Abstracts

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ANIMAL BEHAVIOR AND WELL-BEING

001 Effects of embryonic norepinephrine on juvenile and mature quail behaviors.

J. N. Mengers* and R. L. Dennis, *University of Maryland, College Park.*

Poultry breeding flocks experience stress from numerous sources including feed restrictions, confinement, social aggression, changing environments, transport, and stockperson turnover. Maternal diet and stress can increase catecholamine levels, including norepinephrine (NEP), and alter tyrosine metabolism. Elevated NEP levels impact the embryo and lead to altered survival behaviors in the developed offspring. In order to determine the effects of NEP on feeding and social behaviors, activity level, and fear response, Japanese quail (*Coturnix japonica*) embryos were injected with 10 µL of 0.01 or 0.05 *M* of NEP or saline at ED1 ($n = 130$) and incubated with intact controls ($n = 80$). Weekly behavioral scan samples (AM and PM) were taken from wk 4 (juvenile) to 11 (sexually mature) with rehoming between wk 6 and 7 samplings. Body weights were taken every other week, and organ weights were taken at wk 11. Tonic immobility tests were conducted at 2, 5, and 9 wk. Results showed a greater incidence of eating behavior in birds that received 0.01 or 0.05 *M* of NEP compared with control birds, with eating frequency increasing over time in older NEP-treated birds ($P = 0.019$, wk 5; $P = 0.005$, wk 10; and $P = 0.017$, wk 11). Younger birds that received 0.01 *M* of NEP spent more time drinking compared with birds that received 0.05 *M* of NEP or controls ($P = 0.013$, wk 5, and $P = 0.016$, wk 6). Birds that received 0.05 *M* of NEP foraged more frequently compared with birds that received 0.01 *M* of NEP ($P = 0.002$, wk 6; $P = 0.046$, wk 8; $P = 0.002$, wk 10; and $P = 0.009$, wk 11). Following rehoming, NEP-treated birds exhibited an increase in inactivity compared with control birds ($P = 0.007$, wk 7). Birds that received 0.01 *M* of NEP weighed significantly less than birds that received saline ($P = 0.008$, wk 3; $P = 0.010$, wk 5; $P = 0.006$, wk 7; and $P = 0.006$, wk 9). Relative heart, liver, and spleen weights did not significantly differ ($P = 0.412$, $P = 0.561$, and $P = 0.293$, respectively). We observed no difference in tonic immobility inductions ($P = 0.637$, wk 2; $P = 0.475$, wk 5; and $P = 0.349$, wk 9) or duration ($P = 0.108$, wk 2; $P = 0.426$, wk 5; and $P = 0.730$, wk 9). Our data show that NEP injections during early embryonic development have lasting impacts on feeding and drinking behaviors, activity levels, and weight. These results suggest that maternal and environmental stress, including rehoming, impact both production and behavior with implications for poultry management.

Key Words: norepinephrine, quail, stress
doi:10.2527/asasann.2017.001

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002 Effects of cold temperature and fat supplementation on rumen microbial populations in Korean cattle.

S. W. Na*, H. J. Kang, Y. Kim, and M. Baik, *Department of Agriculture Biotechnology, College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea (South).*

In lower critical temperature, cattle increase their metabolic rate to supply more body heat. This increases nutrient requirements, particularly energy, and may affect rumen fermentation characteristics and thus the rumen microbial ecosystem. This study was performed to examine whether cold temperature and fat supplementation affects rumen microbial populations in Korean cattle. Six Korean cattle steers (average 17 mo of age and 375 kg of BW) were divided into a conventional control diet group ($n = 3$) and a 1.75% fat supplementation group ($n = 3$). Steers were allowed to receive daily a concentrate (1.5% of BW) and 3 kg of tall fescue hay. Steers were raised in metabolic cages in a temperature-controlled room with 2 different temperature conditions. Animals were grown in natural cold condition for 12 d with 2 different diets, and they were then grown in neutral normal temperature for 12 d. There was a 10-d resting period between the 2 temperature conditions in a feedlot with the control diet. The minimum ambient temperature (−6.24°C) of the cold environment was lower ($P < 0.01$) than that (15.8°C) of the normal temperature condition. Rumen fluid samples were obtained via stomach tube on the last day of each of 2 experimental periods 3 h after the morning feeding. Rumen fluids were frozen in liquid nitrogen and stored at −70°C. Genomic DNA was extracted and used for 16S rRNA metagenomics sequencing by an Illumina HiSeq 2000 system. Raw sequencing data was processed by QIIME. Statistical analysis was conducted by 2-way (diet and temperature) ANOVA. Bacteroidetes was the most abundant phylum followed by Firmicutes in all rumen fluid samples. Relative abundances of the genera *Propionibacterium* and *Anaeroplasma* were higher ($P < 0.05$) in cold temperature than in normal temperature, whereas those of *Desulfovibrio* and *Mogibacterium* were lower ($P < 0.05$) in cold temperature. Relative abundance of the family R4-45B was higher ($P < 0.05$) in the fat diet group than in control diet group, whereas that of *Pyramidobacter* was lower ($P < 0.05$) in fat diet group. Real-time PCR was performed to validate the metagenomics data and to identify the changes of microbial population at species levels with 19 microbial primers. *Succinimonas amylolytica* was higher ($P < 0.05$) in cold temperature than in normal temperature. *Ruminococcus albus* was higher ($P < 0.05$) in the fat diet group than in the control diet group. In conclusion, metagenomics and real-time PCR results reveals that cold temperature and fat supplement affect microbial populations in the rumen of beef cattle.

Key Words: cold temperature, fat supplementation, rumen microbial population
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003 Relationship between allogrooming and disease in feedlot steers: Social interactions may provide information about individual animal health.

L. Hoonhout*[1], I. Reimert[1], and C. L. Daigle[2], [1]*Wageningen University, Wageningen, Netherlands,* [2]*Texas A&M University, College Station.*

Social interactions within a group of cattle may provide information about an individual animal's health status. To determine whether social licking (e.g., allogrooming) can be used as an indicator of animal health, *Bos indicus*–cross steers (*n* = 36) were housed in drylots (8–10 steers/pen), individually identified, and video recorded prior to (d −2 and −1) and after (d 1, 2, 4, and 8) inoculation (d 0). Half of the cattle within each pen were inoculated with *Mannheimia haemolytica* (MH) and the other half were inoculated with a phosphate buffer solution (PBSo). We hypothesized that MH cattle would receive more allogrooming after inoculation. Cattle were fed 2 times per day, and video recordings on d −2 and 4 were decoded 2 h before and 2 h after each feeding for the duration of time (s) each steer gave or received allogrooming. The total amount of time on d −2 and 4 spent giving and receiving allogrooming was used to develop 4 behavioral phenotypes: 1) GIVE (*n* = 4; gave > 1 s and received 0), 2) RECEIVE (*n* = 8; gave 0 and received > 1), 3) BOTH (*n* = 23; gave > 1 and received > 1), and 4) NEUTRAL (*n* = 1; gave 0 and received 0). The GIVE steers (130.3 ± 104.3) spent less time (s) allogrooming than BOTH steers (149.4 ± 42.5). The RECEIVE steers (55.3 ± 18.0) spent less time (s) receiving allogrooming than BOTH steers (150.0 ± 26.9). A generalized linear mixed model (PROC MIXED) evaluated the impact of day and treatment on the duration of time spent giving or receiving allogrooming. Neither treatment nor day influenced the duration of time spent giving allogrooming. Treatment (P = 0.13) slightly influenced the duration of time spent receiving allogrooming. *Mannheimia haemolytica* steers (138.3 ± 32.3) spent more time (s) receiving allogrooming than PBSo steers (77.9 ± 21.3). Transition matrices identified that 27% of MH and 16.7% of PBSo steers that were classified as BOTH on d −2 remained BOTH on d 4. Steers classified as GIVE on d −2 were classified as RECEIVE on d 4 for 11.1% of PBSo steers and 0% of MH steers. Of the MH-inoculated steers classified as BOTH on d −2, 27.8% were reclassified as RECIEVE on d 4, whereas no PBSo steers made this transition. Allogrooming is a comfort behavior associated with social dominance and partnership, yet some steers were observed to never give or receive allogrooming. The duration of time individuals receive allogrooming may be a useful metric for identifying sick animals and warrants further investigation.

Key Words: beef cattle, disease detection, social behavior
doi:10.2527/asasann.2017.003

004 Influence of pre- and postnatal stress on the social motivation and fear response in lambs.

X. Averós[1], I. Beltrán de Heredia[1], R. Ruiz[1], and I. Estevez*[1,2], [1]*Neiker-Tecnalia, Vitoria-Gasteiz, Spain,* [2]*IKERBASQUE, Basque Foundation for Science, Bilbao, Spain.*

The impact of maternal separation on the capacity of lambs to respond to social challenges and stressful situations might be modulated by prenatal stressors such as environment conditions experienced by gestating females. In this study, we explored the impact of 2 experimental group sizes (GS) experienced by gestating ewes (prenatal stress) and of early maternal separation (postnatal stress) on the social motivation and fear responses in lambs. Fifty-four pregnant Latxa ewes (Basque Country, Spain) were randomly assigned to 2 experimental prenatal GS treatments of 6 or 12 ewes/pen; GS6 and GS12, respectively). After birth, lambs from each treatment were either left with mothers (MR) or early separated (ES) 24 h after birth. Thirty-two 2- to 8-d-old lambs of similar ages were split into groups of 3, coming from the same pre- and postnatal treatment. Each lamb was sequentially subjected to a novel arena test, a novel object test, and a social motivation test. Lamb behavior, movement patterns, and vocalizations were collected. The effects of pre- and postnatal treatments, their interaction, and male/female differences were determined using the GLIMMIX procedure in SAS. Pen during gestation nested within group size and individual ewe nested within pen during gestation and group size were included as random effects. No significant interactions were detected between pre- and postnatal treatments ($P > 0.05$). Latency to move during the social motivation test was shorter for MR lambs than for ES lambs (3.5 ± 1.6 vs. 7.3 ± 1.7 s for MR and ES lambs, respectively; P = 0.0327), which also had longer inactive periods (38.8 ± 3.6 vs. 15.0 ± 3.0%; P = 0.0278) and explored less (22.1 ± 3.4 vs. 40.9 ± 5.5%; P = 0.0332). The GS6 lambs remained closer to the other test lambs than did GS12 lambs in the social motivation tests (93.9 ± 1.1 vs. 90.08 ± 0.9% of total time; P = 0.0044). Females walked longer net distances than males in the novel arena tests (254.8 ± 7.6 vs. 221.9 ± 8.7 cm, respectively; P = 0.0257). Females also had shorter latencies to move (2.1 ± 1.6 vs. 8.7 ± 2.0 s; P = 0.0488) and walked longer net distances during the social motivation tests (249.6 ± 10.5 vs. 217.5 ± 9.8 cm, respectively; P = 0.0227). No evidences of impact on fear responses were obtained. These results appear to suggest that MR lambs and, to a lower extent, those born from ewes housed at GS6 during pregnancy had increased social motivation. Females appear to show a higher social motivation.

Key Words: group size, lambs, pre- and postnatal stress
doi:10.2527/asasann.2017.004

005 Behavior during human approach and novel object tests and associations with performance from barrows selected for residual feed intake.

S. Azarpajouh*[1], J. D. Colpoys[2], E. K. Arkfeld[3], J. C. M. Dekkers[1], N. K. Gabler[1], E. J. Huff-Lonergan[1], S. M. Lonergan[1], J. F. Patience[3], K. J. Stalder[3], and A. K. Johnson[1], [1]*Department of Animal Science, Iowa State University, Ames,* [2]*Truman State University, Kirksville, MO,* [3]*Iowa State University, Ames.*

The extent to which selection for improved lean accretion and feed efficiency affects livestock behavior and response to stress is not well understood. The objective of this experiment was to examine the behavioral metric correlations and growth performance of barrows divergently selected for residual feed intake (RFI). A human approach test (HAT) and a novel object test (NOT) were used to achieve the objective. Forty low-RFI (LRFI; more feed efficient) and 40 high-RFI (HRFI; less feed efficient) barrows (46.5 ± 8.6 kg) from the eighth generation Yorkshire selection lines were randomly selected and evaluated with HAT (an unfamiliar human) and NOT (an orange traffic cone) over 4 consecutive weeks. Each barrow was individually evaluated within a 4.9 by 2.4 m test arena for 10 min, and frequency of escape attempts (from 2 legs off the ground; may include jump) and freezing (no movement for ≥ 3 s) were determined using video analysis. Performance measures were collected over the grow–finish period and included ADG, feed conversion ratio, live weight, and 10th-rib backfat and loin eye area at the end of the finisher phase. Within lines, Pearson correlations were determined among performance and behavioral metrics during HAT and NOT with the significance level set at $P \leq 0.05$. For HAT, escape and freeze frequencies were not correlated with performance measures for either line ($P \geq 0.33$). Within the LRFI line, freeze frequency during NOT was positively correlated with feed conversion ratio ($r = 0.37$, $P = 0.03$). Escape and freeze frequencies did not have significant correlations with any other performance measures for either line during NOT ($P \geq 0.07$). In conclusion, freeze frequency was weakly correlated with feed conversion ratio in LRFI barrows during NOT, suggesting that more-feed-efficient barrows freeze less in response to novel stimuli. Therefore, within the context of this genetic selection program for improved lean accretion and feed efficiency there were no negative behavioral effects during these fear tests.

Key Words: barrows, fear tests, residual feed intake
doi:10.2527/asasann.2017.005

006 The effect of repeated handling on behavior in beef cattle.

J. T. Parham*[1], A. E. Tanner[2], K. M. Eskridge[1], M. L. Wahlberg[2], W. S. Swecker[3], and R. M. Lewis[1], [1]*University of Nebraska-Lincoln, Lincoln,* [2]*Virginia Tech, Blacksburg,* [3]*College of Veterinary Medicine, Blacksburg, VA.*

Excitable cattle can be detrimental to the health of workers and the cattle themselves, with negative effects on production traits. Acclimation to handling has been proposed to increase docility in excitable cattle as an alternative to culling. The objective of this study is to determine if frequent handling causes a change in docility. A factorial design of 2 groups, frequent (FR) and infrequent (IN), and 3 recording periods, each 1 mo apart, was used. Cattle in the FR group were observed 3 consecutive days within each recording period whereas cattle in the IN group were observed only once. Twenty Angus heifer calves were randomly assigned to each group, and the experiment was repeated over 3 yr. Observations taken on the calves included chute score (1 = docile and 6 = aggressive), exit score (1 = docile and 5 = aggressive), and exit velocity (s). Data were analyzed using ANOVA, with year fitted as a random effect. Recording period, frequency group, and their interaction were compared on d 1 within each period. Recording period and day within recording period were analyzed for the FR group only. There were no differences ($P > 0.24$) among the 2 groups for chute score, exit score, or exit velocity on d 1 of each recording period. Within the FR group, chute score decreased across recording periods ($P < 0.05$), with a tendency to decrease across day within recording period ($P = 0.06$). Exit score and exit velocity were unaffected by recording period ($P > 0.28$) or day within recording period ($P > 0.13$). Although frequent handling decreased chute score within the FR group, there were no differences in docility between the FR and IN groups, suggesting animals did not acclimate to frequent handling.

Key Words: acclimation, beef cattle, temperament
doi:10.2527/asasann.2017.006

007 Impact of exercise on productivity and behavior of weaned *Bos indicus*–cross calves housed in drylots.

C. L. Daigle*[1], B. L. Jackson[1], R. Gill[1], T. A. Wickersham[2], and J. E. Sawyer[1], [1]*Texas A&M University, College Station,* [2]*Department of Animal Science, Texas A&M University, College Station.*

To determine the effects of exercise on cattle productivity and behavior, 2 exercise regimes were evaluated against a control ($n = 4$ pens/treatment) using weaned *Bos indicus*–cross calves ($n = 203$) housed in drylots (16–18 animals/single gender pens). Treatments were applied (3 times/wk for 4 wk) in addition to routine husbandry: 1) programmatic exercise (PRO), in which cattle and stockperson walked in the alleyway behind their home pen for 20 min; 2) free exercise (FREE), in which

cattle were moved into the alleyway behind their home pen and the gate was left open to provide free access to food for 60 min; and control (CON), in which calves left the pen only for routine husbandry. Behavioral observations were conducted on d −2 and −1 relative to treatment implementation (d 0) and on d 5, 6, 12, 13, 19, 20, 26, and 27. Instantaneous scan sampling (48 scans/d; 0800–1200 h and 1300–1700 h at 10-min intervals) was used to create behavioral profiles for cattle (posture [stand, lie, and walk] and behavior [feed, drink, and ruminate]) in the differing treatments. Focal observations (n = 40 min/d per pen) recorded the incidence of social behaviors (allogrooming, social play, and agonistic interactions) and animal–environment interactions (AEI; fencepost licking, rock eating, tongue rolling, and cross-suckling). Body weights were collected on d −10, 10, and 28. A linear mixed model (PROC MIXED) evaluated the impact of treatment, gender, and time on cattle behavior and productivity. Steers (0.96 ± 0.03 kg/d) gained more than heifers (0.85 ± 0.03 kg/d; P = 0.04), and FREE cattle (0.99 ± 0.04) tended (P = 0.06) to have higher ADG (kg/d) than PRO (0.86 ± 0.04) or CON cattle (0.85 ± 0.04). Cattle in the FREE and PRO treatments tended to ruminate more than CON cattle (P = 0.08). Allogrooming (P = 0.05), lying (P = 0.001), AEI (P < 0.01), and rumination (P < 0.01) increased over time. Agonistic interactions increased over time (P = 0.003), and heifers (0.54 ± 0.07) tended (P = 0.09) to engage in more agonistic interactions (proportion of pen/10 min) than steers (0.35 ± 0.07). Anecdotally, PRO cattle became tired after 7 min of walking; shorter programmed exercise regimes may yield production benefits more similar to FREE. Although FREE positively influenced productivity, exercise did not alter behaviors. Comfort-related behaviors increased (e.g., lying, rumination) over the evaluation period, suggesting that calves became acclimated to the environment. However, increases in AEI and agonistic behaviors over the evaluation period suggest that cattle may benefit from periods of increased activity and mental stimulation. Moderate exercise may yield production benefits, does not reduce the performance of production-critical behaviors, and may be beneficial to cattle health and welfare.

Key Words: beef cattle, exercise, welfare
doi:10.2527/asasann.2017.007

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008 Effects of simulated self-enurination on reproductive behavior and endocrinology during the transition into the breeding season in male goats (*Capra hircus*).

W. F. Fritz*, S. E. Becker, and L. S. Katz, *Rutgers University, New Brunswick, NJ.*

The objective of this study was to determine the effects of a simulated self-enurination on the hypothalamo–pituitary–gonadal (HPG) axis in goat bucks. Self-enurination in bucks is androgen dependent and occurs primarily during the breeding season. The behavior is characterized by emission of urine from the erect penis onto the face and front legs; flehmen usually follows. Unpublished work in our lab demonstrated that self-enurination may be used to present attractive cues to females but may also serve as a self-excitatory sexual behavior, whereby urine or chemicals therein stimulate the HPG axis via accessory olfactory system excitation. Previously, our lab conducted experiments to assess this hypothesis by analyzing serum LH and testosterone (T) concentrations in samples taken after simulated self-enurination containing self-enurination urine (SEU) or saline. Results from these studies suggested that simulated self-enurination with SEU may increase LH during the transition into the breeding season and increase T during the transition out of the breeding season. In this study, we assessed both T and LH responses in bucks during the transition into the breeding season. Self-enurination urine for this study was collected during the previous breeding season, pooled, and frozen until needed. Simulated self-enurination involves spraying 1 mL of urine through a modified 22-gauge needle, creating a spritz directed at the buck's nose. Each buck (n = 12) received a total of 4 spritzes, 15 min apart, of either SEU or control (AIR). Air was applied to prevent reliquefying urine residue on the bucks' faces. A switchback was performed in the following 3 wk. Three blood samples were drawn 10 min apart before the first spritz and then 5, 10, 20, 30, 45, and 60 min after the final spritz. Serum LH and T concentrations were determined by RIA. No AIR bucks displayed flehmen. Self-enurination urine bucks displayed flehmen 98% of the time (mean duration 21 s). Treatment with SEU resulted in a greater T increase from baseline than treatment with AIR at 5 min (388 vs. 133%, respectively; P < 0.05) and at 10 min (349 vs. 159%, respectively; P < 0.05). Not sampling blood after each spritz complicated interpretation of the LH data. However, in SEU males, the involvement of the HPG axis is reflected by a decrease in LH area under the curve (57.6 and 74.1 ng/mL × min for SEU and AIR, respectively; P < 0.1) when T was elevated. Our evidence suggests that self-enurination stimulates the HPG axis, thereby facilitating sexual performance.

Key Words: goats, reproductive behavior,
self-enurination
doi:10.2527/asasann.2017.008

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009 Consequences of immunization against GnRF and ractopamine supplementation on behavioral traits of heavy weight market gilts.

L. A. Rodrigues*[1], G. P. Prezotti[2], F. N. Ferreira[1], L. Spricigo[3], L. G. Reis[1], D. M. Junior[1], F. C. Silva[4], W. M. Ferreira[1], and D. O. Fontes[1], [1]*Federal University of Minas Gerais, Belo Horizonte, Brazil,* [2]*Heifer International, Little Rock, AR,* [3]*Zoetis Brazil, São Paulo, Brazil,* [4]*Agricultural Research Corporation from Minas Gerais, Viçosa, Brazil.*

Immunocastration (IM) has recently emerged as an alternative for rearing gilts up to heavier slaughter weights, considering its effects on performance improvement and sexual behavior suppression. The interaction between IM and ractopamine (RAC) supplementation is reported to be beneficial for growth and carcass characteristics. However, some studies reported RAC's adverse effects on swine behavior, mainly increased aggressiveness. Seventy-two gilts (2 gilts/pen) were used in order to measure the interactive effects between IM and RAC on behavioral characteristics and on human–pig interaction during the finishing phase. The factorial arrangement was defined as 2 RAC levels (0 and 10 mg/kg of diet) by 2 immunization categories (nonimmunized and immunized gilts). The first and second immunizations were performed at 15 and 19 wk of age, respectively. Ractopamine supplementation occurred from 21 to 25 wk of age, when all the gilts were exposed to mature boars daily. Animal behavior (on a 24-h basis) and the interaction between gilts and an observer positioned inside a test pen were both evaluated at a single time point (at 23 wk of age). There were no treatment effects on time spent eating, drinking, lying, fighting, or mounting ($P > 0.05$) during the 24-h period. Both RAC (−21.6%; $P < 0.05$) and IM (−32.3%; $P < 0.01$) caused a reduction in standing behavior and there was an interaction between IM and time for sitting behavior ($P < 0.01$), where immunized gilts concentrated this behavior from 1600 to 2000 h (2.11%), with a peak at 1800 h (3.89%). Aiming to assess effects of IM and RAC on human–pig interaction, groups of 4 gilts within each treatment were exposed to an observer standing in the corner of a test pen. Immunized gilts both crossed a line 1 m distant from the observer (−67.38 s; $P < 0.001$) and approached the observer (−125.47 s; $P < 0.001$) in a reduced time compared with nonimmunized gilts, regardless of RAC. The type of interaction between animals and the observer was graded from 1 to 5 (1 = soft contact with the observer and 5 = pigs aggressively tweaking on the observer's clothes) and was not affected by treatments ($P > 0.05$). Immunocastration and RAC did not entail any aggressive behavior on late finishing gilts, and IM improved their willingness to approach and investigate. Assessment of comportment traits in a larger number of animals, under commercial conditions, merits further investigation.

Key Words: human–pig interaction, immunocastration, ractopamine
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010 Effect of different surgical incisions and anesthesia methods on wound healing in recently weaned beef calves.

S. Marti*[1,2], D. M. Meléndez[1,2], E. D. Janzen[1], D. Gellatly[1,2], C. E. M. Heuston[2,3], E. A. Pajor[1], and K. S. Schwartzkopf-Genswein[2], *[1]University of Calgary, Calgary, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]University of Saskatchewan, Saskatoon, SK, Canada.*

A total of 48 recently weaned Angus crossbred bull calves (292 ± 19.1 kg BW) were used to evaluate the effect of types of anesthesia and surgical cuts on scrotal wound healing after castration. Calves were randomly assigned to a 2 × 2 factorial design assessing surgical castration incisions (cut made with Newberry knife [K] vs. bottom cut made with scalpel [B]) and method of anesthesia injected 20 min before castration (local anesthesia injected in the spermatic cord, around the neck of the scrotum and testicles [L; lidocaine HCl 2%] vs. epidural [E; xylazine]) to yield KL, KE, BL, and BE (12 calves/group). Wound healing was assessed in all calves over a 63-d period after castration using maximum scrotal area temperature (MST; °C) assessed via infrared thermography, scrotal circumference (SC; cm), visual evaluation of swelling (SW; 5-point scale in which 0 = no swelling and 5 = increased degree of swelling with presence of pus), and healing of the incision site (HI; 5-point scale in which 1 = incision open without scabbing and 5 = incision completely healed). Data was collected 8 h after castration on d 1, 2, 4, 7, 14, 17, and 21 after castration and weekly thereafter until the end of the study. Pain sensitivity was evaluated using a Von Frey anesthesiometer (g) following the same schedule. Data was analyzed using a mixed-effect model with incision, anesthesia, time, and their interactions as fixed effects and pen within animal as a random effect. An incision × time interaction ($P < 0.05$) was observed for MST, HI, and SW. The MST for B calves was greater ($P < 0.05$) on d 35, 56, and 63 compared with K calves. In addition, B calves tended to have greater HI scores ($P = 0.06$) on d 21, 28, and 35 than K calves, although no differences were observed at the end of the assessment period. In addition, from d 35 to 63, B calves had greater ($P = 0.01$) SW than K calves. Finally, calves administered local anesthesia tended to have greater scores for HI ($P = 0.06$) and lower SC ($P < 0.001$) than calves administered epidural anesthesia. No differences in pain sensitivity were observed between types of surgical incisions or methods of anesthesia. In summary, calves castrated using a Newberry knife and anesthetized using a local anesthetic healed faster and presented less swelling consistent with improved healing.

Key Words: anesthesia, surgical castration incision, wound healing
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011 Effect of lidocaine and meloxicam on indicators of pain and distress after knife castration in weaned beef calves.

D. M. Meléndez*[1,2], S. Marti[1,2], E. D. Janzen[1], D. Moya[2,3], D. Gellatly[1,2], E. A. Pajor[1], and K. S. Schwartzkopf-Genswein[2], *[1]University of Calgary, Calgary, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]Institute of Biological, Environmental and Rural Sciences, Aberystwyth, UK.*

Castration is commonly done without the use of pain mitigation, although previous studies have shown that the combination of an analgesic and an anesthetic drug is more effective at mitigating pain than either drug on its own. The aim of this study was to assess the efficacy of the combination of

a lidocaine (2% with epinephrine) ring block 30 min prior to knife castration in combination with a single dose of subcutaneous meloxicam (Metacam 0.5 mg/kg BW) administered immediately prior to castration. Forty-eight Angus bull calves (301.4 ± 5.8 kg BW) were randomly assigned to a 2 × 2 factorial design assessing administration of meloxicam and lidocaine: no-meloxicam and lactated ringer ring block (NM-NL; n = 12), no-meloxicam and lidocaine ring block (NM-L; n = 12), meloxicam and lactated ringer ring block (M-NL; n = 12), and meloxicam injection and lidocaine ring block (M-L; n = 12). Data was collected on d −1; immediately before castration; at 30, 60, 120, and 240 min after castration; and on d 1, 2, 3, 6, 14, 21, and 28 after castration. Physiological parameters consisted of salivary cortisol (SC), haptoglobin (HP), and scrotal temperature (ST). Behavioral parameters included stride length (SL) and visual analog score (VAS). A lidocaine × time effect ($P < 0.01$) was observed for SC, and L calves had lower concentrations than NL calves 30 and 60 min after castration. In addition, M calves had lower SC concentrations ($P = 0.03$) than NM calves during the first 240 min after castration. A meloxicam × time effect ($P = 0.05$) was observed for HP, with M calves having lower concentrations than NM calves on d 1, 2, and 3 after castration. The L calves had lower VAS scores ($P = 0.01$) than NL calves. No treatment differences were seen in SL ($P > 0.3$) or ST ($P > 0.05$). Despite the fact that there was no interaction between lidocaine and meloxicam, lidocaine was more effective at mitigating the indicators of pain at the time of and up to 1 h after castration, whereas meloxicam was more effective at reducing indicators of pain 3 h and 3 d after castration. In this study, the combination of lidocaine and meloxicam was more effective in controlling pain during and up to 3 d after castration than each drug alone.

Key Words: beef calves, lidocaine, meloxicam
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012 Meloxicam and temperament effects on growth performance and indicators of pain in knife or band castrated calves housed on pasture.

D. Gellatly[1], S. Marti[1], D. M. Meléndez[1], D. Moya[2], E. D. Janzen[1], E. A. Pajor[1], and K. S. Schwartzkopf-Genswein*[3], [1]*University of Calgary, Calgary, AB, Canada,* [2]*Aberystwyth University, Aberystwyth, UK,* [3]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

The objective of this study was to evaluate the effect of castration method, meloxicam, and temperament on growth performance and indicators of pain in band- or knife-castrated beef calves. Seventy-two crossbred Angus calves (76 ± 2 d of age and 134.5 ± 20.30 kg BW) were randomly assigned to treatments according to a 3 × 2 factorial design assessing castration technique (CAST; knife [K], band [B], or sham castration [S]) and drug administration (DRUG; single subcutaneous injection of meloxicam at the time of castration [0.5 mg Metacam/kg BW] or single subcutaneous injection of saline solution as control). Calves were managed in 2 groups (GROUP) of 36 to be castrated on 2 separate days, 2 wk apart. Calves were housed on pasture with ad libitum access to water. Temperament was assessed by measuring flight speed (FS; m/s); faster animals indicated more excitable temperament. Growth performance was assessed using ADG (kg/d). Substance P (SP; pg/mL) and stride length (SL; cm) were used as physiological and behavioral indicators of pain, respectively; greater SP and SL values indicated greater and lower pain levels, respectively. Initial BW and FS were collected on d −6, −1 (prior to castration day), and 0 (immediately prior to castration) as baseline measurements and on d 6, 13, 20, 34, 48, and 62 after castration (DAY). Calves were blocked by the average FS and BW obtained on d −6 and −1. Data was analyzed using a mixed-effects model including CAST, DRUG, DAY, and their interactions as fixed effects and GROUP as a random effect. The average baseline measurements of BW, the average of all FS measurements, and the average of SP or SL obtained on d −1 and 0 were used as covariates. Growth performance was greater ($P < 0.05$) in S (1.33 ± 0.03 kg/d) than in K and B (1.21 ± 0.03 and 1.22 ± 0.03 kg/d, respectively). For every 1 m/s increment in FS, SP decreased by 8.7 pg/mL ($P < 0.05$). There was no effect of CAST, DRUG, or FS on SL. As expected, both knife- and band-castrated calves had reduced ADG compared with S calves. Faster FS was associated with lower pain levels, indicating that temperament can affect physiological measures. A single subcutaneous injection of meloxicam had no effect on growth performance or the indicators of pain used in this study.

Key Words: animal welfare, pain mitigation, reactivity
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013 AWIN mobile apps; animal welfare assessment at your fingertips.

I. Estevez*[1,2], M. Battini[3], E. Canali[3], R. Ruíz[1], G. Stilwell[4], V. Ferrante[3], M. Minero[3], J. Marchewka[1,5], S. Barbieri[3], S. Mattiello[3], I. Beltrán de Heredia[1], C. M. Dwyer[6], and A. Zanella[7], [1]*Neiker-Tecnalia, Vitoria-Gasteiz, Spain,* [2]*IKERBASQUE, Basque Foundation for Science, Bilbao, Spain,* [3]*Department of Veterinary Medicine, University of Milan, Milan, Italy,* [4]*Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal,* [5]*Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Department of Animal Behaviour, Magdalenka, Poland,* [6]*SRUC, Scotland's Rural College, Edinburgh, UK,* [7]*University of São Paulo, Pirassununga, Brazil.*

Animal welfare is an increasingly relevant aspect of livestock farming for societal and economic reasons. It should also be a requirement for high-quality and sustainable production, as assuring optimum welfare helps to minimize losses in animal performance and resource loss. In order to implement these

production models, it is critical to the livestock industry to have access to practical yet sophisticated tools and assessment protocols that ascertain the animals´ welfare status. The development of easy-to-use but effective protocols and supporting tools were one of the main goals of the Animal Welfare Indicators (AWIN; http://www.animal-welfare-indicators.net) project funded within the 7th Framework Programme of the European Union. Animal Welfare Indicators scientists developed assessment protocols for turkeys, sheep, goats, horses, and donkeys that can be effectively applied to commercial conditions with minimal disturbance for the animals. To simplify further the assessment procedures, 4 apps for mobile devices were developed in collaboration with the company Daia. The apps I-WatchTurkey, AWINSheep, AWINGoat, and AWINHorse generated by AWIN scientists are freely available on Google Play Store and allow on-farm data collection of animal-based welfare indicators. The AWIN apps are specifically designed to guide the user step by step during the farm visit. The basic statistical tools included provide an immediate visual output with the results of the assessment, to compare the results with previous evaluations and allow export of the files for further statistical procedures. Potential users of the AWIN apps include farmers for their own self-assessment and to improve competitiveness or veterinary services and technicians in their everyday practice. The real-time output can facilitate dialogue with farmers, suggesting actions to improve the welfare of animals, but can also generate data that can be easily linked to productive performance. The AWIN apps are easy to use; however, basic training on the specific methodologies used, such as the transect approach for turkey welfare assessment, and on how to assess and score the welfare indicators is needed in order to harmonize the assessment and obtain reliable data. Animal Welfare Indicators apps work offline, a feature that contributes to an extensive use of welfare assessment protocols with no geographical limits. These apps increase the efficiency and standardization of on-farm welfare assessment that can promote consumers' acceptance of modern livestock production and social responsibility.

Key Words: animal welfare assessment, protocols, tools
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014 Benchmarking indicators of compromised and unfit conditions in cattle arriving at auctions and abattoirs in Alberta.

C. E. M. Heuston*[1,2], A. Greter[1], N. Diether[1], M. Moggy[1], M. Jelinski[2], C. Windeyer[3], D. Moya[4,5,6], E. A. Pajor[3], E. D. Janzen[3], and K. S. Schwartzkopf-Genswein[4], [1]*Alberta Farm Animal Care Association, High River, AB, Canada,* [2]*University of Saskatchewan, Saskatoon, SK, Canada,* [3]*University of Calgary, Calgary, AB, Canada,* [4]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [5]*Institute of Biological, Environmental and Rural Sciences, Aberystwyth, UK,* [6]*Aberystwyth University, Aberystwyth, UK.*

The transport and sale of compromised and unfit cattle is a major welfare concern. A compromised animal is defined as having reduced capacity to withstand the stress of transport but where transport with special provisions will not result in undue suffering. Currently, there is a lack of information regarding the occurrence and conditions of compromised cattle arriving at central assembly points. A pilot study was conducted to document the incidence of cattle arriving at auctions and abattoirs in a compromised condition within Alberta (Canada) and to characterize which conditions were most prevalent. A total of 8 out of 22 auction markets and 11 out of 43 provincial abattoirs were selected based on annual sale/slaughter volumes and geographic location. Auction volumes were defined as selling $\geq$65,000 cattle/yr (large) and <65,000 cattle/yr (small). Abattoir volumes were defined as slaughtering <275 cattle/yr (low), between 276 and 543 cattle/yr (medium), or >543 cattle/yr (high). Each population was further stratified by age (80% market and 20% cull cattle) based on historical data. Over a 3 mo period, 19 sites were visited once (17 sites were visited by 2 observers and 2 sites were visited by 1 observer) to assess indicators of compromised condition in a representative proportion of cattle (n = 936; 847 auction cattle and 89 abattoir cattle). The conditions assessed included mobility (5 point scale), respiratory signs (modified DART 5 point scale), body condition (BCS; 5-point scale), and heavy lactation (yes/no) and assigned an overall score for compromised condition (5 point scale: normal [1], mild [2], moderate [3], severe [4], and unfit for transport [5]). Cattle were defined as compromised if they had a mobility or respiratory score of $\geq$3, BCS of $\leq$1.5, heavy lactation (yes), or an overall compromised condition score of >3. Data for a particular animal were removed when disagreement between observers was greater than 1 score. The percentage of cattle defined as compromised based on mobility, respiratory signs, BCS, heavy lactation, and overall compromised condition score were 1.26, 0, 0.80, 0.92, and 1.38%, respectively, for auction cattle and 15.7, 2.25, 2.25, 0, and 22.5%, respectively, at abattoirs. Mobility was the most prevalent compromised condition observed in both populations. Except for heavy lactation, the prevalence of all compromised conditions was greater in abattoirs than in auction markets. Characterizing the indicators of compromised conditions in this benchmarking study allows for the identification of important conditions to aid in the development of intervention strategies.

Key Words: abattoir, auction, compromised cattle
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015 Investigation of an animal-in-motion-optical-sensor system for detecting biomechanical patterns in variable cattle gaits.

C. A. Atkins*[1], K. R. Pond[1], and C. K. Madsen[2], [1]*Colorado State University Dept. of Animal Sciences, Fort Collins,* [2]*Ag Tech Optics, LLC, Bryan, TX.*

The primary objective of this study was to assess the use of an animal-in-motion-optical-sensor (AIMOS) system allowing for rapid, real-time assessment of variable biomechanical patterns in live cattle. Biomechanical patterns were categorized into groups of gait type and any variations (jump, trot, walk, slip, kick, and run). Biomechanical patterns were measured (0 to 5 V) using a commercial, standard platform containing 1 AIMOS system. Fifty crossbred and purebred ($n = 20$ Angus, $n = 10$ Hereford, and $n = 10$ Angus × Hereford) steers and heifers ($n = 50$; 292.5 kg average BW) were used in completely randomized design. Over a 2-d period, objective kinetics and subjective kinematics were collected and analyzed. Cattle were run multiple times per test day for a total of 6 runs. Individual cattle exited through a hydraulic chute from which they were guided down a walkway over the AIMOS platform. A signal base unit and computer were placed by the chute to collect near real-time data through integrated fiber optic cabling. Kinetic analog measurements (ratio and amplitude of hoof impacts and ground reaction forces [GRF]) and kinematics (estimated speed and stride length) were recorded from each steer and heifer. Selection variables based on steer and heifer physiological characterizations (breed, sex, and age) were used in linear mixed regression of repeated runs. Visual observations and video analysis were used for categorizing and classifying variable gait patterns after the 2-d period. Temperament traits (excitable, calm, and hesitant) were visually evaluated. Temperature was recorded for each test day (minimum −6°C and maximum 4°C). Individual cattle AIMOS measurements were analyzed for each run, compared with video data, and categorized into pattern groups. The AIMOS system demonstrated differences between and within cattle total vertical GRF ($P < 0.05$) for variable gait types. No differences were noted for temperature effect. Overall, data suggest the AIMOS system could assess variable gait measurements in a repeated study for detecting cattle biomechanical patterns.

Key Words: biomechanical patterns, cattle gait cycle, optical sensors
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016 Exit velocity and feeding behavior of water buffalo: A relationship to be considered during the feedlot adaptation phase.

C. L. Francisco*[1], A. M. Castilhos[1], P. R. L. Meirelles[1], D. C. M. Silva[1], F. M. Silva[1], H. L. Correa[1], A. S. Aranha[1], P. A. C. Luz[1], C. Andrighetto[2], and A. M. Jorge[1], [1]*Universidade Estadual Paulista – FMVZ, Botucatu, Brazil,* [2]*Universidade Estadual Paulista – UNESP, Dracena, Brazil.*

The aim of this study was to evaluate the relationship between exit velocity (EV) and feeding behavior of 75 water buffalo (*Bubalus bubalis*; 13 ± 1 mo of age and 314 ± 117 kg BW) during a 28-d adaptation phase to the diet and feedlot facility. Animals were allocated to 3 pens (26.5 m^2/animal) equipped with artificial shade (2.8 m^2/animal), automatic feeders, and water troughs (Intergado, Minas Gerais, Brazil). Body weight was measured at the beginning and end of the adaptation phase (28 d) to determine total gain (TG) and ADG. Exit velocity was recorded on d 0. The animals had ad libitum access to a total mixed ration (30:70 roughage:concentrate ratio) and water. Dry matter intake and water intake (WI) were recorded daily. The feeding behaviors analyzed were the time to visit the feeder for the first time without DMI, the time for the first 1 kg of DMI, number of total visits to the feeder with DMI, number of total visits to the feeder without DMI, the time to visit the water trough for the first time without WI, number of total visits to the water trough with WI, and number of total visits to the water trough without WI. Data were analyzed with PROC CORR (SAS). Exit velocity was negatively correlated with TG ($r = -0.25$, $P = 0.04$), ADG ($r = -0.24$, $P = 0.04$), DMI ($r = -0.27$, $P = 0.02$), number of total visits at water trough with WI ($r = -0.29$, $P = 0.01$), number of total visits water trough without WI ($r = -0.27$, $P = 0.02$), with a tendency for the number of total visits at feeder with DMI ($r = -0.19$, $P = 0.10$) and total WI ($r = -0.23$, $P = 0.06$). Furthermore, a positive correlation was detected between EV and the time to visit the water trough for the first time without WI ($r = 0.25$, $P = 0.04$). No association was detected ($P > 0.05$) between EV and the other feeding behaviors in this phase. Additionally, total WI was positively correlated with TG ($r = 0.50$, $P < 0.01$) and ADG ($r = 0.51$, $P < 0.01$). In conclusion, exit velocity is correlated with feeding behavior traits during the adaptation phase and can be used as tool to help in the selection of desirable water buffalo in feedlot production. Supported by FAPESP number 2014/05473-7.

Key Words: feeding behavior, feedlot, water buffaloes
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017 Effect of standardized capsicum oleoresin on behavior of feedlot cattle during summer.

C. Oguey[1], T. H. McCullough[*2], G. Parsons[3], E. H. Wall[1], and T. L. Mader[4], [1]*Pancosma, Geneva, Switzerland,* [2]*Gladwin A. Read Co., Waterloo, NE,* [3]*Kansas State University, Saint George,* [4]*Mader Consulting, LLC, Gretna, NE.*

Previous research has shown that low dosages of capsicum oleoresin positively affected individual behavior of cattle housed in small pens. The objective of this trial was to assess the effect of a product standardized with 20% capsicum oleoresin (XT; XTRACT Caps XL, Pancosma) on behavior of feedlot cattle farmed under typical U.S. commercial conditions during the summer. A total of 28 pens regrouping 3,874 cattle (average BW at start of 426 kg) were paired according to pen type and density for 30 d. Within each pair, pens were assigned to either a control total mixed ration diet with monensin (CT) or the same diet supplemented with 250 mg/animal per day XT (XT). Dry matter intake was recorded daily for each pen. Behavior was recorded per pen, once before the trial and then 3 times during the study by 2 examiners. Panting score, percentage of standing versus laying animals, and number of animals at waterers and feed bunk were collected. Dry matter intake was analyzed using the mixed models procedure of SAS, with day, treatment, and their interaction considered fixed effects. Equality of variances for DMI was assessed using a Fisher F-test. Behavior data were analyzed by a χ^2 test. Results showed that the treatments did not affect DMI (mean 10.7 kg/animal per day; $P = 0.57$). However, daily variation of intake tended to be lower in the XT treatment than in the CT group ($P < 0.06$), suggesting that capsicum induced a more homogeneous DMI. The proportion of animals standing versus lying was not affected by the treatments ($P > 0.70$) as well as at the waterer and at the feeder (means of 5.81 and 7.82%, respectively; $P > 0.20$). The proportion of cattle with a panting score greater than 2 was lower in XT than in CT (7.90 vs. 8.10%; $P = 0.15$); however, the biological relevance of this small difference is difficult to interpret. These findings suggest that capsicum supplementation has the potential to modulate intake variation, and this may limit negative effects of a hot season in feedlot cattle raised under commercial conditions.

Key Words: beef cattle, capsicum oleoresin, heat stress
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018 Essential oils in the diet of young bulls: Effect on animal temperament.

M. G. Ornaghi[*1], J. A. Torrecilhas[2], R. A. C. Passetti[1], C. Mottin[1], A. Guerrero[3], C. E. Eiras[1], D. C. Rivaroli[1], T. R. Ramos[1], and I. N. Prado[1], [1]*State University of Maringá, Maringá, Brazil,* [2]*São Paulo State University (UNESP) School of Agricultural and Veterinarian Sciences, Jaboticabal, Jaboticabal, Brazil,* [3]*Instituto Agroalimentario de Aragón-IA2, Zaragoza, Spain.*

Plant extracts and essential oils can be alternative products to antibiotics, because several plants produce secondary metabolites with antimicrobial properties. Additionally, they may act on the olfactory system, which sends signals to the central nervous system releasing endorphins that may affect the feeling of an animal's welfare while altering an animal's temperament. This study was conducted to evaluate the animal temperament of 40 young crossbred bulls (one-half Brown Swiss and one-half Nellore) 10 ± 2.2 mo old with an average BW of 219 ± 11.7 kg. Young bulls were randomly assigned to 1 of 5 diets: control, which had no clove or cinnamon; clove leaf included to supply 3,500 mg/animal per day; clove leaf included to supply 7,000 mg/animal per day; essential oil of leaf cinnamon to supply 3,500 mg/animal per day; or essential oil of leaf cinnamon to supply 7,000 mg/animal per day. The animal temperament was evaluated by calculating the chute score, exit score, and temperament score for periods (each 28 d during 6 periods) and among diets. The data were submitted to an ANOVA using GLM procedures with SAS version 9.0. The diet and period were considered fixed effects, whereas the animals were considered a random effect. Differences between means were evaluated using a Tukey test of 5% of significance. The addition of clove or cinnamon essential oils did not alter ($P > 0.05$) animal temperament. The analysis of temperament score ($P = 0.55$), chute score ($P = 0.71$), and exit score ($P = 0.06$) did not show significant differences among the diets. The exit score was similar among the 6 periods (1.57, 1.80, 2.98, 2.02, 2.73, and 2.66, respectively); however, chute score and temperament score were greater ($P < 0.001$) in the first period compared with other periods. The values for chute score were 1.85, 1.40, 1.35, 1.33, 1.20, 1.17, respectively, and the values for temperament score were 2.31, 1.81, 1.67, 1.69, 1.50, and 1.56, respectively, for periods 1 to 6. The results of this study suggest that clove and cinnamon essential oils can be added as an additive in high-grain finished diets without changing the animal temperament.

Key Words: cinnamon, clove, feedlot
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019 Characterization of piglet losses in regard to boar genetics and management factors.

J. Steinhoff-Wagner* and C. Achten, *University of Bonn, Institute of Animal Science, Bonn, Germany.*

Losses of piglets within the first 5 d are still very high. Reduction of piglet losses requires more information about the dead piglets. The aim of the study was to characterize lost piglets and investigate how reasons recorded by the farmer are related to valid measurable criteria on the dead piglet. On 2 different farms in North Rhine-Westphalia (Germany) with comparable sow genetics but different management systems, piglets were produced in a 2 × 2 Latin square design from the 2 boar genetic lines, PIC408 and German Pietrain (GerPi). Approximately the first 100 dead piglets ($n = 383$) of each boar genetic line on each farm that were lost during the first 5 d of life were bagged and deep frozen. For dissection, piglets were thawed and abdominal girth, crown–rump length, and total and organ weights were specified and external signs of injury, deformities, and fractures were recorded. Effects of the fixed factors sex, farm, and boar line were identified using a Mixed Model of SAS and post hoc Tukey test ($P < 0.05$). Valid measurable parameters were related to recordings from the farms by Spearman rank correlation. Farmer's recordings identified underweight, with 29% on farm A and 40% on farm B, as the most common causes of death. On both farms, the offspring of GerPi boars get older than the offspring of the PIC408 ($P < 0.01$). Crown–rump length was about 3 cm longer in PIC408 piglets than in GerPi ($P < 0.05$). Total and organ weights remained on a comparable level between birth and d 3 but increased to d 4 and 5 ($P < 0.05$), whereby PIC408 offspring showed a higher proportion of organ weights per total weight. Death (or total) weights were closely correlated with recordings of underweight as the cause of death within the same age ($P < 0.05$, $0.5 < r < 1$). The rigidity of the cranial bone was negatively related to low death weights ($P < 0.05$, $-0.5 > r > -1$) and might be a proper indicator for ontogenic age. Different management on the 2 farms affects age at death, whereby results indicate that the closer invasions, for example, castration, were scheduled after birth, the less likely piglets were to survive. Boar genetics seemed to be responsible for differences in anatomy: PIC408 offspring may die earlier because of less muscle and fat storages.

Key Words: dissection, piglet death, piglet loss
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020 Cattle breed and head dimension effects on the performance of a captive bolt stunner equipped with three different length bolts.

D. R. Wagner*[1], H. C. Kline[1], M. S. Martin[1], K. Vogel[2], L. Alexander[3], and T. Grandin[1], [1]*Colorado State University, Fort Collins,* [2]*University of Wisconsin – River Falls, River Falls,* [3]*Cargill Protein Group, Wichita, KS.*

Captive bolt stunning is commonly used as a means of quickly and effectively rendering cattle insensible prior to slaughter. Effective stunning of cattle is partially ensured by proper placement of the device, which may be breed dependent. For Holsteins, stun placement is typically recommended 2.5 cm above common placement for other breeds. The purpose of this study was to determine if head dimensions and brain location differ between Holstein and non-Holstein breeds. This study also examined the effects of different bolt lengths on physical brain damage. It was hypothesized that head size and brain damage would not differ based on bolt length or breed. This study used a randomized, unbalanced block design, with treatment blocked by day. Experimental unit was animal, and analyses were performed using t-tests in SAS 9.4 (SAS Inst. Inc., Cary, NC). The stunner used was a Jarvis USSS-1 (Jarvis Products Corp., Middletown, CT), a penetrating, pneumatic captive bolt gun. For brain damage assessment, 292 heads were randomly sampled across 3 collection periods, with an approximately equal split between Holstein and non-Holstein breeds. Each period was assigned the control bolt (CON), medium bolt (MED), or long bolt (LON), with lengths of 15.2, 16.5, and 17.8 cm, respectively. Heads were collected, immediately measured, and chilled for splitting and damage analysis at the Colorado State University Necrology Laboratory (Colorado State University Veterinary Teaching Hospital, Fort Collins, CO). For head dimension assessment, 426 heads equally distributed between Holstein and non-Holstein breeds were sampled. Head width, poll to orbit, right orbit to poll, and left orbit to poll did not differ between breeds ($P > 0.13$). Head length and orbit to nose length were greater for Holsteins ($P = 0.0046$). Brain size, length, and width as well as skull thickness did not differ between breeds ($P > 0.32$). Stunning metrics included bolt entrance hole diameter, which was greatest for the LON, least for the MED, and intermediate for the CON ($P < 0.0001$). Bolt penetration depth was greatest for the MED ($P < 0.0001$). Sagittal brain damage was least for the CON, with greater damage measured on the MED and LON ($P < 0.0001$). Dorsal damage was least for the CON and increased for the MED and LON ($P < 0.0001$). The data in this study suggest that differing bolt lengths affect brain damage and that head dimensions appear to be different between breeds only in nose length, indicating that current recommendations for differing stun placement based on breed may need to be reevaluated.

Key Words: brain damage, cattle, stunning
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021 Evaluation of different captive bolt lengths and breed influence upon postmortem leg activity in fed cattle.

M. S. Martin*[1], H. C. Kline[1], D. R. Wagner[1], L. Alexander[2], and T. Grandin[1], *[1]Colorado State University, Fort Collins, [2]Cargill Protein Group, Wichita, KS.*

Captive bolt stunning is a widely used means across commercial beef plants to render animals insensible. After stunning, postmortem leg activity poses a safety risk for employees; hence, the objective of this study was to test captive bolt length effects on postmortem leg activity. It was hypothesized that captive bolt length and cattle breed do not influence postmortem leg activity. A total of 2,850 Holstein and non-Holstein Continental/British-bred fed cattle were sampled. The Jarvis USSS-1 (Jarvis Products Corp., Middletown, CT) penetrating pneumatic captive bolt stunner was used with 3 different bolt lengths: 15.24, 16.51, and 17.78 cm, constituting control, medium, and long treatment groups, respectively. The study was an unbalanced, randomized block design, blocked by day, and breed was recorded as Holstein or non-Holstein. The experimental unit was animal and data were analyzed within SAS 9.4 (SAS Inst., Inc., Cary, NC) using *t*-tests. Immediately after knocking, cameras were placed to record postmortem forelimb and hind limb kicking, the number of times each animal was stuck to be exsanguinated, and if the take away belt stopped. Immediately after stunning, cattle fall from the center track restrainer onto the take away belt to be shackled, which influences the stunning-to-exsanguination interval. There were more hind limb kicks using the long bolt ($P = 0.03$) compared with the medium bolt, and more Holstein hind limb kicks were observed relative to non-Holstein ($P = 0.0009$). Forelimb kicks were greater for medium ($P < 0.0001$) and long ($P < 0.0001$) compared with control, and more non-Holstein forelimb kicks occurred relative to Holstein ($P = 0.0002$). The number of take away belt stops was more for control than medium ($P < 0.0001$) as well as long ($P < 0.0001$). Take away belt stops was greater for Holstein relative to non-Holstein ($P < 0.0001$). Righting reflex and number of sticks did not differ regardless of treatment or breed ($P > 0.23$). These data show that captive bolt length and breed play a role in postmortem activity of fed cattle and that breed plays a role in take away belt stops and thus the stun-to-exsanguination interval. Further research is needed to explore the intricacies of these relationships.

Key Words: captive bolt length, cattle, stunning
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022 Correlation between blood proteins and physiological parameters in beef calves under heat stress.

W. S. Kim*[1,2], J. S. Lee[1,2], D. Q. Peng[1,2], Y. S. Kim[1,2], M. H. Bae[1,2], Y. H. Jo[1,2], and H. G. Lee[1,2], *[1]Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea (South), [2]Team of an Educational Program for Specialists in Global Animal Science, Brain Korea 21 Plus Project, Konkuk University, Seoul, Republic of Korea (South).*

Heat stress is an important factor in the cattle industry because it has been directly linked to growth, reproduction, health, and animal welfare. In particular, blood proteins (haptoglobin [HA] and heat shock protein 70 [HSP70]) may play important roles in protein assembly and disassembly, protein folding and unfolding, and suppressing inflammatory responses under heat stress. The objective of this study was to determine the effect of heat stress on blood proteins and to identify the role of proteins through a correlation analysis between blood proteins and physiological parameters. Thirty-two Korean native calves were randomly assigned to 8 groups with 4 animals per group. They were kept in environmental conditions with a temperature–humidity index (THI) ranging from 70.01 to 87.72 in a temperature–humidity controlled chamber for 7 d. According to the ambient temperature, blood was collected after 3 h feeding (at 1100 h). The blood proteins HA and HSP70 and the hormone cortisol as stress-related indicators were analyzed using a commercial bovine ELISA test kit (Life Diagnostics, USA). In addition, HR and RT were measured at the same time points. Data were analyzed by 1-way ANOVA using the Mixed procedure of SAS with THI as the main factor. The HR, RT, serum cortisol, and HSP70 levels were increased ($P < 0.05$) in calves at high THI compared with those at low THI. However, HA level was decreased ($P < 0.05$) in calves at high THI compared with those at low THI. In addition, THI, HR, RT, and cortisol were positively correlated with HSP70 ($R^2 = 0.2241$, $P = 0.0062$; $R^2 = 0.1751$, $P = 0.0171$; $R^2 = 0.2186$, $P = 0.007$; and $R^2 = 0.1822$, $P = 0.0148$, respectively). However, THI and HR were negatively correlated with HA ($R^2 = 0.2157$, $P = 0.02$ and $R^2 = 0.3362$, $P = 0.003$, respectively). Based on these results, blood proteins (HA and HSP70) change under heat stress, which may exert an anti-inflammatory action and protect cells from heat stress damage. Also, blood proteins were used as indexes for the regulation of animal body homeostasis, which is closely associated with physiological parameters in beef calves under heat stress. In addition, these blood proteins can be consolidated to develop a THI chart.

Key Words: beef calves, haptoglobin, heat shock protein 70
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023 Effect of subcutaneous meloxicam on indicators of acute pain and distress after castration and branding in 2-month-old beef calves.

D. M. Meléndez*[1,2], S. Marti[1,2], E. D. Janzen[1], D. Moya[2,3], D. Gellatly[1,2], E. A. Pajor[1], and K. S. Schwartzkopf-Genswein[2], [1]*University of Calgary, Calgary, AB, Canada,* [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Institute of Biological, Environmental and Rural Sciences, Aberystwyth, UK.*

Routine management practices such as vaccination, ear tagging, castration, and branding are procedures commonly done on the same day. The aim of this study was to assess the efficacy of a single dose of subcutaneous meloxicam (Metacam 0.5 mg/kg BW) at mitigating acute pain caused by knife castration or the combination of knife castration and hot-iron branding. Seventy-two 2-mo-old Angus bull calves were randomly assigned to a 3 × 2 factorial design: control (CON), knife (K), and knife and branding (KB) without meloxicam and control, knife (KM), and knife and branding (KBM) with meloxicam. Samples were collected on d −1; immediately before castration (T0); at 60, 90, 120, and 180 min after castration; and 1, 2, 3, and 7 d after castration to determine salivary cortisol (SC), substance P (SP), haptoglobin (HP), stride length, and frequency of tail flicking (TF), foot stamping (FS), and head turning (HT) behaviors. A castration × medication × time interaction was observed for HP ($P = 0.05$) and FS ($P = 0.02$), where KBM calves had greater HP concentrations than KB calves at T0, whereas KB calves had greater HP concentrations on d 1, 2, 3, and 7 and greater FS frequencies than the KBM group on d 1 and 2. The K calves had greater HP concentrations on d 1 and 2 compared with KM calves. A castration × time interaction was observed for SC ($P < 0.01$) and TF ($P < 0.01$). The K and KB calves had greater SC concentrations compared with CON calves 60 min after castration, whereas KB calves had greater concentrations than K calves and both KB and K calves had greater concentrations compared with CON calves 90, 120, and 180 min after castration. The KB and K calves had greater TF frequencies on d 1 and 3 compared with CON calves, whereas KB calves had greater TF than K calves and both groups compared with CON calves on d 2. A castration × medication interaction ($P = 0.01$) was observed for HT, where K calves were found to have greater HT frequencies than KM calves. No treatment or interaction effects were observed for SP. Overall, a single subcutaneous dose of meloxicam administered immediately prior to the procedures conducted was effective at mitigating physiological (HP and SC) and behavioral (TF, FS, and HT) indicators of pain and distress in calves that were castrated and castrated and branded.

Key Words: beef calves, meloxicam, pain mitigation
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024 Timing and frequency of antibiotic and nonsteroidal anti-inflammatory drug administration does not affect wound healing in recently weaned beef calves after band castration.

S. Marti*[1,2], D. M. Meléndez[1,2], E. D. Janzen[1], D. Gellatly[1,2], C. E. M. Heuston[2,3], E. A. Pajor[1], and K. S. Schwartzkopf-Genswein[2], [1]*University of Calgary, Calgary, AB, Canada,* [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*University of Saskatchewan, Saskatoon, SK, Canada.*

The aim of this study was to evaluate if the timing and frequency of administration of an antibiotic (oxytetracycline; 1 mg/10 kg of BW) and a nonsteroidal anti-inflammatory drug (NSAID; meloxicam, 0.5 mg/kg of BW) improved wound healing in band castrated calves. Drugs were administered as a combination. Twenty-four recently weaned Angus crossbred bull calves (292 ± 19.1 kg of BW) were randomly assigned to 1 application of antibiotic and NSAID at the time of banding (CTR); 2 applications, at banding and when the band broke through the skin (SKB); 2 applications, at banding and when the scrotum sloughed off (SSO); or 3 applications, at banding, when the band broke through the skin, and when the scrotum sloughed off (SKSO). Wound healing was assessed in all calves over a 69-d period after band placement. Indicators of wound healing included maximum scrotal area temperature (°C) assessed via infrared thermography, scrotal circumference (cm), visual evaluation of swelling (6-point scale, in which 0 = no swelling and 5 = increased degree of swelling with presence of pus), healing of the wound site (5-point scale in which 1 = incision open without scabbing and 5 = incision completely healed), and pain sensitivity (g) using a Von Frey anesthesiometer. In addition, BW (kg), ADG, and rectal temperature (°C) were recorded. Data was collected the day prior to castration; immediately before castration; 8 h after castration; on d 1, 3, 6, 13, 20, and 27; and weekly thereafter until the end of the study. Data were analyzed using a mixed-effects model, where application of antibiotic and NSAID, time, and their interactions were used as fixed effects and animal within pen was used as a random effect. On d 41 after castration, 100% of the scrotums had sloughed off. However, no differences among treatments were observed for when sloughing occurred. No differences in wound healing ($P = 0.72$) or swelling ($P = 0.13$) were observed among treatments. In addition, no treatment differences were observed for pain sensitivity ($P = 0.71$) after loss of the scrotum (489, 389, 366, and 380 g for CTR, SKB, SSO, and SKSO, respectively), growth ($P = 0.96$), or rectal temperature ($P = 0.91$). Repeated applications of antibiotic and NSAID after band castration did not improve healing or reduce inflammation or pain sensitivity in recently weaned beef calves.

Key Words: band castration, beef, wound healing
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025 Prevalence and characteristics of bruises of beef cattle carcasses from two regions of northwest Mexico. J. N. Sanchez-Perez[*1], F. G. Rios-Rincon[2], K. H. Leyva-Medina[2], J. C. Robles-Estrada[3], and J. J. Portillo-Loera[2], *[1]Universidad Autónoma de Sinaloa, Sinaloa, Mexico, [2]Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [3]Universidad Autonoma de Sinaloa, Culiacan, Mexico.*

Numerous risks associated with transport and handling of livestock cause bruising and poor welfare to animals. The objective of this work was to characterize bruises in bovine carcasses in a Federal Inspection Type slaughter house in the North and Central regions of Sinaloa, México. Four hundred forty-two bovine carcasses were randomly selected in a prospective observational study during 4 mo. Bruises were visually classified into 2 grades according to the amount of tissue affected (subcutaneous tissue [grade 1] and involving muscular tissue and sometimes bone [grade 2], shape (mottled, irregular, linear, circular, and railways), size (small, medium, and large), and location of bruises on the carcass (hindquarter, abdomen, rib, forehead, loin, coccygeal tuberosity, ischial tuberosity, and tail); this assessment was supported by photographs. Data were analyzed with a Fisher test in 2 × 2 contingency tables for 2 categories (Central and North regions). Seventy-six percent of the carcasses presented bruises, 40% from the North region and 36% from the Central region ($P = 0.001$). The anatomical site most affected was the loin (47%) followed by ribs (44%). The most common shape bruises were circular, 29.41% in the North region and 32.81% in the Central region ($P = 0.01$). Small size bruises were the most frequent (26.92 and 31.22%; $P = 0.005$) for the Central and North regions, respectively. Finally, bruises of grade 1 represented 32.58 and 34.84% ($P = 0.02$) for Central and North regions, respectively. It is concluded that the presentation of bruises on carcasses and anatomical sites affected indicates a need to improve transport conditions and personnel skills that result in better welfare for the animals as well as better financial profit.

Key Words: animal welfare, beef cattle, bruises
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026 Evaluation of heat tolerance of Tabapuã bovines in the central region of Brazil. R. Z. Taveira[*1], J. Moraes[2], R. M. D. Silva[1], A. Amaral[1], F. Mendonça[1], F. Ponte[1], F. Carvalho[1], and A. Pereira[3], *[1]Universidade Estadual de Goiás (UEG), São Luís de Montes Belos, Goiás, Brazil, [2]Universidade Federal de Goiás, Jataí, Brazil, [3]Universidade de Évora, Évora, Portugal.*

The aim of this research was to evaluate the heat tolerance of Tabapuã bovines exposed to a heat tolerance test in the central region of Brazil. Eleven male bovines of the Tabapuã breed were used, with average age and average weight of 24 mo and 539.33 ± 59.86 kg, respectively. The experimental design was completely randomized. In the evaluation of heat tolerance, a thermolytic capacity test was used. The thermolytic capacity test was replicated on 5 nonconsecutive hot, sunny, cloudless days. This test consisted of the measurement of rectal temperature (RT) of the animals at 3 different times, obtaining the thermolytic capacity index (TCI). For the calculation of TCI, the following formula was used: $TCI = 10 - [(RT2 - RT1) - (RT3 - RT1)]$. The RT1 was measured at 1300 h, immediately after the animals had remained for 2 h in the shaded corral (1100 to 1300 h). The RT2 was obtained at 1400 h, immediately after the animals had stayed an hour in a corral with incidence of solar radiation (1300 to 1400 h). The RT3 was measured at 1500 h, immediately after the animals had stayed an hour in a shaded corral (1400 to 1500 h). The RT was measured with the aid of a digital clinical thermometer, introduced and kept in the rectum of the animal for 1 min. The mean RT across the 3 schedules evaluated was 38.76°C, indicating good adaptability of Tabapuã breed to the tropical environment. Considering the evaluating of RT, there was a significant difference ($P < 0.05$) between the averages recorded with the animals in the shade (38.35°C) and after 1 h of sun exposure (39.47°C), with an increase of 1.12°C. At the end of the test, after 1 h of exposure to shade, RT numerically decreased ($P > 0.05$) by 1.0°C to 38.47°C. The average TCI was 9.07, with minimum and maximum values of 8.80 and 9.41, respectively, considering the average of all the animals in the 5 d of evaluation. The results obtained in this study showed that the Tabapuã breed has good heat tolerance.

Key Words: adaptation, bovines, well-being
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027 Effect of dehorning and multialleviation treatment on the growth, behavior, and blood parameters of Korean cattle bull calves. S. J. Park[*], H. J. Kim, M. Y. Piao, D. J. S. Jung, S. Y. Kim, S. W. Na, and M. Baik, *Department of Agriculture Biotechnology, College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea (South).*

This study was performed to determine the effects of dehorning and multialleviation treatment (MAT) on growth, behavior, and blood parameters of Korean cattle. Thirty-six Korean cattle bull calves (172.0 kg BW and 223 d of age) were allocated to 4 treatments ($n = 9$/group): no dehorning without MAT injection, no dehorning with MAT injection, dehorning without MAT injection, and dehorning with MAT injection. Multialleviation treatment included 5 mL of 2% lidocaine hydrochloride injection for local anesthesia in each horn and 2 mg/kg BW of 50 mg/mL flunixin meglumine intravenously for anti-inflammation in the neck immediately prior to dehorning. For the no-MAT groups, a 0.9% NaCl placebo solution was used. Dehorning was performed using a Barnes dehorner, and a cautery iron was used to stop bleeding. Blood was collected immediately before and h 0.5, h 5, d 1, d 3, d 7, and d 14 after dehorning and MAT injection. Feed intake was recorded daily, and BW was measured on the day prior to the experiment and at d 14. Behavior was measured between h 0 and 3 after dehorning. All data were analyzed using 2-way ANOVA with the main effects of dehorning and MAT, using the mixed model procedure. Dehorning did not affect ($P > 0.08$) weight gain. Dehorning decreased eating ($P < 0.01$) and increased lying ($P < 0.05$) behaviors, but MAT did not affect these behaviors. A dehorning × MAT interaction was observed ($P = 0.01$) for head shaking. Dehorning tended ($P = 0.06$) to increase head shaking, and MAT decreased head shaking in the dehorning group but not in the no dehorning group. Dehorning increased ($P < 0.001$) circulating cortisol concentrations only at h 0.5, but MAT did not affect cortisol concentrations. Dehorning increased ($P < 0.01$) glucose concentrations at h 0.5 and tended ($P = 0.07$) to increase glucose concentrations at h 5, but MAT did not affect glucose concentrations. In conclusion, dehorning changed behaviors (eating, lying, and head shaking) and increased cortisol concentrations at h 0.5 without affecting growth. Multialleviation treatment decreased frequency of head shaking, but it did not alleviate cortisol concentrations and did not affect eating and lying frequencies. Our study indicates that additional strategy, in addition to the MAT, is recommended for alleviating dehorning stress of male calves.

Key Words: behavior, dehorning, stress
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ANIMAL HEALTH

028 Elevated lipocalin2 expression in vivo protects hosts against bacterial infection.

Q. Wang*,
Feed Science Institute, College of Animal Science, Zhejiang University, Hangzhou, P.R. China.

Lipocalin2, which also known as neutrophil gelatinase-associated lipocalin, is an essential component of the innate antimicrobial immune system. The aim of current study was to determine the distribution of lipocalin2, investigate the expression changes of lipocalin2 after bacterial challenge, and further explore the function of lipocalin2 during bacterial infection. Western blot, real-time quantitative PCR, immunohistochemistry, and ELISA were used to evaluate the temporospatial expression of lipocalin2. Normally, lipocalin2 can be detected mainly in the liver, spleen, kidney, thymus, and intestine. After *Escherichia coli* K88 challenge, both mRNA and protein levels of lipocalin2 were significantly elevated in the liver, spleen, thymus, and jejunum ($P < 0.05$) either in piglets or in mice. Serum lipocalin2 exerted a continuous increase from 8 h after challenge and peaked by 32 h. In addition, we found that the bacterial burden in blood and liver tissues was significantly increased ($P < 0.05$) in lipocalin2-deficient mice. Furthermore, our study revealed that in vitro lipocalin2 exerted obvious bacteriostatic activity, as the proliferation of *E. coli* K88 and *Salmonella typhimurium* CMCC50013 was significantly inhibited ($P < 0.05$) in a dose-dependent manner when treated with lipocalin2. The results suggested that the elevated lipocalin2 expression in vivo was presumed to effectively contribute protection to host innate immunity.

Key Words: bacterial challenge, bacteriostatic ability, lipocalin2
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029 Mitochondrial correlates of signaling processes involved with the cellular response to *Eimeria* infection in broiler chickens.

T. H. Elsasser[*1], S. Kahl[1], A. Martínez[2], K. B. Miska[1], and R. H. Fetterer[3], [1]*USDA-ARS, ABBL, Beltsville, MD,* [2]*Center for Biomedical Research of La Rioja (CIBIR), Logroño, Spain,* [3]*USDA-ARS, APDL, Beltsville, MD.*

Host cellular responses to coccidiosis infection are consistent with elements of apoptosis, autophagy, and necrosis. These processes are enhanced in the cell through cell-directed signaling or repressed through parasite-derived inhibitors of these processes favoring the survival of the parasite. Across all 3 of these cell-based responses, one common factor at the origins of response-initiating signaling is the perturbation of the mitochondria and mitochondria-derived release of superoxide anion and nitric oxide. These reactants can interact to form the potent tyrosine-nitrating reactant peroxynitrite. The objective of our investigation was to determine how mitochondrial dysfunction might arise during the infection-response process and how endogenous biochemical reactions derived from this mitochondrial dysfunction might affect the cell. In the mitochondria, ATP is generated by Complex V ATP synthase, specifically in what is termed the P-loop, a highly ordered hydrophilic pocket. Based on literature citations suggesting that mitochondrial proteins are dysfunctionally nitrated during oxidative stress, we accessed the 3-dimensional structure of the P-loop (PMID: 11509182) and used a computational chemistry algorithm (HyperProtein version 1.0) to model how the nitration of a tyrosine residue (Y-345), significant to the orientation of the ADP, Pi, and Mg^{+2}, might affect the spatial structure of the domain. Analysis revealed that nitration of this specific residue reordered hydrogen bonding and electrostatic charges in the P-loop where the ADP, Pi, and Mg^{+2} were disfavored from interacting. To test if this nitration could be identified during an oxidative stress in vivo, we developed a highly specific mouse monoclonal anti-nitroY-345 P-loop antibody and performed high-resolution fluorescent imaging on duodenal tissues obtained from broilers infected with coccidiosis parasite *Eimeria acervulina*. Imaging revealed that this specific nitration event did occur ($P < 0.05$ vs. noninfected chickens) in villus enterocytes as early as 1 d after infection. This specific P-loop nitration colocalized directly with mitochondria (rabbit-anti-Complex V, C subunit) on d 1 after infection but became more generalized throughout the affected enterocytes as the infection progressed and mitochondria appeared to decrease ($P < 0.04$) in numbers and condense into tight clumps. The nitration mirrored the progression from d 1 to d 3 to d 6 after infection of the parasites down the villus to the crypts, with the nuclei of both the trophozoites and the schizonts showing evidence of strong generalized protein nitration ($P < 0.01$; detected with anti-nitrotyrosine antibody) and membrane disruption. The data suggest that post-translational mitochondrial autonitration of Complex V P-loop may participate in cellular responses to coccidiosis.

Key Words: *Eimeria*, mitochondria, protein nitration
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030 Ovicidal effect of the fruit and leaf of *Caesalpinia coriaria* against *Haemonchus contortus* and *Haemonchus placei*. A. Olmedo-Juarez[1], R. Rojo Rubio[*2], P. Mendoza-de Gives[3], J. F. Vázquez-Armijo[2], B. Albarran-Portillo[2], and C. Garcia-Hernandez[2], [1]*Centro Nacional de Investigacion Disciplinaria en Parasitologia Veterinaria, INIFAP, Cuernavaca, Mexico,* [2]*Universidad Autonoma del Estado del Mexico, Temascaltepec, Mexico,* [3]*Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias, Jiutepec, Mexico.*

The effect of hydroalcoholic extracts of fruits and leaves from *Caesalpinia coriaria* on the egg hatching inhibition of *Haemonchus contortus* and *Haemonchus placei* was evaluated. The tested concentrations were 25.0, 12.5, 6.2, 3.1, and 1.5 mg/mL; likewise, a 4% methanol solution and albendazole were used as negative and positive controls, respectively. The results were analyzed under a 2 × 2 × 6 factorial arrangement of treatments under a completely randomized design, and for the mean comparison, Tukey's test was used. The mean (LC_{50}) and maximum (LC_{90}) lethal concentrations were estimated with Probit analysis of SAS. The hydroalcoholic leaf extract as well as the fruit extract had ovicidal activity (Table 030; $P < 0.05$), inhibiting hatching in around 100% with the concentration of 25.0 mg/mL. The fruit extract had better egg hatching inhibition ($P < 0.001$) in *H. contortus* and *H. placei* than the leaf extract. The LC_{50} for the fruit extract were 1.63 and 3.91 mg/mL and for the leaf were 3.98 and 11.68 mg/mL for *H. contortus* and *H. placei*, respectively. The main compounds contained in both extracts were tannins, flavonoids, gallic acid, and ethyl gallate. It is concluded that the hydroalcoholic extracts from mature fruits and leaves of *C. coriaria* have the ability of inhibit the egg hatching of *H. contortus* and *H. placei*.

Key Words: *Caesalpinia coriaria*, *Haemonchus*, secondary compounds
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Table 030. Percentage of egg hatching inhibition in 2 species of gastrointestinal nematodes exposed to a hydroalcoholic extract of mature fruits and leaves of *Caesalpinia coriaria*

		Egg hatching inhibition, %	
		Nematode	
Extract	Concentration, mg/mL	*Haemonchus contortus*	*Haemonchus placei*
Fruit	25.00	100^{a}	100^{a}
	12.50	100^{a}	100^{a}
	6.25	99.5^{a}	92.75^{a}
	3.15	89.25^{a}	33.75^{cd}
	1.56	58.75^{b}	17.75^{e}
	0.00	3.25^{fg}	2.75^{g}
Leaf	25.00	95.25^{a}	92.50^{a}
	12.50	90.00^{a}	60.75^{b}
	6.25	60.00^{b}	22.75^{de}
	3.15	40.75^{c}	19.75^{de}
	1.56	27.50^{cde}	16.25^{efg}
	0.00	3.25^{fg}	2.75^{g}
Albendazole	10.00	100^{a}	100^{a}
Extract			<0.0001
Nematode			<0.0001
Concentration			<0.0001
Extract × nematode			0.8977
Extract × concentration			<0.0001
Extract × nematode × concentration			<0.0001
SEM			0.10

$^{a–g}$Means within the same column and row with different letters statistically differ ($P < 0.05$).

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031 In vitro evaluation of the antimicrobial activity of several short- and medium-chain fatty acid salts and their combinations. C. Sol[*1], J. M. Oddo[1], M. Puyalto[1], A. Carvajal[2], M. Gómez[2], S. Costillas[2], J. J. Mallo[1], and P. Rubio[2], [1]*NOREL S.A., Madrid, Spain,* [2]*Universidad de León – grupo DIGESPORC, León, Spain.*

Organic acid salts are feed additives used as alternatives to antibiotics for health and growth promotion in animal production. The aim of this study was to investigate the minimum inhibitory concentration (MIC) of organic acid salts against *Salmonella enterica* subsp. *enterica* (7 strains), *Escherichia coli* (9 strains), and *Clostridium perfringens* (6 strains). The products tested were sodium butyrate (BUT), sodium heptanoate (HEP), sodium salt of coconut fatty acid distillate (DIC), and their combinations BUT + DIC (1:1 ratio) and HEP + DIC (1:1 ratio). For each product and each strain, MIC was determined in triplicate using a broth microdilution method at pH 4.8 and 6, and the value that inhibits 50% of the tested isolates was determined (MIC_{50}). The results at pH 4.8 of MIC_{50} against *E. coli* showed that HEP was the most effective (32 ppm) followed by HEP + DIC (128 ppm), BUT (512 ppm), and BUT + DIC (1,024 ppm); DIC could not solubilize at more than 5,000 ppm. Regarding to *Salmonella*, HEP was also the most effective (32 ppm) followed by HEP + DIC and BUT (256 ppm) and DIC and BUT + DIC (512 ppm). *Clostridium* *perfringens* was unable to grow at pH 4.8. The results at pH 6 of MIC_{50} against *E. coli* showed that HEP was again the most effective (3,125 ppm) followed by HEP + DIC (3,500 ppm) and BUT (62,500 ppm). Sodium salt of coconut fatty acid distillate could not solubilize at more than 5,000 ppm and BUT + DIC could not solubilize at more than 9,000 ppm. Regarding to *Salmonella* at pH 6, HEP was also the most effective (1,562 ppm) followed by BUT (125,000 ppm); however, DIC, BUT + DIC, and HEP + DIC could not solubilize at more than 5,000, 9,000, and 14,000 ppm, respectively. Finally, the results against *C. perfringens* showed that DIC was the most effective (15.4 ppm) followed by HEP + DIC (21.5 ppm), BUT + DIC (27.6 ppm), HEP (1,562 ppm), and BUT (31,250 ppm). In summary, the results showed that HEP was the most effective against Gram-negative bacteria, whereas DIC was the most effective against Gram-positive bacteria. The combination HEP + DIC showed an increased effect of DIC against *Salmonella* and also an increased effect of HEP against *C. perfringens*. The combination of BUT with DIC potentiated the effect of BUT against *C. perfringens*. Further studies would be required to better understand these interactions as well as in vivo studies to demonstrate the effects on microbial populations.

Key Words: minimum inhibitory concentration, organic acid salts
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032 Antibacterial activity of different essential oils and their combinations against relevant enteric pathogenic bacteria.

J. M. Oddo*[1], L. Mesas[1], C. Sol[1], M. Gómez[2], S. Costillas[2], A. Carvajal[2], J. J. Mallo[1], P. Rubio[2], and R. Miranda[2], [1]*NOREL S.A., Madrid, Spain,* [2]*Universidad de León – grupo DIGESPORC, León, Spain.*

Essential oils (EO) and their components are being increasingly used in animal feeds for their antibacterial properties. However, in-feed concentrations are usually lower than the effective antibacterial concentrations reported by in vitro assays. Therefore, it is important to study the most efficient EO and synergistic combinations to improve their effectiveness as feed additives. The objective of this study was to test the in vitro antibacterial activity of 3 EO (clove, oregano, and black pepper) and 3 isolated EO components (cinnamaldehyde, thymol, and carvacrol) both individually and in combinations against a collection of reference and field strains of *Escherichia coli*, *Salmonella enterica* subsp. *enterica*, and *Clostridium perfringens*. The minimum inhibitory concentrations (MIC) were studied in triplicate using a broth microdilution method at pH 6. First, MIC of the 6 individual products were determined, whereas in a second step, 11 combinations of the individual products were evaluated. The results indicated that all the individual products, except black pepper, showed antimicrobial activity against all Gram-positive and Gram-negative tested bacterial strains. Minimum inhibitory concentrations that inhibit 50% of the isolates (MIC_{50}) ranged from 300 to 600 mg/L for *E. coli*, 300 to 600 mg/L for *Salmonella*, and 300 to 1,200 mg/L for *C. perfringens*. Carvacrol showed the best antibacterial activity, with a MIC_{50} of 300 mg/L against all 3 bacteria, followed by cinnamaldehyde, with a MIC_{50} of 600 mg/L against *E. coli* and *Salmonella* and a MIC_{50} of 300 mg/L against *C. perfringens*. Most of the combinations showed an increased antibacterial activity compared with their individual components, with a MIC_{50} range from 150 to 300 mg/L for all tested strains of the 3 bacterial species. The combination of cinnamaldehyde, thymol, carvacrol, and clove EO showed the best antibacterial results, with a MIC_{50} of 150 mg/L against all 3 bacteria, followed by the combination of cinnamaldehyde and carvacrol, with a MIC_{50} of 150 mg/L for *E. coli* and *C. perfringens* and a MIC_{50} of 300 mg/L for *Salmonella*. The results of this study confirm that the antibacterial activity of some EO and their components can be increased by their use in combination. Further studies are needed to better understand these interactions as well as in vivo studies to show their effects on microbial populations.

Key Words: combinations, essential oils, minimum inhibitory concentration
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033 Survey of mycotoxins in 2016 United States corn.

E. G. Hendel*[1], P. N. Gott[1], G. R. Murugesan[1], and T. Jenkins[2], [1]*BIOMIN America Inc., San Antonio, TX,* [2]*BIOMIN Holding, GMBH, Getzersdorf, Austria.*

Mycotoxins, toxic secondary metabolites produced by common molds infecting grains and forages, can contaminate feed ingredients. The negative effects on livestock are dependent on the level, type, and duration of exposure as well as the age, species, and general health status of the animal. The current study's objective was to determine the occurrence and potential risk of mycotoxins to livestock species in the 2016 U.S. corn crop in comparison with the previous year. In total, 318 corn samples from 25 states (2015 harvest) and 387 corn samples from 26 states (2016 harvest) were submitted for analysis as part of the annual Biomin PROcheck Mycotoxin Survey. Samples were analyzed by liquid chromatography tandem mass spectrometry for the presence of mycotoxins from 6 major mycotoxin groups: type B trichothecenes including deoxynivalenol (DON), fumonisins (FUM), zearalenone (ZEN), aflatoxins (Afla), type A trichothecenes including T-2 toxin (T-2), and ochratoxin A (OTA). A summary of the results is provided in Table 033. Individual toxin levels and co-occurrence from each year were compared using nonparametric tests (GraphPad Prism). In the 2016 sample pool, 90% of the corn samples had least one mycotoxin detected. Compared with 2015 corn, 2016 corn had higher contamination levels of DON and FUM ($P < 0.001$). Additionally, co-occurrence of more than one mycotoxin increased from 2015 to 2016 (46 vs. 67%; $P < 0.001$). Toxins produced by *Fusarium* fungal species (DON,

Table 033. Summary of mycotoxin analysis

	Year											
	2015						2016					
Parameters	DON	FUM	ZEN	Afla	T-2	OTA	DON	FUM	ZEN	Afla	T-2	OTA
Positive samples, %	72	52	17	1	0.3	2	75	72	42	6	2	0
Median, ppb	400	500	107	23	200	3	785	1,700	163	7	277	NA
90th percentile, ppb	1,500	2,960	600	87	NA	59	4,580	9,340	616	53	400	NA
Maximum contamination, ppb	5,670	16,300	1,200	108	200	100	11,700	119,400	19,000	139	401	NA

FUM, and ZEN) were frequently detected in combination; 21% of samples tested positive for all 3 toxins. Co-occurrence of mycotoxins can result in more severe detrimental impacts on animal health and performance. The high prevalence as well as large number of samples above the U.S. Food and Drug Administration–recommended level (42% of positive samples over 1,000 ppb) positions DON as the greatest mycotoxin threat to livestock from the 2016 U.S. corn harvest. However, the high prevalence of co-occurrence suggests FUM and ZEN also present significant risks to animal health in 2016 corn.

Key Words: deoxynivalenol, mycotoxins, zearalenone
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034 Survey of mycotoxins in United States corn distiller's dried grains with solubles.

E. G. Hendel*[1], P. N. Gott[1], G. R. Murugesan[1], and T. Jenkins[2], *[1]BIOMIN America Inc., San Antonio, TX, [2]BIOMIN Holding, GMBH, Getzersdorf, Austria.*

Distiller's dried grains with solubles (DDGS), a byproduct of the ethanol industry, is commonly used as a feed ingredient for various livestock species. During ethanol production, mycotoxins present in the original corn become concentrated in the resulting DDGS. These secondary metabolites produced by molds infecting crops such as corn can significantly compromise animal health. Severity of the negative effects associated with mycotoxins is dependent on the level, type, and duration of exposure and the age, species, and general health status of animals. The objective of the current study was to determine the occurrence of mycotoxins in samples of U.S. corn DDGS and to evaluate the potential risk posed to livestock. Seventy-nine corn DDGS samples from 14 states were submitted for analysis between 2015 and 2016. Samples were analyzed using liquid chromatography tandem mass spectrometry for the presence of mycotoxins from the following 6 major mycotoxin groups: type B trichothecenes including deoxynivalenol (DON), fumonisins (FUM), zearalenone (ZEN), aflatoxins (Afla), type A trichothecenes including T-2 toxin (T-2), and ochratoxin A (OTA). All samples in the current survey were contaminated with at least one mycotoxin, with 96% having more than one mycotoxin detected. The presence of multiple mycotoxins may intensify the negative effects of each mycotoxin present. The percent positive samples, median, 90th percentile, and maximum contamination level of positive samples for the 6 major mycotoxin groups are presented in Table 034. Deoxynivalenol was detected in 100% of samples, although FUM and ZEN were also highly prevalent. Deoxynivalenol poses the greatest threat from U.S. corn DDGS samples to animal health due to the high prevalence (100%) and large number of samples contaminated beyond the U.S. Food and Drug Administration–recommended level (80% of positive samples above 1,000 ppb).

Table 034. Summary of mycotoxin analysis

Parameters	DON	FUM	ZEN	Afla	T-2	OTA
Positive samples, %	100	88	71	7	0	1
Median of positives, ppb	2,400	2,600	150	6	0	19
90th percentile, ppb	5,420	7,100	431	26	NA	NA
Maximum contamination, ppb	9,800	18,500	666	37	0	19

Key Words: deoxynivalenol, distiller's dried grains with solubles, mycotoxins
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035 Omnigen-AF supplementation may attenuate liver damage during a high concentrate diet in finishing steers.

S. A. Armstrong*[1,2], D. J. McLean[1], M. Bionaz[2], and G. Bobe[2], *[1]Phibro Animal Health Corporation, Teaneck, NJ, [2]Department of Animal and Rangeland Sciences, Oregon State University, Corvallis.*

To determine the effect of OmniGen-AF (OG; a patented nutritional specialty product from Phibro Animal Health Corporation) supplementation on markers of metabolism and liver function in steers during backgrounding, transition, and finishing phases, 9 purebred Angus half-sibling steers were divided into 1 of 2 treatment groups: control (CNTL; *n* = 4) and OG (*n* = 5). Cattle were offered 0 (CNTL) or 56 g/animal per day of OG through a 28-d backgrounding period (limit fed a predominantly forage-based diet), a 14-d transition period, and finished on a high-concentrate diet for 56 d (104 d total). Serum was collected on d 0, 14, 21, 28, 35, 43, 56, 70, 84, 98, and 104 for haptoglobin, metabolites, and markers of liver function as measured by paraoxonase, albumin, aspartate aminotransferase (AST), and gamma-glutamyltransferase (GGT). Data were analyzed using repeated-measures-in-time analysis in PROC MIXED. Fixed effects of the statistical model were treatment (CNTL and OG), dietary phase, day (nested within phase), and their interactions. The values and variation of serum AST and GGT increased at the end of the finishing phase, resulting in a bimodal distribution prior to and at the end of finishing; therefore, we examined AST and GGT concentrations with a separate analysis on d 84, 98, and 104. A diet phase effect was present for metabolites and markers of liver function ($P < 0.05$); the interaction of diet phase and OG supplementation had no effect on metabolites, AST, paraoxonase, or albumin. Gamma-glutamyltransferase tended to increase in OG steers, whereas in CNTL steers, GGT decreased ($P = 0.08$) during the backgrounding phase. OmniGen-AF supplementation during the entire experiment (104 d) increased serum haptoglobin concentrations ($P = 0.0002$) and decreased serum NEFA concentrations ($P = 0.002$). OmniGen-AF supplementation also assuaged the decline in paraoxonase concentrations ($P = 0.02$) and tended to reduce the increase of a marker of liver cell necrosis (AST; $P = 0.07$) at the end of the finishing period (compared with control cattle on d 84, 98, and 104 of supplementation). Based on these data, we conclude that OG supplementation may attenuate liver damage during a high-concentrate diet in finishing steers.

Key Words: finishing steers, liver health, OmniGen-AF
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036 Evaluation of statistical process control procedures to monitor feeding behavior and ruminal temperature changes associated with experimental inoculation of *Mannheimia haemolytica*.

W. C. Kayser*[1], G. E. Carstens[1], W. E. Pinchak[2], I. L. Parsons[1], K. E. Washbun[3], S. D. Lawhon[4], E. Chevaux[5], and A. L. Skidmore[5], *[1]Department of Animal Science, Texas A&M University, College Station, [2]Texas A&M AgriLife Research, Vernon, [3]Department of Large Animal Clinical Sciences, Texas A&M University, College Station, [4]Department of Veterinary Pathobiology, Texas A&M University, College Station, [5]Lallemand Animal Nutrition, Milwaukee, WI.*

Objectives of this experiment were to determine if statistical process control (SPC) procedures coupled with remote collection of rumen temperature (RT) and feeding behavior (FB) patterns could accurately differentiate between animals experimentally inoculated with *Mannheimia haemolytica* (MH) or phosphate buffer solution (PBSo) and to determine if live yeast (LY) supplementation would mitigate responses to MH challenge. Thirty-six crossbred steers (352 ± 23 kg BW) seronegative for MH were allocated within a 2 × 2 factorial treatment arrangement: Factor1 = roughage-based diet with or without LY (*Saccharomyces cerevisiae boulardii* I-1079 at 1×10^{10} cfu/d; Lallemand) and Factor2 = bronchoselective endoscopic inoculation with MH or PBSo. Electronic feed bunks (GrowSafe) were used to measure DMI and FB traits, and ruminal thermo-boluses (Medria) used to measure RT at 5-min intervals. Data were collected 28 d prior to and following inoculation. Steers inoculated with MH exhibited elevated levels of haptoglobin, white blood cells, and neutrophils ($P < 0.02$), indicating that the MH challenge effectively stimulated immunologic responses. However, only 1 animal displayed overt clinical signs of disease. Shewhart charts (SPC procedure) were used in this analysis, and sensitivity, specificity, and accuracy were computed to evaluate univariate and multivariate models based on principal components analysis (PCA). Of the FB traits monitored, time to bunk had the highest model sensitivity (94%) and accuracy (94%), with model accuracies for head-down duration and bunk visit duration and frequency being less (80, 79, and 56%, respectively). Model accuracy for DMI was intermediate at 85%. To address the diurnal nature of RT, data were averaged over 6-h intervals, and quarterly RT models were evaluated separately. Model accuracy for the first quarter RT was more accurate (84%) than the other quarterly RT periods (82, 76, and 79%). Two PCA models were constructed separately using all FB and RT traits. Model sensitivity and accuracy were relatively higher for the FB PCA model (94 and 95%) than for the RT PCA model (78 and 85%), with both PCA models performing slightly better than the best respective univariate trait model. The performance of a combined PCA model (all traits) was intermediate in accuracy at 91%. In this study, LY supplementation did not influence the sensitivity or accuracy of the univariate or PCA models. These results indicate that Shewhart procedures can effectively identify deviations in FB and RT patterns for the purpose of subclinical bovine respiratory disease detection. Furthermore, the PCA models were numerically more accurate than univariate traits and should be more robust in application due to their multivariate nature.

Key Words: animal health monitoring, bovine respiratory disease, statistical process control
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037 Replacing dietary antibiotics with 0.20% L-glutamine in swine nursery diets: Impact on health and productivity of pigs following weaning and transport during the summer.

A. W. Duttlinger*[1], K. R. Kpodo[1], D. C. Lay Jr.[2], B. T. Richert[1], and J. S. Johnson[2], *[1]Purdue University, West Lafayette, IN, [2]USDA-ARS Livestock Behavior Research Unit, West Lafayette, IN.*

Recently, our lab determined that supplementing nursery diets with 0.20% L-glutamine improved health and productivity of weaned and transported piglets in a controlled environment. Therefore, study objectives were to determine the impact of replacing dietary antibiotics with 0.20% L-glutamine on growth performance and health status of piglets following weaning and transport in a production environment during the hot summer months. In July 2016, 246 mixed sex piglets (5.64 ± 0.37 kg BW; Duroc × [Landrace × Yorkshire]) were weaned (19 d of age), loaded onto a trailer, and transported for 12 h.

During transport, ambient temperature (28.5 ± 0.3°C) and relative humidity (61.6 ± 1.1%) in the trailer were monitored in 5-min intervals, feed and water were withheld, and intra-abdominal temperature of 6 sentinel piglets was monitored every 10 min (39.7 ± 0.1°C). Following transport, 240 piglets were unloaded, blocked by BW, and randomly allotted to 1 of 3 dietary treatments (n = 10 pens/treatment [8 piglets/pen]). Treatments were dietary antibiotics (AB; chlortetracycline [441 mg/kg] + tiamulin [38.6 mg/kg]), no dietary antibiotics (NA), or 0.20% L-glutamine (GLU) fed for 14 d (Period 1). Following Period 1, all pigs were provided a common antibiotic-free diet until d 34 (Period 2). Data were analyzed using PROC MIXED in SAS 9.4. In Period 1, ADG tended to be greater (P = 0.06) in AB pigs (234 ± 11 g/d) compared with NA pigs (194 ± 11 g/d), with GLU pigs (213.0 ± 11 g/d) being intermediate and not different from AB and NA pigs. During Period 2, ADG increased (P = 0.03) in AB pigs (455 ± 9 g/d) versus NA pigs (420 ± 9 g/d); however, no differences were observed in GLU pigs (443 ± 9 g/d) compared with AB and NA pigs. Overall, AB and GLU increased ADG (P < 0.01; 359 ± 8 g/d) compared with NA (329 ± 8 g/d), but no differences were detected between AB and GLU pigs. Feed efficiency was improved overall (P = 0.03) for AB piglets (681 ± 13) compared with NA piglets (633 ± 13); however, no G:F difference was detected for GLU pigs (647 ± 13) versus AB and NA pigs. No ADFI differences (P > 0.11; 538 ± 13.1 g/d) were detected. Treatments for enteric challenges were greater overall (P = 0.02) in NA piglets (4.9 ± 1.5%) compared with GLU (1.5 ± 1.5%) and AB piglets (1.5 ± 1.5%). In conclusion, 0.20% L-glutamine supplementation improved piglet health and productivity similarly to dietary antibiotics following weaning and transport during the summer.

Key Words: antibiotics, L-glutamine, piglets
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038 Survey of mycotoxin contamination in feedlot diets in Brazil.

L. Custodio*[1], D. N. Figueira[1], E. M. D. Gloria[2], V. B. Holder[3], A. Yiannikouris[4], J. E. Pettigrew[5], L. N. Kuritza[6], F. D. D. Resende[7], and G. R. Siqueira[7], [1]*FCAV/UNESP, Jaboticabal, Brazil,* [2]*ESALQ/USP, Piracicaba, Brazil,* [3]*Alltech Inc., Nicholasville, KY,* [4]*Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY,* [5]*University of Illinois, Urbana,* [6]*Alltech do Brasil, Araucaria, Brazil,* [7]*APTA – Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil.*

The objective of this survey was to identify mycotoxins and their concentrations in typical total mixed rations (TMR) used in Brazilian feedlots. The survey covered 30 Brazilian feedlots located in 5 major beef-producing states. Total mixed ration samples were collected on site and sent to Agência Paulista de Tecnologia dos Agronegócios (São Paulo, Brazil) to be lyophilized, milled, and subsequently sent to the 37+ Analytical Services Laboratory (Kentucky) for analysis of mycotoxins. The evaluation of mycotoxins comprised 2 distinct steps: In a first step, the absolute quantification of 38 different mycotoxins was performed using a validated and ISO/IEC 17025:2005 accredited method by means of ultraperformance liquid chromatography electrospray ionization tandem mass spectrometry and involving isotopic dilution step and a data normalization process. In a second step, the mycotoxin concentrations were further interpreted according to known species specific sensitivities and normalized according to the principles of toxic equivalent factors, determining the risk equivalency quantities (REQ) expressed in micrograms per kilogram of aflatoxin B1 (AFB1) equivalent. Data were examined and descriptive statistics were obtained using the UNIVARIATE procedure of SAS (9.2). Several toxins were identified in TMR and their average concentrations were determined, such as fumonisins at 2,175 µg/kg, trichothecenes A at 69.5 µg/kg, trichothecenes B at 15.9 µg/kg, fusaric acid at 84.0 µg/kg, aflatoxins at 0.7 µg/kg, and ergot at 1.83 µg/kg. The frequency of occurrence represented 97% for fumonisins, 80% for fusaric acid, 63% for trichothecenes A, 33% for ergot, 20% for trichothecenes B, and 10% for aflatoxins. This survey demonstrates that it is important to consider the combined occurrence of different types of mycotoxins in animal feed that are often neglected in other analytical approaches. Co-occurrences are important because mycotoxins could have an additive effect, potentially further increasing their negative impact. Therefore, in addition to identifying which mycotoxins are present in TMR and at which levels, it is also important to estimate the risks associated with the presence of different types of mycotoxins. The maximum REQ found in the feedlots evaluated in this survey was 230 and the minimum REQ was 1 µg/kg AFB1 equivalent, an REQ of 50, 100, and 150 being considered low (67% of samples), intermediate (27%), and high (7%) risk for beef cattle. In conclusion, fumonisins are the mycotoxins found most frequently and at highest concentrations in TMR fed in Brazilian feedlots. Interestingly, fusaric acid has been reported for the first time in Brazilian feedlots in 80% of the samples investigated.

Key Words: aflatoxins, fumonisins, trichothecenes
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039 Mycotoxin survey of common Bermudagrass in south-central Florida.

P. N. Gott*[1], A. Stam[2], A. Johns[3], B. G. Miller[1], B. Bell[1], T. Jenkins[4], and G. R. Murugesan[1], [1]*BIOMIN America Inc., San Antonio, TX,* [2]*Federally Recognized Tribal Extension Program, Okeechobee, FL,* [3]*Seminole Tribe of Florida, Inc., Okeechobee, FL,* [4]*BIOMIN Holding, GMBH, Getzersdorf, Austria.*

Common Bermudagrass (*Cynodon dactylon* L.) is a warm-season perennial grass found across the southern United States. Evaluation of factors impacting production and reproductive

Table 039. Summary of zearalenone results in pasture samples over time

Month	Total count	Percent positive	Overall mean, ppb[1]	Statistics on positive samples, ppb Mean[1]	Median	90th percentile	Maximum
Mar. 2016	56	78.6[a]	786[a,b]	1,000[a]	270	3,400	9,490
May 2016	62	51.6[b]	489[a,b]	946[a]	140	1,850	10,770
Aug. 2016	24	20.8[b]	27[b]	128[a]	80	270	270
Jan. 2017	15	100.0[a]	1,936[a]	1,936[a]	1,110	5,920	7,930
Combined	157	61.1	664	1,085	290	3,420	10,770

[a,b] Values in the same column sharing a letter were not significantly different (95% confidence level). Percent positive tested with χ^2 and monthly means tested with Bayesian inference (10^6 iterations), R version 3.3.2.

[1] Markov chain Monte Carlo methods used to estimate means of all samples within a month and of samples positive for ZEN within a month.

performance of beef cow–calf pairs grazing pastures on a large ranch in south-central Florida led to the investigation of potential mycotoxin contamination in standing forages. Mycotoxins produced by molds infecting many grains and forages can compromise animal health and performance. Zearalenone (ZEN) is the mycotoxin frequently associated with reproduction-related effects due to its estrogenic activity. The distribution of mycotoxins in pastures at the farm was assessed between paddocks and over time. Samples were hand plucked (25 to 30 samples per paddock) during 4 sampling periods with a total of 157 sampled paddocks over time. Activation Laboratories (Ancaster, ON, Canada) analyzed samples for 15 mycotoxins via liquid chromatography tandem mass spectrometry. Mycotoxin levels were reported on a dry basis in parts per billion (ppb; Table 039). Zearalenone was the predominant mycotoxin, detected in 61.1% of samples. Zearalenone prevalence was lower in May and August samples compared with March and January samples ($P < 0.05$). The concentration of ZEN in positive samples also tended to be lower in August samples. The combination of low prevalence and low concentrations in August meant that the estimated average sample level (overall Markov chain Monte Carlo mean; Table 039) was lower than in January ($P < 0.05$). Other mycotoxins detected included type A trichothecenes (T-2 or HT-2 toxin; 14.6%), type B trichothecenes (deoxynivalenol; 2.5%), sterigmatocystin (2.5%), and fumonisins (0.6%). Mycotoxins were detected in 62.4% of samples whereas 18.5% of samples tested positive for multiple mycotoxins. We conclude that additional sampling across a larger geographic region is needed to determine the wider significance of mycotoxins in common Bermudagrass.

Key Words: Bermudagrass, mycotoxins, zearalenone
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040 Expression galectins in sheep blood during the periparturient period.

B. Osei[*], M. Worku, S. Adjei-Fremah, E. Asiamah, K. Ekwemalor, and H. Ismail, *North Carolina Agricultural and Technical State University, Greensboro.*

In this study, galectin gene expression pre- and postpartum was evaluated in blood. St. Croix sheep are a breed of hair sheep that are parasite resistant and prolific and so are of interest for production. Immunosuppression during the periparturient period occurs in every organ in the sheep's body to enable the ewe support fetal growth and prevent abortion. During this time, sheep become susceptible to diseases and parasite infection. They rely on the effectiveness of their immune system to fight off invading parasites and diseases. Galectins are a family of lectins that have been proposed to promote intra- and intercellular communication impacting immunity. Blood was aseptically collected from 6 pregnant ewes into Paxgene tubes 1 wk before and 1 wk after lambing. Body weight, FAMACHA score, and BCS were collected to ensure they were in good health. Total RNA was isolated from the whole blood and converted into cDNA. Real-time PCR was performed using pooled cDNA samples with 8 different galectin primers (Gal 1, 2, 3, 4, 8, 12, 15 and 16) and B-actin primer served as control. All the galectins were expressed pre- and postpartum except for Gal 2, which was absent prepartum but expressed postpartum. Although all were expressed after lambing, Gal 3, 4, and 16 had a significant fold change increase, with Gal 16 being the highest with a fold change of 4. Periparturient changes in galectin expression may be useful indicator of animal health and welfare and should be characterized further.

Key Words: galectins, periparturient, St. Croix sheep
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041 Biogenic nano-selenium particles effectively attenuate oxidative stress–induced intestinal epithelial barrier injury by activating the Nrf2 antioxidant pathway.

D. Song[*1], Z. Lu[2], F. Wang[1], and Y. Wang[1], [1]*College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China,* [2]*Institute of Feed Science, College of Animal Science, Zhejiang university, Hangzhou, P.R. China.*

Oxidative stress has been implicated in a wide range of animal diseases. Due to frequent enterocyte renewal and continuous exposure to exogenous agents, the intestine is more vulnerable to oxidative stress than other organs, which leads to intestinal inflammation, intestinal barrier injury and dysfunction, and finally decreased animal production efficiency. In the present study, a new form of selenium nanoparticle (biogenic nano-selenium [BNS] particles) was synthesized using bacteria. The protection of BNS particles against oxidative stress–induced intestinal barrier dysfunction and the inherent mechanisms of this process were investigated, and selenomethionine (SeMet) and chemically synthesized nano-selenium (Nano-Se) particles were used for comparison. Characterization of BNS particles revealed that they were monodisperse and homogeneous spheres with an average size of 139.43 ± 7.44 nm. In the mouse model of intestinal oxidative stress, BNS particles were found to protect the mouse intestinal barrier function and preserve intestinal redox homeostasis more efficiently than SeMet and Nano-Se. In vitro experiments with porcine jejunum epithelial (IPEC-J2) cells verified the stronger epithelial barrier-protecting effect of BNS particles against oxidative stress, with reduced cell apoptosis and an improved cell redox state. Biogenic nano-selenium activated nuclear factor (erythroid-derived-2)-like 2 (Nrf2) and increased the expression of its downstream genes, including thioredoxin reductase-1 (TXNRD-1), NADPH dehydrogenase-1, heme oxygenase-1, and thioredoxin, in dose- and time-dependent manners. In contrast, SeMet and Nano-Se merely enhanced the activity of the selenoenzymes TXNRD-1 and glutathione peroxidase-1, indicating the role of selenium donors. Moreover, knockdown of Nrf2 significantly blocked the antioxidative effect of BNS, confirming that BNS protects the intestinal barrier from oxidative stress–induced damage by activating Nrf2 and its downstream genes. Our results suggest that BNS is a promising selenium species with potential application in treating oxidative stress–related intestinal diseases.

Key Words: biogenic nano-selenium particles, intestinal barrier, oxidative stress
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042 Evaluating the metagenome of two sampling locations in the nasal cavity of cattle with bovine respiratory disease complex.

T. G. McDaneld[*], L. A. Kuehn, and J. W. Keele, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Bovine respiratory disease complex (BRDC) is a multifactor disease, and disease incidence may be associated with an animal's commensal microbiota (metagenome). Evaluation of the animal's resident microbiota in the nasal cavity may help us to understand the impact of the metagenome on incidence of BRDC in cattle. Our objective was to determine whether metagenome populations of the nasal cavity vary based on sampling location. Therefore, 2 sampling locations (upper nasal and deep nasal pharyngeal) were evaluated. Nasal swabs from calves were collected when the animal was diagnosed with BRDC after weaning in the feedlot. Samples from healthy cohorts were also collected for each time point evaluated in the feedlot to compare metagenome profiles of healthy and sick animals. For each animal, 1 swab was inserted into the nasal cavity approximately 6 inches for sampling of the upper nasal region and a second swab was inserted approximately 8 inches for sampling of the deep nasal pharyngeal region. Samples were pooled in groups based on when the animal was diagnosed with BRDC (1, 2, or 3 wk after weaning), type of sample (upper nasal or deep pharyngeal), and health status (control or diagnosed with BRDC). To evaluate and compare the metagenome of each pooled sample, the variable region (V1–V3) along the 16S ribosomal RNA gene was amplified by PCR. These amplified products were sequenced using next-generation sequencing (Illumina MiSeq) and sequence reads were analyzed by WebMGA and GreenGenes to identify the bacterial taxa present. In order to assess the similarities or differences between sampling sites, we needed a measure that would reflect changes in the metagenome as a whole, simultaneously accounting for differences in incidence of all detected bacterial taxa. The Jaccard distance between samples is such a measure. Jaccard distances between sampling sites for the same animal group were small relative to the distribution of intersampling site distances between animal groups generated by permutation ($P = 0.00069$). In summary, bacterial populations were similar between upper nasal and deep pharyngeal sampling locations. These results demonstrate that shorter, less invasive nasal swabs produce results similar to those of deep nasal pharyngeal swabs.

Key Words: bovine respiratory disease complex, metagenome, 16S sequence
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043 Metabolomics uncovers serum biomarkers that can predict the risk of retained placenta in transition dairy cows.

E. Dervishi[1], G. Zhang[1], R. Mandal[2], D. S. Wishart[2], and B. N. Ametaj[*1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*University of Alberta, Edmonton, AB, Canada.*

A combination of direct injection and tandem mass spectrometry with a reverse-phase liquid chromatography and tandem mass spectrometry was used to detect serum metabolite signatures in 20 cows that expelled their fetal membranes normally and 6 cows that retained placenta. We aimed to identify serum biomarkers that can predict the risk of retained placenta (RP) in transition dairy cows. Blood samples were obtained from the coccygeal vein once per week at 0700 h before the morning feeding at 8 and 4 wk before parturition, at the week of RP, and at 4 and 8 wk postpartum. We studied perturbation of serum metabolites using an AbsoluteIDQ 180 kit (BIOCRATES Life Science AG, Innsbruck, Austria), which contained metabolites related to AA, acylcarnitines, biogenic amines, glycerophospholipids, sphingolipids, and hexose. Univariate analysis of data was performed using Wilcoxon–Mann–Whitney test provided by R (version 3.0.3; 2008). Metabolomic data were analyzed using the MetaboAnalyst software. Statistical significance was declared at $P < 0.05$. Results showed that cows with RP were characterized by a decrease in lysophosphatidylcholine (LysoPC) a C18:2, C20:3, C20:4, C28:0, and C28:1 at 8 wk before parturition and during the week of diagnosis of RP ($P < 0.01$). At 4 wk prior to calving, LysoPC a C20:4 and C28:0 were decreased. Concentrations of phosphatidylcholines (PC) changed after calving, with 12 and 4 species of PC elevated at 4 and 8 wk after calving, respectively ($P < 0.05$). Cows with RP were characterized by increased concentrations of sphingomyelins in the serum at 8 wk prior to parturition ($P < 0.05$), the week of RP ($P < 0.05$), and at 4 and 8 wk after parturition ($P < 0.05$). Amino acids Lys, Ile, and Leu were greater in cows diagnosed with RP during all experimental time. Biogenic amines, acetylornithine, asymmetric dimethylarginine, total dimethylarginine, carnosine, creatinine, and sarcosine were greater in RP cows during diagnosis week ($P < 0.01$). It is intriguing that pre-RP, RP, and post-RP cows showed an increased concentration of Lys, Ile, Leu, and acetylornithine during all experimental time points studied ($P < 0.01$). Moreover, LysoPC a C20:4 and C28:0, ornithine, and Asn decreased before parturition and at the disease diagnosis week ($P < 0.05$). In conclusion, RP is preceded by and associated with alterations in multiple species of AC, PC, LPC, AA, and BA starting from 8 wk prior to parturition. Alterations of serum Lys, ornithine, acetylornithine, LysoPC a C28:0, Asp, Leu, and Ile might be novel serum biomarkers for prediction of risk of RP in dairy cows.

Key Words: dairy cows, metabolomics, retained placenta
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044 Serum metabolomics fingerprinting during the dry off period identifies metabolite signatures that can predict the risk of metritis.

B. N. Ametaj*, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to screen transition dairy cows during the dry off period for identification of metabolite signatures in the serum that can be used for prediction of risk of metritis and give insights into the pathobiology of the disease. Blood samples were collected from coccygeal vein at 8 and 4 wk prepartum, disease diagnosis week, and 4 and 8 wk postpartum. Gas chromatography mass spectrometry was used to identify and quantify 29 metabolites in the serum of 20 healthy control cows (CON) and 6 cows that were diagnosed with metritis. Data were analyzed using univariate and multivariate analysis. Results showed that 16, 12, 14, 15, and 10 metabolites were significantly altered at −8 and −4 wk, at disease diagnosis, and at +4 and +8 wk around calving in cows diagnosed with metritis versus healthy CON. The multivariate analyses indicated consistent disease-dependent clustering with fairly similar set of metabolites distinguishing premetritis cows from healthy controls at −8 and −4 wk. The utility of these metabolites as biomarkers of risk of disease was assessed by the area under the curve (AUC), and AUC values of 1.0 and 0.969 were observed at −8 and −4 wk, respectively. Overall, results of this study indicated that selected metabolites can be used to early predict the risk of metritis in transition dairy cows. Results indicated significant ($P < 0.05$) metabolite alterations at −8 and −4 wk and at disease diagnosis in premitritis cows and those that developed metritis compared with healthy CON. The multivariate analyses also demonstrated consistent disease-dependent clustering with fairly similar set of metabolites distinguishing premetritis cows from healthy controls at −8 and −4 wk. Among the metabolites that distinguished premetritic cows from healthy CON at −8 wk, oxalate, ornithine, pyroglutamic acid, glutamic acid, and D-mannose were ranked as the top 5 in variable importance in the projection. A similar set of metabolites (except oxalate substituted by phosphoric acid) were ranked as the top 5 at −4 wk, indicating that those top 5 metabolites can be used as predictive biomarkers at −8 and −4 wk before the incidence of postpartum metritis. Intriguingly, multiple metabolites, such as galactose, phosphoric acid, oleic acid, urea, and oxalate, were identified to be different ($P < 0.5$) even at 4 and 8 wk after parturition. The significant alterations of serum metabolite concentrations and disease-dependent clustering around parturition indicate the potential of these metabolites to track the progression and development of metritis in dairy cattle.

Key Words: dairy cows, metabolomics, metritis
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045 Genomic characterization of intrauterine pathogenic *Escherichia coli* from cows with metritis.

Z. Ma*[1,2], A. Ginn[1,2], R. Mir[1,2], M. Kang[1,2], K. N. Galvão[3], and K. Jeong[1,2], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*Emerging Pathogens Institute, University of Florida, Gainesville,* [3]*Department of Large Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville.*

Metritis is a major disease in dairy cows causing animal death, decrease of birth rate and milk production, and economic loss. Antibiotic treatment is generally used to treat such disease, but it is associated with a high failure rate (23–35%). The reason for the treatment failure is not clear. Our hypothesis is that pathogens in the uteri carry extended spectrum β-lactamases (ESBL), which give resistance to ceftiofur, the common antibiotic used to treat the disease. The objective was to investigate the prevalence of ESBL in cows with metritis and characterize the isolated ESBL carriers. Our study investigated the prevalence of ESBL-producing bacteria in uterine samples of cows with metritis ($n = 24$), and whole genomic sequencing of the isolated intrauterine pathogenic *Escherichia coli* (IUPEC) was conducted by Illumina MiSeq for further genomic characterization. We found that the IUPEC-causing metritis had a high prevalence of ESBL (70.8%), which may explain the failure to the treatment. The pathogenicity of these IUPEC isolates was investigated by invasion assay, minimal inhibitory concentration (MIC) test, and antimicrobial susceptibility test.

The strains had strong invasion activity in bovine endometrial cell lines. The MIC of cefotaxime against the ESBL carriers were higher than 64 μg/mL. The ESBL-positive strains had resistance to at least 6 antibiotics across multiple drug classes. In addition, these ESBL-producing IUPEC had high virulence and multidrug resistance according to bioinformatics, which were similar to the reference human clinical *E. coli* isolates, indicating possible transmission to humans and leading to treatment failure in both human and animals.

Key Words: extended spectrum β-lactamases, intrauterine pathogenic *Escherichia coli*, metritis
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046 Serum and urine metallotyping of preketotic and ketotic dairy cows reveals major alterations in multiple mineral elements.

G. Zhang[1], R. Mandal[2], D. S. Wishart[2], and B. N. Ametaj*[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*University of Alberta, Edmonton, AB, Canada.*

Ketotic cows have elevated concentrations of ketone bodies or ketoacids (i.e., β-hydroxybutyric acid [BHBA], acetoacetic acid [AcAc], and acetone) in 3 body fluids including blood, urine, and milk. Both BHBA and AcAc are strong acids that cause ketoacidosis and affect physiological functions of various tissues. The objectives of the current study were to 1) investigate mineral alterations in both serum and urine of preketotic, ketotic, and postketotic cows and 2) identify potential predictive and diagnostic mineral biomarkers for ketosis in serum and urine. Metallotyping was performed in the serum and urine of 6 cases of ketosis and 20 control cows using inductively coupled plasma mass spectrometry at −8 and −4 wk, disease diagnosis week, and +4 and +8 wk relative to parturition. Univariate analysis of data was performed using the Wilcoxon–Mann–Whitney (rank sum) test provided by R (statistical significance: $P < 0.05$). Multivariate data analysis was processed by the MetaboAnalyst software. Results showed disturbances in concentrations of metals in the serum and urine of cows with ketosis at all 5 time points tested. The most important finding of this study was that 4 trace elements including Al, Fe, Mn, and As were persistently elevated in the serum of preketotic, ketotic, and postketotic cows. Moreover, 3 minerals (i.e., B, Al, and Rb) were increased in the urine of preketotic (8 and 4 wk prepartum) cows. It is interesting to point out that Al was the most elevated metal in the serum of preketotic cows at 8 and 4 wk prior to parturition at 91.4-fold (120.6 vs. 1.32 μ*M*) and 78.12-fold (111.34 vs. 1.43 μ*M*), respectively ($P < 0.001$). Similar alterations for Al were also detected in the urine samples of preketotic (i.e., 0.39 vs. 0.05 μ*M*/m*M* creatinine at −8 wk [$P < 0.001$] and 0.16 vs. 0.05 μ*M*/m*M* creatinine at −4 wk [$P < 0.001$]) cows in comparison with control cows. Because preketotic and ketotic cows were on a state of chronic metabolic acidosis, altered mineral elements in both serum and urine are thought to be related to the effects of acidosis on bone metabolism and urine excretion of metals. Findings from the current study might encourage development of early diagnostic biomarkers for risk of ketosis as well as new preventative intervention to lower the risk of ketosis in transition dairy cows.

Key Words: dairy cows, metals, serum and urine
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047 Genetic and environmental components of metabolic diseases and lameness in cattle.

T. M. Goncalves*[1], P. J. Pinedo[2], J. E. P. Santos[3], G. M. Schuenemann[4], G. J. M. Rosa[5], R. O. Gilbert[6], R. C. Bicalho[6], R. Chebel[3], K. N. Galvao[3], C. M. Seabury[7], J. Fetrow[8], W. W. Thatcher[3], and S. L. Rodriguez Zas[1], [1]*University of Illinois, Urbana-Champaign,* [2]*Colorado State University, Fort Collins,* [3]*University of Florida, Gainesville,* [4]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [5]*University of Wisconsin-Madison, Madison,* [6]*Cornell University, Ithaca, NY,* [7]*Department of Veterinary Pathobiology, College of Veterinary Medicine & Biomedical Sciences, Texas A&M University System, College Station,* [8]*University of Minnesota, St. Paul.*

Metabolic diseases including displaced abomasum, ketosis, and lameness have substantial impact on the productivity of beef and dairy cattle herds. Laminitis has been associated to nutritional effects causing metabolic disorders. These diseases are more prevalent in dairy herds and their impact in production is more extreme in dairy cattle than in beef cattle. Therefore, the stronger signal of disease incidence in dairy herds offers a model to further the understanding of the factors influencing the incidence of these diseases in beef cattle. The objective of this study was to assess the impact of nongenetic and genetic factors on the incidence of displaced abomasum, lameness, and ketosis. Health records were analyzed from approximately 6,200 records from Holstein cows across 4 U.S. regions. Two indicators of these diseases were studied: binomial detection of at least 1 disease and multinomial detection of none, at least 1, and at least 2 diseases in 1 lactation. The fixed effects explanatory variables included parity, season, milk yield level (high and low), region, and BCS, and sire was included as a random effect. Parity, season, and milk yield level had significant effects on both disease indicators. The binomial probability of disease and the multinomial probability of multiple diseases were higher with higher parity, in summer relative to winter, and in high producing cows relative to low producing cows. The heritability estimates of the binomial and multinomial disease indicators were 0.28 and 0.3, respectively. The heritability estimates for incidences of displaced abomasum, lameness, and ketosis were 0.33, 0.16, and 0.19, respectively. Our findings suggest that the 3 diseases share both the nongenetic and genetic components and that management practices and genetic selection to reduce the incidence of 1 or 2 of these diseases will reduce the incidence of the remainder diseases. These findings contribute to an animal health project (USDANIFAILLU538909) and a multistate project database (USDANIFAAFRI003542) for direct measures of health and fertility in cattle.

Key Words: heritability, indicators, metabolic disease
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049 Wooden breast disease in commercial broiler chickens: A histologic and RNA sequencing study.

E. L. Fare[1], M. P. Babak[2], and B. Abasht[*2],
[1]Department of Biological Sciences, University of Delaware, Newark, [2]Department of Animal and Food Sciences, University of Delaware, Newark.

Wooden breast disease (WBD) is a myopathy of fast-growing commercial broiler chickens, the most obvious symptom being palpably hard breast muscle (pectoralis major) tissue. The affected breast muscle is both visually and texturally unappealing to consumers, causing economic loss to the poultry industry. Recent research on WBD has focused on understanding the molecular contributors of breast muscle damage, fibrosis, and lipid infiltration resulting from WBD. The current study was conducted to compare gene expression and histology of the liver between WBD-affected and unaffected chickens. Live birds, from a purebred line of commercial broiler chickens, were clinically examined by manual palpation of breast muscle at 47 d of age. Liver tissue samples from 4 affected and 4 unaffected birds were used in high throughput mRNA sequencing using an Illumina 2500 HiSeq platform. After aligning sequence reads to the chicken reference genome (Galgal4) using TopHat, differential gene expression analysis was performed using Cuffdiff. A total of 113 genes were differentially expressed: 71 of these genes were upregulated and 42 were downregulated in affected birds. The differentially expressed genes were used for functional annotation clustering with DAVID Bioinformatics Resources. The most prominent biological pathways enriched with the differentially expressed genes included transmembrane, metabolic, extracellular matrix receptor interaction, and oxidoreductase. Our results indicate that metabolism of bile and cholesterol is disrupted and liver damage and regeneration is occurring more often in affected birds. Histological examination of affected livers presented inflammatory cell infiltration as nodules surrounding veins. In conclusion, this study shows that, in addition to breast muscle, the liver is affected by WBD, indicating further physiological complexities involved in the occurrence of this muscle abnormality in commercial chickens.

Key Words: broiler chickens, liver, wooden breast disease
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050 Effects of nitro treatment on *Salmonella*, *Escherichia coli*, and nitrogen metabolism during composting of poultry litter.

C. Arzola[*1], E. J. Ledezma-Perez[1], R. Anderson[2], M. Hume[2], O. Ruiz-Barrera[1], A. Corral-Luna[1], Y. Castillo-Castillo[3], J. A. Byrd[2], J. Salinas-Chavira[4], M. Ontiveros-Magadan[1], and C. Rodriguez-Muela[1],
[1]Universidad Autonoma de Chihuahua, Chihuahua, Mexico, [2]USDA/ARS, Texas, College Station, [3]Universidad Autonoma de Ciudad Juarez, Cd. Juarez, Mexico, [4]Universidad Autonoma de Tamaulipas, Cd. Victoria, Mexico.

Poultry litter contains appreciable amounts of uric acid, which makes it a good CP supplement for ruminants whose gut microbes transform the nitrogen in uric acid into high-quality microbial protein. However, poultry litter must be treated to kill bacterial pathogens before feeding. Presently, we examined the antimicrobial activity of certain nitrocompounds when administered to early-stage composted poultry litter. The 1-yr-old wood chip litter used in this study had been exposed to 2 to 3 flocks reared without antibiotics. Treatments (ethyl nitroacetate, 3-nitropropionate, ethyl-2 nitropropionate, or nitroethane) were applied to 200 g litter by spraying with 100 mL of each nitro treatment (80 m*M* in 0.4 *M* phosphate buffer, pH 6.4) to achieve 25 µmol/g litter. Control litter was sprayed with buffer alone. After application, the litter was distributed (11 g) to 50-mL tubes (in triplicate) and inoculated with a novobiocin and naladixic acid–resistant *Salmonella* Typhimurium (ST_{NN}) to achieve 3.0 $\log_{10}$ cfu/g. Tubes were closed with caps, sealed with parafilm, and incubated at 37°C for 3 d, after which time the tube contents were diluted and plated on 3 *M Escherichia coli*/coliform petri film and Brilliant Green Agar supplemented with 25 and 20 µg/mL novobiocin and naladixic acid, respectively, for enumeration of wildtype *E. coli* and ST_{NN} strain. Ammonia, uric acid, and urea were colorimetrically measured. Analysis of variance revealed that all nitrocompound treatments decreased ($P < 0.05$) ST_{NN} 1.4 to 1.9 log units compared with controls (6.0 ± 0.2 $\log_{10}$ cfu/g). *Escherichia coli* was decreased ($P < 0.05$) compared with controls (6.5 ± 0.2 $\log_{10}$ cfu/g) by 0.5 log units with ethyl nitroacetate but did not differ otherwise. Accumulations of ammonia were decreased ($P < 0.05$) 21 to 27% by the ethyl derivatives compared with controls (2.8 ± 0.1 µmol/g). Uric acid concentrations were 3.4- to 4.5-fold higher ($P < 0.05$) in litter treated with ethyl 2-nitropropinate and nitroethane than in controls (15.5 ± 1.3 µmol/g). Urea (7.9 ± 2.9 µmol/g) was unaffected by nitro treatment. Results suggest that nitro treatment may help preserve uric acid in composted litter while aiding in *Salmonella* control.

Key Words: *Escherichia coli*, poultry litter, *Salmonella*
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051 Effect of *Eimeria acervulina* infection on cell-specific xanthine oxidase and inducible NO synthase activities and duodenal protein tyrosine nitration (3′-nitrotyrosine proteins) in chickens.

S. Kahl[*1], T. H. Elsasser[1], K. B. Miska[1], and R. H. Fetterer[2], [1]*USDA-ARS, ABBL, Beltsville, MD,* [2]*USDA-ARS, APDL, Beltsville, MD.*

Intracellular generation of nitric oxide (NO) and superoxide anion (O^-_2) during proinflammatory stress can result in the formation of 3′-nitrotyrosine proteins (NTp) that correlate with alteration in protein function and metabolic impairment. Our objective was to determine the cell-specific relationship between xanthine oxidase (XO; an O^-_2–generating enzyme), inducible NO synthase (iNOS; a NO-generating enzyme), and NTp antigens in the chicken duodenum during *Eimeria acervulina* infection. Ross broilers at 21 d of age were either orally infected with 3 × 10^5 oocysts (INF) or noninfected (NOI). At d 1, 3, 6, 7, and 10 after infection (PI), sets of 4 NOI and 4 INF birds were euthanized and blood and tissue samples collected for biochemical analysis and immunofluorescence quantification of antigens (pixel density/cell from quantitative digital image analysis; Q-dia) representative of XO, iNOS, and NTp as stratified between epithelial cells (EC; cytokeratin-18^+) or infiltrating immune cells (IIC; myeloperoxidase$^+$). Compared with NOI birds, there was a reduction in BW gain in INF birds ($P < 0.01$) starting at d 6. Plasma concentrations of nitrate + nitrite (estimate of systemic NO production) was increased in INF birds at d 6 and 7 ($P < 0.01$ vs. NOI) but normalized by d 10 PI. At the peak of infection (d 6), increases in duodenal homogenate iNOS activity were observed ($P < 0.01$ vs. NOI). Homogenate XO activities in INF birds were greater at d 6 PI in the liver ($P < 0.05$) and at d 3 and 6 PI in the ileum ($P < 0.05$) but not the duodenum. In contrast to homogenate iNOS and XO activities, Q-dia, as assessed by cell type, demonstrated increases ($P < 0.05$) in INF birds in iNOS (d 3, 6, and 7) and XO (d 1, 3, 6, and 7) proteins in EC. In IIC, XO was not detected whereas iNOS was highly expressed. Cell pixel densities associated with NTp in EC were greater in INF birds than in NOI birds ($P < 0.01$) at d 1, 3, 6, and 7 PI but returned to NOI levels at d 10 PI. The maximum increases in pixel densities in EC of INF birds for NTp were observed on d 6 PI (13-fold vs. NOI) and for XO were observed on d 3 PI (5-fold). Data indicate that *Eimeria acervulina* infection in chickens results in protein nitration in duodenal EC and that EC themselves are capable of generating the molecular signals that alone or in cooperation with IIC may ultimately lead to protein nitration.

Key Words: coccidiosis, inflammation, protein nitration
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052 Differential expression of intestinal ion transporters and water channel aquaporins in young piglets challenged with enterotoxigenic *Escherichia coli* K88.

C. Zhu[*1], K. Yang[2], J. Ye[1], J. Yang[1], L. Wang[2], R. Liang[1], X. Wu[1], Z. Chen[1], and Z. Jiang[1,2], [1]*Agro-Biological Gene Research Center, Guangdong Academy of Agricultural Sciences, Guangzhou, P.R. China,* [2]*Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, P.R. China.*

Enterotoxigenic *Escherichia coli* (ETEC) K88 can induce severe watery diarrhea and subsequent growth retardation for neonatal and postweaning piglets, which causes great economic loss in swine production. Our previous study has shown that the incidence of diarrhea in young piglets was significantly increased following ETEC K88 challenge. The study was to determine whether the expression of genes involved in water and ion transports would be affected by ETEC K88 both in vitro and in vivo. 1) Thirty-six male piglets (4 d old) were randomly allotted to either the Control or the K88 group. Each group had 6 replicates with 3 piglets in each replicate. All piglets were fed the same diets for 18 d. On d 15, piglets in the K88 group were challenged with ETEC K88 (serotype O149:K91:K88ac) of 1 × 10^8 cfu/pig, whereas those in the Control group received the same volume of sterilized PBS. After challenging with ETEC K88 for 72 h (d 18), 1 piglet from each replicate was selected for slaughter to collect samples from the jejunum, ileum, and colon. The mRNA expression and protein abundance of cystic fibrosis transmembrane conductance regulator (CFTR) in the ileum and colon were significantly increased compared with that in the control group ($P < 0.05$). Furthermore, the mRNA expression of Na–K–Cl cotransporter 1 (NKCC1) in the ileum and colon was significantly increased, whereas in the jejunum, both its mRNA and protein expression were significantly increased by ETEC K88 treatment ($P < 0.05$). 2) Additionally, an established porcine intestinal epithelial cell line (IPEC-J2) was used to investigate the effect and possible mechanism of ETEC K88 on expression of water channel aquaporins (AQP) and ion transporters. Cells (1.17 × 10^6/well) were grown in 6-well plates and treated with ETEC K88 (5.6 × 10^7 cfu/well) for 3 h. AQP3 and AQP11 mRNA were abundantly expressed in IPEC-J2 cells. The mRNA expression of AQP3, AQP11, and Na^+/H^+ exchanger 3 (NHE3) in IPEC-J2 cells was significantly reduced after ETEC K88 treatment ($P < 0.05$). Further analyses by immunofluorescence and western blotting also demonstrated that ETEC K88 significantly decreased the protein expression of AQP3, AQP9, and AQP11 in IPEC-J2 cells ($P < 0.05$). Moreover, the phosphorylation level of protein kinase A (PKA) of the cyclic adenosine monophosphate (cAMP) pathway was significantly decreased by ETEC K88 challenge ($P < 0.05$). The results indicate that the cAMP-PKA signaling pathway might regulate the differential expression of intestinal

ion transporters and AQP, therefore contributing to fluid imbalance and the development of ETEC diarrhea in young piglets.

Key Words: aquaporin, enterotoxigenic *Escherichia coli* K88, ion transporter
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053 Screening the ability of common feed ingredients to reduce enterotoxigenic *Escherichia coli* K88 attachment to porcine epithelial cells.

Y. Zhu, G. González-Ortiz, D. Solà-Oriol, S. López-Vergé*, and S. M. Martín-Orúe, *Animal Nutrition and Welfare Service, Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

The purpose of this study was to evaluate the potential of the feed ingredients commonly used in diets and different kinds of cereal brans to attach enterotoxigenic *Escherichia coli* (ETEC) K88 (adhesion test [AT]) and to reduce the attachment to intestinal porcine epithelial cells (IPEC-J2; blocking test [BT]) in vitro. Tested ingredients included different cereals (wheat, oat, rye, and corn), protein vegetable ingredients (extruded soybean, soybean meal, and rapeseed meal), animal protein ingredients (milk powder, casein glycomacropeptide, and fish meal), and different sources of cereal brans (wheat, spelt, kamut, rye, oat, and rice). All ingredients were finely ground, resuspended in PBS (1:10 [wt/vol]), vortexed, and sonicated 3 times and then centrifuged. The soluble extracts obtained from the supernatant were used in the AT and BT assays. The tests consisted of a miniaturized in vitro system based on high-binding polystyrene microtitration plates. All cereal grains had the ability to adhere ETEC K88 ($P < 0.05$) in the AT compared with PBS. Regarding the protein vegetable ingredients, rapeseed did not adhere ETEC K88 but the extruded soybean and soybean meal attached specifically to ETEC K88 whereas they did not recognize the nonfimbriated (NF) *E. coli*. Milk powder was the only protein source from animal origin that showed the ability to attach ETEC K88, whereas any effect was observed with fish meal compared with PBS. All cereal brans evaluated attached ETEC K88 compared with PBS ($P < 0.001$). Rye and oat reduced the attachment of ETEC K88 to IPEC-J2 cells ($P < 0.01$) in the BT. Wheat soluble extract also had the ability to reduce the attachment of ETEC K88 ($P = 0.05$). Casein glycomacropeptide, included as positive control in the BT, showed a higher inhibition ability of ETEC K88 attachment to IPEC-J2 ($P < 0.001$). All cereal brans, with the exception of rice bran, reduced the attachment of ETEC K88 to IPEC-J2 cells ($P < 0.001$). No difference was observed in the AT with any of the tested ingredients evaluated regarding the NF *E. coli* or the BT, suggesting that the recognition of the soluble extracts to the pathogenic bacteria may be due to the fimbria. Results from these experiments may suggest that some cereals such as rye, oat, and wheat, in addition to their brans, should be further evaluated to ascertain the chemical structure involved recognizing ETEC K88 as a tool to prevent colibacilosis-induced diarrhea in weaned piglets.

Key Words: cereal, enterotoxigenic *Escherichia coli* K88, piglet
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054 The effect of tannin-containing peanut skin supplementation as a natural anthelmintic supplement on drug-resistant *Haemonchus contortus* control and animal performance in meat goats.

B. R. Min*, A. Shipp, J. Byrd, N. Gurung, and W. H. McElhenney, *Tuskegee University, Tuskegee, AL.*

Two trials (indoor [Exp. 1] and grazing trial [Exp. 2]) were conducted to determine the effects of condensed tannin (CT)–containing peanut skin (PS) on animal performance and drug-resistant *Haemonchus contortus* control in meat goats. In Exp. 1, 18 intact male Kiko-crossbreed goats (*Capra hircus*) were randomly assigned to 3 treatments ($n = 6$): 1) control (no-PS), 2) 25% PS, and 3) 50% PS. The diets consisted of concentrates containing varying levels of PS with soybean meal, alfalfa pellet, ground corn, vitamins and minerals mix, and coastal hay at the rate of 450 g/goat per day. Animals were confined indoors for a period of 50 d. In Exp. 2, 32 intact male Kiko-crossbreed goats were randomly assigned to 4 treatments with 2 replicates ($n = 8$) grazing on winter wheat (*Triticum aestivum*) supplemented with 1) control (no-PS), 2) 20 g/d of PS, 3) 80 g/d of PS, and 4) 172 g/d of PS under grazing for a period of 42 d. Animals were dewormed on d −10, and all the goats were artificially inoculated on d 0 with 5,000 infective stage (L3) drug-resistant *H. contortus* larvae. Feed intake and performance were monitored inside the barn and concentrate intakes were recorded in the grazing experiment. Blood samples were taken twice, once at the beginning and once at the end of the experiment. Fecal egg counts (FEC) and FAMACHA scores were determined every 2 wk. Rumen fermentation rate, adult worm counts, and carcass analysis were conducted only in Exp. 2. All analyses were conducted using a GLM procedure of SAS with linear and quadratic effects. In Exp. 2, there were no differences in initial and final BW, ADG, carcass characteristics, ruminal VFA, and FEC. However, adult worm counts score tended to be lower in 80 g PS–supplemented groups ($P = 0.1$). However, in Exp. 1, animals on 25% PS (138.8 g/d) tended to grow 31% faster (quadratic, $P = 0.10$) when compared with the control (95.7 g/d) or 50% PS (110.0 g/d)–supplemented groups. Goats receiving PS supplementation had linearly decreased ($P < 0.05$) FEC, with maximum responses in 25% PS supplementation. There were no differences in DMI and FAMACHA score and blood plasma metabolites. Results indicated that PS supplementation has the potential to improve ADG and the ability to reduce FEC at a moderate level of CT-containing PS supplementation (up

to 25% of DMI); however, additional studies are needed to further validate these findings.

Key Words: goats, *Haemonchus contortus*, peanut skin
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055 The anti-inflammatory effect of cowpea polyphenol in bovine blood.

S. Adjei-Fremah*, E. Asiamah, K. Ekwemalor, B. Osei, H. Ismail, L. E. Jackai, and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

The objective of this study was to investigate the effect of crude cowpea polyphenol extract (CPE) on the expression of genes involved in the inflammatory response in bovine blood in vitro. Plant-derived polyphenols in animal feeds are being used as alternatives to antibiotics to treat and prevent invading microbes. These compounds have antioxidant and anti-inflammatory properties and are able to modulate immune and inflammation responses. Whole blood collected from lactating Holstein-Friesian cows ($n = 10$) were incubated with 10 µg of CPE for 60 min at 37°C and 5% CO_2.Total RNA was extracted from whole blood after incubation and reverse transcribed to cDNA, and quantitative PCR (qPCR) was performed using the cow inflammatory cytokines and receptor array (Qiagen) with 84 genes. The qPCR data were analyzed using Livak's method to calculate fold change in gene expression between CPE-treated and control cows. Normalization of data was performed with GAPDH as an internal control. Out of the 84 genes tested, 81 were expressed, 13 were upregulated and 68 were downregulated, in response to CPE. Treatment with CPE downregulated the expression of proinflammatory cytokine TNFα (fold change [FC; treatment/control] = −43.39), IL1α (FC = −6.19), ILβ (FC = -3.62), and IL8 (FC = −1.25). Expression of chemokines such as CXCL10, CXCL12, and CXCR2 was not altered by treatment with CPE. Interestingly, expression of *IL10RA* (FC = 3.39), a receptor for IL10, a well-known anti-inflammatory cytokine, was upregulated in blood incubated with CPE. IL15, a cytokine that regulates T and natural killer cell activation and proliferation, was upregulated (FC = 2.08) by CPE treatment. The study results demonstrate that polyphenols derived from cowpea have an anti-inflammatory effect in cow blood, and target genes modulated by CPE have been identified for further characterization.

Key Words: anti-inflammatory, bovine, cowpea polyphenol
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056 Probiotic administration modulates the expression of Toll-like receptors in goat blood.

K. Ekwemalor*, S. Adjei-Fremah, E. Asiamah, B. Osei, H. Ismail, and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

The objective of this study was to evaluate the effect of probiotics (FASTtrack microbial pack) on the expression of Toll-like receptors (TLR) in goats. Probiotics are viable microorganisms that have positive effects on growth performance, nutrient synthesis, the microbial ecosystem, absorption, and the reduction in the incidence of intestinal infection and restoration of gut microflora. Following initial screening for infection, 1 wk after weaning, female Spanish × Boer goats were drenched daily with the recommended doses of probiotic (containing *Lactobacillus acidophilus*, *Saccharomyces cerevisae*, *Enterococcus faecium*, *Aspergillus oryza*, and fructooligosacharide) in 10 mL sterile water over an 8-wk period. The control group was given sterile water. Blood samples were collected weekly. Total RNA was isolated from blood collected at the beginning of the study (wk 0) and at the end of the study (wk 8) using Tri-reagent. Ribonucleic acid integrity number (RIN) was determined with a Bioanalyzer, and samples with RIN > 7 for each treatment were reverse transcribed to cDNA using the Ambion RETROscript kit. The RT^2 profiler array was used to determine the expression of 84 genes involved in innate and adaptive immunity. Fold change was calculated using the Livak method with GAPDH as the reference gene for normalization. At wk 0, out of the 84 genes assayed, animals in the control group expressed 25 genes whereas 22 genes were expressed at wk 8. In the treatment group, out of the 84 genes assayed in the treatment group, 41 genes were expressed at wk 0, whereas 67 genes were expressed at wk 8. Probiotics induced the expression of TLR3 and TLR8 and increased the expression of TLR4 (fold change [FC] = 27), TLR6 (FC = 2), TLR7 (FC = 7), and TLR9 (FC = 3). Treatment with probiotics resulted in differential expression of genes related to the TLR signaling pathway. The results from this study will help in the definition of the role of TLR expression in goat blood and the design of therapeutic probiotics and help define the mechanism of action of probiotics.

Key Words: goat, probiotics, Toll-like receptors
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057 The effects of supplementing growing purebred angus heifers with *Bacillus coagulans* during dietary transitions on performance and acute phase proteins.

S. A. Armstrong, V. R. Morrow*, T. H. Schell, and D. J. McLean, *Phibro Animal Health Corporation, Teaneck, NJ.*

The use of direct-fed microbials in animal nutrition is a growing practice to improve animal health and performance. To investigate the effects of supplementing growing beef heifers with a direct fed microbial (*Bacillus coagulans*; Provia 6086; Phibro Animal Health Corporation, Quincy, IL), 16 purebred Angus heifers were trained to eat behind Broadbent Calan gates (American Calan, Northwood, NH) during a 28-d acclimation period. Acclimation diet contained a 20:80 concentrate to forage (C:F) ratio. Heifers were assigned to 1 of 2 treatment groups: control (CNTL; $n = 8$) or direct-fed microbial (Provia 6086 [PV]; $n = 8$). Three basal diets (40:60, 55:45, and 70:30 C:F ratio) were used in this study: diet 1 (40:60 C:F ratio) was offered on d 1 through 7, diet 2 (55:45 C:F ratio) was offered on d 8 through 14, and diet 3 (70:30 C:F ratio) was offered on d 15 through 28 (of supplementation). Cattle enrolled in the PV group were fed product at the rate of 2 billion cfu/animal per day, hand mixed in the top one-third of the presented diet. Dry matter intake was collected 3 times for diets 1 and 2 and 6 times for diet 3. Body weights were collected at baseline and weekly thereafter; BW were used to calculate ADG, and feed efficiency was calculated as G:F. Serum was collected on d 0, 14, and 28 of supplementation, and samples were assayed for lipopolysaccharide binding protein (LBP), haptoglobin (Hp), and serum amyloid A (SAA). Lipopolysaccharide binding protein, Hp, and SAA were analyzed as change from baseline and log transformed prior to analysis. All data were analyzed using PROC GLIMMIX of SAS; $P \leq 0.05$ was considered significant and $0.05 < P \leq 0.10$ was considered trending toward significance. Provia 6086 supplementation improved ADG ($P = 0.007$; 0.73 kg for CNTL and 1.16 ± 0.10 kg for PV) and feed efficiency (G:F; $P = 0.008$; 0.08 for CNTL and 0.13 ± 0.03 for PV) compared with control counterparts. Basal diet influenced BW, DMI, G:F, and ADG ($P < 0.0001$). During diet 1, ADG decreased in all cattle (−0.45 kg/d ± 0.21; $P < 0.0001$); as a result, compensatory gain was seen during diets 2 and 3. Provia 6086 supplementation had no effect on BW and DMI and had a tendency to increase SAA ($P = 0.10$) and LBP concentrations ($P = 0.05$; relative to baseline) when compared with control cattle. This data indicates that providing Provia 6086 during dietary transitions may improve ADG and G:F and modulate the acute phase protein response in growing Angus heifers.

Key Words: animal health, direct-fed microbial, replacement heifers
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058 Impact of neosporosis seropositivity status on some key performance indicators in spring calving beef cow herds in Ireland.

M. H. Parr[1], D. Barrett[2], M. G. Diskin[3], M. McGee[1], and D. A. Kenny*[1], *[1]Teagasc, Co. Meath, Ireland, [2]Department of Agriculture Food and Marine, Co. Kildare, Ireland, [3]Teagasc, Athenry, Ireland.*

Neosporosis in cattle is caused by a coccidian parasite known as *Neospora canium*. This protozoan parasite can be spread vertically from the cow to the fetus during pregnancy or horizontally through contamination of feed from feces of infected canids. To date, there is no published information on the seroprevalence of neosporosis or its impact on reproductive and mortality traits in spring calving beef cow herds in Ireland. The objectives of this study were to quantify the effects, if any, that neosporosis had on 12 wk in-calf rate, calving interval, reappearance rate, and calf mortality (≤28 d). A total of 4,344 cows from 134 spring calving beef cow herds across Ireland were blood sampled to measure the seroprevalence of neosporosis. All serum samples were tested for antibodies against *Neospora canium* using a commercially available diagnostic kit. All cows were ultrasonically scanned to determine pregnancy status at least 30 d after the end of the breeding season. Records for participating herds pertaining to calving interval and calf mortality were extracted from the Irish Cattle Breeding Federation database. Reappearance rate was quantified as the percentage of cows that were scanned pregnant and calved in the following spring calving season. Data were analyzed using the generalized linear models procedure of SAS (version 9.3) with terms for herd, parity, cow breed, sire breed, and animal movements included. The overall prevalence of neosporosis was 5.5% (238/4,344). Overall herd pregnancy rate at the end of the breeding season was 89 (78–100%) and 88% (81–100%) for 2014 and 2015, respectively. There was no difference in 12 wk in-calf rate (87.1 ± 0.9 vs. 83.2 ± 2.5%; $P = 0.13$), calving interval (372.8 ± 1 vs. 369.8 ± 2.9 d; $P = 0.13$), and calf mortality up to 28 d of age (2.9 ± 0.4 vs. 3.2 ± 1.4%; $P = 0.87$) between seronegative and seropositive cows, respectively. However, reappearance was significantly higher (89.6 ± 0.6 vs. 82.4 ± 2.2%; $P = 0.001$) in seronegative cows in comparison with their seropositive compatriots. This was one of the largest studies of its kind to be carried out in beef cattle. The results indicate that there was a significant decrease in reappearance rate in cows determined as seropositive for neosporosis. This may be considered as a measure of fetal loss or abortion in these infected cows. However, there was no negative carryover relationship between neosporosis and other key economically important production indicators.

Key Words: beef cows, neosporosis, reproduction
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059 Validation of candidate markers associated with reproductive performance in porcine respiratory and reproductive syndrome virus naturally infected replacement gilts in southern Sonora Mexico.

C. M. Aguilar-Trejo*[1], K. M. Valerio-Valle[2], R. I. Luna-Ramirez[2], G. Luna-Nevarez[2], J. R. Reyna-Granados[2], J. A. Romo[3], M. A. Sánchez-Castro[4], X. Zeng[4], R. M. Enns[4], S. E. Speidel[4], M. G. Thomas[4], and P. Luna-Nevarez[2], *[1]Universidad Autonoma de Sinaloa, Culiacan Sinaloa, Mexico, [2]Instituto Tecnologico de Sonora, Ciudad Obregon Sonora, Mexico, [3]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico, [4]Department of Animal Sciences, Colorado State University, Fort Collins.*

Porcine respiratory and reproductive syndrome virus (PRRSV) in replacement gilts is an infection that decreases reproductive performance in breeding females and affects the economy of the Mexican swine industry. The objective of this study was to validate the associative relationship among average number of piglets alive (NPA) at first and second farrowing with genotypes in PRRSV early-infected gilts. The experiment included seventy-five 8-mo-old females with breed composition of three-fourths Landrace × one-fourth Yorkshire. All gilts were exposed to a wild strain of PRRSV once they arrived into the breeding area, and blood samples were collected 2 wk later to confirm virus infection by real-time PCR (Tetracore Nextgen Real-Time PCR). Gilts observed in estrus received 2 natural services with fertility-tested boars. Females confirmed as pregnant were maintained in a gestation area and then moved to the farrowing area the day before parturition. Blood samples were collected on each individual and spotted onto FTA cards for genotyping using a 8,826 low-density SNP chip (Infinium BeadChip; Illumina, San Diego, CA). Previous analysis of these genomic data identified 12 SNP associated with average NPA ($P < 0.001$), using multilocus mixed models, which were performed in SNP Variation Suite 7 of Golden Helix, Inc. A mixed effects model was used to validate the associative relationship between these SNP and reproductive phenotypes; this model included SNP genotype and age of dam as fixed effects and sire as a random effect. An allele substitution effect was also calculated using a regression model that included genotype term as a covariate. Mean values for average NPA were 10.61 ± 0.38. From the SNP previously identified, only ALGA0056378 (rs81422969) and MARC0036292 (rs81229798) were associated with average NPA ($P < 0.01$). Least squares means among ALGA0056378 genotypes CC, CT, and TT were 11.93 ± 0.62, 9.45 ± 0.59, and 8.59 ± 2.51, respectively, and among MARC0036292 genotypes AA, AG, and GG were 6.22 ± 2.40, 8.69 ± 0.71, and 11.47 ± 0.51, respectively. The most favorable alleles increased NPA by 1.71 ± 0.88 and 2.73 ± 0.67 for ALGA0056378 and MARC0036292, respectively. In conclusion, a phenotype to genotype association analyses validated 2 specific genetic markers that explain genetic variation in the average number of piglets alive from gilts early infected with PRRSV. Therefore, we propose such SNP as candidates to focus our study on the genetic basis that underlies reproductive performance in gilts infected with a wild PRRSV strain in southern Sonora.

Key Words: gilts, porcine respiratory and reproductive syndrome virus, reproductive performance
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060 The nasopharyngeal microbiota of beef cattle before and after transport to a feedlot.

D. B. Holman[1], J. Hallewell*[2], and T. W. Alexander[3], *[1]USDA, National Animal Disease Center, Ames, IA, [2]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB, Canada, [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

The nasopharyngeal (NP) microbiota plays an important role in bovine health, comprising a rich and diverse microbial community. The nasopharynx is also the niche for potentially pathogenic agents, which are associated with bovine respiratory disease (BRD), a serious and costly illness in feedlot cattle. We used 14 beef heifers from a closed and disease-free herd to assess the dynamics of the NP microbiota of cattle that are transported to a feedlot. Cattle were sampled prior to transport to the feedlot (d 0) and at d 2, 7, and 14. The structure of the NP microbiota significantly changed over the course of the study, with the largest shift occurring between d 0 (prior to transport) and 2 ($P < 0.001$). Phylogenetic diversity and richness increased following feedlot placement (d 2; $P < 0.05$). The genera *Pasteurella*, *Bacillus*, and *Proteus* were enriched at d 0, *Streptococcus* and *Acinetobacter* at d 2, *Bifidobacterium* at d 7, and *Mycoplasma* at d 14. The functional potential of the NP microbiota was assessed using PICRUSt, revealing that replication and repair, as well as translation pathways, were more relatively abundant in d-14 samples. These differences were driven mostly by *Mycoplasma*. Although 8 cattle were culture positive for the BRD-associated bacterium *Pasteurella multocida* at one or more sampling times, none were culture positive for *Mannheimia haemolytica* or *Histophilus somni*. This study investigated the effect that feedlot placement has on the NP microbiota of beef cattle over a 14-d period. Within 2 d of transport to the feedlot, the NP microbiota significantly changed, increasing in both phylogenetic diversity and phylogenetic richness. These results demonstrate that there is an abrupt shift in the NP microbiota of cattle after transportation to a feedlot. This may have importance for understanding why cattle are most susceptible to BRD after feedlot placement.

Key Words: bovine respiratory disease, nasopharyngeal microbiota, 16S ribosomal ribonucleic acid gene
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061 Chronic hypobaric hypoxia induces high expression of nitric oxide in Holstein heifers in Tibet.

S. Wang[*1], Y. J. Wang[2], Z. J. Cao[2], and S. LI[1], *[1]State Key Laboratory of Animal Nutrition, Beijing Engineering Technology Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, P.R. China Agricultural University, Beijing, P.R. China, [2]State Key Laboratory of Animal Nutrition/Beijing Engineering Technology Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, P.R. China Agricultural University, Beijing, P.R. China.*

This study aimed to evaluate the adaptation of Holstein dairy cattle to the atmospheric pressure of Tibet (Lhasa city; 3,658 m altitude and 13.33 kPa atmospheric partial pressure of oxygen). To our knowledge, this was the first report of Holstein dairy cattle adaptation to chronic hypobaric hypoxia in Tibet. Unlike original highland animals, Holstein heifers were transported from the plains to Lhasa and both healthily adapted and sick individuals were found after 1 yr of exposure. Comparisons were made between healthy Holstein heifers and those with brisket disease. Heifers (age = 16 ± 2 mo) were transported to Lhasa; after 1 yr, 10 heifers with brisket disease (480 ± 18 kg BW) and 10 healthy heifers (557 ± 14 kg BW) were chosen to evaluate the physiological effects of chronic hypoxia on Holstein heifers. Plasma samples were analyzed for endothelial nitric oxide synthases (eNOS), inducible NOS (iNOS), total NOS (TNOS), and circulating NO and nitrite/nitrate (NOx). Immunohistochemistry was performed to detect remodeling of small pulmonary arteries. RT-PCR and western blots were used to determine the expression of lung eNOS and endothelin-1 (EDN-1). Respiratory rates ($P < 0.001$), oxygen saturation ($P < 0.001$), and blood velocity ($P < 0.001$) were significantly higher in healthy heifers. However, heart rates were higher in heifers with brisket disease ($P < 0.05$). Peripheral arterial pressures were significantly higher in healthy heifers than that in heifers with brisket disease (systolic pressure, $P < 0.0001$; diastolic pressure, $P < 0.01$; and mean arterial pressures, $P < 0.01$). Plasma eNOS ($P < 0.001$), iNOS ($P < 0.001$), TNOS ($P < 0.05$), and NOx ($P < 0.0001$) levels were higher in healthy heifers than in heifers with brisket disease. Moreover, *eNOS* mRNA ($P < 0.01$) and protein ($P < 0.01$) were more highly expressed in healthy lungs. Immunostaining revealed that eNOS was highly expressed in the intima of pulmonary arterioles ($P < 0.01$). In addition, *EDN-1* mRNA ($P < 0.05$) and protein ($P < 0.01$) levels were both reduced in healthy heifers compared with heifers with brisket disease. Heifers with brisket disease displayed small pulmonary arterial (diameter < 100 µm) adventitial thickening ($P < 0.001$), proliferation of smooth muscle cells ($P < 0.001$), and low eNOS expression in the intima ($P < 0.01$) compared with healthy heifers. In conclusion, it is possible that highly expressed NOS dilate reconstruction of vasculature, maintain blood pressure, and attenuate vascular remodeling to protect against the progression of pulmonary hypertension.

Key Words: brisket disease, endothelia nitric oxide synthases, Holstein heifer
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455 *L. plantarum*-treated NK cells protect intestinal epithelial cells from barrier disruption caused by enterotoxigenic *Escherichia coli.*

X. Yang[*1,2], Y. Qiu[1,2], S. Hu[1,2], L. Wang[1,2], X. Wen[1,2], X. Ma[1,2], Z. Wang[1,2], and Z. Jiang[1,2], *[1]Ministry of Agriculture Key Laboratory of Animal Nutrition and Feed Science in South China, Guangzhou, China, [2]Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, China.*

Natural killing (NK) cells play a central role in host defense against pathogenic bacteria. Probiotics are able to modulate mucosal immune system in the intestine by maintaining intestinal homeostasis and tolerance towards resident microbiota. We previously found a strain of probiotics, *Lactobacillus plantarum* (*L. plantarum*), to significantly improve mucosal barrier integrity and function of the small intestine in a pig model. The present study is designed to investigate the anti-inflammatory potential of *L. plantarum* in NK cell-mediated intestinal epithelial barrier function under Escherichia coli (ETEC) K88 infection. To study the effect of *L. plantarum* on the function of NK cells, a *L. plantarum* strain CGMCC1258 was cultured with NK-92MI cells without direct contact using a transwell system for 2 to 6 hours before collection of NK cells for mRNA and protein expression analysis. To study the anti-inflammatory potential of L. plantarum in NK cell-mediated epithelial cell integrity, NCM460 (an epithelial cell line) was exposed to ETEC K88 for 2 hours using transwell culturing system and subsequently stimulated in a cell-cell contact manner with NK-92MI cells pre-treated with *L. plantarum* for 4 hours. *L. plantarum* efficiently increased the protein and mRNA levels of *NCRs*, and the mRNA abundance of *IL-10*, *perforin*, *INF-ɤ*, *TNF-α*, *IL-8* and IL-26. In addition, the protein levels of IL-10, LIF and IL-22 were increased by *L. plantarum*. Protein level of IL-22 was increased in the *L. plantarum*-treated NK cells supernatant. Transfer of *L. plantarum*-treated NK cells conferred protection against ETEC K88-induced intestinal epithelial barrier damages in NCM460 cells. Protection was associated with an increased expression of *ZO-1* and *occludin* mRAN and protein in ETEC K88-infected NCM460 cells. Furthermore, adding *L. plantarum*-treated NK cells to ETEC K88-infected NCM460 cells, the protein and mRNA levels of *IL-22R1* was increased in NCM460. *L .plantarum*-treated NK cells were also observed to induce an augmentation in protein levels of phosphorylated p38, JAK1, Stat3 and Tyk2 in ETEC K88-infected NCM460 cells. *L. plantarum*-treated NK cells

improved intestinal epithelial barrier function via IL-22-IL-22R pathway in NCM460 cells during ETEC-K88 infection.

Key Words: NK cells, *Lactobacillus plantarum*, intestinal epithelial barrier
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911 Improving calving rates in dairy cows by infusion of seminal proteins at insemination.

L. A. Ibrahim*, *Gainesville, FL.*

Seminal fluid is conventionally thought to have a single purpose, which is the carriage of spermatozoa to the oocyte to achieve conception and commence pregnancy. However, its role is now recognized to extend beyond this to targeting female tissues. The cellular and molecular environment of the uterus during the pre- and peri-implantation period of early pregnancy is critical for implantation success and optimal fetal and placental development. Recent studies in rodents, livestock species, and humans show that seminal fluid contains active moieties that interact with epithelial cells lining the female reproductive tract to influence the uterine environment, through activating a cascade of cytokine- and leukocyte-mediated events that appear to contribute to endometrial receptivity for embryo implantation. Epithelial cytokines activated by seminal plasma are also secreted into the luminal fluid, where they exert embryotrophic actions on the developing preimplantation embryo. It is unknown if seminal plasma from the bovine contains such immunoregulatory molecules or has the ability to modulate the uterine environment following insemination. Evaluation of the endometrium following seminal plasma exposure (or seminal proteins) provides us novel information on the endometrial environment, which is potentially lacking after traditional AI. Taking together all that, we hypothesize that infusion of seminal plasma during bovine AI will increase pregnancy rates and decrease pregnancy loss in dairy cows by altering the molecular and cellular environment of the early pregnant uterus. The objective of our current project is to identify active signaling factors in bovine seminal fluid and examine their contribution to modulating the cellular and molecular environment of the early pregnant reproductive tract and to enrich these factors in AI to prevent problems such as miscarriage and implantation failure. In Exp. 1, we evaluated bovine seminal plasma for the presence and concentration of significant seminal proteins identified in other species, namely TGFβ and PGE2. In Exp. 2, by using a developed endometrial explant model, bovine endometrium explants were collected using a sterile 8-mm punch biopsy and cultured for 24 h with seminal plasma, semen, cell pellet, or medium and RNA was extracted and used for RT-PCR and qPCR. Finally, we evaluated the responsiveness of the endometrium epithelium and stromal cells following seminal plasma exposure. qPCR data confirmed that seminal fluid induces endometrial synthesis of several cytokines and chemokines including GM-CSF(CSF2), IFNE, and cyclooxygenase-2 (COX-2) mRNA transcription. This is postulated to induce uterine synthesis of prostaglandins PGE and PGF2α. However, the expression of IL 6 and IL8 was decreased. What is clear is that seminal fluid is far more than a proteinaceous liquid. It is a substance full of chemical signals entering into communication with the uterine tract. Proper communication leads to a supportive embryonic environment. Ultimately, we aim to develop a new protocol whereby targeted seminal proteins can be added back to semen at the time of AI to optimize reproductive outcomes in commercial dairy herds.

Key words: seminal plasma, endometrium, inflammation
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ASAS GRADUATE STUDENT POSTER COMPETITION: MS DIVISION

062 Identification of the MUC2 promoter as a strong promoter for intestinal gene expression through generation of transgenic quail expressing GFP in gut epithelial cells.

R. M. Woodfint*, *The Ohio State University, Columbus.*

Identification of tissue- and stage-specific gene promoters is valuable for delineating the functional roles of specific genes in genetically engineered animals. Here, through the comparison of gene expression in different tissues by analysis of a microarray database, the intestinal specificity of mucin 2 (MUC2) expression was identified in mice and humans and further confirmed in chickens by reverse-transcription PCR analysis. An analysis of *cis*-acting elements in avian MUC2 gene promoters revealed conservation of binding sites, within a 2.9-kb proximal promoter region, for transcription factors such as caudal type homeobox 2 (CDX2), GATA binding protein 4 (GATA4), hepatocyte nuclear factor 4 α (HNF4A), and transcription factor 4 (TCF4) that are important for maintaining intestinal homeostasis and functional integrity. By generating transgenic quail, we demonstrated that the 2.9-kb chicken MUC2 promoter could drive green fluorescent protein (GFP) reporter expression exclusively in the small intestine, large intestine, and ceca. Fluorescence image analysis further revealed GFP expression in intestine epithelial cells. The GFP expression was barely detectable in the embryonic intestine but increased during posthatch development. The spatiotemporal expression pattern of the reporter gene confirmed that the 2.9-kb MUC2 promoter could retain the regulatory element to drive expression of target genes in intestinal tissues after hatching. This new transgene expression system, using the MUC2 promoter, will provide a new method of overexpressing target genes to study gene function in the avian intestine.

Key Words: Japanese quail, mucin 2, transgenic
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063 The effects of age at weaning and length of lipid supplementation on growth, metabolites, and carcass quality of young steers.

J. E. Tipton*, L. K. Lewis, and N. M. Long, *Clemson University, Clemson, SC.*

The objective of this study was to determine how weaning age and length of lipid supplementation effected growth, circulating metabolites, and carcass quality of young steers. Calves from a single AI sire were early weaned (EW; $n = 24$) at 150 ± 11 d of age or traditionally weaned (TW; $n = 24$) at 210 ± 11 d of age. Following a 2-wk adaptation period, steers were assigned to control (CON; $n = 12$/weaning group) or rumen bypass lipid (RB; Essentiom; $n = 12$/weaning group) treatment and then fed for either 45 ($n = 6$/treatment) or 90 d ($n = 6$/treatment). Treatments were formulated to be isocaloric and isonitrogenous. Steer BW was recorded on d −14 and −7 (relative to treatment), and then BW and blood samples were taken on d 0, 22, 45, 66, and 90. After treatment, steers were harvested at a commercial processing plant. The right rib section of each animal was collected for proximate analysis. Data was analyzed in a 2 × 2 × 2 factorial with all significant interactions in the model using SAS. Circulating metabolites were analyzed as repeated measures. Steers fed RB had increased plasma glucose compared with CON steers ($P = 0.03$; 72.1 and 67.9 ± 1.7 mg/dL, respectively). Serum triglyceride concentrations were increased in RB steers vs. CON steers ($P = 0.02$) and in TW steers compared with EW steers ($P = 0.03$; 14.3 ± 1.5). Serum cholesterol concentrations were increased (treatment × day, $P = 0.01$) in RB steers over CON steers from d 22 to 90 of treatment. Traditionally weaned steers had a greater HCW than EW steers (143.7 ± 2.8 and 142.0 ± 2.8 kg, respectively; $P < 0.0001$). Steers fed for 90 d also had greater HCW than 45-d steers (153.4 ± 2.8 and 132.3 ± 2.8 kg, respectively; $P < 0.0001$). The longissimus dorsi from RB steers had an increased EE compared with CON steers (3.6 ± 0. 2 vs. 2.4 ± 0. 2% on a wet basis; $P < 0.0001$). Also, longissimus dorsi from 90-d steers had greater ($P = 0.02$) concentration (3.3 ± 0.2%) of lipid than those fed for 45 d (2.7 ± 0.2%). These data show that RB supplementation increases circulating glucose, cholesterol, and triglyceride concentrations as well as marbling content of the longissimus dorsi in young steers. Furthermore, a longer period of supplementation results in increased IM adipose concentration and increased HCW.

Key Words: early weaning, fat supplementation, metabolites

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064 Effects of dietary supplementation of β-mannanase on immune responses in nursery pigs.

K. Jang*[1,2], K. Kim[1], S. Kim[1], J. Kim[1], B. Kim[1], S. Park[1], J. J. Lee[1], J. H. Lee[3], S. W. Kim[2], and M. Song[1], *[1]Chungnam National University, Daejeon, Republic of Korea (South), [2]North Carolina State University, Raleigh, [3]CTCBIO Inc., Seoul, Republic of Korea (South).*

Feed enzymes targeting nonstarch polysaccharides (NSPases) can bring positive effects for pigs through improving nutrient digestion and utilization by releasing nutrients trapped in nonstarch polysaccharides such as mannans and xylans. However, little information about NSPases effects on pig health and immunity is available. The objective of this study was to evaluate effects of dietary supplementation of β-mannanase on immune responses in newly weaned pigs. A total of 72 weaned pigs (5.9 ± 0.5 kg BW and 21 d old) were randomly allotted to 4 dietary treatments (3 pigs/pen and 6 replicates/treatment) in a randomized complete block design (block = BW). Dietary treatments were in a factorial arrangement: 0 or 0.05% β-mannanase (CTCBIO Inc., Seoul, Korea) and 0 or 0.05% cocktail enzyme (combination of xylanase, α-amylase, protease, β-glucanase, and pectinase; CTCBIO Inc.). Pigs were fed for 6 wk using a 2-phase feeding program with each phase of 3 wk. Dietary treatments did not include antibiotics, fish meal, blood plasma, and zinc oxide. Blood samples were collected from randomly selected 2 pigs in each pen on d 1, 2, 3, 7, and 14 after weaning. Measurements were cortisol, tumor necrosis factor-β (TNF-β), transforming growth factor-β (TGF-β), C-reactive protein (CRP), and IgG, IgM, and IgA by ELISA. Data were analyzed using PROC MIXED of SAS. The statistical model included effects of 2 factors and their interaction as fixed effects and block as a random effect. Supplemental β-mannanase decreased ($P < 0.05$) cortisol on d 14 (3.29 vs. 6.40 ng/mL), TNF-β on d 3 (0.74 vs. 1.06 ng/mL) and 7 (0.75 vs. 1.18 ng/mL), TGF-β on d 2 (1.27 vs. 1.62 ng/mL), and CRP on d 7 (4.02 vs. 4.87 ng/mL) and 14 (3.44 vs. 4.58 ng/mL) after weaning and increased ($P < 0.05$) IgG on d 7 (27.2 vs. 18.5 mg/mL) after weaning compared with diets without β-mannanase, but there were no β-mannanase effects on IgM and IgA. No effects of cocktail enzyme and interaction between β-mannanase and cocktail enzyme were found for all measured variables. In conclusion, dietary supplementation of β-mannanase in nursery diets reduced stress and inflammation indicators and increased IgG in nursery pigs.

Key Words: β-mannanase, immune responses, nursery pigs

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065 Studies on innate immune characteristics of Baylis and Low Country Spanish goats on pasture.

H. L. Thompson*, M. Worku, A. M. Hamilton,
B. Osei, E. Asiamah, and K. Ekwemalor, *North Carolina Agricultural and Technical State University, Greensboro.*

The objective of this study was to evaluate resilience to parasites in Baylis and Low Country Spanish goat bloodlines. Spanish goats have adapted to the Southeastern United States. They are known for their meat, ability to thrive on forage and clear brush in harsh environments, and good fertility. About 8,000 purebred Spanish goats from 15 bloodlines have been reported in the United States. This unique genetic resource has not been characterized. The Baylis and Low Country bloodlines are originally from the southeast and are considered parasite resistant. Eight adult female goats, 4 each from the Low Country and Baylis lines, were monitored on pasture at the North Carolina Agricultural and Technical State University farm. Blood and fecal samples were collected monthly for lab analysis. The average of data collected is presented during the 3 summer months, June, July, and August. Body weight, BCS, and FAMACHA scores were determined. The packed cell volume (PCV) and total cell count were determined. Parasite eggs per gram (EPG) was determined using the modified McMaster technique. Low Country had a higher *Haemonchus contortus* egg count during the summer season. The average coccidia oocyte count was about the same overall between the 2 bloodlines. On average, Baylis had a higher BW (+5.4 kg), a slightly higher BCS (+0.25), a higher PCV (+2.75%), and less *H. contortus* (−45.84 EPG) compared with the Low Country line. The Low Country goats had a PCV of 36.88%, a total cell count of 3.35×10^6, and a *H. contortus* count of 116.67 EPG. FAMACHA scores were the same for both lines, at 1.7. Both lines had low parasite burdens for animals maintained on pasture. However, under the same management conditions, the Baylis bloodline tended to show higher resilience to *H. contortus* as indicated by PCV, BW, and BCS when compared with the Low Country line. Further studies using a larger population are needed to determine the impact of genetic variation and breed effects for parasite susceptibility.

Key Words: Baylis, Low Country
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066 Goat parasite incidence and host resilience in North Carolina during the fall season.

A. M. Hamilton*, M. Worku, H. L. Thompson,
and S. Adjei-Fremah, *North Carolina Agricultural and Technical State University, Greensboro.*

This study aims to address concerns regarding the incidence of goat parasites and host resilience during the fall season in North Carolina. Due to an increase in anthelmintic resistance and climate change, producers are plagued with increasing difficulties stabilizing herd health, especially around the time of parturition. During the periparturient period, goats succumb to haemonchosis, due to the combined assault of larvae emerging from hypobiosis and the immunosuppression of late pregnancy. Twenty periparturient Boer and BoerX goats ($n = 20$), managed on pasture, were randomly selected from 4 farms in North Carolina. Body weight, BCS, and FAMACHA score were evaluated on the farm. Blood and fecal samples were collected once a week for 5 wk pre- and postpartum. Strongyle eggs per gram (EPG) and Coccidia oocyte counts were conducted using the modified McMaster technique. The packed cell volume was determined from collected blood samples, and plasma was separated and stored at −20°C. Total plasma protein concentration was determined using the bicinchoninic acid assay. The 5-wk averages were computed. The prepartum Strongyle and Coccidia oocyte EPG were 891.3 and 232.9, respectively. The postpartum Strongyle and Coccidia oocyte EPG were 983.5 and 342.5, respectively. The BW was 113.5 and 90.7 kg pre- and postpartum, respectively. The BCS pre- and postpartum was 3.2 and 2.4, respectively. The FAMACHA score pre- and postpartum was 3.7 and 4.2, respectively. The packed cell volume was 22.8 and 18.6% pre- and postpartum, respectively. The average total plasma protein concentration pre- and postpartum was 77.8 and 75.9 mg/mL, respectively. Gastrointestinal nematodes and Coccidia were present in all farms tested. The observed incidence of parasites and associated anemia have implications for a necessity of new strategies for parasite control and herd management.

Key Words: autumn, goat, periparturient rise
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067 Evaluation of body condition index in comparison with body condition score in horses and ponies.

K. DeLano*[1], B. McIntosh[1], K. Kaufman[1], and
P. Harris[2], *[1]Virginia Polytechnic and State University, Blacksburg, [2]WALTHAM Centre for Pet Nutrition, Melton Mowbray, Leicestershire, UK.*

Objective assessment of adiposity may be useful in monitoring health and fitness in performance horses. Although relatively accurate and useful for experienced investigators, body condition scoring systems can be subjective and unreliable for inexperienced owners or assessors, underscoring a need for a quantitative, rather than qualitative, index to measure condition. The purpose of this study was to compare the more subjective body condition scoring system (BCSS) with the newly developed body condition index (BCI), similar to the body mass index (BMI) used in humans. The BCI was derived iteratively using objective measurements (cm): $BCI = [(HB^{0.5} + BG + NC^{1.2})/H^{1.05}]^{2.2}$, in which HG = heart girth, BG = belly girth, NC = neck circumference, and H = height to the withers. In the current study, 126 horses and ponies of varying ages (1 to 26 yr) and breed types (23 Thoroughbred or Thoroughbred crosses, 11 ponies, and 92 warmbloods) were used to compare the BCSS and the BMI. Body condition scores (using the modified Henneke scoring system and assessed by experienced investigators) ranged from 3.5 to 8 out of 9. Body condition index scores ranged from 4.7 to 8.4 out of 9. Scores were different between the BCI and BCSS (*P* < 0.0001); BCI scores were generally higher, with a mean difference of 0.65. Although the BCI and BCSS were not meant to be exact matches (*r* = 0.34), it is useful to understand the potential causes of variation between the 2 systems, and where room for improvement may exist. Mean differences were similar between Thoroughbreds, ponies, and warmblood breeds (0.67, 0.71, and 0.67, respectively), suggesting the BCI does not have a breed bias and can cross over different confirmation types. Much of the variation may arise from animals with lower BCS scores. In horses and ponies with a BCS greater than or equal to 5, the mean difference between BCI and BCS was 0.51, but in horses with a BCS less than 5, the mean difference was 1.49. These data suggest the BCI equation may need to be adjusted in order to better fit horses with a BCS less than 5.

Key Words: body condition, equine, nutrition
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068 Environmental impacts from cattle consuming tannin-containing hays.

E. K. Stewart[*1], K. A. Beauchemin[2], J. W. MacAdam[3], and J. J. Villalba[1], [1]*Utah State University, Logan,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Department of Plants, Soils, and Climate, Utah State University, Logan.*

The cow–calf phase counts for approximately 80% of the total beef production system greenhouse gas emissions. There is potential for tannin-containing hays to reduce these environmental impacts. Fifteen mature beef brood cows and 9 yearling beef heifers were blocked by weight and randomly assigned to 3 groups of 5 cows or 3 heifers and fed tannin-containing (birdsfoot trefoil [BFT], sainfoin [SAN], and small burnet [SML]) or non-tannin-containing (alfalfa [ALF], cicer milkvetch [CMV], and meadow bromegrass [MB]) hays in 4 trials. Groups of cows were fed BFT, CMV, or MB in Trial 1 and ALF, SAN, or SML in Trial 3. Groups of heifers were fed ALF, MB, or SAN in Trial 2 and BFT, CMV, or SML in Trial 4. Each trial used a completely randomized block design with repeated measures during 5 d following a 14-d adjustment period. Nine cows and 9 heifers were selected for total collection of enteric methane using the SF6 methodology, feces, and urine whereas intake was measured for all animals. Methane emission from cows was lower for SML than ALF (*P* = 0.04) or SAN (*P* = 0.03; Table 068). Additionally, cows and heifers fed tannin-containing hays showed lower urine (UUN) and blood urea nitrogen (BUN) than animals fed non-tannin-containing hays (Table 068), suggesting a shift in nitrogen excretion from urine to feces. In conclusion, tannin-containing legumes consumed as hays have the potential to reduce environmental impacts of cattle fed in confinement.

Key Words: legumes, methane emissions, urinary urea
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Table 068.

	Trial 1					Trial 3				
Items	BFT	CMV	MB	SEM	*P*-value	ALF	SAN	SML	SEM	*P*-value
Treatments (cows)										
BUN, mg/dL	6.9^{a}	16.5^{b}	10.0^{a}	1.6	0.0033	18.7^{a}	13.4^{b}	4.2^{c}	1.8	0.0003
UUN, g/d	81.7^{ac}	228.7^{b}	82.9^{c}	19.9	0.0043	216.8	98.6^{a}	24.4^{b}	26.6	0.0084
CH$_4$, L/d	46.29^{a}	44.84^{a}	55.12^{a}	5.97	0.51	52.79^{a}	51.37^{a}	28.72^{b}	5.79	0.048
Intake, g intake/kg BW	15.5^{a}	15.19^{a}	12.27^{a}	1.94	0.45	15.92^{ab}	12.82^{a}	18.29^{b}	1.44	0.062
	Trial 2					Trial 4				
Items	ALF	MB	SAN	SEM	*P*-value	BFT	CMV	SML	SEM	P-value
Treatments (heifers)										
BUN, mg/dL	27.9^{a}	10.9^{b}	14.9^{b}	16.1	0.0007	14.8^{a}	19.2^{a}	4.5^{b}	27.7	0.023
UUN, mg/d	238.7^{a}	32.8^{b}	44.1^{b}	17.5	0.0003	119.6^{a}	183.9^{b}	23.8^{c}	8.2	<0.0001
CH$_4$, L/d	54.11^{a}	52.58^{a}	37.09^{a}	7.57	0.26	37.25^{a}	39.08^{a}	36.11^{a}	5.15	0.91
Intake, g intake/kg BW	24.42^{a}	16.95^{b}	19.86^{ab}	0.95	0.0043	23.0^{a}	19.78^{b}	16.96^{c}	0.68	0.0021

Means in a row with different superscripts differ (*P* < 0.1).

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069 Effects of dietary β-glucan on growth performance, diarrhea, and gut permeability of weanling pigs experimentally infected with a pathogenic *Escherichia coli.*

K. Kim[*1], A. Ehrlich[1], V. Perng[1], J. Chase[1], H. Raybould[1], X. Li[1], E. R. Atwill[1], R. Whelan[2], A. Sokale[3], and Y. Liu[1], [1]*University of California, Davis,* [2]*Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany,* [3]*Evonik Corporation, Kennesaw, GA.*

ProGlucan is 100% dried algae, *Euglena gracillus*, which contains approximately 54% β-1,3-glucan. The objective of this experiment was to investigate the influence of dietary supplementation of ProGlucan on growth performance, diarrhea score, and gut permeability of weaned pigs experimentally infected with a pathogenic F-18 *Escherichia coli.* Weaned pigs (*n* = 36; 7.69 ± 0.77 kg BW) were individually housed in disease containment rooms and randomly allotted to 1 of 3 dietary treatments with 12 replicate pigs in each treatment. The 3 diets were a nursery basal diet (control) and 2 additional diets containing either 100 or 200 mg/kg of ProGlucan in the basal diet. The experiment lasted 17 d (5 d before and 12 d after the first inoculation [d 0]). The inoculum used in this experiment was F-18 *E. coli*, containing LT, STb, and SLT-2 toxins. The inoculation doses were 10^{10} cfu/3 mL oral dose daily for 3 d. The growth performance was measured on d 0 to 5, d 5 to 12, and d 0 to 12 after inoculation (PI). Diarrhea score (DS; 1, normal, to 5, watery diarrhea) was recorded for each pig daily. Frequency of diarrhea was the percentage of pig days with DS of 4 or higher. Rectal temperature was measured for each pig daily after first inoculation. On d 5 and 12, jejunum were collected from 4 pigs in the control group and high-dose ProGlucan group for transcellular and paracellular permeability analysis. All data were analyzed by ANOVA using the PROC MIXED of SAS with pig as the experimental unit. The χ^2 test was used for the frequency of diarrhea analysis. No differences were observed in growth rate and feed intake of *E. coli*–challenged pigs throughout the experiment. Pigs fed 100 mg/kg ProGlucan had lower ($P < 0.05$) rectal temperature compared with pigs fed the control diet on d 5 and 7 PI. Inclusion of 200 mg/kg ProGlucan reduced ($P < 0.05$) frequency of diarrhea (9.26 vs. 17.90%) for the entire experimental period and decreased ($P < 0.05$) transcellular permeability on d 12 PI compared with the control diet. In conclusion, supplementation of ProGlucan may enhance disease resistance of weaned pigs, as indicated by reducing frequency of diarrhea and gut permeability.

Key Words: diarrhea, ProGlucan, weaned pigs
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070 Ruminal microbes of adult steers extensively degrade l-glutamine but not l-glutamate or l-citrulline.

K. R. Gilbreath*[1], G. Nawaratna[1], T. A. Wickersham[2], M. C. Satterfield[1], F. W. Bazer[1], and G. Wu[1], [1]*Texas A&M University, College Station,* [2]*Department of Animal Science, Texas A&M University, College Station.*

The microbial population within the rumen has long been considered to have the capability of extensively degrading all dietary AA. Results from our feeding trial showed that this view might not be accurate. In vivo and in vitro studies were conducted to test the hypothesis that certain AA undergo little degradation by ruminal microbes. In the in vivo experiment, at 0.5 h before and 0, 0.5, 1, 2, and 4 h after cannulated adult steers (approximately 500 kg; $n = 6$) consumed 0.56 kg dried distiller's grain mixed with 70 g l-glutamine plus 70 g l-citrulline, samples of rumen fluid and plasma were collected for AA analysis using HPLC. Results showed that the concentrations of glutamine in the rumen fluid declined rapidly but that of glutamate (a product of glutamine catabolism) gradually increased between 0.5 and 4 h after consumption of the meal. In contrast, the concentration of citrulline in the rumen fluid was constant through the 4-h period after steers consuming the meal. The concentrations of l-citrulline and l-arginine, but not l-glutamine or l-glutamate, were increased in the steers at 1 and 2 h after the meal, respectively, when compared with the values at 0 h. In the in vitro experiments, whole rumen fluid (3 mL) from the steers was incubated at 37°C with 5 m*M* l-glutamine, 5 m*M* l-glutamate, or 5 m*M* l-citrulline for 0.5, 1, 2 or 4 h, and 20 µL samples were collected at the predetermined time points for AA analyses. Results showed extensive hydrolysis of l-glutamine into l-glutamate but little degradation of either l-glutamate or l-citrulline by rumen microbes during the 4-h period of incubation. Collectively, these in vivo and in vitro results indicate that rumen microbes of adult steers extensively degrade l-glutamine but not l-glutamate or l-citrulline. We suggest that l-citrulline without any encapsulation or protection from rumen microbes can be effectively supplemented to the diets of ruminants to increase its concentrations and of l-arginine in plasma for utilization and metabolism by various organs and tissues. Supported by funds from Texas A&M AgriLife Research.

Key Words: arginine, citrulline, glutamine
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071 Effect of melatonin supplementation from mid to late gestation on hair growth and skin temperature of beef cattle.

K. J. McCarty*, M. P. T. Owen, C. G. Hart, K. C. Yankey, T. Smith, and C. O. Lemley, *Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

Melatonin has been previously shown to increase distal skin temperature and decrease core body temperature in humans. However, limited research is available on the impact of melatonin on skin temperature in cattle. Therefore, the objective was to examine effects of supplemental melatonin treatments on core body temperature, skin temperature, and hair growth during mid to late gestation in cattle. Commercial beef heifers ($n = 32$) and cows ($n = 25$) were artificially inseminated and delegated to receive melatonin implants (MEL) or nonimplant control (CON). Animals in the MEL ($n = 29$) treatment group received two 24-mg melatonin ear implants at d 180, 210, and 240 of gestation. Maternal BW, rectal temperature, ambient temperature, humidity, thermal images, and hair weight were collected on d 180 (baseline) and 240 of gestation. Thermal imaging was collected using a Flir ThermaCAM S60 (FLIR Systems, Boston, MA) infrared thermography camera. A sample of hair was collected from a 5.08 by 10.16 cm area on the left thoracic region right behind the shoulder, and images were taken. Temperatures of both the shaved and unshaved areas were analyzed using ThermaCAM Researcher PRO 2.7 software (FLIR Systems). Data were analyzed using MIXED procedure of SAS. The model statement included melatonin treatment, parity, and breed. Maternal BW was not different between MEL vs. CON on d 180 ($P = 0.92$) or 240 ($P = 0.95$). Similarly, rectal temperature was not different between MEL vs. CON on d 180 ($P = 0.34$) or 240 ($P = 0.54$). The ambient temperature was not different ($P = 0.27$) and averaged 31 ± 1°C; however, average humidity was increased on d 240 (82 ± 4%) vs. d 180 (67 ± 5%). Temperature of the shaved areas on d 180 ($P = 0.92$) and 240 ($P = 0.28$) were not different between treatments. Temperature of the unshaved area was not different on d 180 ($P = 0.75$); however, on d 240, the temperature of the unshaved area was decreased ($P = 0.05$) in MEL (32.7 ± 0.4°C) vs. CON (33.5 ± 0.3°C). Hair weight of the shaved areas on d 180 ($P = 0.91$) and 240 ($P = 0.63$) were not different between treatments. In summary, melatonin supplementation did not alter BW, rectal temperature, or temperature of the shaved area. However, temperature of the unshaved area was decreased during melatonin supplementation.

Key Words: gestation, melatonin, thermal imaging
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072 Insect larvae fed mycotoxin-contaminated wheat – A possible safe, sustainable protein source for animal feed?

Carlos Ochoa Sanabria[1]*, N.S. Hogan[1,2], K.M. Madder[1], and F.C. Buchanan[1], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, [2]Toxicology Centre, University of Saskatchewan, Saskatoon, SK.*

Demand for increased food production, particularly protein, is increasing with the world's growing population. Alternative and sustainable sources of animal protein will be required to reduce environmental impacts of conventional livestock production. Historically, insects have been typical dietary components within eastern countries, and their nutritional value is proportionally comparable to that of conventional meat. The yellow mealworm (*Tenebrio molitor*) is an edible insect, rich in CP and crude fat. Moreover, there is evidence that mealworms are able to use mycotoxin-contaminated wheat as a food source without accumulating the mycotoxins, thus providing a value for low-grade wheat along with a more sustainable and cheaper source of CP for animal feed. The aim of this study was to measure production traits and survivability and to determine whether mealworms can detoxify mycotoxins (specifically deoxynivalenol [DON]) when fed *Fusarium*-damaged, high-mycotoxin wheat. To achieve these objectives, naturally contaminated grain was sorted to obtain 4 levels of DON: control (0.2 ppm), low (2 ppm), medium (10 ppm), and high (12 ppm). These levels were fed to larvae (seventh to ninth instar) per replicate for feeding ($n = 300$) and breeding ($n = 200$) trials. Each treatment was replicated 5 times and the endpoint for both experiments was when 2 pupae where observed (mean = 32.8 ± 3.2 d). Larvae were fasted for 24 h and frozen prior to mycotoxin analysis by HPLC/mass spectrometry. *Fusarium graminearum* was culture isolated from highly chalky damaged kernels. Survival rate tended to be higher in the high diet treatment than the other treatments ($P = 0.0534$) when using the GLIMMIX procedure in SAS. Mean ADG was estimated as 604.9542 mg/d per replicate (300 larvae), and there was no significant difference between treatments ($P = 0.1489$). Nevertheless, the feed conversion ratio was significantly higher for the low mycotoxin diet (mean = 84.6141, $P = 0.0001$) when compared with other treatments. Conversely, DON was measurable within the mealworms across all replicates with a mean of 0.1291 ppm and a range of 0.0977 to 0.1902 ppm with 6.3, 1.2, and 1.1% of ingested DON detected in dry bodies from low, medium, and high mycotoxin diets, respectively. Notably, DON concentrations were not significantly different between diets ($P = 0.8828$) and are far below the regulatory limits for food or feed. From our research, *Tenebrio molitor* does not appear to accumulate harmful mycotoxins when fed highly contaminated grain and, with further research, could conceivably be used as a sustainable, safe protein source in animal feed.

Key Words: fusarium, insects, mycotoxins
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073 The effects of a low vitamin A diet on the mechanism of intramuscular fat development.

E. E. Knutson*[1], A. B. P. Fontoura[1], J. J. Gaspers[1], P. P. Borowicz[2], K. C. Swanson[2], M. L. Bauer[1], J. A. Clapper[3], and A. K. Ward[2], *[1]North Dakota State University, Fargo, [2]Department of Animal Sciences, North Dakota State University, Fargo, [3]South Dakota State University, Brookings.*

Commercial steers consisting of a minimum of 75% Angus genetics and purebred Simmental steers were used to evaluate the effect of a low vitamin A (LVA) diet on marbling in cattle in a 2 × 2 factorial design. After 3 mo of backgrounding on a LVA diet (1,017 IU/kg DM), 64 steers (32 Angus crosses and 32 Simmentals) were allocated 1 of 2 dietary treatments for finishing. The LVA diet contained 723 IU vitamin A/kg DM; the control diet (CON) consisted of the LVA diet supplemented with 2,200 IU/kg DM vitamin A. At the completion of finishing, steers were slaughtered at a commercial abattoir. Muscle biopsies were collected from the longissimus dorsi at the beginning, middle, and end of finishing. Histology was used to visualize the protein fatty acid binding protein 4 (FABP4). Ribonucleic acid was extracted from the biopsy tissue and reverse transcribed to cDNA. Gene expression was measured by qPCR. Target genes include *FABP4*, *PREF-1*, *PPARγ*, *ADH1C*, *RALDH1a1*, *C/EBPα*, and *RXR-α*, *RXR-β*, and *RXR-γ*. Blood samples were collected at the beginning and end of finishing. These were used for retinol quantification (via HPLC) and hormone analysis (via RIA) for IGF-1 and GH. There was an interaction ($P < 0.01$) between treatment and breed for marbling score. The LVA treatment resulted in a 16% increase in marbling in the LVA treatment compared with the CON within the Angus-cross group but had no effect in Simmental cattle. No difference was found in FABP4 protein expression. Serum retinol displayed a treatment × time interaction ($P = 0.01$), with LVA levels lower than those of the CON at both time points. There was a difference ($P = 0.01$) in GH between breeds, with Simmentals having greater levels. The LVA treatment tended ($P = 0.09$) to result in lower IGF-1 serum concentrations when compared with the CON group. Angus-cross cattle had greater ($P = 0.001$) expression of *FABP4* as well as a tendency ($P < 0.10$) for greater expression of *RXR-α*, *RXR-β*, and *RXR-γ*. The CON group showed a significantly ($P = 0.04$) higher expression of *FABP4* and a tendency ($P < 0.10$) for higher expression of *RXR-α*, *C/EBPα, PREF-1*, and *ADH1C*. There were no differences in *PPARγ* or *RALDH1a1* expression. Therefore, we conclude that in steers of moderate to high marbling potential (such as Angus crosses), vitamin A restriction is associated with increased marbling and differential expression of adipogenic genes within the vitamin A pathway.

Key Words: marbling, nutrition, vitamin A
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074 Dietary supplementation with arginine between days 14 and 30 of gestation enhances survival and development of conceptuses in gilts. C. M. Herring*, *Texas A&M University, College Station.*

Most embryonic loss in pigs occurs before d 30 of gestation during the peri-implantation period. We conducted this study to test the hypothesis that dietary arginine supplementation between d 14 and 30 of gestation can enhance survival and development of the conceptus (embryo and its extraembryonic membranes) in gilts. Gilts were fed 1 kg of a corn and soybean meal–based diet containing 12% CP twice daily beginning on d 0 of gestation (the day of breeding). Either 0.4% L-arginine (as L-arginine HCl; $n = 7$) or an isonitrogenous amount of L-alanine ($n = 6$) was supplemented to the basal diet between d 14 and 30 of gestation. On d 30 of gestation, gilts were fed either L-arginine HCl or L-alanine and hysterectomized 30 min later. Uterine tissue, embryos, fetal membranes, and fetal fluids were collected. Data were analyzed by χ^2 analysis or the unpaired *t*-test. Compared with the control group, arginine supplementation increased ($P < 0.05$) embryonic survival by 28% (75.5% in the control group vs. 96.5% in the arginine group), increased allantoic fluid volume by 25.3%, and increased amniotic fluid volume by 48.1%. The placentae of arginine-supplemented gilts were more vascularized in terms of the number and size of blood vessels. Maternal BW, uterine weight, maternal liver weight, number of corpora lutea, and relative weights of fetal livers were not different between the 0.4% arginine-treated and control gilts. We conclude that dietary arginine supplementation to pigs between d 14 and 30 of gestation improves survival and development of the conceptuses. Supported by USDA National Institute of Food and Agriculture grants.

Key Words: arginine, conceptus, embryonic survival
doi:10.2527/asasann.2017.074

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075 Effects of poor maternal nutrition and gender on satellite cell metabolism in lambs. D. E. Martin*, 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.*

Poor maternal nutrition during gestation alters offspring muscle composition, mass, fiber number, postnatal growth, and satellite cell function. Satellite cells are quiescent myogenic cells located adjacent to mature muscle fibers that contribute to pre- and postnatal muscle growth. We hypothesized that over- or underfeeding ewes during gestation would negatively impact the metabolic function of muscle satellite cells in the offspring. Pregnant western white-faced ewes ($n = 78$) were individually fed 60, 100, or 140% of NRC requirements for TDN from d 30.2 ± 0.2 of gestation until parturition. Within 24 h of birth, lambs were euthanized for LM collection. Satellite cells were isolated and cultured from the LM of 24 lambs (9 males and 15 females; $n = 8$ lambs per diet). The glycolytic and mitochondrial respiration of satellite cells was determined using the Seahorse Bioscience XF analyzer. Proliferative cells were seeded at a density of 7.5×10^4 in triplicate wells. Respiration data were normalized based on DNA content. Data were analyzed as a completely randomized design using PROC MIXED in SAS with main effects and interaction of gender and maternal diet. There was a main effect of gender for maximal respiration and spare respiratory capacity. Maximal respiration was 46% greater in females than males (411.3 ± 35.1 and 281.9 ± 29.7 pmol $O_2 \cdot min^{-1} \cdot \mu g\ DNA^{-1}$ for females and males, respectively; $P = 0.04$) and spare respiratory capacity was 89% greater in females than males (259.5 ± 26.4 and 122.0 ± 23.7 pmol $O_2 \cdot min^{-1} \cdot \mu g\ DNA^{-1}$ for females and males, respectively; $P = 0.03$). There was no interaction of gender × maternal diet for the mitochondrial stress variables analyzed (nonmitochondrial respiration, basal respiration, ATP production, proton leak, maximal respiration, and spare respiratory capacity; $P \geq 0.15$). There was no interaction or main effects of gender or maternal diet on the variables analyzed for glycolytic stress (nonglycolytic acidification, glycolysis, glycolytic capacity, and glycolytic reserve; $P \geq 0.34$). In conclusion, the mitochondrial respiration of satellite cells differs based on offspring gender but not maternal diet. Increased maximal respiration and spare respiratory capacity may give female lambs a greater ability to meet metabolic challenges and face energetic demands.

Key Words: maternal nutrition, satellite cells, sheep
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076 Estimation of the effects of mutations causing complex vertebral malformation and brachyspina on milk production, milk composition, and fertility traits in Holstein Friesian dairy cattle.

L. Ratcliffe*[1], M. Mullen[1], F. Kearney[2], M. C. McClure[2], and J. McClure[2], [1]*Bioscience Research Institute, Athlone, Ireland,* [2]*Irish Cattle Breeding Federation, Bandon, Ireland.*

The frequencies of mutations with lethal effects are of significant economic importance in cattle production. The elimination or at least management of such mutations in the national breeding herd is a desirable objective; however, estimation of the potential pleiotropic effects on other traits of economic importance would ascertain if strategic matings of carrier animals would be advantageous. Therefore, the objective of the current study was to estimate the effects of 2 such lethal recessives, complex vertebral malformation (CVM) and brachyspina (BY), on milk and fertility traits in Holstein-Friesian dairy cattle. Complex vertebral malformation and BY SNP genotypes and phenotypes (expressed as predicted transmitting abilities [PTA]) on 10,707 dairy cows were obtained through the Irish Cattle Breeding Federation. The association between each SNP and deregressed PTA was analyzed in ASREML using a weighted mixed animal model. Only cows with an adjusted reliability of >10% were included in the analysis and included $n = 6{,}876$ for milk yield and composition traits and $n = 1{,}193$, $n = 264$, $n = 4{,}566$, $n = 8{,}564$, $n = 152$, and $n = 2{,}380$ cows for calving interval, survival, calving difficulty, gestation length, calf mortality, and maternal calving difficulty, respectively. Complex vertebral malformation (minor allele frequency of 1.7%) was associated with both increased milk protein (0.019 [SE 0.006]; $P < 0.01$) and increased milk fat concentration (0.039 [SE 0.0132]; $P < 0.01$) whereas no associations ($P > 0.05$) were observed between CVM and any of the other milk traits (milk yield, milk fat yield, and milk protein yield) or fertility traits (calving interval, survival, calving difficulty, gestation length, calf mortality, and maternal calving difficulty). Significant associations were observed between BY (<1%) and decreased milk protein concentration (0.024 [SE 0.008]; $P < 0.01$) and increased milk yield (73.21 kg [SE 30.12]; $P < 0.05$). No associations ($P > 0.05$) were observed between BY and any of the fertility traits considered. These results provide additional evidence that carriers of these recessive mutations exhibit effects on milk production and/or composition in Holstein Friesian cattle, however, with no evidence of effects on the fertility traits examined. Cognizance and monitoring of the potential pleiotrophic effects of lethal recessives such as examined in this study will aid livestock breeders when considering elimination of carriers to minimize reduction of the genetic merit of farm enterprises and inform the benefits of strategic matings in controlling these mutations in the population while also sustaining productivity.

Key Words: fertility, lethal recessives, milk
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077 Effects of dietary protease on gut microbiota of weaned pigs.

B. Kim*[1], I. H. Park[2], J. Kim[1], S. Kim[1], J. J. Lee[1], K. Kim[1], K. Jang[1], S. Oh[3], S. Oh[4], Y. Kim[4], J. Y. Cho[2], S. H. Cho[2], and M. Song[1], [1]*Chungnam National University, Daejeon, Republic of Korea (South),* [2]*DSM Nutrition Korea Ltd., Seoul, Republic of Korea (South),* [3]*Chonnam National University, Gwangju, Republic of Korea (South),* [4]*Chonbuk National University, Jeonju, Republic of Korea (South).*

This experiment was conducted to investigate effects of dietary protease on gut microbiota of weaned pigs. A total of 75 weaned pigs (7.06 ± 0.18 kg BW and 28 d old) were randomly assigned to 3 dietary treatments (5 pigs/pen and 5 pens/treatment) in a randomized complete block design (block = BW). The dietary treatments were 1) a diet based on corn and soybean meal to meet or exceed the requirement of CP as a positive control (PC; CP = 24.17%), 2) a low protein diet as a negative control (NC; CP = 23.51%), and 3) NC + 0.02% protease (PRO). The protease used in this experiment was a commercial product (Ronozyme ProAct; DSM nutrition products, Kaiseraugst, Switzerland) containing 75,000 protease units/g derived from *Bacillus licheniformis*. The dietary treatments did not include spray dried plasma, fishmeal, zinc oxide, and antibiotics to avoid their antibacterial or physiological effects. Pigs were fed each treatment for 6 wk. Three weaned pigs per dietary treatment were randomly selected to collect feces on the last day of the experiment to verify their gut microbiota by metagenomic analysis with pyrosequencing. The pyrosequencing data was analyzed using CLcommunity program. The PRO treatment increased ($P < 0.05$) phylum Firmicutes and genus *Lactobacillus* in gut microbiota of weaned pigs compared with PC or NC. However, PRO decreased ($P < 0.05$) phylum Bacteroidetes and genera *Clostridium* and *Streptococcus* in gut microbiota of weaned pigs compared with PC or NC. In conclusion, addition of protease in nursery diets modulated gut microbiota of weaned pigs.

Key Words: gut microbiota, protease, weaned pigs
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078 The induction and synchronization of estrus in meat goats during the fall and late spring (season and out of season) using controlled internal drug release devices on Delmarva.

E. N. Escobar[1], E. Kassa*[1], D. O'Brien[2], and H. Taylor[1], [1]*University of Maryland Eastern Shore, Princess Anne,* [2]*Virginia State University, Petersburg.*

Changes in U.S. demographics have increased chèvon (goat meat) demand. The USDA National Agricultural Statistics Service reported annual chèvon imports > $129 million. During the year, demand follows traditions and festivals, which change from year to year. It is challenging for meat-goat producers to cater to consumer demand because goats are seasonal breeders. The U.S. Food and Drug Administration (FDA)–approved controlled internal drug release (CIDR) devices (2009) for sheep estrus synchronization; however, the FDA's approval of CIDR devices for goats is still pending. This demonstration's objective was not to determine CIDR efficacy in meat goats but to resolve applicability and practicality of CIDR device use to reduce kidding periods and target peak chèvon demands. From 2012 to 2015, crossbred does (n = 183) were separated into 2 groups, synchronized (CIDR) or not (CONTROL), for breeding in late *Spring* (anestrus season) or *Fall* (natural breeding season). At each breeding event, CIDR devices were inserted for 12 to 18 d. At the time of CIDR device removal, does were clustered in single buck mating groups of no more than 6 does/group. The goat protocol proposed for FDA approval (12 to 18 d) was followed because pretrials at this station gave inconsistent results following the sheep's label CIDR device insertion and removal time (5 d). At birth, goat kids were tagged, weighed, and sexed and litter size was recorded (LSZ; kids/doe exposed). Data was analyzed using χ^2 and ANOVA (SAS software package) for the effect of synchronization and season on pregnancy rates (PR; pregnant does/exposed does) and LSZ at birth. Overall, PR did not differ from one year to the other in CIDR or CONTROL does. Also, during the trial, PR were similar in CIDR does and in CONTROL does (40.6 and 30.0%, respectively). Pregnancy rates did not differ in *Spring* (17.8 and 19.5% for CIDR and CONTROL, respectively), but PR were significantly different ($P < 0.03$) in *Fall* for CIDR and CONTROL does (60.8 and 39.1%, respectively). Overall, doe LSZ was influenced by season bred and use of CIDR devices, with CIDR-*Fall*-bred does having a higher ($P < 0.0001$) LSZ (1.6 ± 0.2) compared with CONTROL-*Fall*-, CONTROL-*Spring*-, and CIDR-*Spring*-bred does (0.8 ± 0.2, 0.4 ± 0.2, and 0.4 ± 0.2, respectively). These results do not encourage the use of CIDR devices in commercial meat-goat herds for increasing pregnancy rates. Further targeted studies will be useful to confirm LSZ increase in fall bred CIDR does. Controlled internal drug release synchronization in our station reduced a 60- to 90-d kidding period to 10 d, allowing operators to arrange facilities, labor, and supplies accordingly, enhancing kid survival and does welfare.

Key Words: meat goats, pregnancy rates, seasonal anestrous
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079 The effects of supplementing ad libitum olive pomace on serum fatty acid composition in Spanish goats.

P. Urso*, M. M. Beverly, S. F. Kelley, M. J. Anderson, and K. J. Stutts, *Sam Houston State University, Huntsville, TX.*

In the livestock industry, the feedstuffs that are offered to livestock can alter the biochemical composition of blood and muscle tissue. Specifically, feedstuffs high in specific fatty acids can potentially create healthier meat and help reduce high-density lipoprotein cholesterol in humans. Olive pomace is a byproduct of the olive oil industry and could be considered as a potential livestock feedstuff to be used to promote these fatty acids due to its high C18:1 content (74%). The objective of this study was to determine if olive pomace could be supplemented at a level that increases the C18:1 concentration in blood. To accomplish this, mature Spanish-influence goats (n = 14; 41.6 kg) were fed ad libitum olive pomace, starting at 2% of their BW, for 28 d to determine if this byproduct would alter circulating fatty acid content, and molasses was mixed with the ration at 0.5% BW to improve the palatability of the feed. Does were fed in herringbone-style runs every afternoon, and BW and blood samples were collected every 2 wk. All data were analyzed using PROC GLM in SAS. There were significant changes in C18:1 and C18:2 over time, with mean consumption of 0.55 kg/d over the duration of the trial. From d 0 to 28, the serum concentration of C18:1 increased ($P < 0.001$) by 8.67% and C18:2 increased ($P < 0.03$) by an average of 4.38%. Serum concentration of C18:0 increased by 3.59%, but this was not significant. There was also no significant increase in C16:0. C18:1 and C18:0 followed a similar pattern of change (r = 0.682), with a marked increase in concentration of C18:1 and C18:0 occurring from d 14 to 28. This rise in concentration combined with the linear increase of C18:2 may indicate that C18:2 is saturated into C18:1 and then further into C18:0. No significant difference in C16:0 concentration indicates that although saturation occurs with the 18-carbon fatty acids, the loss of carbons is not as prevalent. If C18:1 is deposited in the muscle tissue as a result of increased concentration in the blood, then feeding olive pomace can be a healthy alternative to high starch ingredients such as corn and barley.

Key Words: nutrition, olives, ruminant
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080 The effect of conjugated linoleic acid supplementation on fat deposition and lean muscle mass in horses.

E. F. Miller*[1], J. L. Leatherwood[2], M. J. Anderson[1], and M. M. Beverly[1], [1]*Sam Houston State University, Huntsville, TX,* [2]*Department of Animal Science, Texas A&M University, College Station.*

Fatty acids are used within the equine industry to increase the caloric density of a diet as well as replace soluble carbohydrates. Omega-3 fatty acids are the most commonly supplemented fatty acids due to their potential health benefits; however, palatability limitations have spurred an investigation into alternative fatty acids such as CLA. Conjugated linoleic acid has shown health benefits similar to that of omega-3s, but the effect of CLA on equine fat deposition and lean muscle mass has yet to be established. The purpose of this investigation was to evaluate the effects of supplementing elevated levels of CLA on both lean muscle mass and fat deposition in young growing horses. In phase I of this study, 10 Quarter horses were fed between 5.0 and 10.0% of the concentrate diet, increasing the supplementation level every 3 d to determine the maximum inclusion rate of CLA in horses. In phase II, 9 Quarter horses were separated into 2 treatment groups fed either a control diet of soybean oil or CLA ($n = 4$ and $n = 5$ per group, respectively) for 12 wk, with BW and sex evenly distributed across treatments. Diets were formulated to be isocaloric and isonitrogenous, and each treatment was offered at 0.015% BW/d. Growth measurements were collected weekly; rump fat thickness, rib eye area (REA), and intermuscular fat were measured on d 7, 42, and 84 of the feeding period. The MIXED procedure in SAS was used with repeated measures to detect differences in growth performance and ultrasound measurements. There were no differences in performance characteristics or fat content between treatment groups ($P > 0.05$). In order to account for initial differences between treatments ($P < 0.05$), REA between the 17th and 18th ribs (REA17) was run with d 7 as a covariate. Mean REA17 tended to be higher in CLA-supplemented horses ($P < 0.07$) when compared with controls. These results suggest that in an equine model, CLA does not affect growth performance or fat deposition but may increase lean muscle mass in young growing horses. Further studies examining these effects over longer supplementation periods or in obese or insulin-resistant horses may offer insight to potential benefits of CLA in the horse.

Key Words: body composition, conjugated linoleic acid, horses
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081 Assessment of bovine ruminal and mesenteric vascular serotonin receptor populations.

M. A. Snider*[1], D. L. Harmon[1], and J. L. Klotz[2], [1]*University of Kentucky, Lexington,* [2]*USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY.*

A previous study using a contractility bioassay determined that $5HT_{2A}$ receptors in bovine lateral saphenous veins play a role in ergot alkaloid-induced vascular contraction in steers grazing endophyte-infected (*Epichloë coenophiala*) tall fescue (*Lolium arundinaceum*). Ergot alkaloids have also been shown to be vasoactive in gut vasculature. To determine what 5HT receptors are involved in vasoconstriction of gut vasculature, contractility of ruminal and mesenteric arteries and veins collected from cattle were evaluated in the presence of agonists selective for $5HT_{1D}$ (L694-247), $5HT_{2A}$ (TCB-2), $5HT_{2B}$ (BW723C86), and $5HT_7$ (LP44) receptors. Segments of vein and artery were collected from 18 mixed-breed and -gender animals between 10 and 30 mo of age (531 ± 29 kg). Vessels were sliced into 2- to 3-mm cross-sections and suspended in a multimyograph containing 5 mL of continuously oxygenated Krebs–Henseleit buffer (95% O_2/5% CO_2, pH = 7.4, and 37°C). Vessels were equilibrated to 1.0 g for 90 min followed by the addition of 120 m*M* KCl. Tissues were exposed to increasing concentrations of 5HT agonists every 15 min. Contractile response data were normalized as a percentage of the maximum contractile response induced by KCl. Analysis of variance was evaluated using mixed models procedure of SAS for effects of agonist concentration for each vessel type. BW723C86, L694-247, and LP44 did not induce a contractile response for ruminal or mesenteric vasculature. However, when exposed to BW723C86 or L694-247, mesenteric veins relaxed ($P < 0.05$). There was a trend for BW723C86 ($P < 0.05$), L694-257 ($P = 0.06$), and LP44 ($P < 0.05$) to induce a contractile response for ruminal arteries but at the lowest agonist concentration. This is an indication that the ruminal artery is still relaxing from exposure to KCl. Exposure of gut vasculature to TCB-2 induced vasoactivity. Onset was observed at addition of 5×10^{-5} *M* TCB-2 for the mesenteric artery and vein and the ruminal vein ($P < 0.05$). The mesenteric artery reached a maximal response when exposed to 5×10^{-5} *M* TCB-2 and did not differ from the highest (1×10^{-4} *M*) TCB-2 concentration addition ($P > 0.05$). For the ruminal artery, a contractile response was observed at 5×10^{-6} *M* TCB-2 ($P < 0.05$). The findings of this study indicate that $5HT_{1D}$ and $5HT_{2B}$ are present in mesenteric veins and may play a role in vasorelaxation. Furthermore, $5HT_{2A}$ is present in ruminal and mesenteric vasculature, plays a role in vasoconstriction of blood flow, and could be influenced by ergot alkaloid exposure as has been demonstrated in peripheral blood vessels.

Key Words: bovine, serotonin, vasoconstriction
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082 The effects of poor maternal nutrition during gestation on the number of Pax7-positive myogenic progenitor cells.

M. C. Wynn*, A. K. Jones, M. L. Hoffman, S. M. Pillai, K. K. McFadden, S. A. Reed, S. A. Zinn, and K. E. Govoni, *Department of Animal Science, University of Connecticut, Storrs.*

Poor maternal nutrition during gestation can negatively affect fetal muscle development by altering the development of myogenic progenitor cells. We hypothesized that maternal nutrient restriction feeding and overfeeding during gestation would decrease the number of myogenic progenitor cells expressing the transcription factor paired box 7 (Pax7) in the LM of offspring. Pregnant western white-faced ewes ($n = 78$) were fed 60, 100, or 140% of NRC requirements for TDN starting at d 30 ± 0.2 of gestation and offspring are referred to as RES, CON, and OVER, respectively. At d 45, 90, and 135 of gestation, ewes were euthanized for fetal muscle collection ($n = 10$ to 15 fetuses per treatment per time point). Another group of ewes was allowed to undergo parturition, and lambs were necropsied within 24 h (birth; $n = 10$ to 13 per treatment). The LM was sampled from each fetus, cryosectioned (10 μm thickness), immunostained with Pax7 antibody and Hoechst (nuclei stain), and imaged ($n = 5$ per fetus), and Pax7 positive [Pax7(+)] cells were quantified using ImageJ. Data were analyzed using PROC MIXED in SAS with main effects of maternal diet, litter size, and time point. An interaction of maternal diet × litter size ($P = 0.04$) was observed such that within OVER offspring, the number of Pax7(+) cells in triplets was 72 and 67% greater compared with singletons and twins, respectively ($P \leq 0.04$). Between diets, the number of Pax7(+) cells was 76 and 49% greater in OVER triplets compared with CON and RES triplets, respectively ($P \leq 0.03$). No differences in the number of Pax7(+) cells were observed between litter sizes within RES and CON ($P \geq 0.77$) or within a litter size between CON and RES ($P \geq 0.08$). An interaction of time point × litter size was observed ($P = 0.04$) such that at d 45, triplet offspring Pax7(+) cells were 24 and 45% greater compared with singletons and twins, respectively ($P \leq 0.05$). However, no differences in the number of Pax7(+) cells were observed between litter sizes at d 90 and 135 of gestation or birth ($P \geq 0.16$). In conclusion, triplets exhibit more Pax7(+) cells at early gestation and due to maternal overfeeding, which may delay their progression through myogenesis.

Key Words: maternal nutrition, muscle, sheep
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083 Egg production and quality from laying quails fed three levels of moringa meal.

K. M. Degollado Aguayo*[1], H. Bernal Barragán[1], E. Olivares Sáenz[1], F. Sánchez Dávila[1], M. Cervantes Ramírez[2], A. Morales[2], and N. C. Vásquez Aguilar[1], [1]*Universidad Autonoma de Nuevo Leon, San Nicolás de los Garza, Mexico,* [2]*ICA – Universidad Autónoma de Baja California, Mexicali, Mexico.*

This study was conducted to evaluate the effect of adding 0 (T0), 5 (T5), and 10% (T10) moringa leaf (*Moringa oleifera*) meal to a soybean meal–sorghum–based diet on egg production and quality from laying quails (*Coturnix japonica*). Eighteen 7-wk-old laying quails, with an initial live weight (LW) of 140 ± 5 g, were individually housed and randomly assigned to the 3 treatments (TRT; $n = 6$). Diets were isoproteic and isoenergetic. During the first 8 wk of the laying cycle, quail LW and feed intake were recorded weekly. Produced eggs ($n = 530$) were identified and weighed, and egg mass production was recorded. Egg shape index was calculated as their relative width by length ratio. Egg energy and protein concentrations were measured ($n = 6$). Shell thickness (μm); the proportions of albumen, yolk, and shell (gravimetrically); and egg yolk color (using reflectance chroma meter) were determined ($n = 60$/treatment). The experiment was a completely randomized design; statistical analyses were performed with SPSS software, and mean comparisons were performed using Tukey. Average quail LW was higher for T0 (160.9 g) than for diets with moringa (average 151.9 g; $P < 0.05$). There was no difference among TRT in feed intake (136.37 g/wk), egg quantity (3.68 eggs/wk), or egg mass (35.55 g/wk; $P > 0.05$). Nevertheless, egg weight was higher for T0 (9.87 vs. 9.14 g; $P < 0.05$). Feed efficiency of egg production (0.240 g egg/g feed) was similar among TRT ($P = 0.102$). No differences were observed ($P > 0.05$) in egg energy (6,692 cal/g) and protein (12.28%) concentration or in the efficiency of protein (0.042; $n = 144$) and energy (0.102; $n = 144$) deposition among TRT. Egg shell was thicker (313 vs. 278 μm; $P < 0.05$) in T0. Egg shape index (80.0 vs. average 77.5%) and the proportion of egg shell (16.6 vs. average 15.3%) were higher in T10 ($P < 0.05$). The proportion of yolk (34.5%) and albumen (49.8%) were similar among TRT ($P > 0.05$). Eggs from T5 and T10 had higher "A" and "B" color parameter values ($P < 0.001$). The "L" parameter was higher ($P < 0.001$) for T0. In conclusion, including moringa leaf meal up to 10% in quail diets at the beginning of the laying cycle had positive effects on the pigmentation of quail egg yolk, without affecting efficiency of egg protein and energy deposition and without reducing egg production parameters.

Key Words: dietary moringa, egg production and quality, quails
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084 Effect of Omnigen-AF on the preweaning performance of beef calves.

T. S. Crook*[1], J. E. Koltes[2], B. Stewart[3], C. Shelton[3], M. B. Sims[3], D. J. McLean[4], J. D. Chapman[4], and P. A. Beck[3], *[1]University of Arkansas Department of Animal Science, Fayetteville, [2]Department of Animal Science, University of Arkansas, Fayetteville, [3]University of Arkansas Division of Agriculture SWREC, Hope, [4]Phibro Animal Health Corporation, Quincy, IL.*

The objective of this research was to determine the effects of feeding OmniGen-AF (OG; Phibro Animal Health Corp., Teaneck, NJ) to mature cows ($n = 112$) and primiparous heifers ($n = 48$) from 60 d before calving to breeding and to their calves in creep feeds for 90 d before weaning on calf performance. Mature cows were randomized into 16 pasture groups by age and heifers were randomized into 4 pasture groups at the University of Arkansas Southwest Research and Extension Center from 60 d prior projected calving to breeding (December 15, 2015, through May 2, 2016). Corn gluten feed was supplemented to all cows at 1.4 $\text{kg}\cdot\text{cow}^{-1}\cdot\text{d}^{-1}$, prorated for 5 d/wk feeding (2.5 kg/cow). Cows were fed OG a daily rate of 4 g/45.4 kg. Calves ($n = 146$) were born between February 10 and April 15, with an average calving date of March 1. Creep feed (67% soybean hulls and 33% corn gluten feed, as-fed basis) was offered at 1% BW from July 14 through October 7, 2016. Calves were offered OG at a daily rate of 4 g/45.4 kg in the creep feed. A subset of heifer calves in each pasture ($n = 3$/pasture) were inserted with an intravaginal device containing a temperature data recorder for a 9-d period during September, and core body temperatures (CBT) were recorded every 20 min. Birth date, birth weight, BW, and BW change of calves were recorded and analyzed as CRD by ANOVA, using the mixed procedure of SAS. Fixed effects included treatment, parity group, and the treatment × parity interaction, with sire (AI vs. natural service) and birth date included as covariables and pasture within treatment as the random effect. Analysis of CBT was conducted as a repeated measures analysis by hour with day as the repeated measure and calf as the subject. Calves supplemented with OG gained more BW ($P = 0.03$) than control calves during the creep feeding period (80.7 vs. 72.5 kg, respectively); however, BW at weaning did not differ ($P = 0.27$). A treatment × hour interaction ($P < 0.01$) for CBT was observed, with OG-supplemented heifers having numerically lower CBT (−0.7°C; $P = 0.19$) at 1400 h than control heifers. Providing OG in the creep diet of calves was shown to have a positive influence on BW gain before weaning. Numerically lower CBT may indicate less heat stress in OG-supplemented calves, but more research is needed to further substantiate these effects.

Key Words: beef cows, body temperature, calf performance
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085 Effects of vaccine treatment and temperament classification on intake and feeding behavior responses to bovine viral diarrhea virus challenge in beef steers.

P. S. Smith*[1], G. E. Carstens[1], C. A. Runyan[2], J. F. Ridpath[3], J. E. Sawyer[4], and A. D. Herring[1], *[1]Department of Animal Science, Texas A&M University, College Station, [2]Angelo State University, San Angelo, TX, [3]National Animal Disease Center, USDA-ARS & Ridpath Consulting, Ames, IA, [4]Texas A&M University, College Station.*

Objectives of this study were to examine the effects of multiviral bovine respiratory disease vaccine treatment (VT) and temperament classification on DMI and feeding behavior responses following a bovine viral diarrhea virus (BVDV) challenge. Nellore–Angus F_2 and F_3 steers ($n = 364$; 330 ± 48 kg BW) were assigned to 1 of 3 vaccine treatments within sire groups: nonvaccinated (NON), modified live (MLV), and killed (KV). Performance, DMI, and feeding behavior traits (bunk visit [BV] duration, BV eating rate, and meal duration) were monitored for 56 d during four 14-d periods, using a GrowSafe system. All steers were intranasally inoculated with BVDV type 1b field strain at the end of the first 14-d period. Exit velocity (EV) was measured and used to assign steers to 1 of 3 temperament classifications (TC; calm, moderate, or excitable) based on mean EV ± 0.5 SD. As expected, DMI, ADG, G:F, BV, and meal durations all decreased ($P < 0.01$) during period 2 after BVDV challenge and subsequently increased during periods 3 and 4. Average daily gain and G:F were not affected by VT or VT × period interaction. However, the BVDV-induced reduction in DMI was less for MLV steers than for KV and NON steers (VT × period, $P < 0.05$). Although there was not a VT × period interaction ($P > 0.2$), MLV steers had increased BV and meal durations ($P < 0.01$) and slower ($P < 0.01$) BV eating rate compared with KV and NON steers. Calm steers consumed more ($P < 0.01$) DMI (9.23 vs. 8.63 ± 0.23 kg/d) and had a numerically higher ADG (1.12 vs. 1.01 ± 0.11 kg/d) than excitable steers. Calm steers had 10% higher ($P < 0.01$) BV duration, 17% higher ($P < 0.01$) meal duration, and a 5% slower ($P < 0.01$) BV eating rate compared with excitable steers. The VT × TC interaction was not significant for DMI and ADG but was for feeding behavior traits. Compared with KV and NON steers, MLV steers had higher ($P < 0.01$) BV and meal durations in both calm steers (11 and 13%, respectively) and excitable steers (6 and 13%, respectfully) but not in moderate-temperament steers. These results suggest that the MLV vaccine mitigated the negative effects of BVDV challenge on DMI, which supports previous immune response findings. Moreover, VT appeared to alter feeding behavior patterns, with MLV steers having longer BV and meal durations and slower eating rates compared with KV and NON steers.

Key Words: bovine respiratory disease, feeding behavior, vaccine treatment
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086 Effects of dietary methionine deficiency on the growth performance and plasma concentrations of selected metabolites in growing pigs.

Z. Yang*[1], M. S. Hasan[1], R. C. Thompson[1], M. A. Crenshaw[1], D. D. Burnett[1], J. K. Htoo[2], and S. F. Liao[1], *[1]Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State, [2]Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany.*

Methionine is the second or third limiting AA in a typical grain-based swine diet and plays a very important role in promoting growth performance, especially the muscle growth of pigs. This study was conducted to evaluate the effects of a dietary Met deficiency on the growth performance and blood plasma concentrations of selected metabolites that include total protein, albumin, urea nitrogen, glucose, triglycerides, and cholesterol in growing pigs. Twenty individually penned crossbred barrows (Yorkshire × Landrace; 23.6 ± 2.41 kg initial BW) were assigned to 2 dietary treatments according to a completely randomized design. A basal corn–soybean meal diet (Diet 1; Met deficient) was formulated using analyzed ingredient AA contents and published standardized ileal digestible (SID) coefficients to contain 0.22% SID Met and 0.52% SID Met + Cys but to meet or exceed the NRC (2012) recommendations for other essential AA (e.g., 1.08% SID Lys), energy (2,545 kcal/kg NE), minerals, and vitamins. Crystalline DL-Met was supplemented to the basal diet at the expense of corn (0.15%) to create Diet 2 adequate in Met (0.37% SID Met and 0.67% SID Met + Cys). During the 4 wk of the ad libitum feeding trial, the BW and feed intake were measured weekly and the ADG, ADFI, and G:F were calculated weekly as well as for the overall feeding period. Immediately before and after the feeding trial, jugular vein blood was collected for plasma sample analyses. The plasma concentrations of the selected metabolites were determined using an ACE Clinical Chemistry System (Alfa Wassermann, Inc.). Data were analyzed using Student's *t*-test. After the 4-wk trial, pigs fed Diet 1 had a lower ($P < 0.001$) ADG (870 vs. 980 g/d) and G:F (0.45 vs. 0.50) than the pigs fed Diet 2. Pigs fed Diet 1 had a higher ($P < 0.001$) plasma concentration of urea nitrogen than those fed Diet 2 (6.6 vs. 4.2 mg/dL). Pigs fed Diet 1 tended to have a higher ($P = 0.085$) plasma albumin concentration. There were no differences ($P > 0.10$) between the 2 treatments in all other parameters measured. These findings indicated that dietary Met deficiency can reduce the rate of body protein synthesis or growth performance as suggested by the plasma urea nitrogen level. Increasing plasma urea nitrogen concentration will lead to increased nitrogen excretion to the environment. However, what mechanisms at the cell signaling level are responsible for the AA utilization warrants further investigation.

Key Words: deficiency, methionine, plasma metabolite
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087 Evaluation of passive transfer immunity and predicting survivability in newborn white-tailed deer fawns.

E. E. Evers*[1], K. J. Stutts[1], J. L. Leatherwood[2], C. R. Stewart[1], C. J. Hammer[3], and M. J. Anderson[1], *[1]Sam Houston State University, Huntsville, TX, [2]Department of Animal Science, Texas A&M University, College Station, [3]North Dakota State University, Fargo.*

Immunoglobulin gamma is used as a marker for the success or failure of passive transfer in neonates that rely on the maternal transfer of immunoglobulins through the consumption of colostrum. Industry standards for successful passive transfer have been established for major livestock species; however, benchmarks have yet to be determined for pen-raised white-tailed deer fawns (*Odocoileus virginianus*). The objectives of this study were to determine an on-farm methodology to indicate successful passive transfer of immunity and to identify methods to characterize physical status that may be used to predict the survivability of pen-raised white-tailed deer fawns. Fawns ($n = 153$) born to 88 white-tailed does (1.5 to 7.5 yr and 40–80 kg) from an established herd (3-S Whitetails, Bedias, TX) were used in this study. Measurements including BW, body length, and cannon bone length were obtained biweekly from birth to 6 wk of age. At 24 h of age, blood samples (6 mL) were obtained via jugular venipuncture. Blood was analyzed on farm using a handheld digital refractometer (MISCO PA201). Both whole blood and serum were analyzed for total protein concentration, IgG concentration, and a Brix value, which was determined using a scale adapted for on-farm use on dairies. Serum IgG concentration was also quantified by radial immunodiffusion (RID) that was validated for use in cervids. Data were analyzed using the LOGISTIC, MIXED, and CORR procedures of SAS. During the trial, fawn morbidity rate was 75.8% and mortality rate was 21.6%. The logistic procedure indicated that serum Brix values ($P < 0.01$) and serum IgG concentration ($P < 0.02$) at birth were useful for predicting survivability of fawns. Fawns that survived had greater serum Brix values (8.93 ± 0.17 vs. 7.55 ± 0.35 °Brix) and serum IgG concentrations (9.51 ± 0.66 vs. 6.80 ± 1.40 g/L) than fawns that died. In addition, there was a strong positive relationship ($P < 0.01$) between all on-farm serum measurements and results of the RID ($r = 0.87$). Body measurements obtained were not predictors of survivability ($P \geq 0.12$); however, there were differences between fawns that survived and those that died. Fawns that survived had a greater ($P < 0.02$) cannon bone length (18.39 ± 0.10 vs. 17.79 ± 0.23 cm) and BW (2.74 ± 0.05 vs. 2.33 ± 0.12 kg) at birth than fawns that died. These results indicate that serum IgG concentration and Brix values measured on farm using a handheld electronic refractometer may be used to help predict passive transfer of immunity and survivability in white-tailed deer fawns. These

results also indicate that certain physical characteristics of newborn fawns may be related to survivability.

Key Words: passive transfer, survivability, white-tailed deer
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088 Effect of level of dietary sulfur on in vitro true digestibility of a commercial ration fed to Dorper wethers.

V. Garza*[1], K. C. McCuistion[1], G. Faz[1], C. L. Lara[2], J. J. Martinez[1], L. P. Sastre[1], and N. L. Bell[1], [1]*Texas A&M University – Kingsville, Kingsville,* [2]*Texas A&M University-Kingsville, Rio Grande City, TX.*

It is believed that sulfur may reduce palatability of lamb, but the resulting effect on digestibility is not clear. The primary objective of this study was to evaluate the effect of dietary sulfur on in vitro true digestibility (IVTD) of a commercial ration fed to 8 Dorper wethers (29.87 ± 0.52 kg BW). A secondary objective was to determine the effect of sulfur-treated rumen fluid on digestibility of diets containing 2 levels of sulfur. Treatments consisted of 0 (CON) or 0.3% (SUL) sulfur mixed into the ration of 8 Dorper wethers (29.87 ± 0.52 kg BW) consuming a commercial growing ration (Purina Honor Show Chow Show lamb Grower 15% DX Medicated feed) with chopped coastal hay mixed at 90:10%. Wethers were individually housed for the duration of the 56-d trial. Ground feedstuff samples containing CON or SUL treatments were weighed into F57 nylon filter bags in quadruplicate. Sheep were slaughtered 56 d after commencing sulfur inclusion. Gastrointestinal tracts were collected during slaughter to allow for rumen fluid collection. Rumen fluid was processed and IVTD protocol performed in accordance with ANKOM (2005) using an ANKOM Daisy^{II} Incubator. Data were analyzed using the MIXED procedure of SAS 9.3 (SAS Inst. Inc., Cary, NC). Sulfur had no effect ($P = 0.16$; 85.20 vs. 83.00% IVTD, respectively) on IVTD of CON vs. SUL feedstuffs. Rumen fluid from SUL sheep did not differ in its ability to degrade feedstuffs when compared with rumen fluid from CON sheep ($P = 0.81$; 84.37 vs. 83.83% IVTD for CON vs. SUL rumen fluid, respectively). Results suggest that dietary sulfur could be altered to benefit lamb palatability without affecting digestibility.

Key Words: digestibility, Dorper, sulfur
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089 Two days of adaptation period may be enough for measuring ileal amino acid digestibility using chromium or titanium as an indigestible index in swine diets.

B. G. Kim[1], S. A. Lee*[2], and H. H. Stein[2], [1]*Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea (South),* [2]*University of Illinois at Urbana-Champaign, Urbana.*

The objective was to determine a minimum adaptation period in ileal AA digestibility experiments. Eight barrows with an initial BW of 58.1 kg (SD 4.3) fitted with a T-cannula in the distal ileum were randomly allotted to a 2-period crossover design with 2 diets and 8 pigs in each period. A soybean meal–based diet and an N-free diet were prepared. Both diets contained 0.4% chromium oxide, 0.4% titanium dioxide, and 0.4% Celite as indigestible indexes. A washout diet with no index was provided ad libitum for 7 d before each 9-d experimental period. The diets were provided at 3 times the estimated daily maintenance requirement for energy. In the same experiment, we found that the minimum adaptation period before ileal digesta collection to have constant index concentrations was 3 to 4 d. Therefore, the digestibility and endogenous loss of AA data were pooled from d 5 to 9 (i.e., true values) to compare with the data from d 1, 2, 3, or 4. On d 1, the apparent ileal digestibility (AID) and the standardized ileal digestibility (SID) of all indispensable AA except Met and Trp calculated using Cr were less (mean difference = 4.1 and 3.9% for AID and SID, respectively; $P < 0.05$) than the true values. Except for His on d 2 and Phe on d 4, the AID and SID of all indispensable AA on d 2, 3, and 4 did not differ from the Cr-based true values. On d 1, the AID and SID of all indispensable AA except Ile, Lys, Met, Thr, and Trp calculated using Ti were less (mean difference = 3.2 and 2.5% for AID and SID, respectively; $P < 0.05$) than the true values. Except for His on d 2 and Phe on d 4, the AID and SID of all AA on d 2, 3, and 4 did not differ from the Ti-based true values. The AIA-based AID and SID of all indispensable AA did not differ from the true values, likely due to the large variability in the AIA-based AID and SID of AA (mean SEM of indispensable AA = 7.9%) compared with Cr- or Ti-based AA digestibility (mean SEM of indispensable AA = 1.5 or 1.2%, respectively). In conclusion, 2 d of adaptation period may be sufficient for ileal AA digestibility experiments with Cr or Ti as an indigestible index.

Key Words: adaptation period, ileal digestibility, indigestible index
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ASAS GRADUATE STUDENT POSTER COMPETITION: PhD DIVISION

090 The hydroxyproline–glycine pathway for gl.ycine synthesis in neonatal pigs.

S. Hu[*1], G. Nawaratna[1], B. D. Long[1], F. W. Bazer[1], G. A. Johnson[1], J. T. Brosnan[2], and G. Wu[1], *[1]Texas A&M University, College Station, [2]Memorial University of Newfoundland, St. John's, NF, Canada.*

Glycine has crucial roles in nutrition and metabolism and is the most abundant AA in the plasma of newborn pigs (approximately 1 m*M*; 2- to 3-fold greater concentrations than in plasma of other species). Quantitative analysis has shown that the classic pathways for glycine synthesis (from serine, threonine, and choline) are insufficient to meet the metabolic requirements of neonatal pigs. Therefore, we hypothesized that there is an additional pathway for endogenous synthesis of glycine. On d 1, 7, 14, and 21 of lactation, milk samples were obtained from 6 sows. Six piglets were euthanized on each of those days to obtain plasma and tissue samples for analyses of AA, enzyme activities, and expression of proteins and mRNA. Data were analyzed by 1-way ANOVA. Our results indicated high concentrations of hydroxyproline as a tripeptide in sow's milk and plasma from piglets. The specific activities of hydroxyproline oxidase (OH-POX), alanine:glyoxylate aminotransferase, and 4-hydroxy-2-oxoglutarate aldolase, which are key enzymes for synthesis of glycine from hydroxyproline, decreased ($P < 0.05$) in the liver and kidneys between d 1 and 21 but increased ($P < 0.05$) in the pancreas and small intestine. Similar results were obtained for the expression of mRNA for those enzymes and for proline oxidase (POX). For the serine- and threonine-dependent glycine pathways, specific activities and expression of mRNA for serine hydroxymethyltransferase and threonine dehydrogenase increased ($P < 0.05$) between d 1 and 21. Immunohistochemistry (IHC) revealed that the localization of OH-POX and POX proteins in the liver switched from periportal to perivenous hepatocytes with age, which indicated a change in hepatic catabolism of hydroxyproline and proline. In the kidneys, the abundance of OH-POX and POX proteins appeared to decrease with age. Results of IHC also revealed the presence of OH-POX and POX in the pancreas, small intestine, stomach, skeletal muscle, and gallbladder. These findings indicate the presence of the hydroxyproline–glycine pathway for the synthesis of glycine from milk- and endogenous collagen–derived hydroxyproline via interorgan metabolism in neonatal pigs, which may compensate for a severe deficiency of glycine in sow's milk. Supported by funds from the USDA National Institute of Food and Agriculture.

Key Words: endogenous synthesis, glycine, hydroxyproline
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091 Relationship between body weight and growth rate of healthy gilts with osteochondrosis lesions.

L. Fabà[*1], D. Solà-Oriol[1], E. Varella[2], and J. Gasa[1], *[1]Animal Nutrition and Welfare Service, Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Tecnología & Vitaminas, S.L., Alforja, Spain.*

Growth rate and BW of gilts may have an impact on lameness and osteochondrosis. The aim of this study was to evaluate cartilage lesions on gilts (around service BW) and their relationship with previous performance traits. Among 120 gilts (Landrace × Yorkshire) between 210 to 235 d of age, 40 were randomly selected and blocked by BW: heavy (HG; 177.7 ± 4.8 kg) and light (LG; 165.3 ± 5.2 kg). Gilts were previously monitored from 35.8 ± 5.9 kg of BW. Gilts were fed ad libitum to meet nutrient requirements for growth (11.9 MJ ME/kg, 160 g CP/kg, and 9.7 g Lys/kg CP). Individual BW and gait observations were performed on trial d 0, 22, 42, 69, 94, 116, and 137 to detect noninfectious lameness. Gilts were slaughtered on d 137 and shoulder, elbow, carpal, femoro-iliac, knee, and tarsal joints of the left half carcass were examined. All joints were evaluated by gross examination of abnormalities in cartilage surfaces and osteochondrosis lesions (OL): erosions, ulcerations, repair reactions, and infolding of the joint cartilage. Because none of the gilts showed more than 3 surfaces with OL, the classification was defined as Tibia, Femur, and Other. Macroscopic evaluation was performed on each surface: 1) presence or absence of OL (0–1); 2) severity: none (0), small (1; involved less than 5%), moderate (2; 5–10%), and severe (3; exceeded 10%); 3) generally, number of surfaces with OL (nOL); 4) presence or absence of severe OL (SevOL); and 5) a total score (Tscore; sum of severities in all surfaces [0–9]). Prevalence of OL was 80%, and 52.5% of all gilts showed a moderate or severe OL (SevOL, 15%). Five percent showed lameness and eventually recovered (161.8 ± 20.1 kg BW at detection), all showing moderate OL. The LG showed increased severity in Tibia, 8 times higher incidence in Tibia, and more nOL than HG ($P < 0.10$). Similarly, a higher severity in Other joints and, overall, a higher Tscore (2.29) was observed in LG compared with HG (1.19; $P < 0.05$). Average daily gain and age did not influence any parameter of cartilage evaluation; however, when gilts were classified by ADG from 100 kg to final BW (high or low), low ADG showed greater Tscore (0.70) than high ADG ($P < 0.10$). In conclusion, cartilage OL is not directly related to clinical lameness. Within a homogeneous herd of grown gilts, a lower BW indicated higher probabilities of osteochondrosis prevalence and severity independently of age differences.

Key Words: growth performance, lameness, leg weakness
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092 Life cycle assessment of sheep meat and wool production in Northern California.

H. C. Dougherty*[1], J. W. Oltjen[1], F. M. Mitloehner[1], K. A. Rodrigues[2], and E. Kebreab[1], [1]*University of California, Davis, Davis,* [2]*University of California Agriculture and Natural Resources – Hopland Research & Extension Center, Hopland.*

A partial life cycle assessment (LCA) of a sheep production system in California was conducted to better understand the environmental impacts of sheep production in the United States. This cradle-to-farm-gate LCA analyzed emissions from sheep–lamb, stocker, and finishing stages of lamb production within the same market chain. Our objective was to calculate the carbon footprint associated with commercial sheep production in northern California and to compare the impact of allocation methods for 1 kg of live weight lamb (LWT), 1 kg cull adult (LWT), and 1 kg of greasy wool at the farm gate. Primary data was collected from on-farm records wherever possible and secondary data from published literature. Whole-system emissions totaled 474.7 Mt carbon dioxide equivalent (CO_2e), of which 42.2% were from animal emissions, 52.6% from feed production and transport, and 5.2% due to animal transport and on-farm operations. Enteric methane was responsible for 34% of total emissions. The sheep–lamb, backgrounding, and feedlot phases were responsible for 86.1, 4.18, and 9.72%, of overall emissions, respectively. Emissions were allocated 100% to meat or between lamb, wool, and cull adult meat on a mass basis. The production system studied for this analysis focused on producing market lambs, with final live weights of 56.4 kg and carcass yield grade 2. Cull adults averaged 54.4 and 68 kg for ewes and rams, respectively, and whole-farm wool production was 2.05 Mt greasy wool. When all emissions were allocated to lamb production, carbon footprints were 28.6 kg CO_2e/kg LWT. When emissions were allocated on a mass basis between lamb, wool, and cull adult meat, 65, 27, and 8% were allocated to lamb, cull adults, and wool, respectively. Carbon footprints were 19 kg CO_2e/kg lamb, 8.0 kg CO_2e/kg cull adult, and 2.5 CO_2e/kg wool. These values highlight the importance of meat production to Californian sheep producers, compared with wool-focused systems found in Australia and the United Kingdom. Whilst lamb has a higher carbon footprint compared with beef regardless of allocation method, coproduct allocation methods also play a significant role in assigning environmental impacts. This analysis is a first step in assessing the overall impact of small ruminant supply chains in the country and identifying aspects that contribute to environmental impacts of production. The results provide baseline data on emissions from sheep production that may be useful in future efforts by the California lamb industry.

Key Words: carbon footprint, sheep, sustainability
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093 16S characterization of liver abscesses in Western United States feedlot cattle.

M. D. Weinroth*, C. R. Carlson, J. N. Martin, J. L. Metcalf, P. S. Morley, and K. E. Belk, *Colorado State University, Fort Collins.*

Liver abscesses are a major economic burden to beef producers. Although different causative organisms have been isolated from purulent material, there is a knowledge gap concerning the complete characterization of the polymicrobial community of a liver abscess. The objective of this study was to characterize liver purulent material across common beef cattle production systems in the western United States using the 16S rRNA gene. Sixteen pens of cattle, from 5 different feedlots, were identified to represent 2 exposure groups: tylosin fed and no tylosin (8 pens per exposure group). From each pen, up to 5 liver abscesses were collected at harvest. Due to sampling limitations (some pens had fewer than 5 abscesses) and the variability in purulent material volume (resulting from the stage and size of the abscess), DNA from 36 liver samples was successfully extracted. Libraries from DNA samples were prepared and sequenced on an Illumina HiSeq 2500 using the 515F/806R primer set for amplification of the V4 region of the 16S rRNA. Sequenced forward and reverse reads were concatenated into 1 contig and raw sequencing reads were clustered into operational taxonomic units. Through 16S characterization, 5 phyla, 11 classes, and 13 orders were identified in the DNA extracted from an abscess. The phyla identified were Bacteroidetes (30.4%), Fusobacteria (30.1%), Proteobacteria (21.9%), Firmicutes (10.6%) and Actinobacteria (5%), with the remaining 2% unclassified. Fusobacterium and Trueperella were both present in the abscess communities, and both are known causative agents of liver abscesses. Of note, the top 3 phyla, which make up 82% of the abscess community, were Gram-negative. This result is surprising, as tylosin, a macrolide, is primarily active against Gram-positive bacteria. Although the isolation of Gram-negative bacteria from liver abscesses is commonly observed, the concentration of Gram-negative bacteria in the microbial community suggests that conventional mechanisms of prevention may not always result in the absence of an abscess. Despite significant effects of variables such as treatment ($P = 0.026$) and geographic region ($P = 0.002$) on the microbiome phylogenetic composition, the overall composition at the phylum level was very similar across samples and the 5 most abundant taxa were present in all samples. Because our goal was to describe overall microbiome of purulent material, treatment and region were not considered for final summary analyses. This is the first time the complex community of liver purulent material has been described. These data may suggest a more targeted approach to liver abscess prevention and treatment.

Key Words: liver abscess, 16S, tylosin
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094 The effect of two additives on ruminal fermentation using a semicontinuous culture system.

M. Capelari*[1], K. A. Johnson[2], B. Latack[1], J. Roth[1], and W. Powers[3], [1]*Michigan State University, East Lansing,* [2]*Washington State University, Pullman,* [3]*University of California, Oakland.*

Seven 37-d trials tested the effect of nitrate (NIT) and monensin (MON) in diets commonly fed to beef cattle (BEEF; 10:90 forage to concentrate ratio; 3 trials) and dairy cattle (DAIRY; 50:50 forage to concentrate ratio; 4 trials) on rumen fermentation and CH_4 emissions. Additives (0, 1.25, and 2.5% diet DM of NIT and 0 and 4 mg/L of MON) were tested alone and combined (NIT + MON; 6 total treatments; 3 replicates per treatment). Rumen fluid was pooled from 5 nonadapted lactating cows fed a 50:50 forage to concentrate ratio diet 3 h after the morning feeding, and 1 L of processed inoculum was transferred to 2.2-L vessels. Treatment diets were added to nylon bags, which remained in the anaerobic fermentation system for 48 h. Buffer was infused into vessels at 70 mL/h. Gas production and composition and VFA were measured daily. Ammonia nitrogen (NH_3–N) and DMD were measured twice weekly. For BEEF and DAIRY trials, when compared with control, NIT reduced CH_4 production (33.5 vs. 43.5 and 24.7 vs. 32.1 m*M*/d, respectively; $P < 0.01$, SEM 1.5) and NH_3–N (6.6 vs. 8.1 and 17.1 vs. 21.0 mg/dL, respectively; $P < 0.01$, SEM 0.6) whereas MON reduced CH_4 production (26.6 vs. 43.5 and 26.3 vs. 32.1 m*M*/d, respectively; $P < 0.01$), butyrate (12.6 vs. 14.9 and 16.1 vs. 19.4 m*M*/d, respectively; $P < 0.01$, SEM 0.5), and acetate to propionate ratio (1.6 vs. 1.9 and 1.6 vs. 2.0, respectively; $P < 0.01$, SEM 0.06) and increased propionate (29.6 vs. 26.2 and 26.8 vs. 22.2 m*M*/d, respectively; $P < 0.01$, SEM 0.6) and total VFA (50.7 vs. 48.1 and 38.3 vs. 35.4 m*M*/d, respectively; $P < 0.01$, SEM 1.9). The combination of NIT + MON in BEEF and DAIRY trials further reduced CH_4 (19.3 vs. 43.5 and 21.3 vs. 32.1 m*M*/d, respectively; $P < 0.01$) and increased acetate (51.2 vs. 49.5 m*M*/d [$P = 0.07$] and 53.7 vs. 49.9 m*M*/d [$P < 0.01$], respectively; SEM 0.9). For BEEF only, compared with the control, NIT reduced DMD at higher doses (72.3 vs. 74.3 g/100 g DM; $P < 0.05$, SEM 1.4) and NIT + MON increased total VFA at lower doses (55.4 vs. 48.1 m*M*; $P < 0.01$). For DAIRY, butyrate was reduced by NIT (16.1 vs. 19.4 m*M*/d; $P < 0.01$) and further reduced by NIT + MON (15.2 vs. 19.4 m*M*/d; $P < 0.01$). The combination of NIT + MON enhanced CH_4 reduction and increased acetate molar ratio. When NIT was present at higher doses, DMD was reduced. The combination of NIT + MON reduced butyrate in DAIRY trials and, at lower doses, increased total VFA production in BEEF trials.

Key Words: in vitro, methane, volatile fatty acid
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095 Influence of supplemental copper, manganese, and zinc source on reproduction, mineral status, and performance in a grazing beef cow–calf herd over a two-year period.

S. Jalali*[1], K. Lippolis[2], J. K. Ahola[1], J. J. Wagner[1], K. Sellins[1], S. B. Laudert[3], J. S. Heldt[3], J. Spears[4], and T. E. Engle[1], [1]*Colorado State University, Fort Collins,* [2]*Oregon State University – EOARC Burns, Burns,* [3]*Micronutrients, Indianapolis, IN,* [4]*North Carolina State University, Raleigh.*

The objective of this experiment was to evaluate the effects of supplemental Cu, Mn, and Zn source on reproduction, trace mineral (TM) status, and performance in a grazing cow–calf herd in eastern Colorado over a 2-yr period. Crossbred (Angus and Angus × Hereford; $n = 261$) 3-yr-old beef cows were stratified by expected calving date, BW, BCS, and liver TM status and randomly assigned to 1 of 6 pastures. Pastures were then assigned to 1 of 2 free-choice mineral treatments (n = 40–45 cows per pasture; experimental unit = pasture), resulting in 3 replicate pastures per treatment for each year of the 2-yr experiment. Treatments consisted of 1) hydroxychloride TM (HTM; 100% of the Cu, Mn, and Zn from IntelliBond C, M, and Z, respectively) and 2) inorganic + organic TM (IOTM; 75% of Cu, Mn, and Zn from sulfate TM and 25% of Cu, Mn, and Zn from AA complexes of Cu, Mn, and Zn). Replicates were rotated among pastures approximately every 28 d in order to minimize pasture effects. Free-choice mineral feeders were used to continuously provide current NRC-recommended concentrations of Cu, Mn, and Zn for 2 yr. Blood samples and liver biopsies were obtained from every cow before the initiation of the experiment and then from a subgroup of animals (20 random animals/replicate) at the end of yr 1 and the same 20 animals/replicate at the end of yr 2. At the end of yr 1, liver Cu and Zn concentrations were greater ($P < 0.05$) in HTM-supplemented cows compared with IOTM-supplemented cows. At the end of yr 2, liver Cu concentrations were greater ($P < 0.05$) and Zn concentrations tended ($P < 0.06$) to be greater in HTM-supplemented cows compared with IOTM-supplemented cows. However, over the 2-yr experiment, mineral intake, BW, BCS, pregnancy rate to AI, overall pregnancy rate, 205-d adjusted weaning weight, kilograms of calf weaned per cow exposed, and plasma Cu, Mn, and Zn concentrations were similar across treatments. These data indicate that under conditions of this experiment, source of TM had no impact on beef cattle production parameters but TM source did impact liver Cu and Zn concentrations over the 2-yr experiment.

Key Words: beef cows, reproduction, trace mineral
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096 Maternal restricted and overfeeding during gestation alters offspring gene expression of inflammatory markers in the liver at day 135 of gestation and at birth.

A. K. Jones*, S. M. Pillai, M. L. Hoffman, K. K. McFadden, K. E. Govoni, S. A. Zinn, S. A. Reed, *Department of Animal Science, University of Connecticut, Storrs.*

The fetal liver facilitates hematopoiesis and development of both liver-resident and peripheral tissue macrophages, priming innate postnatal immunity. We hypothesized that in the fetal liver, the expression of genes mediating inflammation would be disrupted by exposure to poor maternal nutrition during gestation. To test this hypothesis, pregnant western white-faced ewes were fed 100, 60, or 140% of NRC requirements for TDN beginning at d 30.2 ± 0.2 of gestation, with offspring referred to as CON, RES, and OVER, respectively. Ewes ($n = 3$ to 5 per diet per time point) were euthanized at d 135 of gestation for fetal tissue collection or underwent parturition and lambs were euthanized within 24 h of birth. Ribonucleic acid was isolated from the liver of 6 offspring per diet at each time point. The expression of 84 genes mediating inflammation was profiled using real-time RT-PCR arrays. Data were analyzed using PROC MIXED in SAS for main effects and interaction of maternal diet and gender. At d 135 of gestation, maternal diet decreased expression of *lymphotoxin-β* 1.5-fold in OVER compared with CON ($P \leq 0.03$). *Chemokine (C-C motif) ligand 16* (*CCL16*) expression increased 1.9-fold in RES compared with CON ($P \leq 0.02$). At d 135 in males, *tumor necrosis factor (TNF) superfamily (SF)14* expression increased 2.9-fold, whereas expression of *chemokine (C-C motif) receptor 6* (*CCR6*), *CCR4*, *CCL3*, *IL2 receptor-γ*, and *TNFSF receptor 11B* decreased 5.0-, 4.0-, 1.9-, 1.2-, and 1.2-fold, respectively ($P \leq 0.05$), compared with females. At birth, *TNF-α* increased 4.5-fold in RES compared with CON ($P \leq 0.05$), whereas *bone morphogenetic protein 2*, *chemokine (CXC motif) ligand 12* (*CXCL12*), and *CXCL10* were reduced by 3.0-, 2.6-, and 1.8-fold, respectively, in OVER compared with CON ($P \leq 0.04$). A main effect of gender was also observed at birth such that in males, *CCL1* expression increased 6.8-fold but *CXCL9*, *CXCL10*, *TNFSF10*, *IL15*, and *IL5* expression decreased 3.0-, 2.1-, 2.0-, 1.6-, and 1.6-fold, respectively ($P \leq 0.02$), compared with females. Additionally, 10 genes at d 135 and 5 genes at birth exhibited an interaction of maternal diet × gender ($P \leq 0.05$). In conclusion, expression of genes related to inflammation in the fetal liver is differentially affected by maternal restriction and overfeeding during gestation, with the effects of maternal diet differing at d 135 of gestation and after parturition. This may be a mechanism by which poor maternal nutrition causes unfavorable postnatal growth, metabolism, and survival in lambs.

Key Words: inflammation, liver, maternal nutrition
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097 Evaluation of methods for determining cleaning performance in pig stables.

C. Heinemann*, B. Petersen, and J. Steinhoff-Wagner, *University of Bonn, Institute of Animal Science, Bonn, Germany.*

All-in-all-out production systems are well established for pig fatting, but without proper cleaning and disinfection, carryover of microorganisms cannot be avoided. Thus, advantages of an all-in-all-out system are made void and diseases can be easily transmitted to new arriving pigs. To our knowledge, reliable methods for determination of the cleaning and disinfection performance in pig stable besides visual control are lacking. The aim of this study was to identify critical control points in pig pens and compare 5 different methods that are routinely applied for cleaning control in food processing or hospitals. Samples were collected in a randomly chosen cleaned pen of 6 different fattening farms with swabs or agar contact plates at 15 defined locations (entrance door, side wall, back wall, ceiling, slatted floor, dumping area, floor in front of the feeder, feeder outside, feeder inside, windowsill, 2 toys, 2 nipple drinkers, and pipe). All farms differ in cleaning and disinfection procedure. Swabs samples were used for measurement of protein and ATP content as well as for the microbiological parameters total aerobic count, MRSA, and ESBL. Three different contact plates were applied (violet red bile dextrose agar [VRBD] for Enterobacteriaceae, plate count [PC] agar for total aerobic count, and Dey Engley agar for aerobic count on surfaces with disinfectant residues). Additionally, visually, cleanliness of the sampled area was recorded using a 4-score grading scheme. Contact plates were applicable to only 12 of the 15 locations, whereby VRBD showed good performances to control cleanliness in pig stables. Dey Engley agar and PC agar showed a very high bacterial load that was not quantifiable. We found high Spearman rank correlations within protein content, ATP value, total aerobic count, and ESBL ($0.38 \geq r \geq 0.82$, $P < 0.003$). Based on additional criteria such as time between sampling and result as well as handling, protein swabs seem very useful as a semiquantitative method for rapid detection of cleaning performance and ATP analysis for rapid identification of hygienic problems. Additionally, comparison among sampling locations in pens showed that highest bacterial load was found on nipple drinkers, independent of farm and previous cleaning and disinfection process. This can cause serious problems if bacterial load contains pathogens, which are than transmitted to new arriving pigs.

Key Words: hygiene, monitoring, pig health
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098 The regulation of proline on cell proliferation involved in polyamine metabolism in porcine enterocyte IPEC-J2.

J. Wang*, *Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, P.R. China.*

Increased levels of cellular polyamines are essential for stimulation of intestinal epithelial cell proliferation. Proline is one of precursors of ornithine, which is converted into polyamines via ornithine decarboxylase (ODC). The aim of this study was to investigate the effect of Pro on the polyamine metabolism and cell proliferation in the porcine enterocyte IPEC-J2. Cells cultured with DMEM-H containing 10% FBS and were exposed to 400 μ*M* L-Pro or 400 μ*M* L-Pro + 10 m*M* α-difluoromethylornithine (DFMO) for 4 d. The results showed that the ODC protein level and spermidine and spermine contents was increased by L-Pro, but combined addition of L-Pro and DFMO prevented the expression of ODC protein and thus decreased the concentrations of putrescine, spermidine, and spermine in the IPEC-J2 cells ($P < 0.05$). The percentage of cells in the S phase was increased in response to L-Pro treatment and depletion of cellular polyamines by exposure to DFMO caused the G_1 phase growth arrest ($P < 0.05$). Meanwhile, the mRNA expressions of c-fos and c-myc were elevated in the L-Pro treated IPEC-J2 cells but significantly inhibited by DFMO, and inhibition of polyamine synthesis with DFMO increased p53 mRNA level ($P < 0.05$). Interestingly, compared with L-Pro supplementation, the combination of L-Pro and DFMO decreased cell apoptosis and the levels of associated proteins, including Bax and cytochrome C ($P < 0.05$). These findings indicated that Pro promote polyamine synthesis by mediating ODC expression and plays an important role in cell-cycle progression and cell proliferation in the porcine enterocyte IPEC-J2, and polyamine-deficient IPEC-J2 cells may be protected from apoptosis, thereby provided useful information for dietary Pro or polyamine supplementation to improve the health and development of small intestinal mucosa in piglets.

Key Words: polyamines metabolism, porcine enterocyte, proline
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099 Effects of dietary lysine restriction on the concentrations of free amino acids and other selected metabolites in the blood plasma of growing pigs.

M. S. Hasan*, M. A. Crenshaw, J. M. Feugang, and S. F. Liao, *Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

Growth performance, especially muscle growth, of pigs is dependent on the constant supply of balanced AA and other nutrients from the blood circulation. Lysine is typically the first limiting AA in grain-based swine diets. This project was conducted to study how dietary lysine restriction affects plasma concentrations of AA and other metabolites in growing pigs. Twelve individually penned crossbred barrows (Yorkshire × Landrace; 22.6 ± 2.04 kg initial BW) were assigned to 2 dietary treatments according to a completely randomized design ($n = 6$). Two corn and soybean meal–based diets were formulated to contain 0.65% (lysine deficient; Diet I) and 0.98% (lysine adequate; Diet II) standardized ileal digestible lysine. During the 8-wk feeding trial, pigs had ad libitum access to their respective diets and fresh water. Pigs' BW and feed intake were measured biweekly, and ADG, ADFI, and G:F were calculated biweekly as well as for the overall feeding period. Immediately after the feeding trial, jugular vein blood was collected for plasma sample preparation. The plasma AA contents were analyzed with the established HPLC method, and plasma contents of selected metabolites were determined using Alfa Wassermann's ACE Clinical Chemistry System. Data were statistically analyzed using Student's *t*-test. Overall, the final BW and ADG in pigs fed Diet I were lower ($P < 0.01$) than in pigs fed Diet II. However, no difference in ADFI was found between the 2 groups. Therefore, the G:F of Diet I pigs was lower than that of Diet II pigs ($P = 0.04$). Although the plasma concentration of b-alanine in Diet I pigs was higher ($P < 0.01$) than in Diet II pigs, the plasma concentrations of lysine, methionine, leucine, arginine, tyrosine, and total protein in Diet I pigs was lower ($P < 0.05$) than in Diet II pigs. The plasma concentrations of all other AA and metabolites (including urea nitrogen, albumin, glucose, and cholesterol) were not different ($P > 0.10$) between the 2 groups. Based on these results and nutrition knowledge, dietary lysine restriction is responsible for the reduced plasma lysine level and growth performance of Diet I pigs. Reduced levels of plasma methionine, leucine, arginine, tyrosine, and total protein indicate that pigs consuming a lysine-deficient diet may utilize these metabolites for other metabolic functions. In conclusion, dietary lysine restriction can affect the plasma profile of free AA and other metabolites in addition to free lysine in growing pigs.

Key Words: lysine, nutrients metabolite, swine
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100 Big data analysis of beef production and quality: An example with the Brazilian cattle industry.

V. Cardoso Ferreira*, J. R. R. Dórea, and G. J. M. Rosa, *University of Wisconsin-Madison, Madison.*

"Big data" represents the new era in data exploration and use in livestock systems. With recent developments in data recording technology and analytics tools, it is now possible to get important insight regarding management practices and environmental effects affecting livestock productivity and product quality on a much larger scale. Even though analyzing big data is challenging (as it requires cautious data curation, large computer memory, and specific data mining tools), it can be extremely valuable. In this analysis, data from Brazilian beef cattle was available from 2 sources: JBS S.A. (81,053 farms) and DSM Produtos Nutricionais (22,223 farms). After merging, the final data set comprised information from 7,248 farms and 1,571,023 carcasses slaughtered in the years 2014 through 2016. Three outcome variables were analyzed: BW at slaughter (BWS; kg), carcass fat index (FI; 1–5), and age at slaughter (AS; yr). Covariates included in all models were AS (except when it was an outcome), season (dry or rainy in each year), animal category (steer, bull, cull bull, heifer, and cow), frequent technical consulting (FTC; binary), regional sales team (RST; 17 levels), type of feedlot premix (no feedlot premix [NFP], finishing grazing cattle [FGC], feedlot without additives [FWA], and feedlot with additives [FA]) and farm (random effect). After extensive data mining, mixed model analyses were performed for all outcomes. The use of FA premix decreased AS and increased BWS and FI in comparison with NFP (0.55 yr [$P < 0.00$], −1.78 kg [$P < 0.00$], and −0.13 [$P < 0.00$], respectively), FGC (0.34 yr [$P < 0.00$], −3.58 kg [$P < 0.00$], and −0.12 [$P < 0.00$], respectively), and FWA (0.72 yr [$P = 0.04$], −21.09 kg [$P = 0.05$], and −0.25 [$P = 0.02$], respectively). Adopting FTC increased BWS (6.38 kg; $P < 0.01$) and FI (0.07; $P < 0.01$) and reduced AS (−0.13 yr; $P < 0.01$). Bulls presented greater BWS (26.51 kg; $P < 0.01$) and lower AS (−0.46 yr; $P < 0.01$) but presented lower FI (−0.51; $P < 0.00$) in comparison with steers. Differences in BWS were observed for different RST and seasons (most $P < 0.01$). Age at slaughter was reduced and BWS and FI increased for rainy seasons of 2014 through 2016 ($P < 0.01$). Combining FTC and FA was capable of increasing BWS by 27.4 kg and reducing AS in approximately 10 mo in comparison with FWA and non-FTC, suggesting that this approach might be favorable for production. Results presented here provided a wide snapshot of beef production in Brazil under a big data perspective never explored before. They provide also useful insight to validate experimental findings and aid decision-making at the farm level.

Key Words: beef cattle, big data, feedlot
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101 Effects of dietary protease on immune responses of weaned pigs.

J. Kim*[1], I. H. Park[2], S. Kim[1], J. J. Lee[1], K. Jang[1], B. Kim[1], S. Park[1], D. Mun[1], J. Choe[1], J. Kang[1], J. Baek[1], J. Y. Cho[2], S. H. Cho[2], and M. Song[1], *[1]Chungnam National University, Daejeon, Republic of Korea (South), [2]DSM Nutrition Korea Ltd., Seoul, Republic of Korea (South).*

This experiment was conducted to investigate effects of dietary protease on immune responses of weaned pigs. A total of 75 weaned pigs (7.06 ± 0.18 kg BW and 28 d old) were randomly assigned to 3 dietary treatments (5 pigs/pen and 5 pens/treatment) in a randomized complete block design (block = BW). The dietary treatments were 1) a diet based on corn and soybean meal to meet or exceed the requirement of CP as a positive control (PC; CP = 24.17%), 2) a low-protein diet as a negative control (NC; CP = 23.51%), and 3) NC + 0.02% protease (PRO). The protease used in this experiment was a commercial product (Ronozyme ProAct; DSM nutrition products, Kaiseraugst, Switzerland) containing 75,000 protease units/g derived from *Bacillus licheniformis*. The dietary treatments did not include spray dried plasma, fishmeal, zinc oxide, and antibiotics to avoid their antibacterial or physiological effects. Pigs were fed each treatment for 6 wk. Blood was collected from 1 randomly selected pig in each pen on d 1, 3, 7, and 14 after weaning. Measurements were number of white blood cells (WBC) by an automated hematology analyzer calibrated for porcine blood and tumor necrosis factor-α (TNF-α), transforming growth factor-β (TGF-β), and C-reactive protein (CRP) by the ELISA. Data were analyzed using PROC GLM of SAS. The statistical model for every measurement included dietary effect and BW as a covariate. Pigs fed PRO had lower WBC on d 7 (14.84 vs. 20.42 × 10^3/μL; $P < 0.05$) and TNF-α on d 7 (618 vs. 889 pg/mL; $P = 0.085$) and 14 (437 vs. 576 pg/mL; $P = 0.069$) than those fed NC, but there were no differences in WBC and TNF-α between pigs fed PC and pigs fed PRO. Pigs fed PRO had lower TGF-β on d 3 (630 vs. 1,588 and 1,396 pg/mL; $P < 0.05$) than those fed PC and NC. However, no differences were found on CRP among dietary treatments. In conclusion, addition of protease may reduce inflammatory responses of weaned pigs.

Key Words: immune response, protease, weaned pigs
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102 Effects of substitution of corn with brown rice on growth performance, nutrient digestibility, and blood profiles of weaned pigs.

S. Kim*[1], K. Jang[1], J. Kang[1], D. Mun[1], B. Kim[1], J. Kim[1], S. Park[1], J. J. Lee[1], J. Choe[1], Y. Kim[2], J. Park[2], and M. Song[1], *[1]Chungnam National University, Daejeon, Republic of Korea (South), [2]National Institute of Animal Science, Cheonan, Republic of Korea (South).*

A study was conducted to evaluate effects of substitution of corn with brown rice on growth performance, nutrient digestibility, and blood profiles of weaned pigs. A total of 144 weaned pigs (7.06 ± 0.57 kg BW and 28 d old) were randomly allotted to 4 dietary treatments (6 pigs/pen and 6 replicates/treatment) in a randomized complete block design (blocks = BW). Dietary treatments were a nursery diet based on a corn–soybean meal basal diet (CON) and 3 additional diets formulated by replacing corn with 50 (BR50), 75 (BR75), and 100% of brown rice (BR100). The diets did not include animal plasma, fish meal, zinc oxide, or antibiotics to avoid their antibacterial or physiological effects. Pigs were fed respective dietary treatments for 6 wk. For the last week of the experiment period, pigs were fed respective dietary treatments containing 0.3% chromic oxide as an indigestible marker. Fecal samples were collected from 1 randomly selected pig in each pen daily for the last 3 d after the 4-d adjustment period. Blood was collected from 1 randomly selected pig in each pen on d 1, 3, 7, and 14 after weaning. Measurements were growth performance, frequency of diarrhea, nutrient digestibility by an index method, and blood profiles by an automated hematology analyzer calibrated for porcine blood. Data were analyzed using PROC GLM of SAS. The statistical model for every measurement except frequency of diarrhea included dietary effect as a fixed effect and BW as a covariate. The χ^2 test was used for the frequency of diarrhea. There were no differences on growth performance (ADG were 448, 479, 456, and 479 g/d and ADFI were 697,710,718, and 704 g/d for CON, BR50, BR75, and BR100, respectively) during the overall experimental period, and frequency of diarrhea, number of white blood cells, and packed cell volume for the first 2 wk after weaning among dietary treatments. However, BR50, BR75, and BR100 increased ($P < 0.05$) apparent total tract digestibility (ATTD) of DM (90.26, 90.51, and 89.88 vs. 86.33%) and energy (90.40, 90.02, and 89.52 vs. 84.60%) compared with CON but did not affect ATTD of CP. In conclusion, substitution of corn with brown rice in nursery diets had no negative effects on growth performance, nutrient digestibility, and blood profiles of weaned pigs.

Key Words: brown rice, growth performance, weaned pig
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103 Effect of energy source, level, sex, and age on meat characteristics of lambs.

J. R. Jaborek[*1], H. N. Zerby[1], S. J. Moeller[1], and F. L. Fluharty[2], *[1]The Ohio State University, Columbus, [2]The Ohio State University, Wooster.*

The objective of the study was to compare ad libitum whole shelled corn (AC), 85% of ad libitum whole shelled corn (LC), and ad libitum alfalfa pellets (AAlf) and lamb sex and age on meat characteristics. Ewe ($n = 48$) and wether ($n = 48$) lambs were blocked by sex and age and stratified by initial weight to pen. Typical market age (TM) ewe ($n = 24$) and wether ($n = 24$) lambs were removed from the study when pens reached an average weight of 59.0 and 63.5 kg, respectively. The remaining long-fed ewe ($n = 24$) and wether ($n = 24$) lambs remained on feed for an average of 218 d total and then were removed from the study on a pen basis. Statistical analysis was conducted using the PROC MIXED statement in SAS with diet, sex, age, and 2- and 3-way interactions as fixed effects, diet, sex, and age nested within pen as the random effect, with significance established at $P < 0.05$. There was an age × sex interaction ($P < 0.05$) for the ultimate pH of the longissimus dorsi from lambs. Ultimate pH of the longissimus dorsi was greater from TM ewe lambs compared with TM wether lambs and long-fed ewe lambs and tended to be greater compared with long-fed wether lambs. Loin Minolta L* values were greater ($P < 0.05$) in TM lambs compared with long-fed lambs. There was a diet × sex interaction ($P < 0.05$) for lean Minolta a* values, indicating that wethers offered AC or AAlf had a greater lean Minolta a* value compared with ewes offered AC and wethers offered LC. Wethers tended ($P = 0.06$) to have a greater lean Minolta b* value when compared with ewe lambs. Minolta L* measurements of fat over the rack were greater ($P < 0.05$) from long-fed lambs compared with TM lambs. Minolta a* values of carcass fat were greater ($P < 0.05$) for AC lambs compared with fat from AAlf lambs, with LC lambs being intermediate. The total lipid percent in the longissimus dorsi and ground shoulder patty was greater ($P < 0.01$) for long-fed lambs compared with TM lambs. Ground shoulder patties from lambs offered AC had a greater ($P < 0.05$) percentage of total lipid compared with lambs offered LC or AAlf. Long-fed lambs produced fatter carcasses with darker lean and brighter colored fat and a lower ultimate pH. Lambs offered AC produced fatter carcasses with redder colored fat compared with AAlf and LC lambs.

Key Words: energy source, lambs, meat characteristics
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104 Effects of carbohydrase on productive performance and white blood cells of lactating sows.

J. J. Lee[*1], J. Kim[1], B. Kim[1], S. Kim[1], K. Kim[1], J. Choe[1], Y. Kim[2], J. Park[2], I. H. Park[3], J. Y. Cho[3], and M. Song[1], *[1]Chungnam National University, Daejeon, Republic of Korea (South), [2]National Institute of Animal Science, Cheonan, Republic of Korea (South), [3]DSM Nutrition Korea Ltd., Seoul, Republic of Korea (South).*

The present study was conducted to evaluate effects of multigrain carbohydrases (DSM Nutrition Korea Ltd., Seoul, Republic of Korea) on productive performance and white blood cells of lactating sows. A total of 12 sows (218.37 ± 5.5 kg BW; 2 parity) were randomly assigned to 2 dietary treatments: a diet based on corn–soybean meal (CON) and CON supplemented with 0.01% multigrain carbohydrase (MCS). The MCS contained xylanase (2,700 units/g), glucanase (700 units/g), and cellulase (800 units/g). Sows were fed the dietary treatments for 28 d (weaning) after farrowing. Blood samples were collected from sows on d 0, 3, and 7 after farrowing and 2 randomly selected nursing piglets in each sow on d 3, 7, and 14 after birth. Measurements were performances and number of white blood cells (WBC) of sows and litter by an automated hematology analyzer calibrated for porcine blood and frequency of diarrhea of litter. Data were analyzed using PROC GLM of SAS. The statistical model for every measurement except frequency of diarrhea included dietary effect and parity as a covariate. The χ^2 test was used for the frequency of diarrhea. Sows fed MCS had less BW change during lactation (−7.85 vs. −15.47 kg; $P < 0.05$) than those fed CON, but ADFI and backfat depth change of sows was not different between CON and MCS. Nursing piglets from sows fed MCS had greater ADG during lactation (210.91 vs. 183.49 g/d; $P < 0.05$) than those from sows fed CON. However, no differences were found on preweaning mortality and frequency of diarrhea of nursing piglets from sows fed either CON or MCS. Sows fed MCS had lower WBC on d 3 after farrowing (11.36 vs. 13.70 $10^3/\mu L$; $P < 0.05$) than those fed CON. Moreover, nursing piglets from sows fed MCS had lower WBC on d 7 after birth (13.22 vs. 17.77 $10^3/\mu L$; $P < 0.05$) than those from sows fed CON. In conclusion, addition of multigrain carbohydrase in the lactation diet decreased BW change of sows and increased ADG of their litter.

Key Words: carbohydrases, lactating sows, productive performance
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105 Effects of biweekly administration of recombinant bovine somatotropin on steroid metabolizing enzymes during early gestation.

M. P. T. Owen*[1], K. J. McCarty[1], M. M. Steichen[1], C. D. Sanford[2], L. B. Canal[2], P. L. P. Fontes[2], N. Oosthuizen[2], N. DiLorenzo[2], K. Vonnahme[3], G. C. Lamb[4], and C. O. Lemley[1], [1]*Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State,* [2]*University of Florida, North Florida Research and Education Center, Marianna,* [3]*North Dakota State University, Fargo,* [4]*Texas A&M University, Department of Animal Science, College Station.*

Previous research has shown that cattle treated with recombinant bovine somatotropin (rBST) yielded greater circulating steroid hormone concentrations, which led us to hypothesize that cattle treated with rBST would have decreased activity of steroid and eicosanoid metabolizing enzymes. Ninety-seven Angus heifers were assigned to receive either rBST (BST; 500 mg/14 d) or no rBST (CONT) immediately prior to fixed-timed AI (TAI) following the 7-d Co-Synch + controlled internal drug release ovulation control protocol. Administration of rBST (sometribove zinc, Posilac; Elanco Animal Health, Indianapolis, IN) was by a single subcutaneous neck injection on d 0, 15, 29, 43, and 57 of gestation. Pregnancy was diagnosed by transrectal ultrasonography on d 29 and verified 64 d after TAI. Subsequently, a subset of pregnant heifers ($n = 7$ BST and $n = 5$ CONT) were harvested on d 80 of pregnancy for collection of the maternal liver, fetal liver, and corpus luteum. Placentomes were separated into caruncle and cotyledon portions. Cytochrome P450 1A (CYP1A), 2C (CYP2C), and 3A (CYP3A) and uridine 5′-diphospho-glucuronosyltransferase (UGT) activities were determined via luminogenic substrates. Activities were expressed per milligram of protein, and data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC), using the Wilcoxon rank sum test, with significance declared at $P \leq 0.05$. Activity of CYP1A was not different between treatments within maternal liver ($P = 0.19$), fetal liver ($P = 0.53$), caruncle ($P = 0.32$), cotyledon ($P = 0.63$), or corpus luteum ($P = 0.76$). Activity of CYP2C was greater ($P = 0.01$) in the maternal liver of BST vs. CONT heifers; however, activity was not different between treatments in caruncle ($P = 0.91$) or corpus luteum ($P = 0.97$). Activity of CYP2C was not detected in the fetal liver or cotyledon. Activity of CYP3A was observed only in the maternal liver and was not different between treatments ($P = 0.82$). Activity of UGT was greater ($P = 0.02$) in corpora lutea samples from BST compared with CONT; however, activity was not different between treatments in the maternal liver ($P = 0.49$) or the fetal liver ($P = 0.95$) and was not detected in the caruncle or cotyledon. In conclusion, administration of rBST during the first 60 d of pregnancy increased activity of CYP2C in the maternal liver and UGT in corpora lutea tissues compared with CONT. Therefore, the previously observed increase in peripheral concentrations of steroids is not associated with a decrease in steroid-metabolizing enzymes.

Key Words: caruncle, corpus luteum, cotyledon
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106 Effect of β-hydroxybutyrate on gene expression in the hypothalamus and pituitary of sheep.

E. R. Cope*[1], B. H. Voy[2], M. Staton[1], T. Lane[1], J. Davitt[1], and J. T. Mulliniks[1], [1]*University of Tennessee, Knoxville,* [2]*Department of Animal Science, University of Tennessee, Knoxville.*

Negative energy balance (NEB) and metabolic dysfunctions have been shown to impair reproduction; however, the mechanisms and molecular pathways that couple energy status to reproductive function are poorly defined. Previous studies have indicated an association between elevated beta-hydroxybutyrate (BHB) and reproduction efficiency. To identify molecular pathways that couple metabolic dysfunctions to reproduction, 10 wethers were randomly assigned to be centrally injected into the lateral ventricle through intracerebroventricular cannulas with 1 mL of β-hydroxybutyric acid sodium salt solution (BHB; 12,800 μmol/L) or saline solution (0.9% NaCl). Two hours after injection, wethers were humanely euthanized and the hypothalamus and pituitary were harvested for transcriptome characterization using RNA sequencing. Ribonucleic acid was extracted from the hypothalamus and pituitary and deeply sequenced (468,912,732 reads from the hypothalamus and 515,106,092 reads from the pituitary) using an Illumina Hi-Seq platform and aligned to the *Bos taurus* and *Ovis aries* genomes using BLAST. Of the total raw reads, 87% (hypothalamus) and 90.5% (pituitary) mapped to the reference *Ovis aries* genome. Within these 2 sets of reads, approximately 56% in the hypothalamus and 69% in the pituitary mapped to either known or putative genes. Fragments per kilobase of transcripts per million normalized counts were averaged and ranked to identify the transcript expression level. Gene Ontology analysis of these 2 gene sets (using DAVID

Bioinformatics Resources) identified biological process functions related to genes shared between tissues as well as functional categories with tissue-specific enrichment. Injection of BHB altered ($P < 0.05$) expression of 11 genes in the pituitary and 44 genes in the hypothalamus. Three genes (zinc finger and BTB domain containing 16 [ZBTB16], FK506 binding protein 5 [FKBP5], and eukaryotic elongation factor 2 kinase [EEF2K]) were influenced ($P < 0.05$) by BHB injection in both tissues. Of these 3 genes, FKBP5 is of particular interest as a mediator of fertility during NEB, due to its role in modulating stress at the hypothalamus–pituitary–adrenal axis. Functional enrichment analyses revealed that BHB injection altered expression of genes in pathways related to stimulus perception, inflammation, and cell cycle control. The set of genes altered by BHB creates a foundation from which to identify the signaling pathways that suppress fertility during NEB or periods of metabolic dysfunctions.

Key Words: gene expression, metabolic dysfunction, reproduction
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107 Validation of primary antibodies for multiple immunofluorescent labeling of horse skeletal muscle fiber type.

C. M. Latham*[1] and S. H. White[2], [1]*Texas A&M University, College Station,* [2]*Texas A&M AgriLife Research and Department of Animal Science, College Station.*

Immunohistochemical analysis offers the ability to evaluate muscle fiber type, fiber type-specific cross-sectional area, organization of fibers, and fiber hybridization. Currently, few primary antibodies have been validated for fiber type analysis in horse skeletal muscle, and those that are available can be cost prohibitive and laborious to perform on the same sample. The objective of this experiment was to validate a more efficient method of immunofluorescent fiber type staining in horse skeletal muscle. Samples from the gluteus medius and triceps brachii from a mature mare and her fetus in late gestation were embedded in OCT, frozen in liquid nitrogen-cooled isopentane, and stored at −80°C. Seven-micrometer cross sections were cut in a cryostat, allowed to dry at room temperature for 1 h, and stored at −20°C until analysis. One of 2 protocols was then used to determine fiber type. The first protocol used a previously validated method of immunofluorescent fiber type analysis in horse skeletal muscle (Tulloch et al., 2011), whereas the second protocol used isoform-specific primary antibodies that are commonly used in human and rodent skeletal muscle samples. Protocol 1 used primary antibodies against slow (MAB1628; Millpore, Darmstadt, Germany) and fast muscle fibers (MHCf; Leica Biosystems, Wetzlar, Germany). Protocol 2 used primary antibodies against myosin heavy chain type I (MyHC1; BA-D5), MyHC2a (SC-71), and MyHC2x (6H1), all from Developmental Studies Hybridoma Bank (DSHB; Iowa City, IA). Following incubation in primary antibodies, sections were incubated in fluorescent secondary antibodies, mounted with fluorescent mounting media, and imaged using a fluorescent microscope (Nikon Instruments, Melville, NY). At least 50 muscle fibers were compared for each sample. Myosin heavy chain type 1 BA-D5 and slow MAB1628 identified the same fibers for all fibers counted. To confirm that the 6H1 antibody labeled type 2x fibers and not type 2a fibers, sections were incubated in a previously validated antibody for type 2a fibers (SC-71; DSHB) as well as the proposed primary antibodies (BA.D5 and 6H1; DSHB). Together, 6H1 and SC-71 labeled the same fibers as MHCf, confirming 6H1 and SC-71 label all fast-twitch fibers. Therefore, the primary antibodies BA.D5 and 6H1, in combination with SC-71, allow for immunofluorescent labeling of multiple fiber types on a single section, using isoform-specific secondary fluorescent labels.

Tulloch, L., J. Perkins, and R. Piercy. 2011. Multiple immunofluorescence labelling enables simultaneous identification of all mature fibre types in a single equine skeletal muscle cryosection. Equine Vet. J. 43:500–503.

Key Words: horse, immunofluorescence, muscle fiber type
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108 Effects of Omnigen-AF supplementation on in vitro embryo development and gene expression in superovulated donor beef cows.

A. P. Snider*[1,2], S. A. Armstrong[1], D. J. McLean[1], and A. R. Menino[2], [1]*Phibro Animal Health Corporation, Teaneck, NJ,* [2]*Department of Animal and Rangeland Sciences, Oregon State University, Corvallis.*

Embryo quality is a crucial factor when selecting embryos for transfer. Variation in embryo quality can be attributed to poor oocytes and semen, inflammation, and potential immune system dysregulation. OmniGen-AF (OG) supplementation supports immune system function and animal health. Previously, we observed that feeding beef cattle donors OG during superovulation decreased percent degenerate embryos recovered, decreased cortisol, and increased progesterone concentrations. Therefore, we evaluated the effects of OG supplementation on in vitro embryo development and gene expression of 2 immune system markers in superovulated beef cattle. Twenty-four crossbred beef cows that had never been superovulated were randomly assigned to 4 treatment groups: 0 g OG/animal per day and 200 mg FSH (0/200), 0 g OG/animal per day and 400 mg FSH (0/400), 56 g OG/animal per day and 200 mg FSH (56/200), and 56 g OG/animal per day and 400 mg FSH (56/400). Cows were fed OG for 49 d (where d 0 = start of the feeding period). Superovulation was started on d 28 and ova were nonsurgically recovered on d 49. Good to excellent quality morulae and blastocysts were cultured for 8 d to evaluate in vitro embryo development. Blood samples for evaluating *CD62L* (L-selectin) and *CXCR2* (IL-8R) gene expression in circulating immune cells were collected on d 0, 10, 14, 21, 28, 38, 42, and 49. The protocol was repeated on all cows 90 to 120 d later with cows reassigned in original groups and fed OG for 49 d. In the first superovulation, percent blastocysts hatching was greater in embryos recovered from 0/200 and 56/400 cows compared with those recovered from 0/400 cows ($P < 0.05$). Greater ($P < 0.05$) embryo volumes were attained by embryos recovered from cows treated with 200 vs. 400 mg FSH. Although similar trends were observed in the second superovulation, feeding OG had no significant effects on in vitro embryo development. *CD62L* and *CXCR2* expression was not affected ($P > 0.10$) by OG feeding in the first superovulation; however, *CD62L* was upregulated ($P < 0.05$) and *CXCR2* tended to be upregulated ($P = 0.07$) in cows fed OG in the second superovulation. In summary, OG supplementation improved in vitro development in embryos recovered from cows first superovulated with the standard 400 mg FSH dose and, during second feeding experimental period, induced expression of immune system markers.

Key Words: cattle, OmniGen-AF, reproduction
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109 Effect of delayed wrapping and wrapping source on nitrogen balance and blood urea nitrogen in gestating sheep offered alfalfa silage.

V. Niyigena*[1], K. P. Coffey[2], W. K. Coblentz[3], D. Philipp[2], A. N. Young[1], 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.*

Exposing ensiled forage to oxygen can result in DM deterioration and reduce silage intake by animals. This study was conducted to investigate the effects of 2 different wrapping sources and time intervals between baling and wrapping on N balance and blood urea N in gestating sheep offered alfalfa silage. Alfalfa forage was baled in large round bales and then wrapped in stretch plastic film with (KURA) or without an oxygen-limiting barrier embedded in the plastic wrap. Bales were wrapped on the day of baling or after a 1-, 2-, or 3-d delay. Beginning in January 2016, silages were chopped and packed into plastic-lined trash containers and then offered randomly for ad libitum intake to 16 gestating ewes (63.5 ± 1.71 kg BW) to provide 2 observations per treatment for 3 experimental periods. Each period consisted of a 10-d dietary adaptation period followed by 7 d of total fecal and urine collection. Blood samples were harvested the last day of each period immediately prior to feeding and 4 and 8 h after feeding. Data were analyzed using PROC MIXED of SAS for a 2 × 4 factorial arrangement of treatments, and blood data were treated as repeated measures. No interactions were detected ($P \geq 0.05$) between wrap type and time delay after baling for N balance and blood urea nitrogen (BUN). Retained N (% of N intake and % of absorbed N) was greater ($P < 0.05$) from silage wrapped with KURA. Nitrogen absorption (%) and N apparently absorbed (g/d) linearly decreased ($P < 0.05$) as wrapping was delayed after baling. Total N intake (g/d and g/kg BW), urinary N (g/d), and N retained (g/d and g/kg BW) were not affected ($P \geq 0.05$) by wrap type and time delay between baling and wrapping. Concentrations of BUN (mg/dL) were quadratically affected ($P < 0.05$) by delay between baling and wrapping and were greater ($P < 0.05$) 4 h after feeding than immediately prior to feeding. In general, wrap type and time delay after baling affected N utilization, but N intake and N excreted in urine were not affected by wrap type and time delay after baling. Therefore, delaying wrapping alfalfa silage bales after baling may have negative effects on forage protein utilization by animals. The study was supported in part by USDA-ARS specific cooperative agreement 58-3655-4-052.

Key Words: alfalfa, nitrogen, sheep
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110 Effect of forage species and supplement type on rumen kinetics and serum metabolites in developing beef heifers grazing winter forage.

Z. D. McFarlane*[1], R. P. Barbero[2], R. L. Nave[3], and J. T. Mulliniks[1], [1]*University of Tennessee, Knoxville,* [2]*Sao Paulo State University, Jaboticabal, Brazil,* [3]*University of Tennessee, Crossville.*

The objective was to determine the effect of stockpiled forage type and protein supplementation on VFA production, serum metabolites, and heifer BW. Over 2 yr, spring-born, crossbred heifers (*n* = 45) were stratified by BW at weaning and randomly assigned to 1 of 3 forage treatments: 1) endophyte-infected tall fescue (TF; *Festuca arundinacea*), 2) big bluestem (*Andropogon gerardi* Vitman) and indiangrass (*Sorghastrum nutans* L.) combination (BI), or 3) switchgrass (SG; *Panicum virgatum* L.). Forage treatments were then randomly assigned to receive 1 of 2 supplement types: 1) 0.68 $kg \cdot heifer^{-1} \cdot d^{-1}$ of dried distiller's grains with solubles (DDGS; 28% CP, 74% RUP, and 88% TDN) or 2) 0.22 $kg \cdot heifer^{-1} \cdot d^{-1}$ of blood meal and fish meal (BF; 72.5% CP, 67.5% RUP, and 69.5% TDN), resulting in a 3 × 2 factorial arrangement of treatments. Treatments were initiated every year in January and terminated in April at the onset of a 60-d breeding season. Body weights and serum samples were collected approximately every 28 d from initiation of grazing until breeding. Serum glucose concentrations were greater ($P = 0.05$) for heifers grazing SG. Circulating NEFA concentrations were greater ($P = 0.04$) in TF heifers. Serum urea N (SUN) was not influenced ($P = 0.37$) by forage type. Ruminal acetate concentration and acetate:propionate ratio were greater ($P = 0.04$) in heifers grazing SG pastures. Heifer BW change from January to February and overall BW change were greater ($P < 0.01$) for TF heifers. However, BW change from March to April was not different ($P = 0.84$) among forage types. Serum glucose and SUN concentrations exhibited ($P < 0.05$) supplement type × sampling time interactions. Ruminal acetate tended to be greater ($P = 0.09$) and butyrate concentrations were greater ($P < 0.01$) for BF-supplemented heifers. The acetate:propionate ratio was not influenced ($P = 0.15$) by supplement type. Supplement type did not influence ($P > 0.13$) BW or BW change from January to February and January to April; however, heifers fed DDGS gained ($P = 0.03$) more BW from March to April. Heifer BW change from February to March exhibited ($P < 0.05$) a forage type × supplement interaction with BF heifers gaining more BW on BI pastures than DDGS heifers. Overall, developing heifers on low-quality native forages initially delayed BW gain; however, heifers seemed to quickly adapt to the lower-quality forage, resulting in similar BW gains in March and April.

Key Words: heifer development, rumen fermentation, serum metabolites
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111 Effect of oil source, cooking method, and storage time on lipid oxidation in ground beef patties from Nellore cattle.

A. R. Cabral[*1], F. S. Costa[2], M. E. Groto[3], A. S. C. Pereira[4], and S. L. Silva[3], [1]*Texas A&M University, College Station,* [2]*Agencia Paulista de Tecnologia dos Agronegocios – APTA, Sao Jose do Rio Preto, Brazil,* [3]*University of Sao Paulo/FZEA, Pirassununga, Brazil,* [4]*University of Sao Paulo (USP), School of Veterinary Medicine and Animal Science (FMVZ), Department of Animal Science (VNP), Pirassununga, Brazil.*

The aim of this study was to evaluate the effects of feeding vegetable oil sources (sunflower [SU], linseed [LO], and soybean [SO]) in lipid oxidation of raw and cooked beef patties stored for 0 and 90 d. Ninety-six Nellore steers were fed for 82 d with diets containing 3.5% of vegetable oils (DM basis). After 82 d on feed, animals were harvested and samples of longissimus muscle and subcutaneous fat were collected to prepare 40 hamburger patties per treatment (100 g each). Patties were prepared using a commercial formulation (85.4% meat, 12% fat, 2% salt, 0.3% garlic, and 0.3% emulsifier) and packaged in oxygen-permeable plastic bags and then immediately frozen at −18°C and stored for 0 and 90 d. The patties were evaluated raw and cooked. The cooked patties were grilled at 170°C for 4 min on each side (internal temperature 70°C). Lipid oxidation was estimated as thiobarbituric acid–reactive substances (TBARS) and measured as milligrams of malonaldehyde (MDA) per kilogram. The data was analyzed as a completely randomized design in a $4 \times 2 \times 2$ factorial arrangement (3 oil sources plus control × 2 storage time × raw and cooked) using a mixed model (MIXED procedure of SAS), including the fixed effects of oil source, storage time, cooking method, and the interaction between the treatments. There was an interaction between storage times, cooking methods, and oil source ($P < 0.0001$). There was an increase of TBARS values after 90 d for all oil sources ($P < 0.0001$). For both 0 and 90 d, LO and SU were higher in MDA than SO ($P < 0.0001$); the same happened for both raw and cooked patties ($P < 0.0001$). The TBARS values were higher in cooked samples compared with the raw patties for the control treatment ($P = 0.013$), were smaller for SU ($P < 0.0001$), and no effect for LO ($P = 0.7785$) or SO ($P = 0.7949$). There was an increase of TBARS values after 90 d for the raw samples ($P < 0.0001$) but there was no effect for those that were cooked ($P < 0.0001$). When the patties were compared at 0 d, those that were raw had lower concentrations of MDA compared with the cooked samples ($P < 0.0001$); however, at 90 d, the raw samples had higher concentrations of MDA than cooked samples ($P < 0.0001$). In conclusion, storage time and cooking method increase lipid oxidation in beef patties and the use of soybean oil would result in less lipid oxidation compared with the other treatments.

Key Words: hamburger patties, soybean oil, thiobarbituric acid–reactive substances
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112 Evaluation of fecal near-infrared reflectance spectroscopy profiling technology to predict forage intake estimated using *n*-alkane markers in grazing cattle.

J. R. Johnson[*1], G. E. Carstens[2], S. D. Prince[3], K. H. Ominski[4], K. M. Wittenberg[5], M. Undi[6], D. A. Forbes[7], A. N. Hafla[8], D. R. Tolleson[9], and J. A. Basarab[10], [1]*Texas A&M University, College Station,* [2]*Department of Animal Science, Texas A&M University, College Station,* [3]*Texas A&M AgriLife Research, Temple,* [4]*Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada,* [5]*University of Manitoba, Winnipeg, MB, Canada,* [6]*NDSU Central Grasslands Research Extension Center, Streeter, ND,* [7]*Texas AgriLife Research, Uvalde, TX,* [8]*Agri-King, Inc., Fulton, IL,* [9]*Senora Research Station, Sonora, TX,* [10]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Improved methodology to estimate intake of grazing animals is needed for better-informed management strategies, as current techniques are limited. The objective of this study was to evaluate the accuracy of fecal near-infrared reflectance spectroscopy (NIRS) to predict forage intake estimated using *n*-alkane markers in grazing animals. Fecal samples were collected from individual animals across 11 trials ($n = 260$) in which forage DMI was predicted using the alkane-ratio technique. For each trial, fecal samples were collected 2 times daily for 5 consecutive days and composite samples were subjected to NIRS analysis by a Foss NIRS 6500 scanning monochromator (Foss, Eden, Prairie, MN). Fecal spectra were used to develop equations to predict fecal alkane concentration (8 trials; $n =$

Table 112.[1]

Item	No.	Range	Mean (SEL)	Calibration		Validation	
				R^2_c	SEC	R^2_{cv}	SECV
Fecal alkane concentration							
C_{31}, mg/kg	212	222–1,564	986.4 (3.3)	0.99	54.7	0.98	67.1
C_{32}, mg/kg	212	60–333	182.9 (2.5)	0.90	20.6	0.87	23.2
n-Alkane predicted DMI							
DMI, kg/d	260	2.93–16.9	7.40 (0.16)	0.90	0.74	0.87	0.84

[1] SEL = standard laboratory error; SEC = SE of calibration; SECV = SE of cross-validation.

212) and *n*-alkane predicted DMI (11 trials; $n = 260$). For the prediction of fecal alkane concentrations, coefficients of determination for calibration (R^2_c) and cross-validation (R^2_{cv}) were 0.90 and 0.87, respectively, for fecal C_{32} concentration and 0.99 and 0.98, respectively, for fecal C_{31} concentration. Calibration and cross-validation accuracies (R^2_c and R^2_{cv}) for the prediction of forage DMI estimated using the *n*-alkane method were 0.90 and 0.87, respectively. These results indicate the presence of strong associations between fecal NIRS spectra and fecal alkane concentrations but do not provide information regarding the robustness of these equations, which is necessary for industry application. To evaluate the robustness of the equations in this study, independent-trial validation was performed. This type of validation was accomplished by removing a single trial from the database and using the remaining 10 trials to develop the calibration equation to predict the independent trial. For this study, independent-trial validation results for the prediction of fecal alkane concentrations and forage DMI estimated using the *n*-alkane method were poor ($R^2_v < 0.15$). Although cross-validation results indicate the potential of this technology to predict forage intake of grazing animals, the independent-trial validation results suggest that a larger database will be needed to enhance robustness of predictive equations across diverse production systems.

Key Words: beef cattle, feed intake, near-infrared reflectance spectroscopy
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113 Supplementation of blackberry pomace during the transition phase may improve health and immune function of dairy cows in the week before calving.

K. Swanson*[1], S. Akers[1], K. Estenson[1], R. Wilson[1], M. Keller[1], and G. Bobe[2], [1]*Oregon State University, Corvallis,* [2]*Department of Animal and Rangeland Sciences, Oregon State University, Corvallis.*

Blackberry pomace, the waste from blackberry processing, is rich in polyphenolic compounds that have anti-inflammatory and antioxidative properties. More than 80% of dairy cows become sick after calving with diseases such as mastitis and ketosis, which in turn have a negative effect on their production and reproductive health. In this study, the effectiveness of blackberry pomace as a natural supplement to improve the overall health of transition dairy cattle was assessed. We hypothesized that the addition of blackberry pomace would help improve metabolic status (lower free fatty acids [FFA], lower β-hydroxybutyrate [BHB], and increase glucose) and overall health around the time of calving. Using completely randomized block design, 24 cows were assigned to 3 groups and received between 4 wk before and after calving no supplement (Control), 57 g/d of dried blackberry pomace (Low Blackberry), or 114 g/d of dried blackberry pomace (High Blackberry) as a top dressing to their standard total mixed ration. Blood samples were collected on approximately d 28, 21, 14, 9, 7, 5, 3, and 1 prepartum, and both blood and milk samples were collected on d 0, 1, 3, 7, 14, 21, and 28 postpartum. Upon completion of the study, blood samples were analyzed for BHB, glucose, phosphorus, and FFA concentrations. In addition, we collected BCS weekly and feed intake data daily. All data was analyzed using PROC MIXED and PROC GLIMMIX in SAS version 9.4. There was a significant decrease ($P < 0.05$) in BHB for d −1 and blood urea nitrogen d −3 relative to calving in the Low Blackberry cows when compared with the Control cows. In addition, there was a significant increase ($P < 0.05$) for glucose on d 0 relative to calving for High Blackberry cows compared with Control cows. Serum phosphorus concentration at d −1 relative to calving significantly increased ($P < 0.05$) for both blackberry groups when compared with the Control group. The average BCS for the High Blackberry cows was significantly higher ($P < 0.05$) than that of the Control cows in the week prior to calving. There were no differences observed in milk yield or feed intake when comparing the groups. In conclusion, the supplementation of blackberry pomace to multiparous transition cows helped to improve metabolic status and health in the week leading up to calving.

Key Words: blackberry pomace, health, transition cow
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ASAS UNDERGRADUATE STUDENT POSTER COMPETITION

114 Effects of medicated feed on Coccidia rates in early gestation goats.

J. Eier*, C. R. Fisher, and T. L. Bova, *University of Findlay, Findlay, OH.*

The objective of the current study was to examine the effects on a decoquinate medicated feed compared with a control feed on the coccidia rates in early gestation goats. Coccidia, especially common in goats, are microscopic parasites that destroy the epithelial cells in the lining of the small intestine. Damage to the intestinal lining impairs digestive function and slows growth rate of the goat (Luginbuhl, 2015). The clinical form of coccidiosis is accompanied by severe diarrhea and eventually death. Medications, such as decoquinate, have been used in animal feed to prevent coccidiosis. Medicated products, such as decoquinate, decreased shedding of oocyst into the intestinal environment and aided in the prevention of coccidiosis (Schoenian, 2005). Does in early gestation (n = 10) were fed a nonmedicated control feed or medicated feed (decoquinate recommendation at 22.7 mg/45.4 kg of BW) in a CR design. Groups were fed at a rate of 0.91 kg of feed/45.4 kg of BW per day for 44 d. Fecal grab samples were collected on d 1, 30, 37, and 44 for each group. Fecal grab samples were analyzed for coccidia oocysts numbers through a flotation technique similar that of to Zajac et al. (2012). Data was analyzed through PROC GLM in SAS 9.1 with significance at $P < 0.05$. Goats fed the decoquinate medicated feed had a significant decrease in eggs per gram ($P < 0.0015$). Results indicate that decoquinate reduced rates of coccidiosis ($P = 0.0011$) and, overall, decreased oocysts numbers.

Key Words: coccidia, decoquinate, oocyst
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115 Oral administration of L-arginine hydrochloride to low-birth-weight piglets improves their growth and survival.

D. W. Long*, N. Wu, W. He, G. Nawaratna, B. D. Long, W. Bin, S. Hu, and G. Wu, *Texas A&M University, College Station.*

Pigs exhibit severe naturally occurring intrauterine growth restriction (IUGR). Under current feeding programs, approximately 20 to 25% of piglets are born with a birth weight of <1.1 kg. Intrauterine growth restriction accounts for 76% of preweaning deaths. To date, IUGR piglets are culled on farms and there are no effective nutritional means to prevent their death or enhance their growth. In the present study, we conducted an experiment to determine the effects of L-arginine supplementation on the growth and survival of IUGR piglets. In this experiment, 88 IUGR piglets (with a mean birth weight of 0.85 kg) from 22 sows (4 IUGR piglets/sow) were randomly assigned into 4 groups. They were nursed by sows and orally administered 0, 0.1, 0.2, or 0.4 g L-arginine (in the form of L-arginine HCl) per kilogram BW twice daily. The total doses of L-arginine were 0, 0.2, 0.4, or 0.8 g/d per kilogram BW. Appropriate amounts of L-alanine were added to the oral L-arginine solutions so that all groups of piglets received the same amount of nitrogen. Piglets were weighed on d 1, 7, and 14 of age. On d 14, blood samples (1 mL) were obtained from the jugular vein of piglets at 1 h after suckling, and their milk consumption was measured over a 9-h period using the weigh–suckle–weigh technique. Milk intake did not differ ($P > 0.05$) among the 4 groups of piglets. Oral administration of Arg increased ($P < 0.05$) Arg concentrations in the plasma in a dose-dependent manner. When compared with the control group (ADG = 152 g/d between d 1 and 14), IUGR piglets administered 0.2 and 0.4 g L-arginine/d per kilogram BW increased ($P < 0.05$) by 19 and 31%, respectively. The ADG did not differ ($P > 0.05$) between the controls and the IUGR piglets receiving 0.8 g L-arginine/d per kilogram BW. The survival rates of the IUGR piglets were 50, 75, 90, and 90%, respectively, for the 0, 0.2, 0.4, and 0.8 g L-arginine/d per kilogram BW groups. Growth and survival of IUGR piglets can be improved through supplementation of L-arginine HCl. Supported by USDA National Institute of Food and Agriculture grants and Texas A&M University.

Key Words: alanine, arginine, intrauterine growth restriction
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116 Chemical composition of enzymatically digested food waste byproducts.

C. Jinno*[1], D. Morash[2], E. McNamara[2], A. King[1], and Y. Liu[1], *[1]University of California, Davis, [2]California Safe Soil, LLC, McClellan, CA.*

Fruit, vegetable, meat, and dairy food waste was collected from supermarkets and processed using enzymatic digestion, pasteurization, and stabilization. The screened and separated final byproduct was 90% liquid food waste (LFW) and 10% solid food waste (SFW). Chemical composition of the LFW and SFW was determined as a first step for their use in diets of pigs. Therefore, 11 batches of each of LFW and SFW were collected and analyzed for DM, CP, AA, ash, ether extract (EE), crude fiber (CF), ADF, NDF, ADL, fructose, glucose, sucrose, maltose, stachyose, verbascose, starch, macrominerals, microminerals, and fatty acids. On a DM basis, LFW contained 22.05% DM, 22.05% CP, 36.58% EE, 0.48% Ca, 0.33% P, 7.50% glucose, 5.14% fructose, 3.38% ADF, 5.81% NDF, and 65.48% unsaturated fatty acids. Solid food waste contained 28.98% DM, 19.53% CP, 34.43% EE, 2.69% Ca, 1.12% P, 5.61% glucose, 3.71% fructose, 17.27% ADF, 25.51% NDF, 63.63% unsaturated fatty acids on a DM basis. Concentrations of these components in LFW were compared with those in SFW using a t-test in SAS. Results indicated that DM, ash,

CF, Ca, P, Mg, S, Cu, Zn, Mn, starch, ADF, NDF, ADL, hemicellulose and cellulose were greater ($P < 0.05$) in SFW than in LFW. Concentrations of all indispensable AA and all dispensable AA except for glycine were greater ($P < 0.05$) in LFW than in SFW. Although both LFW and SFW contain enriched nutrients for nonruminant animals, the high concentration of fiber components in SFW will limit the use of this byproduct in nursery pigs. However, the combination of LFW and SFW will dilute the fiber content and thereby balance nutrients for both nursery and growing pigs. The relatively high concentration of fat will probably limit the inclusion rate of both byproducts in late-finishing pig diets. Further research will be conducted to evaluate the growth performance of nursery and growing–finishing pigs by feeding the combination of LFW and SFW.

Key Words: chemical composition, enzymatically digested food waste, nutrients
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117 Prediction models for standardized total tract digestible phosphorus in swine diets.

J. Y. Sung* and B. G. Kim, *Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea (South).*

The objectives of the present study were to develop equations for predicting the standardized total tract digestible (STTD) P based on total P and phytate P and supplemental phytase concentrations in swine diets and to evaluate the accuracy of the prediction models for STTD P using recently published data. A total of 414 data from 65 experiments that used supplemental phytase and determined P digestibility were used to develop equations for predicting STTD P in swine diets. The CORR procedure of SAS was used to determine correlation coefficients among variables and the NLMIXED procedure was used to generate prediction equations. The STTD P was positively correlated with total P ($r = 0.73$, $P < 0.001$), phytate P ($r = 0.21$, $P < 0.001$), and supplemental phytase ($r = 0.36$, $P < 0.001$) concentrations. Three equations for predicting the STTD P were as follows: in the linear model, STTD P (g/kg, as-fed basis) = 0.244 + 0.660 × total P − 0.432 × phytate P + 0.224 × phytate P × phytase, with Akaike information criterion (AIC) = 503.5 and Bayesian information criterion (BIC) = 523.6; in the quadratic model, STTD P (g/kg, as-fed basis) = 0.179 + 0.662 × total P − 0.422 × phytate P + 0.286 × phytate P × phytase − 0.011 × (phytate P × phytase)^2, with AIC = 498.8 and BIC = 523.0; and in the exponential model, STTD P (g/kg, as-fed basis) = 0.214 + 0.664 × total P − 0.444 × phytate P + 0.581 × phytate P × ($1 - e^{-0.603 \times \text{phytase}}$), with AIC = 498.6 and BIC = 522.8, in which total P ranged from 1.05 to 7.90 g/kg, as-fed basis; phytate P ranged from 0.40 to 6.18 g/kg, as-fed basis; and phytase ranged from 0 to 2.22 FTU/g, as-fed basis. According to the regression analysis for testing the accuracy of the developed quadratic model using 42 recently published STTD P data, the intercept (0.014 ± 0.041; $P = 0.739$) representing the mean bias and slope (−0.009 ± 0.051; $P = 0.865$) representing the linear bias were not different from 0. When validating the exponential model with the same method, the intercept (0.021 ± 0.038; $P = 0.582$) and slope (0.004 ± 0.048; $P = 0.935$) were also not different from 0. In conclusion, the equations suggested herein can fairly accurately predict STTD P concentrations using total P, phytate P, and supplemental phytase concentrations as independent variables in swine diets.

Key Words: phytase, pigs, prediction equation
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118 Is the time of insemination linked with the reproductive response of the animal? Assessment of follicular size at fixed-time artificial insemination and behavioral patterns in beef cattle following seven-day CO-Synch + controlled internal drug release estrus synchronization protocol.

M. R. Corpron*[1], R. Griffiths[1], S. Parish[2], and M. G. Maquivar[1], [1]*Department of Animal Sciences, Washington State University, Pullman,* [2]*Washington State University, Pullman.*

The objective of the present study was to evaluate follicular size at insemination, pregnancy rate, and sexual behavioral patterns in beef heifers and cows synchronized with a fixed-time AI (FTAI) protocol. Heifers ($n = 38$) and cows ($n = 117$) were synchronized using a 7-d CO-Synch + controlled internal drug release (CIDR). At d −7, an administration of 100 µg of GnRH and an intravaginal CIDR device were given to all animals. At d 0, the CIDR device was withdrawn and 1 dose of PGF2a (25 mg) was administered. Animals were continuously observed for behavioral signs of heat after CIDR device removal until either 64 (FTAI for heifers) or 66 h (FTAI for cows). Ovarian follicle size was determined at FTAI via ultrasonography. Estrus was classified as passive (animal receiving a behavior) and active (animal conducting the behavior) and characterized by display of mounting, attempted mounting, sniffing or licking genitalia, head butting, chin resting, flehmen, and following with sexual intent. Peak of estrus was determined when behaviors per hour (number of behaviors/h) were the highest in comparison with the animal's own behavioral patterns. Pregnancy rates were 47.4% (18/38) for the heifers and 58.9% (69/117) for the cows. Estrus expression was 86.8% (33/38) for heifers and 59% (69/117) for cows. On average, heifers exhibited a quicker ($P < 0.001$) onset of passive (43.7 ± 9.2 h) and active estrus (37.7 ± 6.4 h) after CIDR device removal compared with cows (passive, 52.9 ± 7.1 h, and active, 49.7 ± 6.8 h). Heifers peaked faster ($P < 0.001$; 52.2 ± 7.2 h) compared with cows (57.7 ± 5.8 h) and had fewer ($P < 0.001$) mounts per hour (0.99 ± 0.8) compared with cows (3.43 ± 2.4). It was observed that heifers exhibited longer ($P < 0.001$) sexual behavior (active, 20.0 ± 9.4 h, or passive, 14.6 ± 7.2 h) compared with cows (active, 12.1 ± 6.2 h, or passive, 8.9 ± 5.0 h). Average ovulatory follicle size was also different ($P = 0.02$) for heifers (12.01 ± 2.5 mm) compared with cows (13.1 ± 2.6 mm). Based on these results, it is concluded that under the influence of FTAI protocol, the type of animal greatly influences the timing of the onset of heat, estrus response, intensity of estrus, and ovulatory follicle size at the time of insemination. For mature cows, the time of insemination appears to be appropriate; however, for heifers, it remains to be determined if altering the time of AI relative to the onset estrus can impact their fertility.

Key Words: beef cattle, estrous behavior, fixed-time artificial insemination
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119 Evaluation of circulating plasma amino acid concentrations in beef heifers supplemented protein in a low- to medium-quality forage diet.

E. L. Stephenson*[1], A. L. Jones[2], J. S. Luther[1], and A. E. Radunz[1], [1]*University of Wisconsin-River Falls, River Falls,* [2]*University of Wisconsin-Madison, Madison.*

Angus, Hereford, and Angus-cross yearling beef heifers (409 ± 35 kg; $n = 39$) were used to evaluate protein supplementation strategies in low- to medium-quality forage diets on circulating AA concentrations. Heifers were stratified by BW and BCS and then randomly assigned to 1 of 4 protein supplements: 1) no supplementation (CON), 2) low-fat dried distiller's grains (LDG; 7.4% fat; 0.8% BW), 3) high-fat dried distiller's grains (HDG; 9.5% fat; 0.8% BW), and 4) cottonseed meal (CSM; 2.2% fat; 0.4% BW) to provide similar CP intake. Heifers were individually fed by means of a Calan gate system (American Calan Inc., Northwood, NH). Hay was fed twice daily 7 h apart to provide low- to medium-quality chopped grass hay (8.6% CP and 70% NDF; 1.13 Mcal NEm/kg) ad libitum, and 1 h prior to hay feeding, supplements were provided. Supplementation began 7 d prior to timed AI (d 0) and ended 30 d later. A subset of heifers (3 per treatment) were randomly selected to evaluate circulating AA concentrations after feeding on d 26 and were fed protein supplements prior to AM hay feeding, and then coccygeal blood samples were collected at −2, 2, 4, 6, 8, 10, 12, and 14 h after supplementation. Overall plasma total AA (TAA), branched-chain AA (BCAA), and essential AA (EAA) concentrations were lower ($P \leq 0.003$) for CON than for CSM, HDG, and LDG, whereas overall plasma nonessential AA (NEAA) concentrations were not different ($P = 0.22$) among treatments. At 8 h after feeding, plasma TAA, BCAA, and EAA concentrations were lowest ($P \leq 0.03$) compared with all other hours. Within h 8, HDG had greater ($P \leq 0.04$) plasma TAA, BCAA, NEAA, and EAA concentrations compared with CON, CSM, and LDG. Plasma EAA concentrations were lower ($P \leq 0.03$) for h 6, 12, and 14 and plasma BCAA concentrations were lower for h 2, 4 10, 12, and 14 in CON heifers compared with LDG- and HDG-supplemented heifers; however, plasma NEAA concentrations were not different ($P \geq 0.05$) among treatments 4 and 14 h after feeding. Plasma Asp and Trp were not different ($P \geq 0.33$) among supplementation strategies for treatment or treatment × hour. Greater plasma Arg concentrations were observed ($P \leq 0.03$) in CSM vs. HDG, LDG, and CON at h 6, 10, 12, and 14 h after feeding. Overall, protein supplementation increased circulating AA concentrations compared with no supplementation and the lowest AA concentrations were observed at 8 h after feeding.

Key Words: amino acids, beef cattle, protein supplementation
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120 Effect of body condition score on steroid and eicosanoid metabolizing enzymes in various horse tissues.

K. C. Yankey*, M. P. T. Owen, E. N. Ferjak, C. A. Cavinder, K. J. McCarty, C. G. Hart, D. D. Burnett, T. T. N. Dinh, and C. O. Lemley, *Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

Alterations in BCS have been shown to directly affect reproductive efficiency in mammalian species. This variation in nutritional status has been shown to alter production and metabolism of hormones within the body, which are vital throughout the estrous cycle and gestation. Our objective was to determine the activity of steroid and eicosanoid metabolizing enzymes in horses with varying BCS. In addition, we examined tissue distribution of steroid and eicosanoid metabolizing enzymes in horses. We hypothesized a concomitant increase in BCS and activity of steroidogenic enzymes. The BCS of 20 nonpregnant, anestrous mares were established by 2 trained individuals and recorded prior to euthanasia, and tissue samples were collected from the liver, kidney, adrenal gland, ovary, and endometrium for later analysis. Cytochrome P450 1A (CYP1A), 2C (CYP2C), and 3A (CYP3A) and uridine 5′-diphospho-glucuronosyltransferase (UGT) activities were determined using luminogenic substrates and expressed per milligram of protein. The MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) was used to test effect of BCS within a given tissue with age and BW as covariates. Main effect of tissue was tested using the Wilcoxon rank sum test, and statistical significance was declared at $P < 0.05$. Activity of CYP1A was not different across BCS except in adrenal tissues ($P = 0.03$), where BCS 5 was greater than BCS 4 and 6, which were similar. Activity of CYP1A was 100-fold greater ($P < 0.0001$) in the liver than in the adrenal, ovary, and kidney, whereas activity of CYP1A was undetectable in the endometrium. Activity of CYP2C was 100-fold greater ($P < 0.0001$) in the liver than in the adrenal, ovary, and endometrium, whereas activity of CYP2C was undetectable in the kidney. Activity of CYP3A was detectable only in the liver. Activity of UGT was not different across BCS except in the kidney ($P = 0.02$), where BCS 4 was lesser than BCS 5 and 6, which were similar. Activity of UGT was 3-fold greater ($P < 0.0001$) in the liver than in

the kidney, whereas activity of UGT was 9-fold greater ($P < 0.0001$) in the kidney vs. the ovary and endometrium. In general, BCS did not alter the activity of steroid and eicosanoid metabolizing enzymes in horses. However, tissue differences of these enzymes indicated abundant hepatic metabolism in horses. Based on these findings, further research is warranted to comprehend the relationship between BCS and hormone metabolizing enzymes in livestock.

Key Words: cytochrome P450, hormone metabolism, uridine 5′-diphospho-glucuronosyltransferase
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121 Characterizing fetal liver and placental steroid and eicosanoid metabolizing enzymes from dams supplemented with melatonin.

C. N. McGee*[1], M. P. T. Owen[1], K. J. McCarty[1], C. G. Hart[1], K. C. Yankey[1], E. H. King[2], R. M. Hopper[2], D. D. Burnett[1], and C. O. Lemley[1], *[1]Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State, [2]Department of Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Mississippi State.*

Melatonin is a strong antioxidant that contributes to circadian rhythm in several mammalian species. Melatonin has been shown to influence uteroplacental hemodynamics in both sheep and cattle. The objective was to examine fetal liver and placental steroid and eicosanoid enzyme activity during maternal melatonin supplementation. Commercial beef heifers ($n = 12$) were bred via AI and delegated to receive two 24-mg subdermal melatonin implants (MEL; $n = 6$) or act as part of a nonimplant control group (CON; $n = 6$). All treatments were applied at d 180, 210, and 240 of gestation, and heifers underwent Caesarian removal of the fetus at 243 ± 2 d of gestation. Placental samples were collected and separated into maternal (caruncle [CAR]) and fetal (cotyledon [COT]) portions. Additionally, the fetal liver was harvested. Cytochrome P450 1A (CYP1A), 2C (CYP2C), and 3A (CYP3A) and uridine 5′-diphospho-glucuronosyltransferase (UGT) activities were determined via luminogenic substrates. Activities were expressed per milligram of protein, and data were analyzed, using the Wilcoxon rank sum test, within tissue using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) with treatment, fetal sex, and the interaction thereof in the model. Statistical significance was declared at $P \le 0.05$. Activity of CYP1A in CAR was decreased ($P = 0.02$) in male vs. female fetuses from CON dams. Activity of CYP1A was not different ($P \ge 0.25$) in COT tissues; however, activity of CYP1A in the fetal liver was increased ($P = 0.01$) in male vs. female fetuses. Activity of CYP2C was observed only in CAR and was not different between treatments ($P \ge 0.59$). Activity of CYP3A was observed only in the fetal liver and was not different between treatments ($P \ge 0.41$). Activity of UGT in COT was decreased ($P = 0.03$) in male fetuses from MEL dams vs. female fetuses from MEL dams and male fetuses from CON dams. Activity of UGT was not different ($P \ge 0.34$) between treatments in CAR; however, activity of UGT was increased ($P = 0.002$) in the fetal liver from MEL dams compared with the fetal liver from CON dams. In conclusion, melatonin supplementation did alter hormone metabolizing enzymes in fetal liver and placental tissues of gestating cattle. Moreover, the difference in activity of steroid and eicosanoid metabolizing enzymes in male and female fetuses may indicate a physiological adaptation to decrease excessive exposure.

Key Words: caruncle, cotyledon, fetal liver
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122 Traits influencing sale price of performance-tested beef bulls in Michigan.

K. M. Rizzolo* and D. D. Buskirk, *Michigan State University, East Lansing.*

For business and breeding decisions, bull producers need information on the phenotypic and genetic qualities most demanded by their markets. This study used data from the Michigan Cattlemen's Association/Michigan State University Bull Evaluation Program, which evaluates bulls from consignors throughout Michigan and Indiana, raising them in a central location for 5 mo, while standardizing their environmental and feeding conditions. Bulls meeting the program criteria are offered for sale at auction. Traits listed in the sale catalog that influence the variation in sale price (SP) were analyzed for Angus, Simmental, and SimAngus bulls that sold through the program from 2010 to 2016 ($n = 466$). For Simmental and SimAngus bulls, PROC GLM of SAS was used to examine the categorical traits of coat color, horned status, birth type (single, twin, or embryo transfer), and purebred or percentage status. The average SP for purebred Simmental bulls was \$693.92 more than for SimAngus bulls ($P = 0.011$). No other categorical traits were significant in explaining variation in SP. A multiple linear regression analysis (PROC REG of SAS), using the stepwise procedure (entry level, $P \le 0.05$, and stay level, $P \le 0.10$), was completed to examine the continuous variable traits of bull age, sire, birth weight (BiW), weaning weight, final weight (FWT), ADG, weight per day of age (WDA), frame score, intramuscular fat (IMF), rib eye area (RE), scrotal circumference, and pelvic area; EPD percentiles for calving ease (CE%), birth weight (BiW%), weaning weight, yearling weight (YW%), maternal milk (MM%), marbling (MAR%), fat thickness, and rib eye area (RE%); Angus EPD indices for weaned calf value and beef value; and Simmental EPD indices for terminal index (TI%) and all-purpose index. For Angus, $\mathrm{SP} = \$2{,}017.39 - \$1{,}057.39(\mathrm{CE\%}) - \$790.07(\mathrm{BiW\%}) - \$1{,}932.70(\mathrm{YW\%}) - \$1{,}943.89(\mathrm{MAR\%}) + \$1{,}303.92(\mathrm{MAR\%}^2) - \$728.30(\mathrm{RE\%}) + \$0.00067(\mathrm{FWT}^2) + \$60.40(\mathrm{ADG}^2) + \$121.64(\mathrm{RE}) - \$26.18(\mathrm{IMF}^2)$ ($R^2 = 0.6927$, $P < 0.0001$). For Simmental, $\mathrm{SP} = -\$15{,}291 - \$832.21(\mathrm{CE\%}) - \$758.18(\mathrm{MM\%}) + \$348.55(\mathrm{BiW}) - \$2.20(\mathrm{BiW}^2) - \$2{,}955.34(\mathrm{TI\%}) + \$2{,}055.26(\mathrm{TI\%}^2) +$

$0.00134(FWT^2) + $154.82(WDA^2) + $174.17(RE) ($R^2 = 0.7326$, $P < 0.0001$). By understanding the monetary impacts of individual traits on sale price, bull producers can focus on breeding objectives that either emphasize or deemphasize particular traits, based on current market demand.

Key Words: bull, expected progeny difference, price
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123 Transcriptional regulation of genes involved in calcium and phosphate metabolism in neonatal pigs fed with different levels of dietary calcium and phosphate.

R. Gagliardi*[1], W. Zhang[1], R. L. Murray[1], L. Zhao[2], K. Kroscher[2], R. P. Rhoads[2], and C. H. Stahl[1], *[1]University of Maryland, College Park, [2]Virginia Tech, Blacksburg.*

Dietary calcium and phosphate intake during the neonatal period may be of critical importance for lifetime skeletal development. In older animals, calcium and phosphate homeostasis is orchestrated by intestinal absorption, bone turnover, and kidney excretion, which are regulated by several hormones such as parathyroid hormone (PTH), calcitonin, fibroblast growth factor 23 (FGF23), and calcitriol [1,25(OH)$_2$D$_3$]. In older animals, the PTH/calcitriol system appears to be the major regulator of calcium and phosphate homeostasis; however, in neonates, this system is not fully developed. We hypothesized that dietary calcium and phosphate concentrations would affect the expression of genes involved in calcium and phosphate homeostasis in neonatal pigs. Twenty-seven neonatal pigs (24 ± 6 h old) were randomly assigned into 1 of 3 treatment groups. Groups received a milk replacer diet for 16 d that contained calcium and phosphate at a 25% deficiency, adequate, or 25% excess (NRC standard). At the completion of the feeding trial, samples of the liver and kidney were obtained for total RNA isolation. Gene expression of vitamin D receptor (VDR), parathyroid hormone receptor (PTHR), type II sodium-dependent phosphate cotransporter (NPT2), vitamin D-activating enzyme 1α-hydroxylase (Cyp27B1), and 1,25-dihydroxy vitamin D3-24-hydroxylase (Cyp24A1) were determined by real-time PCR. Data, adjusted by housekeeping gene ribosomal protein L4 (RPL4), were normalized back to the deficient group and then analyzed by ANOVA using the GLIMMIX procedure of SAS 9.4. Both PTHR and NPT2 were significantly higher in the calcium- and phosphate-deficient group than in the adequate group (1.01 ± 0.07 vs. 0.75 ± 0.08 for PTHR and 1.01 ± 0.09 vs. 0.65 ± 0.09 for NPT2; $P < 0.05$). No significant differences were detected between the excess group and any other 2 groups. Similarly, expression of Cyp27B1 was significantly higher in the deficient group than in both the adequate and excess groups (1.10 ± 0.13 in the deficient group, 0.60 ± 0.13 in the adequate group, and 0.55 ± 0.13 in the excess group). These results provide some clues into the homeostatic regulation of calcium and phosphate in neonates. Based on these results, even a small deficiency in dietary calcium and phosphate intake can initiate transcriptional changes of key regulatory gene pathways to maintain homeostatic conditions.

Key Words: calcium and phosphate, gene expression, neonatal pigs
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124 High-fiber high-lipid by-product pellets are an effective replace ment for barley grain in diets for finishing beef cattle.

J. A. Johnson* and G. B. Penner, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada.*

This study was conducted to evaluate the effects of treating oat hulls with CaO prior to inclusion in a high-lipid by-product pellet (HLP) on DMI, ruminal fermentation, and total tract digestibility (Study 1) and growth performance (Study 2). In Study 1, 6 ruminally cannulated crossbred Hereford heifers (374 kg ± 18 kg BW) were used in a replicated 3 × 3 Latin square design. Periods consisted of 25 d, with the last 5 d used for sample collection. Dietary treatments included a barley-based control diet (CON) composed of 90% concentrate:10% barley silage. The barley grain and canola meal in the CON were replaced with HLP (30% DM basis) that were not treated (HLP-NT) or a treatment where pelleted oat hulls were treated with 7.5% CaO (HLP-CaO). Study 2 used 210 steers assigned to 21 pens in a 113-d finishing study to evaluate DMI, ADG, and gain:feed (G:F). Steers were fed diets similar to Study 1. Data from Study 1 were analyzed with the mixed model of SAS including the fixed effects of treatment, period, and square and the random effect of heifer nested in square. Data from Study 2 included treatment as a fixed effect. For Study 1, DMI and ruminal short-chain fatty acid concentration were not affected. For individual short-chain fatty acids, the molar proportion of isobutyrate was greatest ($P \leq 0.018$) for HLP-NT, intermediate but not different for CON, and least for HLP-CaO. Ruminal pH was not affected ($P > 0.10$). Apparent total-tract digestibility of DM ($P < 0.05$) and OM ($P < 0.001$) was greatest for the CON (70.7, 79.0%) compared to HLP-NT (68.9, 66.3%), and HLP-CaO (68.4, 65.4%). Digestibility of CP was greater ($P = 0.02$) for the HLP-NT (65.7%) compared to the CON (64.0%) but was not different from HLP-CaO (65.7%). Ether extract digestibility was greater for the HLP-NT (82.6%) and HLP-CaO (79.1%) treatments compared to CON (85.5%; $P < 0.01$). In Study 2, starting BW (424 kg), ending BW (645 kg), and ADG (2.0 kg/d) were not different. However, DMI (kg/d) was greater ($P < 0.01$) for HLP-CaO (12.5) and HLP-NT (12.6) than CON (11.5), and G:F tended to be reduced ($P = 0.08$; 0.15, 0.15, and 0.16 kg/kg, respectively). Calcium oxide treatment of oat hulls did not improve digestibility, but the inclusion of HLP is an effective partial replacement of barley grain without negatively affecting ruminal fermentation and ADG.

Key Words: beef, by-product pellets, calcium oxide
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125 Effect of monensin and protein supplementation on in situ degradability of low-quality forage fed to cattle.

J. I. Solis*[1], J. L. Foster[2], C. A. Loest[3], J. J. Martinez[1], L. P. Sastre[1], and N. L. Bell[1], *[1]Texas A&M University Kingsville, Kingsville, [2]Texas A&M AgriLife Research, Beeville, [3]New Mexico State University, Las Cruces.*

The effect of including monensin in a protein supplement fed to cattle consuming low-quality forage is not well defined. The objective of this study was to evaluate the effects of monensin and protein supplementation on *in situ* disappearance kinetics of low-quality forage (LQF; 4.1% CP). Four cannulated cows were used in a 4 × 4 Latin Square design with treatments arranged as a 2 × 2 factorial: the first factor was monensin (0 or 200 $\text{mg}\cdot\text{hd}^{-1}\cdot\text{d}^{-1}$), and the second factor was protein supplement (0 or 0.64 $\text{kg}\cdot\text{hd}^{-1}\cdot\text{d}^{-1}$ CP provided as cottonseed meal; CSM). A premix (0.23 $\text{kg}\cdot\text{hd}^{-1}\cdot\text{d}^{-1}$) consisting of ground hay, cracked corn, molasses, salt, dicalcium phosphate, and a commercial mineral mix, was provided to all animals and allowed for monensin inclusion. Animals were individually housed and fed at 0600 h daily. Prior to sampling, 14 d were required to prevent carryover effects from previous monensin feeding. However, only 10 days of treatment adaptation was required for optimal monensin response. Thus, d 1 to 4 of each period, all animals were provided LQF with no treatment. Day 5 to 14 served as treatment adaptation, and sampling occurred d 15 to 20. Samples of LQF were weighed into 10- by 20-cm polyester bags in replicates of six for each hour. On d 15, bags were placed into the ventral area of rumen and replicates removed after 0, 4, 8, 16, 24, 48, 72, and 96 h of incubation. Upon removal from the rumen, bags were placed in ice water, rinsed, and then frozen until final bag removal. Bags were washed in a commercial washing machine and then dried at 55°C to a constant weight. Dried residues were analyzed for DM. In situ rumen DM degradation data were fitted to the first-order exponential model with discrete lag using the iterative Marquardt method and NLIN procedure of SAS 9.3. There was no interaction ($P \geq 0.16$) between protein and monensin for any DM disappearance parameters measured. Protein had a tendency ($P = 0.07$) to reduce potentially degradable DM (from 58.60 to 50.42%) likely due to the increased ($P \leq 0.01$) rate of DM degradation (from 1.87 to 4.76%/h) that it caused. Monensin had no effect ($P = 0.12$) on potentially degradable DM but increased ($P = 0.03$) rate of degradation from 3.06 to 3.57%/h. Protein or monensin supplementation had no effect on lag time or residue ($P \geq 0.11$). It is likely that the increased rate of degradation caused by protein and monensin will allow increased intake of LQF, thus improving its use in production operations.

Key Words: low-quality forage, monensin, protein
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126 Evaluation of protein supplementation on protein digestibility in beef cattle fed a low to medium quality forage diet.

C. M. Rawson*[1], J. R. Pukrop[1], S. Day[2], A. L. Jones[3], J. S. Luther[1], and A. E. Radunz[1], *[1]University of Wisconsin-River Falls, River Falls, [2]BioZyme, Inc., St. Joseph, MO, [3]University of Wisconsin-Madison, Madison.*

Four ruminally and duodenally fistulated steers (469 ± 37 kg initial BW) were housed individually and arranged in a 4 × 4 Latin square to evaluate protein digestibility in steers fed a low to medium quality forage in response to protein supplementation. Steers were fed a chopped grass hay ad libitum (8.3% CP, 64.9% NDF) twice daily, plus (1) high-fat dried corn distillers grains (HDG, 10.8% fat, 0.8% of BW), (2) low-fat dried corn distillers grains (LDG, 5.7% fat, 0.7% of BW), (3) cotton seed meal (CSM, 3.0% fat, 0.4% of BW), or no supplement (CON). Supplements were formulated to provide isonitrogenous intake and to increase post-ruminal ARG supply. Each 21-d experimental period had 16 d of adaptation and a 5-d collection period. From d 12 to 20, 8 g of chromic oxide was dosed ruminally twice daily at h 0 and h 12 via gelatin capsule for use as a digesta flow marker. Grab duodenal and fecal samples were collected over 3 d in a manner that allowed for digesta to be sampled every other h in a 24-h period. Protein supplementation resulted in greater ($P \leq 0.0027$) total OM and CP intake compared to CON. Intake of NDF was not different ($P = 0.43$) among treatments, whereas ADF intake was greater ($P \leq 0.0001$) for CSM vs. CON, LDG, and HDG. Fat intake was greatest ($P = 0.001$) for HDG and lowest for CON, and CSM and LDG were intermediate. Greater ($P \leq 0.014$) OM and CP duodenal flow rate was observed with protein supplementation vs. CON whereas differences were not ($P \geq 0.14$) observed for NDF and ADF. Duodenal flow rate was greater ($P = 0.005$) for TAA with protein supplementation vs. CON, and ARG duodenal flow rate was greatest ($P = 0.008$) with CSM, lowest for CON, and intermediate for HDG and LDG. Apparent total tract digestibility for OM and EE was greater ($P \leq 0.03$) with HDG, LDG, and CSM compared to CON, and NDF and ADF apparent total tract digestibility tended ($P \leq 0.07$) to be greater with protein supplements than CON. Apparent total tract digestibility of CP, TAA, and ARG was lower ($P \leq 0.02$) in CON than in protein-supplemented treatments. Post-ruminal supply of TAA and ARG was greater with vs. without protein supplementation. Overall fiber and protein digestibility improved with protein supplementation in low to medium quality forage diets.

Key Words: beef cattle, protein digestibility, protein supplementation
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127 Impact of two-stage weaning on calf growth parameters.

L. L. Seim*, P. L. Harrelson, and F. W. Harrelson, *Morehead State University, Morehead, KY.*

Removal of the dam and change in the source of nutrition at weaning results in increased stress and frustration for calves. In an effort to minimize stress, two-stage weaning may be utilized. An anti-suckling device is placed in the calf's nostrils 4 to 7 d prior to weaning based upon manufacturer recommended guidelines. Previous research involving the two-stage weaning method has shown calf weight loss prior to weaning. The objective of the study was to evaluate if the use of anti-suckling devices would impact calf growth when placed at 2 or 4 d prior to weaning. Data were collected over two years using registered Angus heifer and bull calves. Calves (n = 48 in yr 1 and n = 51 in yr 2) were utilized in a completely randomized design. Calves were stratified by weight and randomly assigned to 1 of 3 treatments: control (CON), 2 d with device prior to weaning (2D), or 4 d with device prior to weaning (4D). All calves were weaned using fenceline weaning on d 0. Calf growth performance were measured weekly from 7 d preweaning through 28 d postweaning. For the 28 d postweaning period, all calves were fed together in the same pen. Data were analyzed using the MIXED procedure of SAS with sex, treatment, and year as fixed effects. Corresponding interactions were also analyzed, but none were identified as significant. No differences ($P > 0.37$) were observed for any growth parameters based upon treatment. Sex significantly impacted ($P < 0.01$) calf weight, as bull calves were consistently heavier than heifers. Interestingly, no differences ($P = 0.84$) were observed between sexes in the preweaning period; however, during postweaning, bulls gained faster ($P < 0.01$) than heifers (1.26 kg/d vs. 1.00 kg/d, respectively). We also found that all calves in yr 2 grew at a significantly ($P < 0.01$) lower rate compared to yr 1 both pre- and postweaning. Results from this trial indicate that bull calves gain weight at a faster rate following weaning compared to heifers. Further, application of the two-stage weaning method with device placement at either 2 or 4 d prior to weaning does not impact calf growth rate.

Key Words: beef cattle, growth, weaning
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128 Flaxseed containing lipid supplement increases omega-3 content in bovine serum more than ground flaxseed.

R. Wilson*[1], S. Akers[1], K. Swanson[1], M. Keller[1], L. Goddik[1], G. Cherian[1], R. Day[2], and G. Bobe[3], [1]*Oregon State University, Corvallis,* [2]*N3Feed, Tualatin, OR,* [3]*Department of Animal and Rangeland Sciences, Oregon State University, Corvallis.*

The transfer efficiency of lipid supplements rich in PUFAs such as flaxseed into blood is often poor because PUFAs are hydrogenated in the rumen. To prevent ruminal biohydrogenation of PUFA, various methods of PUFA protection have been tested with limited success. In this study, a novel method to "rumen-protect" flaxseed is proposed, which encapsulates flaxseed using a proprietary method (12BT40; *N3*Feed® LLC; Tualatin, OR). To determine whether 12BT40 increases omega-3 concentrations in bovine serum more than its ingredients alone, we used a double 3 × 3 Latin square design; 6 mid- to late-lactation, pregnant Holstein cows (1 block each for primiparous and multiparous cows) were fed 0 kg/d (Negative Control), 3 kg/d of 12BT40 (Treatment), and 3 kg/d of the unprocessed ingredients of 12BT40 (Treatment Control) as top-dressing for 2-week periods each. Serum samples were collected at the end of each 2-week treatment period and analyzed for their fatty acid profile, respectively. Data were analyzed using PROC MIXED in SAS version 9.4. Fixed effects were treatment, period, and parity. Repeated measures within cows were modeled with the random statement. Compared with Treatment Control, 12BT40 increased total serum fatty acid concentrations from 148 ± 18 to 183 ± 18 μg/mL ($P = 0.03$) (Negative Control, 138 ± 18 μg/mL). 12BT40 supplementation increased serum omega-3 concentrations from 25.4 ± 2.9 μg/mL to 34.6 ± 2.9 μg/mL ($P = 0.01$) (Negative Control, 16.4 ± 2.9 μg/mL). Thus, we conclude that 12BT40 is effective in increasing total fatty acid concentrations and omega-3 concentrations in bovine serum beyond what can be achieved with feeding an equal amount of ground flaxseed.

Key Words: fatty acid profile, flaxseed, serum
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BEEF SPECIES

129 Maternal plane of nutrition during mid-gestation affects the skeletal muscle transcriptome in beef cattle progeny.

J. C. McCann*[1], T. B. Wilson[1], L. L. Guan[2], D. W. Shike[1], and J. J. Loor[1], [1]*Department of Animal Sciences, University of Illinois, Urbana,* [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The objective was to determine the effect of maternal nutrition management during mid-gestation on the skeletal muscle transcriptome in progeny using 3 dietary treatments. Spring-calving, multiparous cows (n = 25) were limit-fed a common diet at three levels of intake to achieve 70% NRC requirement (70%REQ; 5.2 kg DMI), 100% NRC energy and protein requirements (REQ; 7.4 kg DMI), and 130% NRC requirements (130%REQ; 9.7 kg DMI). Diet composition included soy hulls, corn silage, and alfalfa haylage. Treatment diets were fed during mid-gestation (d 88 to 171 of gestation), and a common diet formulated to meet 100% NRC requirements was fed during the remainder of gestation. After calving, all cows and calves were managed similarly as a single contemporary group. Longissimus muscle biopsies were taken on 99 and 392 d of age. Extracted RNA was used in paired-end RNA sequencing on the Illumina HiSeq 2500 platform to analyze the transcriptome at d 99 and 392. Transcriptomic data were mapped to the UMD3.1.1 bovine reference genome and analyzed using a mixed model approach within the R-package limma. Over 7,000 expressed genes were included in weighted gene co-expression network analysis (WGCNA), which clustered genes into 11 modules including 4 that correlated to phenotypic measures. The largest module included over 2,000 co-expressed genes and was downregulated ($P < 0.01$) in progeny born to 130%REQ-fed compared with REQ-fed dams. The Dynamic Impact Approach annotated genes within this module to KEGG pathways. The pathways most impacted by maternal plane of nutrition were mainly lipid-associated including steroid and steroid hormone biosynthesis, sulfur metabolism, retinol metabolism, ketone synthesis and degradation, fat digestion and absorption, and PPAR signaling pathways. Module 7 (342 genes) was correlated positively with Warner-Bratzler shear force and negatively with marbling score. Major pathways in module 7 centered on glycolysis/gluconeogenesis, energy metabolism, and calcium signaling. These genes and associated pathways support increased glycolytic muscle fibers (type 2x) in progeny born to 130%REQ-fed compared with 70%REQ-fed dams. Results indicate the skeletal muscle transcriptome and associated metabolic functions prior to slaughter are affected by mid-gestation maternal plane of nutrition and may be regulated by epigenetic factors.

Key Words: fetal programming, skeletal muscle, transcriptome
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130 Changes in feed intake, growth, feed efficiency, and body composition of beef cattle fed forage then concentrate diets.

A. P. Foote*, R. G. Tait, Jr., and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

The objective of this experiment was to determine changes in production traits and body composition of beef steers and heifers when fed a forage-based ration followed by a concentrate-based ration. Cattle were progeny of composite breed cows bred to Charolais, Simmental, and Red Angus bulls. Approximately 4 wks after weaning, steers (n = 71) and heifers (n = 79) were placed on a ration containing (DM basis) 69.8% corn silage, 30% alfalfa hay, and 0.2% salt. Feed intake was measured for 84 d, and BW were measured at 7 time points to calculate ADG using a quadratic regression of BW on time. Cattle were then transitioned to a concentrate-based finishing ration containing (DM basis) 67.8% dry-rolled corn, 20% wet distillers grains with solubles, 8% alfalfa hay, and 4.2% vitamin/mineral supplement. Data were analyzed using a mixed model (SAS) with sex, sire breed, dam breed, period (forage vs. concentrate), and sex × period as fixed factors, sire as a random variable, and period treated as a repeated variable. This allowed the calculation of correlations among residuals from within periods. Cattle consumed approximately 30% more DM on the concentrate ration compared to the forage ration ($P < 0.01$), and steers consumed about 10% more DM than heifers ($P < 0.01$). The residual correlation between forage and concentrate DMI was r = 0.51, indicating a positive association of DMI between the 2 rations. Regardless of sex, ADG was greater on the concentrate ration (0.9 vs. 2.1 kg/d; $P < 0.01$); however, the residual correlation was r = −0.09. The residual correlation coefficient for G:F was r = −0.17 and RFI was r = 0.38. Increase in LM area was greater for heifers ($P < 0.01$) and was greater during the concentrate ration feeding period ($P < 0.01$), and the residual correlation was r = −0.35. There was a sex × feeding period interaction for back fat change ($P < 0.01$), indicating that steers had a greater increase in fat thickness on the forage ration while heifers had a greater fat thickness increase on the concentrate ration. The residual correlation for back fat gain was r = −0.27. There was a sex × feeding period interaction ($P < 0.01$) for change in intramuscular fat (IMF), with steers gaining more IMF on the forage ration (0.50 vs. 0.33%) but heifers gaining more IMF on the concentrate ration (1.64 vs. 0.65%). Data indicate that there is correlation across different diets for feed intake and composition of growth traits in beef cattle. USDA is an equal opportunity provider and employer.

Key Words: feed efficiency, feed intake, growth
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131 Alteration in gene expression in the jejunum mucosa of Angus steers with divergent ADG.

A. P. Foote*, B. N. Keel, and A. K. Lindholm-Perry, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

The objective of this study was to determine the association of differentially expressed genes in the jejunum of steers with average DMI and high or low ADG. Feed intake and growth were measured in a cohort of 144 commercial Angus steers consuming a finishing ration containing (on a DM basis) 67.8% dry-rolled corn, 20% wet distillers grains with solubles, 8% alfalfa hay, and 4.2% vitamin/mineral supplement. From the cohort, a subset of steers with DMI within ± 0.32 SD of the mean for DMI and the greatest (high ADG) and least (low ADG) steers were chosen for slaughter and jejunum mucosa collection (*n* = 8 for each group). Dry matter intake (10.1 ± 0.05 kg/d) was not different ($P = 0.41$) but ADG was greater in the high gain group (1.72 and 2.17 ± 0.02 kg/d for the low and high ADG groups, respectively; $P < 0.01$). At slaughter, jejunal mucosa was collected and scraped and mRNA was isolated for sequencing. Differentially expressed genes (DEG) were identified using Tophat2/Cuffdiff software.

Gene ontology and pathway analyses were performed using the iPathwayGuide software. A total of 13,747 genes were found to be expressed in the jejunum, of which 64 genes were differentially expressed between the 2 groups (corrected $P < 0.05$). Ten of the genes were upregulated in the low ADG group, and 54 were upregulated in the high ADG group. Gene ontology analysis resulted in 24 biological process terms found to be over-represented ($P < 0.05$). Biological process terms included digestion, drug and xenobiotic metabolism, and carbohydrate metabolism. Additionally, 89 molecular function terms were found ($P < 0.05$) and included metallopeptidase activity, transporter activity, steroid hydrolase activity, glutathione transferase activity, and chemokine receptor binding. Metabolic pathways ($n = 28$) impacted ($P < 0.05$) by the DEG included drug and xenobiotic metabolism by cytochrome P450, carbohydrate digestion and absorption, vitamin digestion and absorption, galactose metabolism, linoleic acid metabolism, and mucin type O-glycan biosynthesis. Results from this experiment indicate that cattle with average DMI and greater ADG likely have a greater capacity to handle foreign substances. It is also possible that these cattle with a greater ADG have a greater number of transporters for vital nutrients, such as glucose and phosphate. USDA is an equal opportunity provider and employer.

Key Words: feed efficiency, gut physiology, RNA-seq
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132 Performance and carcass traits of Nellore and Nellore × Angus steers fed whole shelled corn diets.

M. M. Ladeira*[1], A. C. Rodrigues[1], P. V. R. Paulino[2], S. A. Ferreira[3], L. R. Santos[1], and T. C. Coelho[1], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]Nutron Alimentos Ltda, Campinas, Brazil, [3]IF Sudeste MG, Lavras, Brazil.*

Diets with a high proportion of concentrate or even diets without inclusion of forage began to be used on a larger scale in South American feedlots. Moreover, the number of Angus and Nellore crossbred steers is increasing in Brazil to produce better quality beef. Therefore, the objective of this study was to evaluate performance and carcass traits of Nellore and Nellore × Angus steers fed whole shelled corn diets. Thirty-two animals, with average BW of 353 ± 25.3 kg were housed in individual pens and used in a completely randomized design using a 2 × 2 factorial arrangement (2 breeds and 2 diets). One diet contained 80% whole shelled corn and 20% of a pellet based on soybean meal and minerals (WSC; 15.1% CP and 2.84 Mcal/kg of ME). The other diet had 74% whole shelled corn, 20% of the same protein-mineral pellet, and 6% of sugarcane bagasse (WSCB; 14.7% CP and 2.75 Mcal/kg of ME). Feeding period was 116 d, with 20 d of adaptation period and 96 d of experimental period. Steers were fed individually and initial and final weighing was measured after 16 h of fasting. At the end of the feedlot, steers were slaughtered using cerebral concussion and slitting of the jugular vein, and then carcass traits were measured. Statistical model included the effects of breed, diet, and breed × diet interaction. Nellore × Angus steers had greater DMI, ADG, LM area, and backfat thickness (BF; Table 132). However, Nellore steers had greater dressing percentage (DP; Table 132). Steers fed WSCB had greater DMI and tended to have greater ADG (Table 132). In conclusion, Angus × Nellore steers have greater ADG than Nellore, but they are not more efficient. The use of bagasse in WSC diets increases DMI and therefore ADG in feedlot steers. Funded by Fapemig and CNPq.

Key Words: *Bos indicus*, crossbred, feedlot
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Table 132. Performance and carcass traits of Nellore and Nellore × Angus steers fed whole shelled corn diets

	Nellore		Angus × Nellore			*P* value		
Item	WSC[1]	WSCB[2]	WSC	WSCB	SEM	Breed (B)	Diet (D)	B*D
DMI, kg	6.75	7.87	7.60	8.89	0.35	0.01	<0.01	0.82
ADG, kg day^{-1}	0.841	0.901	0.959	1.196	0.07	0.01	0.06	0.25
G:F	0.122	0.114	0.125	0.134	0.008	0.15	0.90	0.30
HCW, kg	246.18	246.44	247.25	253.87	6.90	0.53	0.61	0.64
LMA, cm^2	72.17	68.10	75.89	77.17	3.12	0.04	0.65	0.39
BF, mm	6.80	5.55	8.20	7.77	0.58	<0.01	0.15	0.48
DP, %	57.90	56.41	54.88	53.63	0.53	<0.01	0.01	0.82

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133 Effects of intermittent feeding of tylosin phosphate on feedlot performance, carcass characteristics, and incidence of liver abscesses in steers.

H. C. Muller*[1], R. G. Amachawadi[1], H. M. Scott[2], C. L. Van Bibber-Krueger[1], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]Texas A&M University, College Station.*

Liver abscesses (LA) are a source of economic loss in feedlot cattle, and tylosin phosphate historically has been fed to decrease LA incidence and severity. This study was conducted to evaluate intermittent feeding of tylosin phosphate as a strategy to decrease usage of a medically important antibiotic and to study impact on cattle performance and incidence of liver abscesses. Steers (n = 312; 411 ± 6.7 kg initial BW) were blocked by weight and randomly assigned, within block, to one of 3 treatments in a randomized complete block experiment. Treatments included no tylosin (NC), tylosin fed continuously (CT) at 10 g/T diet DM, and tylosin fed on an intermittent basis (IT; 1 wk on, 2 wk off). Steers were housed

Table 133.

Item	Treatment			SEM	P-value
	No Tylosin	Continuous Tylosin	Intermittent Tylosin		
ADG, kg	1.82	1.86	1.79	0.037	0.207
DMI, kg/d	10.88	11.20	10.85	0.236	0.278
Gain:feed	0.1673	0.1661	0.1650	0.0027	0.752
HCW, kg	380.3	383.1	380.3	7.58	0.512
USDA Choice + Prime, %	76.0	73.4	78.7	5.88	0.671
Total LA, %	21.4	7.8	9.6	4.65	0.012

in 24 dirt-surfaced pens with 13 steers/pen and fed once daily ad libitum. Finishing diets contained 57.7% steam-flaked corn, 30% wet corn gluten feed, 8% corn silage, and 2.3% supplement (DM basis) and supplied 33 g/T monensin and either 0 or 10 g/T tylosin. At the start of the trial, steers were weighed, vaccinated against clostridial and viral pathogens, treated with a topical parasiticide, and implanted with estradiol-trenbolone acetate implants. Steers were harvested after 119 d. No differences were observed among treatments for ADG, DMI, or feed efficiency ($P > 0.20$). Marbling score was lower for CT compared to IT and NC (Sm^{29}, Sm^{58}, and Sm^{55}, respectively; $P = 0.022$), but no other differences were observed for carcass traits ($P > 0.10$). Incidence of LA was greater for NC compared to IT and CT treatments ($P = 0.012$), but IT and CT were not different ($P > 0.50$). Intermittent feeding of tylosin decreases overall use of antibiotics in feedlot cattle without compromising cattle performance or incidence of liver abscesses.

Key Words: feedlot, intermittent feeding, liver abscess
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134 Effect of two-stage weaning duration on behavior in beef calves.

F. W. Harrelson* and P. L. Harrelson, *Morehead State University, Morehead, KY.*

In beef cattle, weaning is a stressful time for both the dam and calf. Calves experience physical separation from their dam and typically experience a change in diet. One recent method developed to counteract the stress of weaning is the two-stage weaning process. This procedure incorporates a nose flap which prevents suckling. Based on the recommendation from the manufacturer, it should be used for 4 to 7 d prior to separation from the dam. Previous research has shown that cattle weaned in this manner exhibit fewer stress-related behaviors. The objective of this study was to evaluate if nose flap placement 2 or 4 d prior to weaning would affect the behavior of beef calves. Data were collected over 2 consecutive years utilizing 48 registered Angus bull and heifer calves (256 ± 6 kg) in a completely randomized design. Calves were stratified by BW and randomly assigned to 1 of 3 treatments: control (CON), 2 d with nose flap prior to weaning (2D), or 4 d with nose flap prior to weaning (4D). All calves were subsequently weaned via fence-line weaning on d 0. Behavior observations were collected for 6 d pre- and post-weaning in 2-h blocks starting at 0730, 1200 (yr 1 only), and 1700 h. Activities observed were classified as eating (EA), suckling/attempting (SU), walking (WA), or inactive (IA) which included lying, standing, and ruminating. Individual observations were compiled into a percentage of the day spent doing each activity, and these were analyzed using the MIXED procedure of SAS. Analysis of EA resulted in a day × treatment interaction ($P < 0.01$), whereby prior to weaning, CON calves generally spent less time eating than either 2D or 4D but more time eating than 2D calves post-weaning. For IA, no interaction ($P > 0.27$) was present; however, there was a significant day effect ($P < 0.01$). Results for SU showed a day × treatment interaction ($P < 0.01$), as calves suckled/attempted to suckle less following application of treatment than CON calves. Similar to other activities, WA showed a day × treatment interaction ($P = 0.02$) in which CON calves spend a greater amount of time walking after weaning compared to 2D and 4D calves while spending less time walking pre-weaning. Results from the current study suggest that utilization of the two-stage weaning method may impact stress-associated behaviors often observed prior to and immediately following weaning.

Key Words: beef cattle, behavior, weaning
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135 Productivity measures in beef cows and calves following a single subcutaneous injection of long acting eprinomectin.

C. E. Andresen* and P. J. Gunn, *Department of Animal Science, Iowa State University, Ames.*

The objective of this study was to elucidate the effects of a single injection of long-acting eprinomectin on economically relevant production variables in beef cows and calves. Animals from 13 cooperator herds across 7 states were stratified within herd by cow age, calf birth date, calf birth BW, and calf sex and assigned to 1 of 2 treatments: injectable doramectin (DOR; Dectomax, Zoetis, Animal Health, Parsippany, NJ; n = 756) or injectable eprinomectin (EPR; Longrange, Merial, Duluth, GA; n = 770) at a rate of 1 cc/50 kg. Average duration between treatment and the end of the grazing season was 133 ± 36 d. Fecal samples were randomly collected from 20 cows from 4 cooperator herds and consisted of both spring- and fall-calving herds. Fecal samples were collected at treatment and again at the end of the grazing season to evaluate fecal egg count (FEC). Continuous and categorical data were analyzed using the MIXED and GLIMMIX procedures of SAS, respectively. Cow treatment BW and end of grazing season BW were not different ($P = 0.32$) between treatments. However, there was a treatment × season interaction for both cow change in BW ($P = 0.05$) and percent change in BW ($P = 0.08$), as spring-calving EPR cows tended to have greater increases in BW over the course of the treatment period. Initial and final BCS did not differ between treatments ($P = 0.76$). While FEC at treatment did not differ (DOR = 2.60; EPR = 2.75; $P = 0.86$), cows treated with EPR had less FEC at the end of the treatment period (DOR = 2.03; EPR = 0.71; $P = 0.03$) and tended to have a greater reduction of FEC over the course of the grazing season ($P = 0.08$). Calf treatment BW, weaning BW, and ADG did not differ between treatments ($P = 0.49$). Calves treated with DOR had a tendency ($P = 0.08$) for a lesser incidence of pinkeye. Incidence of pinkeye tended to be less ($P = 0.06$) for cows treated with EPR. Fly counts were not different between treatments ($P = 0.14$). Pregnancy rates and expected calving interval based on ultrasound were not different between treatments ($P = 0.25$). Lack of differences observed in the current study may likely be a function of low fecal egg counts in participating herds. As part of this ongoing study, calving interval, calf feedlot, and carcass performance will be assessed.

Key Words: anthelmintic, fecal egg count, pregnancy
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136 Administration of recombinant bovine somatotropin prior to fixed-time artificial insemination and the effects on pregnancy rates and conceptus development in beef heifers.

N. Oosthuizen*[1], P. L. P. Fontes[1], D. D. Henry[1], C. D. Sanford[1], F. M. Ciriaco[1], L. B. Canal[1], N. DiLorenzo[1], V. R. G. Mercadante[2], and G. C. Lamb[3], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]Virginia Tech, Animal and Poultry Sciences, Blacksburg, [3]Department of Animal Science, Texas A&M University, College Station.*

To determine the effects of recombinant bovine somatotropin (bST; sometribove zinc, Posilac, Elanco Animal Health, Indianapolis, IN) administration at the initiation of a fixed-time artificial insemination (TAI) protocol on pregnancy rates and conceptus development in replacement beef heifers, 412 *Bos taurus* beef heifers were enrolled in a complete randomized design at 4 locations from January to July of 2016. All heifers were exposed to the 7-day CO-Synch + CIDR protocol where they received a 100-µg injection of GnRH (Factrel; gonadorelin hydrochloride; Zoetis Animal Health) and a controlled internal drug releasing (EAZI-BREED CIDR; 1.38 g of progesterone; Zoetis Animal Health) insert on d −9, heifers received 25 mg of $PGF_{2\alpha}$ (Lutalyse; dinoprost tromethamine; Zoetis Animal Health) at CIDR removal on d −2, followed by a 100-µg injection of GnRH and TAI 54 ± 2 h later on d 0. Within location, all heifers were randomly assigned to one of two treatments: (1) BST (n = 191), heifers received 650 mg bST on d −9; or (2) CONTROL (n = 223), heifers received no bST on d −9. Blood samples were collected on d −9, −2, 0, 28, and 60 to determine concentrations of IGF-1. Pregnancy was diagnosed via transrectal ultrasonography on d 28 and 60 after TAI by determining the presence of a viable fetus. Conceptus development was assessed by measuring crown to rump length (CRL) on d 28 at the time of pregnancy diagnosis. Concentrations of IGF-1 were similar ($P > 0.05$) between treatments on d −9, 28, and 60; however, concentrations of IGF-1 were greater ($P < 0.001$) in bST-treated heifers at TAI (372.4 vs. 193.7 ng/ml). Pregnancy rates to TAI (PR/AI) were greater ($P = 0.028$) in CONTROL compared with BST heifers (42.5 vs. 29.9%). Overall breeding season pregnancy rates did not differ ($P = 0.967$) between treatments. No differences ($P = 0.668$) in CRL (8.8 ± 1.7 mm) were determined on d 28 between CONTROL and BST heifers. Administration of bST at the initiation of a TAI protocol increased IGF-1 concentrations at TAI, failed to increase embryo size, but decreased PR/AI.

Key Words: beef heifers, fixed-time artificial insemination, recombinant bovine somatotropin
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137 Effect of a single dose of long acting eprinomectin on bull reproductive performance.

C. E. Andresen* and P. J. Gunn, *Department of Animal Science, Iowa State University, Ames.*

The objective was to examine the effects of a single injection of long-acting eprinomectin on performance parameters and semen quality of reproductively-active bulls. To study these effects, 11 bulls were allocated by breeding group and assigned to one of two treatments: injectable doramectin (DOR; Dectomax™, Zoetis, Animal Health, Parsippany, NJ; n = 6; BW = 833 ± 60 kg) or injectable eprinomectin (EPR; Longrange™, Merial, Duluth, GA; n = 5; BW = 783 ± 73 kg) at a dosage rate of 1 mL/50 kg of BW. At time of treatment, initial BW, BCS, and fecal samples were taken and a breeding soundness exam (BSE) was conducted. The BSE included a general health and locomotion evaluation, assessment of scrotal tone (ST), scrotal circumference (SC), external palpation of sex organs (scrotum, testes, and epididymis), internal palpation of accessory sex glands, visual assessment of penis and prepuce, and collection of a semen sample via electroejaculation. A drop of ejaculate was placed on two warmed slides, one of which received a cover slip in order to assess progressive motility and the other stained with Eosin-Nigrosin for assessment of morphology. Morphological abnormalities were classified as primary or secondary and broken down by head, proximal droplet, distal droplet, and tail defects. Following a 46-d breeding season, final BW, BCS, and fecal samples were taken and BSE were again conducted. Results were analyzed using PROC MIXED of SAS. Initial and final BW and BCS did not differ between treatments ($P > 0.18$). Change in BW, BCS, and ADG during treatment period were also not different between groups ($P > 0.32$). No differences ($P > 0.18$) in motility, ST, or SC were noted between treatments. No differences in sperm morphology were noted between treatments. While there was a tendency ($P = 0.07$) for EPR bulls to have a greater reduction in fecal egg count over the course of the treatment period, this is mostly a function of EPR bulls tending ($P = 0.06$) to have a greater internal parasite load at treatment administration (DOR = 2.72; EPR = 19.72 eggs/g). Overall, use of long acting eprinomectin for internal parasite control did not have a negative impact on sperm quality and bull fertility over the course of the breeding season. While limitations in observational units are acknowledged, data from this study suggest that a single injection of long acting eprinomectin is not detrimental to bull reproductive function.

Key Words: anthelmintic, fecal egg count, fertility
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138 Analysis of serial vaginal temperature measurements in crossbred beef cattle grazing novel or toxic fescue.

S. Chewning*[1], D. A. Koltes[1,2], J. G. Powell[1], L. R. Meyer[1], J. D. Tucker[1,3], D. S. Hubbell, III[1,3], J. J. Chewning[4], and J. E. Koltes[1], [1]*Department of Animal Science, University of Arkansas, Fayetteville,* [2]*Department of Poultry Science, Division of Agriculture, University of Arkansas, Fayetteville,* [3]*University of Arkansas, Division of Agriculture Livestock and Forestry Research Station, Batesville,* [4]*Swine Research Services, Inc., Springdale, AR.*

Fescue toxicosis causes hyperthermia, reduced hair shedding, decreased weight gain, and reproductive success in cattle. The objective of this study was to determine if grazing toxic vs. novel (non-toxic) fescue changed the heating and cooling cycles during hot weather. An equal number (N = 50) of animals were grazed on novel or toxic fescue for 6 mo (March through August) as part of a larger trial examining chronic effects of toxic fescue. Half of the animals on toxic and half on novel were given access to a pond. All animals had shade access. Pastures were monitored monthly for toxic levels of ergot valine mycotoxins (>300 ppb). In early August, intravaginal devices containing an iButton thermosensor were placed in each cow to measure vaginal temperatures every 5 min for 1 wk (max THI > 100/day). Data from only 5 d were analyzed to exclude the impact of animal handling stress on body temperature. One pasture was excluded due to toxic fescue contamination. In addition, intravaginal devices from 3 animals were lost on pasture during the trial. A total of 71 cows were analyzed from 1 of 3 remaining pasture treatments, including: toxic no pond (TF-NP; n = 26), toxic with pond (TF-P; n = 23), and novel with pond (NF-P; n = 22). Temperatures were averaged by hour each day for each animal. Vaginal temperature was analyzed using a repeated measures model with Proc Mixed of SAS, including pasture treatment, breed (Charolais, Hereford), hide color (black, red, white, smoke), parity (2,3, 4), day, hour of the day, treatment-by-hour, treatment-by-sire, and treatment-by-sire-by-hour interactions. Hours within a day were fit as repeated. All variables in the model were significant ($P < 0.002$). Animals on NF-P were 0.15°C warmer than animals on TF-P ($P < 0.0001$) and 0.06°C cooler than animals on TF-NP ($P < 0.0001$). Animals grazing TF-P were 0.18°C cooler than those with no pond access ($P < 0.0001$). Hours of the day showed significant difference in hour of day-by-treatment interaction ($P < 0.0001$). Additionally, NF-P appear cooler than TF-P from 7 to 11 AM, while TF-P showed decreasing temperatures during some of the hottest times of the day (3 to 10 PM). A significant breed-by-treatment interaction was identified, indicating that Charolais cattle on TF-P were significantly hotter than Herefords on the same pasture after 3 PM ($P < 0.0001$). This study indicates that toxic fescue increases body temperature even during cool morning hours, though ponds may reduce body temperature. Additional studies are needed to determine impact on hair shedding, weight gain, and grazing time.

Key Words: cattle, fescue, serial temperature measurements
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139 Zinc injection as a novel castration method in beef bulls: effects on performance, behavior and testosterone and haptoglobin concentration.

J. J. Ball*[1], J. T. Richeson[2], E. B. Kegley[1], T. E. Lawrence[2], S. L. Roberts[2], and J. G. Powell[1], [1]*Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville,* [2]*West Texas A&M University, Canyon.*

One hundred and eighty bulls (BW = 337 ± 10.9 kg) were blocked by BW (6 blocks) and assigned randomly to 1 of 3 treatments on d 0: (1) INJ [received 1 mL (100 mg Zn) of a Zn solution in each testis], (2) BAN (received blood-restrictive rubber band placed upon the dorsal aspect of the scrotum), or (3) BUL (bulls with testicles remaining intact) in a randomized complete block design (3 pens/block and 10 cattle/pen). A random subset of 54 animals (n = 3/pen) were fitted with accelerometers on d 0 for 28 d. The subset also had testis width and scrotal circumference determined and were bled via jugular venipuncture to assess serum haptoglobin and testosterone concentrations every 28 d until slaughter. At slaughter, INJ and BUL were castrated at chain speed to assess final testes weight and for histopathological evaluation. Data were analyzed using PROC MIXED with an alpha of 0.05, and pen served as the experimental unit for all dependent variables. Final BW was greater in INJ and BUL compared to BAN cattle ($P < 0.01$). Overall ADG and G:F were greater ($P \leq 0.03$) in INJ and BUL than BAN; whereas, DMI was similar between treatments for the study duration ($P = 0.46$). Histopathological results (n = 13; INJ = 7; BUL = 6) indicated that INJ testes were degenerative and not viable while BUL testes were normal. Final serum testosterone concentrations on d 168 were similar ($P = 0.14$) between INJ and BUL, while after d 14, BAN were non-detectable. Serum haptoglobin concentration was greater in INJ than BUL and BAN on d 1, 3, 5, and 7 ($P < 0.01$). Scrotal circumference ($P = 0.08$) and testis width ($P = 0.07$) on d 168 tended to be greater in BUL compared to INJ. Motion index was greater in BUL and INJ compared to BAN

cattle during the d 0 to 28 monitoring period ($P \leq 0.02$). There were no differences in standing or lying time ($P \geq 0.85$) or lying bouts ($P = 0.35$); however, step count was greater ($P = 0.04$) in BUL and INJ. The injection of Zn appeared to cause sterilization but did not cause complete cessation of testicular function as evidenced by testosterone concentration more similar to BUL than BAN. This resulted in increased BW and G:F compared to BAN, yet the acute phase response was markedly greater directly after injection.

Key Words: castration, injectable castration, zinc
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140 The combination of ß-carotene and vitamins improves the pregnancy rate at fixed time artificial insemination (FTAI) in grazing beef cows.

M. H. A. Colli[1], W. A. Gonçales Junior[1], J. C. Motta[1], V. N. D. Gouvea*[2], T. S. Acedo[2], L. F. M. Tamassia[2], F. M. Ellif[1], R. D. Mingoti[1], and P. S. Baruselli[1], [1]*Universidade de Sao Paulo, Sao Paulo, Brazil,* [2]*DSM Produtos Nutricionais Brasil SA, Sao Paulo, Brazil.*

This experiment was conducted in a commercial beef farm located in Rio Brilhante, MS, Brazil during the spring/summer breeding season (September to October 2016). A total of 430 suckled multiparous beef cows (Nellore; *Bos indicus*, 417.2 ± 57.9 kg) were used. Cows were maintained on 4 paddocks of *Brachiaria brizantha* with ad libitum access to water. At the beginning of the trial (30 d before the first timed-AI), animals were assigned according to calving date, stratified by BCS (mean of 2.5 ± 0.5, 1 to 5 scale) and ß-carotene blood concentration (mean of 4.2 ± 1.8 mg/L), and randomly assigned to treatments: Control (mineral supplement: no ß-carotene nor vitamins) and Treated (combination of 500 mg ß-carotene, 70,000 IU Vit. A, 10,000 IU Vit. D3, 500 mg Vit. E, and 10 mg biotin/cow/d in the mineral supplement). The mineral supplement (8% Na; 30% TDN; 35% CP; 22.5% NPN) was daily offered to the animals in collective feeders at an amount of 200 g/cow/d. The ß-carotene, vitamins, and minerals used were from DSM® Produtos Nutricionais Brasil SA. Cows were rotated through the paddocks every 8 d to avoid effects related to pasture amount and quality. Animals were synchronized using an estradiol/progesterone-based timed-AI protocol: d 0, insertion of the progesterone device and 2.0 mg of estradiol benzoate i.m.; d 9, treatment with 0.15 mg of PGF2α analogue (D-cloprostenol), 300 IU eCG, and 1.0-mg estradiol cypionate i.m., and the intravaginal progesterone device was removed; d 11, FTAI. Blood samples were collected at the beginning of the experiment and at the moment of the FTAI. Serum ß-carotene was quantified using portable photometer (iCheck®; BioAnalyt, GmbH, Teltow, Germany). Data were analyzed using the GLIMMIX 9.3 procedure of SAS. The conception rate at FTAI was greater ($P = 0.04$) in cows supplemented with ß-carotene and vitamins (66.6%; 142/213) than control group (57.6%; 125/217). The blood ß-carotene concentration at the beginning of the experiment was 4.2 ± 1.7 mg/L for the control group and 4.3 ± 2.0 ng/mL for the ß-carotene and vitamins group ($P > 0.05$). At FTAI, the blood ß-carotene concentration was 5.1 ± 1.5 mg/L for the control group and 4.8 ± 1.5 mg/L for treated cows ($P > 0.05$). In conclusion, despite no difference in blood ß-carotene concentration, feeding grazing beef cows with the combination of ß-carotene and vitamins A, D, E, and biotin in the mineral supplement increased conception rate to timed-AI by 15.6%.

Key Words: fertility, mineral, pasture
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141 Effect of method of breeding and season on pregnancy rate, cumulative embryonic and fetal losses in lactating Nili-Ravi buffalo.

N. Ahmad*, A. Qayyum, and U. Arshad, *Department of Theriogenology, University of Veterinary and Animal Sciences, Lahore, Pakistan.*

Buffalo reproductive efficiency is challenging due to seasonal anestrus, lowered fertility, and higher embryonic losses. Basic information on reproductive norms is generally lacking in buffalo. The objective of this study was to determine the effect of method of breeding and season on pregnancy rate and cumulative embryonic and fetal losses in Nili-Ravi buffalo. Buffalo (n = 130) ranging from 4 to 8 years of age, having 350 to 550 kg body weight and 60 to 200 days post-partum were enrolled in this study. Oestrus detection was performed twice a day by an apronized teaser buffalo bull for one hour each. A 2 × 2 factorial design was used to address method of breeding and season. Buffalo (n = 130) exhibiting oestrus along with the presence of a large sized (>12 mm) follicle were randomly assigned to be bred either in peak breeding season (PBS; n = 80) or low breeding season (LBS; n = 50). Within each season, buffalo were divided to receive either natural service (NS; n = 65) or artificial insemination (AI; n = 65). For natural service, a buffalo, in oestrus, was allowed to remain with the bull until mating. Artificial insemination was achieved using the frozen thawed semen of a bull of known fertility, 24 hours after the onset of standing oestrus. PBS comprised of September to December, and LBS were from May to July. Serial ultrasonography was done on Day 30, 45, 60, and 90 after breeding (Day 0) to monitor pregnancy rate, embryonic mortality, and fetal losses. Results revealed that the pregnancy rate when determined on Day 30 after breeding was higher in NS as compared to the AI group (63% vs. 43%; $P < 0.05$) during PBS while it did not differ (48% vs. 32%; $P > 0.05$) in LBS. The cumulative embryonic and fetal losses between Day 31 and 90 were significantly lower in PBS than LBS (33% vs. 60%; $P < 0.05$), ignoring breeding method. In conclusion, pregnancy rates were better with natural service in peak breeding season, and cumulative embryonic fetal losses were higher in low breeding season in Nili-Ravi buffalo. It is implied that this base line information can help in devising

strategies to improve reproduction in buffalo. **[Editor: Please check < and > signs in this abstract, as abnormal coding (< and >) was originally used throughout.   was also used but was deleted as it appeared only between complete sentences (perhaps to indicate a space).]**

Key Words: breeding method and season, Nili-Ravi buffalo, pregnancy rate
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143 Price differences due to preconditioning of beef calves compared to traditional marking in Alabama from 2012-2016.

F. W. Abrahamsen*, A. W. Elliott, N. K. Gurung, B. R. Min, and W. H. McElhenney, *Tuskegee University, Tuskegee, AL.*

Preconditioning has potential to bring higher economic returns for cow-calf producers from feeder calves if preconditioning is cost-effective. The objective of this study was to find out the price differences between traditional marketing and value added marketing (preconditioning or board sales) of beef calves in Alabama from 2012 to 2016. The sales data were collected from the USDA-AMS (Agricultural Marketing Services) field office at Montgomery, Alabama for both traditional marketing (auctions) and value added marketing. There were 20 locations for traditional marketing while board sales data were collected from 3 locations. Of the total calf sales, only 23% of calves were sold through board sales. Sales data were collected from 585 lots (farmers) representing 118,125 head of calves sold between January 2012 and December 2016 at different auctions and board sales. The data consisted of auction types, gender, muscle scores, and average weight (range, 250 kg to 386 kg), but the breeds of feeder calves were not considered. Data were analyzed by the General Linear Model Procedures of SAS to determine the price difference associated with sales type including all variables listed above. However, the economic values of preconditioning were not determined. The analyzed data showed that beef calf prices differed significantly ($P < 0.05$) between market types (auction vs. board sales), years, gender, muscle scores, and average weights. The overall yearly averages were $121.48, 137.40, 211.32, 206.37, and 126.52 for 45.4 kg live weights for years 2012, 2013, 2014, 2015, and 2016, respectively. Steers sold at board sales with an average body weight of 250 kg brought $32/45.4 kg more than those sold traditionally at the same body weight, but the difference narrowed as body weight increased to 318 kg body weight with a difference of only $21.44/45.4 kg. When values for market types (auction and board sales) were combined, the values for muscle scores were $164.25, 168.02, 158.99, and 151.19 for 1, 1 and 2 combined, 2, and 3 muscle scores, respectively. Similarly, the values for gender were $157.60, 156.11, and 168.13 for bulls, heifers, and steers, respectively. The year 2014 was the best year for beef calf prices in Alabama regardless of auction types. The results of this study suggest that there are price differences between the traditional marketing and board sales (preconditioning) of calves; however, the net profits due to auction types need to be investigated further to demonstrate the economic benefits of preconditioning calves.

Key Words: beef calves, preconditioning, price differences
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144 A meta-analytical approach to evaluate the relative effectiveness of virginiamycin for veal calf performance is maximized after ten weeks of administration.

M. A. Gorocica*[1] and L. O. Tedeschi[2], [1]*Phibro Animal Health, Teaneck, NJ,* [2]*Texas A&M University, College Station.*

The objective of this analysis was to evaluate the growth performance and feed conversion ratio (FCR) of veal calves receiving 80 mg/kg DM of virginiamycin (Vmax) alone or in combination with 50 mg/kg DM of furazolidone for up to 18 wk of life. Eight studies that were conducted in the Netherlands (five studies, n = 901 calves), Mexico (one study, n = 47 calves), and Czech Republic (two studies, n = 30 calves) evaluated the impact of different timing and length of administration of treatments (TRT). The statistical model had TRT as the fixed effect and the period of administration of the TRT (PHASE: initial, final, whole) within studies as the random effect. The number of calves in the pens was used as a weight variable in the PROC GLIMMIX of SAS. For multiple comparisons, the LSMEANS and PDIFF statements were used, and different subscript letters indicate statistical difference at $P < 0.05$. The unadjusted ADG for Vmax plus furazolidone and Vmax alone were 40 and 32.8% greater than the control group (1.084, 1.028, and 0.774 kg/d, respectively). When ADG was adjusted for the effect of the random variable phase within the study, Vmax plus furazolidone and Vmax alone had greater ADG than the control group (1.045^{a}, 1.026^{a}, 0.918^{b}, respectively; $P < 0.05$). When we analyzed the ADG adjustment for phase within study, relative to the average ADG, the relative adjustments for ADG during the early period of medication (initial phase; less than 10 wk) were negative (down to −0.4 kg/d) whereas for the later period of medication (final phase; greater than 10 wk) they were positive (up to 0.3 kg/d). When we regressed the relative adjustment of ADG for phase within study on length of medication using the *lm* of R, the quadratic response ($R^2 = 0.5$; N = 16; $P = 0.0198$) indicated the maximum relative adjustment of ADG occurred at 14 wk of medication with Vmax alone, though greater ADG adjustments were observed between 10 and 12.5 wk of medication. There was no TRT effect on FCR ($P = 0.3736$), and veal calves that received Vmax had greater feed intake than control ones (1.56 versus 1.46 kg/d, respectively; $P < 0.001$). Vmax alone or in combination with furazolidone enhanced ADG of veal calves. Longer administration of the medication (at least 10 wk) seems to be beneficial, with a maximum increase on ADG at 14 wk of medication.

Key Words: calves, growth, virginiamycin
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145 A meta-analytical approach to evaluate the performance of cattle fed virginiamycin or monensin under feedlot conditions from seven European countries.

M. A. Gorocica*[1] and L. O. Tedeschi[2], [1]*Phibro Animal Health, Teaneck, NJ,* [2]*Texas A&M University, College Station.*

This meta-analysis evaluated the growth performance of feedlot cattle fed virginiamycin (Vmax) or monensin (MON) in Europe. Twelve trials from seven European countries (Spain, Belgium, UK, Italy, Ireland, Germany, and France) conducted prior to 1999 were selected. Vmax dosage varied from 74 to 210 mg/hd/d with a median of 150 mg/hd/d and MON ranged from 150 to 210 mg/hd/d with a median of 150 mg/hd/d. Not all trials had complete data, and the analysis was conducted with the average data representing 763 animals distributed among control (CON, n = 150), Vmax (n = 347), and MON (n = 266) treatments. The PROC GLIMMIX and PROC MIXED of SAS were used to analyze the random coefficients model in which treatment (CON, Vmax, or MON) was the only fixed effect and study was the random effect. Pen was the experimental unit, and the number of animals per treatment within study was used in the WEIGHT statement. For multiple comparisons, the LSMEANS and PDIFF statements were used. Initial BW and dose were tested as covariates and removed from the statistical model if not significant ($P < 0.10$). The variation of ADG for CON animals was almost two times greater than for MON- and Vmax-treated animals. The ADG adjusted for study effect were 1.279, 1.336, and 1.361 kg/d for CON, MON, and Vmax, respectively ($P = 0.08$). Animals receiving Vmax had a greater ADG than CON animals ($P = 0.03$) but not different from monensin ($P = 0.25$). However, when adjusted for dose ($P = 0.03$), Vmax had significantly greater ADG ($P = 0.02$) than MON (1.355 vs. 1.288 kg/d, respectively) at the mean dose (123 mg/hd/d). Nonetheless, caution should be used when interpreting this result because their optimum dosage might differ. Despite a lower FCR of Vmax compared to MON (6.56 vs. 7.87, respectively), neither DMI ($P = 0.93$) nor FCR ($P = 0.17$) were different among treatments. We concluded that under European feedlot conditions, after adjusting for study effect, there is evidence that Vmax might increase ADG compared to CON (1.361 vs. 1.336 kg/d, respectively; $P = 0.03$). Furthermore, when compared with MON at the same dose (mg/an/d), Vmax significantly increased ADG without affecting DMI or FCR.

Key Words: feedlot, growth, virginiamycin
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146 EPNIX® and liver abscess treatment effects on the performance, health, and carcass characteristics of feedlot steers.

V. B. Holder*[1], B. P. Holland[2], and A. B. Word[2,3], [1]*Alltech Inc, Nicholasville, KY,* [2]*Cactus Feeders, Amarillo, TX,* [3]*Texas Tech University, Lubbock.*

A trial was conducted using 3,360 crossbred beef steers in 48 pens to evaluate the effects of feeding EPNIX® products (Alltech Inc.) on the growth performance, carcass characteristics, and health outcomes of feedlot steers. Four treatments were evaluated: (1) control (CON+MT), standard commercial feedlot ration including monensin and tylosin; (2) EPNIX® without monensin and tylosin (EPNIX); (3) EPNIX® with the inclusion of monensin and tylosin (EPNIX+MT); and (4) EPNIX® 2 without monensin and tylosin (EPNIX 2). The base finishing diet was similar between treatments and included steam-flaked corn, wet corn gluten feed, wet distillers grains with solubles, and chopped corn stalks. Data were analyzed as a randomized complete block design in the GLM procedure of Minitab 17. Dry matter intake and live performance were not different between treatment groups ($P \geq 0.174$), although final BW tended to be greatest in the EPNIX+MT and EPNIX 2 treatments compared to CON+MT and EPNIX when dead and removed steers were included (651.0 and 647.9 kg vs. 645.1 and 639.7 kg, respectively; $P = 0.059$). Additionally, when dead and removed steers were included, feed efficiency was improved in the CON+MT, EPNIX+MT, and EPNIX 2 treatments compared to EPNIX (6.00, 5.97, and 6.10 vs. 6.22, respectively; $P = 0.046$). Digestive-related deaths were greatest in EPNIX and least in EPNIX+MT (0.95% vs. 0.12%; $P = 0.043$). Contrasts revealed that inclusion of EPNIX increased HCW ($P = 0.031$). Dressing percentage was greatest in EPNIX and EPNIX 2 and least in CON+MT and EPNIX+MT (64.7 or 64.8% vs. 64.5 or 64.6%, respectively; $P = 0.002$). A greater percentage of carcasses were graded Choice for CON+MT and EPNIX+MT treatments than for EPNIX or EPNIX 2 (74 or 73% vs. 66 or 68%, respectively; $P < 0.001$). Total liver abscesses were greatest in EPNIX and EPNIX 2 treatments compared to CON+MT or EPNIX+MT (24 or 19% vs. 14 or 10%, respectively; $P < 0.001$), although EPNIX 2 had tended to have fewer abscesses than EPNIX ($P < 0.1$). These data indicate that EPNIX® inclusion in finishing diets increased HCW, improved carcass transfer, and had the greatest effect on the prevention of digestive disorders and liver abscesses when fed in combination with monensin and tylosin.

Key Words: antibiotics, carcass, liver
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147 Efficiency measures and feedlot performance of growing buffaloes (*Bubalus bubalis*).

F. M. Silva[1], A. M. Castilhos[1], P. R. L. Meirelles[1], D. C. M. Silva[1], H. L. Correa[1], A. S. Aranha[1], M. A. Paschoa[1], B. C. Agustinho[2], P. A. C. Luz[1], L. M. Zeoula[2], C. L. Francisco[1], and A. M. Jorge*[1], [1]*Universidade Estadual Paulista - FMVZ, Botucatu, Brazil,* [2]*Universidade Estadual de Maringá - UEM, Maringá, Brazil.*

Identifying animals that stand out in efficiency and performance is important for animal production; therefore, the purpose of this study was to evaluate efficiency measures, feedlot performance, and ultrasound measures of water buffaloes (*Bubalus bubalis*). The data were collected during 84 d from 75 animals (non-castrated; 314 ± 117 kg of initial BW and 390 ± 58 dof age) of 3 genetic groups (GG; n = 25 for each: Jafarabadi, Mediterranean, and Murrah). The animals were allocated into 3 feedlot pens by GG. Total mixed ration (30:70 corn silage:concentrate) and water were offered in automated feeding and water stations (Intergado®, MG, Brazil). Individual DMI was recorded daily, and ADG was calculated from the difference of final and initial BW divided by 84 d. Data were analyzed using the MIXED procedure (SAS Inst. Inc., Cary, NC), and the statistical model included the fixed effect of GG. Jafarabadi group had greater values for final BW (473.47, 423.54, 418.76 kg for Jafarabadi, Mediterranean, and Murrah, respectively; $P = 0.03$), ADG (1.72, 1.41, 1.34 kg for Jafarabadi, Mediterranean, and Murrah, respectively; $P < 0.01$), and hip height (1.36, 1.29, 1.28 m for Jafarabadi, Mediterranean, and Murrah, respectively; $P < 0.01$), and no differences were observed between Mediterranean and Murrah groups. Dry matter intake did not differ ($P > 0.28$) among GG. However, group effects were detected for G:F (0.20, 0.17, 0.16 kg/kg for Jafarabadi, Mediterranean, and Murrah, respectively; $P < 0.01$), residual feed intake (−0.40, 0.12, 0.13 kg of DMI/d for Jafarabadi, Mediterranean, and Murrah, respectively; $P = 0.01$), residual gain (0.22, −0.05, −0.08 kg/d for Jafarabadi, Mediterranean, and Murrah, respectively; $P < 0.01$), and residual intake and gain (0.48, −0.17, 0.11 for Jafarabadi, Mediterranean, and Murrah, respectively; $P = 0.01$), which were all greater for the Jafarabadi group whereas no differences were found between Mediterranean and Murrah groups. The Jafarabadi and Murrah groups differ from the Mediterranean group for ribeye area (49.04, 43.73, 48.09 cm^2 for Jafarabadi, Mediterranean, and Murrah, respectively; $P = 0.03$) and rump fat thickness (7.88, 6.10, 7.64 mm for Jafarabadi, Mediterranean, and Murrah, respectively; $P = 0.03$). No group effect was observed ($P = 0.14$) for backfat thickness. In conclusion, the results indicate that the genetic group has an effect on efficiency measures and feedlot performance of water buffaloes. The Jafarabadi group had greater values for feed efficiency measures and feedlot performance. Supported by FAPESP #2014/05473-7 and #2015/04542-8.

Key Words: digestibility, feed efficiency, water buffaloes
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148 Use of infrared thermography to evaluate the residual feed intake in water buffaloes.

D. C. M. Silva, C. L. Francisco, A. M. Castilhos, F. M. Silva, H. L. Correa, A. S. Aranha, A. A. Longuini, P. A. C. Luz, P. R. L. Meirelles, and A. M. Jorge*, *Universidade Estadual Paulista - FMVZ, Botucatu, Brazil.*

The aim of this study was to evaluate the use of infrared thermography and the relationship with residual feed intake (RFI) in water buffaloes of three genetic groups during the growth phase in feedlot. Sixty-five water buffaloes of 3 genetics groups (Jafarabadi, Mediterranean, and Murrah, non-castrated male; 10 ± 1 mo of age; 314 ± 117 kg initial BW) were allocated in collective pens for 28 d of adaptation and 84 d of data collection. Diet was composed of corn silage (30%) and concentrate based on corn grain, cottonseed meal, mineral salt, urea, and calcitic limestone (70%). Total mixed ration was offered daily by automatic feeding system (Intergado®, MG, Brazil) to assess individual feed intake. Residual feed intake was determined as the difference between the observed and predicted feed intake of the animal based on its metabolic BW and ADG over 84 d. Animals were classified into Low (<0.5 SD mean), Medium (within ±0.5 SD), and High (>0.5 SD mean) RFI groups. Infrared thermography images were collected at a distance of approximately 1.5 m from regions of the animal's body (eye, face, ribs, scrotum, forelegs, brisket) using an infrared thermographic camera and analyzed by software (Testo 882, thermal imager software IRSoft). Data were analyzed with MIXED procedure (SAS, Inst. Inc., Cary, NC) with RFI group as fixed effect of the model. No group effects were detected ($P > 0.05$) for eye, face, ribs, scrotum, and forelegs. Only the brisket showed group effect ($P = 0.02$). Estimated brisket temperature of the Low RFI group was lower (29.14 ± 0.43°C) than those of the High and Medium groups of RFI (30.33 ± 0.43°C vs. 29.97 ± 0.43°C, respectively). In conclusion, these results provide evidence of the relationship between thermal images of brisket and feed efficiency in growing water buffaloes under tropical conditions. Furthermore, it is important to note that the brisket is a region of prominent fat deposition in water buffalo and additional studies within this subject are warranted. Supported by FAPESP #2014/05473-7.

Key Words: infrared thermography, residual feed intake, water buffaloes
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149 Quantitative carcass characteristics of water buffaloes: a great option for meat producers.

A. S. Aranha[1], C. L. Francisco[1], A. M. Castilhos[1], M. H. M. P. Narciso[1], F. M. Silva[1], H. L. Correa[1], D. C. M. Silva[1], P. A. C. Luz[1], C. Andrighetto[2], P. R. L. Meirelles[1], and A. M. Jorge*[1], [1]*Universidade Estadual Paulista - FMVZ, Botucatu, Brazil,* [2]*Universidade Estadual Paulista - UNESP, Dracena, Brazil.*

The objective of this study was to evaluate potential differences among carcass characteristics of water buffaloes (*Bubalus bubalis*) of 3 genetic groups (Jafarabadi, Mediterranean, and Murrah) and to demonstrate the potential of the species for meat production. Seventy-five animals (n = 25 animals of each genetic group) were finished on feedlot and slaughtered at 587 ± 58 d of age. Diet was offered as total mixed ration (30:70 corn silage:concentrate). After slaughter, total blood and gastrointestinal tract (with and without contents) were weighted to determine the empty body weight (EBW). The half-carcasses were weighted to obtain values HCW and hot carcass yield (HCY). Fat in the abdominal cavity (KPH) was collected and weighted, and the results were expressed as kilograms (KPH) and as percentage of HCW (KPH%). The carcasses were chilled at 0°C for 24 hours. After chilling, measure of the rib fat thickness (RFT; *Longissimus* muscle; 12th to 13th ribs) was recorded. The carcass length was collected to calculate the carcass index (CI = weight/length; $kg.cm^{-1}$). The hindquarter proportion (HQP, %) and the carcass edible portion (CEP, %) were calculated and expressed as percentage of carcass weight. Data were analyzed with MIXED procedure (SAS Inst. Inc., Cary, NC) and Satterthwaite approximation to determine the denominator degrees of freedom for the tests of fixed effects. The animal was considered the experimental unit. The model statement included genetic groups (GG) as fixed effect. No GG effects were detected for EBW ($P = 0.20$), HCW ($P = 0.44$), KPH ($P = 0.42$), KPH% ($P = 0.48$), HQP ($P = 0.44$), CEP ($P = 0.42$), and CI ($P = 0.11$). There was a difference among the three GG for HCY (50.93%, 49.89%, 49.07% for Murrah, Jafarabadi, and Mediterranean, respectively; $P < 0.01$). The Murrah group showed a greater value for RFT ($P < 0.01$), whereas the others GG did not differ (10.17 mm, 6.86 mm, 5.81 mm for Murrah, Mediterranean, and Jafarabadi, respectively; $P > 0.10$). In conclusion, the animals from the Murrah genetic group presented better carcass characteristics compared to the animals of the genetic groups Jafarabadi and Mediterranean. However, the 3 genetic groups of water buffaloes have great potential for meat production. Supported by FAPESP #2014/05473-7.

Key Words: carcass, hot carcass yield, water buffaloes
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150 Efficiency measures and feedlot performance of water buffaloes for meat production.

A. M. Castilhos, C. L. Francisco, P. R. L. Meirelles, H. L. Correa, A. S. Aranha, F. M. Silva, D. C. M. Silva, C. M. Pariz, P. A. C. Luz, and A. M. Jorge*, *Universidade Estadual Paulista - FMVZ, Botucatu, Brazil.*

There is an increasing interest in the use of measures of efficiency as a tool to improve the profitability of producers; however, in water buffaloes, this measure is still unknown. The objective of this study was to compare growth performance with measures of efficiency in 75 non-castrated male buffalos (314 ± 117 kg BW and 390 ± 58 d of age) of 3 genetic groups (GG): Jafarabadi (n = 25), Mediterranean (n = 25), and Murrah (n = 25). Dry matter intake was recorded using an automated feeding system (Intergado®, MG, Brazil) for 84 d. The measures of efficiency (EF) evaluated were residual feed intake (RFI) and residual BW gain (RG). The animals were classified for each EF into Low (<0.5 SD mean) and High (>0.5 SD mean) groups, and then High and Low groups were compared using Proc MIXED (SAS) with GG and EF groups as fixed effects. The performance traits were ADG, DMI, final BW, and carcass characteristics evaluated by ultrasound [ribeye area and backfat thickness (BF); 12th-rib]. There was no interaction ($P > 0.10$) between GG and EF groups. High and Low groups had similar ($P > 0.41$) initial and final BW and ultrasound measures for all EF. As expected, RFI groups did not differ for ADG ($P = 0.68$); however, RFI group effect was detected for DMI ($P = 0.02$). For the RG groups, the behavior was the reverse; it did not differ for DMI ($P = 0.91$) but differed for ADG ($P < 0.01$). The EF measures (G:F, RFI, RG)

Table 150.

	RFI				RG			
Traits	High	Low	SEM	*P*	High	Low	SEM	*P*
Initial BW, kg	313.13	324.99	22.51	0.60	313.11	331.61	22.39	0.41
Final BW, kg	432.41	447.73	24.92	0.54	453.65	437.91	24.39	0.52
Ribeye area, cm^2	42.18	43.16	2.15	0.65	43.74	42.25	2.16	0.49
Backfat thickness, mm	5.47	5.09	0.55	0.49	5.39	5.83	0.58	0.45
ADG, kg/d	1.42	1.46	0.10	0.68	1.67	1.27	0.09	<0.01
DMI, kg/d	8.75	7.67	0.45	0.02	8.43	8.38	0.48	0.91
G:F, kg/kg	0.16	0.19	0.01	<0.001	0.20	0.15	0.01	<0.01
RFI, kg/d	0.55	−0.81	0.09	<0.001	−0.49	0.36	0.16	<0.01
RG, kg/d	−0.14	0.15	0.04	<0.001	0.20	−0.22	0.03	<0.01

differed ($P < 0.05$) for all divergent groups. In conclusion, the RFI and RG demonstrated high phenotypic variability, did not alter the characteristics of the carcass assessed by ultrasound, and have potential to be included in selection programs for water buffalos. Supported by FAPESP #2014/05473-7.

Key Words: residual body weight gain, residual intake and body weight gain, water buffaloes
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151 Apparent diet digestibility and morphometric measurements of ruminal papillae of water buffaloes finished in feedlot.

H. L. Correa, P. R. L. Meirelles, F. M. Silva, D. C. M. Silva, A. S. Aranha, M. A. Paschoa, M. H. M. P. Narciso, A. A. Longuini, P. A. C. Luz, A. M. Castilhos, C. L. Francisco, and A. M. Jorge*, *Universidade Estadual Paulista - FMVZ, Botucatu, Brazil.*

The objective of this study was to evaluate the relationship between parameters of apparent diet digestibility and morphometric measurements of ruminal papillae of water buffaloes (*Bubalus bubalis*) finished in feedlot. Sixty-five non-castrated males (BW and mean age of 314 ± 117 kg and 390 ± 58 d, respectively) were used. The animals were allocated in collective pens and received a diet based on corn silage (30%), milled grain (53.19%), cotton meal (12.99%), urea (0.76%), calcitic lime (0.75%), and mineral salt (2.24%). Diets were offered in an automatic feeder system (Intergado®, MG, Brazil) with ad libitum access. Animal DMI and ADG were recorded. In order to estimate the apparent digestibility of nutrients (DM, CP, NDF, ADF, TDN, and OM), fecal collection was used to calculate fecal excretion from the internal indigestible neutral detergent fiber marker (iNDF). A fragment (1 cm², approximately) of each rumen from cranial sac (atrium ruminis) was collected for the study of macroscopic morphological variables, such as number of papillae (NOP; n/cm² of rumen wall); papillae surface area (PSA; mm^2); papillae width (W); papillae length (L); absorptive surface area (ASA; cm^2/cm^2 of rumen wall) calculated as follows: $[1 + (NOP \times PSA) - (NOP \times 0.002)]$; and proportion of the papillae on absorptive surface (PPAS; %) calculated as follows: $[(NOP \times PSA/ASA) \times 100]$. Data were obtained from captures and analysis of the images by software (Image J, National Institutes of Health, Bethesda, MD, USA). Subsequently, data were analyzed with PROC CORR (SAS, Inst. Inc., Cary, NC). There were associations among the nutrient digestibilities ($P < 0.05$) with ASA, PPAS, and W, except to W and DigCP ($P > 0.05$). Relationships were observed ($P < 0.05$) among papillae length, ADG, and DMI. The relationship between papillary morphometric characteristics and nutrient digestibility illustrates the efficiency of water buffaloes in the utilization of the feed. Supported by FAPESP #2014/05473-7 and #2016/01109-4.

Key Words: digestibility, ruminal papillae, water buffaloes
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Table 151.

	NOP	PSA	ASA	PPAS	HEIGHT	WIDTH	LENGTH
DM digestibility	−0.14	−0.24**	−0.37*	−0.29*	−0.14	−0.29*	−0.09
CP digestibility	−0.15	−0.16	−0.32*	−0.27*	−0.12	−0.20	−0.06
NDF digestibility	−0.12	−0.23**	−0.35*	−0.32*	−0.13	−0.32*	−0.04
ADF digestibility	−0.07	−0.23**	−0.35*	−0.33*	−0.16	−0.28*	0.04
TDN digestibility	−0.10	−0.23**	−0.34*	−0.24*	−0.12	−0.29*	−0.08
OM digestibility	−0.13	−0.23**	−0.35*	−0.27*	−0.13	−0.29*	−0.13
ADG	−0,13	−0.06	−0.21**	−0.20	−0.12	0.01	0.29*
DMI	−0.11	−0.002	−0.08	−0.10	0.04	−0.09	0.48*

$^*P < 0.05$, $^{**}P < 0.10$

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152 Effects of frequency of supplementation during peri and postpartum of grazing primiparous Nellore cows.

F. H. de Moura*[1,2], M. Fonseca[1], M. F. Paulino[2], M. M. Lopes[2], and M. S. Duarte[2], *[1]University of Nevada, Reno, [2]Universidade Federal de Viçosa, Viçosa, Brazil*

The goal of this study was to evaluate the effects of supplementation frequency during pre (105 d from parturition) and postpartum (105 d from parturition) of Nellore primiparous cows on performance and physiological responses. Twenty-five pregnant heifers with an average BW of 408 ± 2 kg and 172 ± 2 d of gestation were used in this trial. Animals were housed in 6 paddocks with full access to water, and stocking rate was defined on the basis of potentially digestible DM availability (DMpd). Evaluated treatments were: control (ad libitum mineral mix); daily supplementation (1.5 kg of concentrate/animal); and supplementation every 3 d (4.5 kg of concentrate/animal). Two 9-d digestibility trials were performed at 55 d before parturition and 55 d after parturition. Plasma concentrations of glucose, IGF-1, NEFA, and beta-hydroxybutyrate (BHB) were used as indicators of energy state and collected at 27 and 9 d before parturition, on the day of parturition, and 9 and 27 d after parturition. The response variables were analyzed using PROC MIXED in SAS 9.4 (SAS Inst., Cary, NC) assuming a completely randomized design with 3 treatments and 2 replicates per treatments. Treatment was considered a fixed effect whereas treatment within paddock was considered random. The DMpd observed during the experiment for pre and postpartum was 4.4 t/ha and 2.9 t/ha, respectively, which

corresponded to the momentary mean availability of 78.6 and 52.9 g/kg BW. The DMI was not affected by supplementation frequency during peripartum (*P* > 0.10) or postpartum (*P* > 0.10). The supplementation frequency did not affect BW at 10 d before parturition (*P* > 0.10) or at 105 d after parturition (*P* > 0.10). Glucose concentration was affected by supplementation frequency (72.27 vs. 65.62 mg/dL for pre and postpartum respectively; *P* < 0.10). Most likely, daily supplementation reduces oscillation and increases circulating concentrations of glucose. Circulating concentrations of IGF-1 (206 vs. 222 vs. 201 ng/mL for pre and postpartum respectively; *P* > 0.10), NEFA (0.21 vs. 0.23 vs. 0.18 mmol/L for pre and postpartum respectively; *P* > 0.10), and BHB (0.45 vs. 0.52 vs. 0.45 mmol/L for pre and postpartum respectively; *P* > 0.10) did not differ among treatments. The forage availability associated with lack of supplementation frequency effect on intake may have contributed to no changes in performance and physiological responses. These results suggest that when there is non-restriction on forage availability, supplementation frequency during pre and postpartum does not affect performance or physiological responses of primiparous Nellore cows.

Key Words: metabolism, periparturient,
supplementation frequency
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153 Cryoprotectant effect of different antioxidants added to bovine sperm.

J. M. Valdez-Torres*[1], M. E. Burrola-Barraza[1], J. A. Grado Ahuir[1], J. Antillon-Ruiz[1], B. Sanchez-Ramirez[1], N. Hernandez-Parra[2], and H. Hernandez-Cano[1], *[1]Universidad Autónoma de Chihuahua, Chihuahua, Mexico, [2]Union Ganadera Regional de Chihuahua, Chihuahua, Mexico.*

The cryopreservation-thawing process of bovine sperm is associated with generation of elevated amounts of reactive oxygen species (ROS). These ROS cause harmful effects on sperm. Therefore, the objective of this study was to evaluate the cryoprotectant potential effects of cysteine (CYS), caffeine (CAF), ascorbic acid (AA), and *Rhus trilobata* plant extract (RT) added to extender for cryopreservation of bull semen on post-thawed semen traits. Semen from six bulls (5 Angus, 1 Charolais) was obtained, and each ejaculate was diluted to a final concentration of 40 × 10^6 spermatozoa per mL and divided into five equal aliquots corresponding to each of the treatments: Control (CT), CYS (2 mM/ml), CAF (5 mM/ml), AA (4.5 mg/ml), and RT (16.6 µg/ml). Samples were packed in 0.5-mL straws and frozen in liquid nitrogen and then thawed for evaluation. Cellular viability (VIT) was assessed through nigrosin eosin smears. A hypo-osmotic swelling test (HOST) was used to assess the functional integrity of the sperm membrane. Computer-assisted sperm analysis (CASA) systems were used to measure motility parameters: spermatic motility (%, MT) and progressive motility (%, MP) as well as spermatic kinematics: average path distance (DAP, µm), curved line distance (DCL, µm), straight line distance (DSL, µm), average path velocity (VAP, µm/s), straight line velocity (VSL, µm/s), curvilinear velocity (VCL, µm/s), straightness (%, STR), linearity (%, LIN), wobble (%, WOB), amplitude of the lateral head displacement (ALH, µm), and frequency of head displacement (BCF, Hz). Data were analyzed using the MIXED procedure of SAS, with a model including treatment as a fixed effect and bull as a random effect. Results indicated that the addition of RT extract to the extender for cryopreservation of bull semen preserves better the viability and integrity of the sperm membrane compared to the other treatments (*P* < 0.05). The MT and MP were improved (*P* < 0.05) with RT treatment compared to the other groups. The characteristics of spermatic kinematics DAP, DSL, DCL, VAP, VSL, VCL, and BCF were affected in a positive way (*P* < 0.05) by the addition of RT and CAF treatments in comparison with CT, CYS, and AA. In contrast, no statistical difference (*P* > 0.05) was observed between the different treatments. In conclusion, our results indicate that the addition of RT to the extender for cryopreservation of bull semen allows better preservation of both the cellular characteristics and the motility parameters of post-thawed bovine sperm.

Key Words: antioxidant, bovine sperm,
cryopreservation
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154 Effect of sperm dose on pregnancy per timed AI in Brazilian beef cattle.

S. Menegatti Zoca*[1], B. Shafii[1], W. Price[1], M. D. Utt[2], L. H. Cruppe[2], M. DeJarnette[2], L. D. Peters[2], J. L. M. Vasconcelos[3], and J. Dalton[4], *[1]University of Idaho, Moscow, [2]Select Sires Inc, Plain City, OH, [3]Sao Paulo State University, Botucatu, Brazil, [4]University of Idaho, Caldwell.*

The objective of this study was to determine if beef bull fertility varied with the dose of sperm used for insemination. Pregnancy per timed AI (P/TAI) of bulls was investigated in large Brazilian beef herds. Ejaculates were collected from 5 Angus bulls by artificial vagina and diluted to 10, 20, 20, or 40 × 10^6 sperm per straw in a milk-based extender. Each sperm dose was loaded into color-coded 0.5-mL straws (colors were alternated within bull among treatments), cryopreserved, and stored in liquid nitrogen. Use of two 20 × 10^6 sperm per straw treatments was an attempt to illustrate the potential impact of random variation, as these treatments differed only in straw color. Beef cows (n = 5,290) on 11 farms were synchronized for TAI using an intravaginal progesterone device-based protocol and were randomly assigned to treatments. Each bull (dose combination) was represented in each farm, with farm personnel blind to treatments. Bull identification and straw color were recorded at the time of AI. The proportion pregnant were analyzed using generalized linear mixed models to estimate the fixed effects of bull, dose, and the bull by dose

Table 154. Pregnancy per timed AI (P/TAI) for 5 Angus bulls

Bull	n	P/TAI, %	SEM
A	1,148	46.8^{a}	1.94
B	1,136	47.7^{a}	1.95
C	1,301	39.5^{c}	1.83
D	807	45.6^{ab}	2.18
E	898	42.3^{bc}	2.06

[a,b,c] Means within the same column not sharing a common superscript are different, $P < 0.05$.

interaction. Farms were considered as a random blocking effect. Means were compared using pairwise comparisons. No interaction between bull and sperm dose was detected ($P = 0.56$). The P/TAI was different between bulls ($P < 0.05$: Table 154). No effect of sperm dose on P/TAI was revealed (43%, 45%, 43%, and 46.5% for 10, 20, 20, and 40×10^6 sperm dosages, respectively; $P = 0.22$). The numeric range in P/TAI between the two control doses (20×10^6 sperm per straw) was 0.3 (Bull E; 434 total doses; 44.3% vs. 44.6%) to 6.4 percentage points (Bull D; 415 total doses; 47.2% vs. 40.8%), providing evidence that the potential impact of random variation cannot be ignored. In conclusion, fertility differences (P/TAI) between bulls were detected (Table 154); however, dose per straw (10, 20, and 40×10^6 sperm) did not impact P/TAI.

Key Words: bull, fertility, sperm dose
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155 Repeatability of number of progeny born to bulls used in group mating of cows.

G. L. Bennett*, R. G. Tait, Jr., L. A. Kuehn, W. M. Snelling, and T. G. McDaneld, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

The group mating of bulls in pasture situations is a management practice that might be more efficient if an individual bull's ability to sire calves could be predicted. Retrospective data on numbers of progeny born to bulls from 4 populations (Angus and 3 composite breeds) in 4 consecutive years of spring calving were used to estimate repeatability of number of calves born per bull per season. Data only included bulls and cows 2 yr of age and older. Bulls were mated in cohort groups of 5 to 11 (median = 9) bulls assigned to 17 groups of 65 to 267 (median = 214) cows. The median ratio of cows to bulls was 22.8 (range = 10.8 to 26.0). The breeding season was 60 to 63 d for 3 yr and 49 d for the last year. Only bulls that remained in breeding pastures for the entire season were used for data analysis. Of these, 19 bulls were used in each of 2 populations and 20 were used in each of the other 2. Thirty-eight bulls were used for a single season, 23 were used for 2 consecutive seasons, 12 were used for 3 seasons, and 5 were used for all 4 years. Parentage was determined by SNP genotyping. Ten bulls sired 0, 1, or 2 calves in a breeding season, 11 sired 42 to 56 calves in a season, and the median number was 17. Variances for number of calves and square root of number of calves sired by a bull in a season were estimated from a mixed model with bull as the random effect and mating group (confounded with year and population) as fixed effects. Repeatability was the ratio of bull variance to bull plus residual variance. Repeatability estimates were 0.62 for number and 0.60 for square root of number using all populations in a single analysis. Estimates ranged from 0.39 to 0.86 for number and 0.36 to 0.86 for square root of number when estimated within population. Number of calves sired by bulls used in groups of up to 11 bulls in one breeding season is a good indicator of the number sired in a subsequent season if bull health and fitness are not factors.

Key Words: cattle, group mating, repeatability
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156 Relationships between DMI fluctuation and feeding behavior at the beginning and end of the finishing phase in feedlot cattle.

J. C. McCann*[1], L. M. Shoup[2], M. D. Miller[3], G. E. Carstens[4], and D. W. Shike[1], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]University of Illinois, Urbana, [3]Texas A&M University, College Station, [4]Department of Animal Science, Texas A&M University, College Station.*

The objectives of this study were to (1) determine the relationships between daily individual DMI fluctuation and feeding behavior at the beginning and end of the finishing phase and (2) determine the ability of feeding behavior traits and DMI fluctuation during the initial 28 d to predict overall growth performance. Over 2 yr, calf-fed, crossbred Angus steers (n = 222) were fed on similar finishing diets within a year. Individual DMI and feeding behavior traits were recorded using the GrowSafe (Airdrie, AB) system. At the beginning and end of the finishing phase, 28 d were selected for characterization of DMI fluctuation and 10 feeding behavior traits. Daily fluctuation in DMI was calculated for each steer as the percent of days where DMI variation exceeded 30% from the DMI of the previous day. Non-feeding interval frequency (NFIF) at the beginning and end of the finishing phase was correlated ($r = 0.50$; $P < 0.001$). Bunk visit duration (BVDUR) and meal size at the beginning and end of the finishing phase were also repeatable ($r = 0.80$; $P < 0.001$ and $r = 0.35$; $P < 0.001$, respectively). Variation in meal intake and head-down duration expressed as the SD of each at the beginning and end of the finishing phase was correlated ($r = 0.36$; $P < 0.001$ and $r = 0.38$; $P < 0.001$, respectively). Meal size variation was not associated with fluctuation in DMI during the beginning of the finishing phase ($P = 0.60$), suggesting they are independent measures of feeding behavior. Meal size and variation in head-down duration were the most strongly correlated ($r = 0.26$; $P < 0.001$ and $r = 0.28$; $P < 0.001$, respectively) traits with ADG over the entire finishing phase. During the early finishing phase, BVDUR was the most correlated trait with G:F ($r = 0.25$; $P < 0.001$). Stepwise regression selected 4 feeding behaviors traits (meal size SD, DMI fluctuation, head-down duration SD, and NFIF; $P < 0.05$) in the beginning of the finishing phase that were able to predict 19% of the variation in ADG during the entire finishing phase. Overall, data suggest some feeding behaviors are highly repeatable during the finishing phase and may increase their utility for making management decisions or in cattle selection.

Key Words: feeding behavior, feedlot,
intake fluctuation
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157 Accounting for backfat thickness on the prediction of residual feed intake of young beef bulls influences its relationship to breeding soundness examination traits.

J. Antillon-Ruiz*, J. J. Molina-Cardenas, F. A. Rodríguez-Almeida, and M. E. Burrola-Barraza, *Universidad Autónoma de Chihuahua, Chihuahua, Mexico.*

During the last decade, there have been great efforts to improve feed efficiency in beef cattle. Although, the use of residual feed intake (RFI) as an indicator of net feed efficiency has been the measurement of choice, there are still some concerns about potential antagonistic related effects on reproductive traits, such as age at puberty and fertility traits in young animals. The objective of this study was to examine the relationship between two alternative RFI measures and breeding soundness examination traits in Angus young bulls. Twenty-five animals were examined at the end of a 70-d feed efficiency performance test for sperm concentration (SPC) and percentages of motile spermatozoa (PM), progressive motility (PPM), and normal spermatozoa fraction (NSF). The semen sample was obtained by the electroejaculation method and analyzed by the computer-assisted sperm analysis (CASA) system. The backfat thickness (BFT) was measured using an Aloka 500 ultrasound with a 17-cm linear transducer. The images were taken by a certified technician and then sent to the Centralized Ultrasound Processing Lab (CUP) for interpretation. The two RFI measures were: RFI_{Koch}, computed as the residuals from linear regression of DMI on mid-test body weight ($BW^{0.75}$) and ADG; and RFI_{fat}, which included the additional adjustment for BFT. Animals were classified into those with the greatest (least efficient, n = 8), intermediate (n = 9), and least (most efficient, n = 8) RFI values. Two separate one-way ANOVA were performed to evaluate the class effects of feed efficiency as determined by RFI_{Koch} or RFI_{fat}. For significant ANOVA results, a Tukey's range test was run for means comparisons of efficiency groups. Under the RFI_{Koch} classification, SPC and NSF tended to be greater ($P = 0.10$) for the least efficient group (418.2 ± 97.9 millions/ml and 89.6 ± 3.0%) than for the intermediate (146.2 ± 92.3 millions/ml and 80 ± 2.8%) and most efficient (245.8 ± 97.9 millions/ml and 83.2 ± 3.0%) groups. Those differences disappeared when accounting for BFT under the RFI_{fat} classification. We concluded that inclusion of backfat in the model to predict RFI for feed efficiency evaluation statistically eliminates its antagonistic relationship with breeding soundness examination traits in young Angus bulls, but the study of potential biological implications deserves further research efforts.

Key Words: beef cattle, feed efficiency,
reproductive traits
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158 Effects of an AI plastic sheath with three semen outputs on AI pregnancy rates of beef heifers enrolled in estrus synchronization protocols.

C. L. Timlin*[1], N. W. Dias[1], J. F. Currin[2], S. Clark[2], and V. R. G. Mercadante[1], [1]*Virginia Tech, Animal and Poultry Sciences, Blacksburg,* [2]*Virginia-Maryland Regional College of Veterinary Medicine, Blacksburg.*

We determined whether a newly designed AI plastic sheath with three outputs for semen deposition would reduce semen reflux into the sheath and increase pregnancy rates of beef females enrolled in estrus synchronization protocols. A total of 881 Angus and Angus crossed beef heifers (13 ± 1.5 m of age) at 7 different locations were enrolled in this study. Heifers from locations 1, 2, 4, and 5 were enrolled in the 14-day+CIDR-PG estrus synchronization protocol, and heifers from locations 3, 6, and 7 were enrolled in the 7-day CO-Synch+CIDR estrus synchronization protocol. Individual BCS were determined 2 d (locations 3, 6, and 7) and 3 d (locations 1, 2, 4, and 5) prior to AI. Within location, heifers were stratified by BCS and randomly assigned to two treatments: (1) fixed-time AI using an AI plastic sheath with three semen outputs (Tri; n = 440) or (2) fixed-time AI using an AI plastic sheath with a single semen output (Single; n = 441). After each insemination, the AI plastic sheaths were examined for signs of semen reflux into the sheath. Pregnancy data were analyzed using GLIMMIX procedure of SAS with heifers as the experimental unit, including the fixed effects of treatment, location, BCS, and random effects of sire and AI technician. Heifer BCS differed ($P < 0.001$) among locations but was similar ($P = 0.606$) between treatments (5.5 ± 0.03) and no treatment × location interaction was detected ($P = 0.647$). Pregnancy rate was similar ($P = 0.696$) between treatments (52.9 ± 0.02% and 54.4 ± 0.02%, for Single and Tri heifers, respectively). There was a location effect ($P < 0.001$) on pregnancy rate, ranging from 43.4% to 68.6%, and no treatment × location interaction was detected ($P = 0.352$). There was a difference ($P < 0.001$) between AI sheaths on percentage of sheaths with signs of semen reflux after insemination (13.8 vs. 4.8 ± 0.01% for Single and Tri AI sheaths, respectively). However, signs of reflux in the AI sheath were not correlated ($P = 0.7225$; R = 0.0001) with pregnancy outcome. We conclude that the AI plastic sheath with three semen outputs decreased the percentage of

AI sheaths with signs of semen reflux but failed to increase fixed-time AI pregnancy rates of beef heifers.

Key Words: AI sheath, artificial insemination, fixed-time AI
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159 The effect of fescue toxicosis on semen quality and fertility of young growing beef bulls.

S. L. Pratt*[1], C. Burnett[1], N. M. Long[1], F. N. Schrick[2], and G. S. Sell[1], [1]*Clemson University, Clemson, SC,* [2]*University of Tennessee, Knoxville, Knoxville.*

The objective of this study was to evaluate semen quality and fertility in young growing beef bulls grazing the ergot alkaloid (EA) producing tall fescue cultivar Kentucky 31 (KY31) compared to a novel endophyte cultivar lacking EA (NE). Angus bulls (n = 54 over 2 yr, 12 to 16 mo of age) were stratified by BW, BCS, and scrotal circumference (SC) and then allotted to graze either KY31 or NE for 56 d. Bulls were subjected to venipuncture and electroejaculation at the start of treatment (TRT; d 0) and every 28 d to the end of the study. Semen was evaluated for quality and blood samples harvested for use in prolactin (PRL) RIA. Bull BW, BCS, and SC were measured on d 0, 28, and 56. On d 56, semen from bulls (n = 4 per treatment) with similar and acceptable quality was extended, kept at 19°C, and used for artificial insemination within 30 h of collection. Angus and Angus crossbred females were stratified by age, calving date, BCS and BW and allotted to be timed inseminated (TAI) with KY31 (n = 78) or NE (n = 73) semen. Pregnancy was evaluated 30 d post-timed insemination via transrectal ultrasound to determine TAI pregnancy rates. Bull BW, BCS, serum PRL concentration, and all semen quality parameters were subjected to analysis using JMP (SAS Institute, Cary, NC) with the LS Means procedure to test for effects of TRT, day, and TRT × day interactions. Serum PRL concentrations showed a TRT × day effect ($P = 0.001$) with values for bulls grazing KY31 decreased at 28 and 56 d of grazing compared to NE. Bull BW and BCS were affected by d ($P = 0.001$). Neither the ejaculate volume, sperm concentration, nor sperm velocity differed due to TRT. Both percent motile sperm ($P = 0.03$) and progressively motile sperm ($P = 0.04$) were lower in the KY31 at d 0 compared to the other TRT × day combinations; however, no difference was observed in the percentage of bulls passing a breeding soundness exam due to TRT. Timed AI pregnancy rates were 46 and 43% for KY31 and NE, respectively ($P = 0.655$). Grazing KY31 negatively impacts serum PRL concentrations and supports previous observations; however, consuming KY31 had no effect on growth, semen quality, or fertility of young growing beef bulls.

Key Words: artificial insemination, breeding soundness exam, fescue toxicosis
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160 Breeding soundness evaluations of beef bulls at approximately 14 and 20 months of age developed on forage.

S. L. Pratt* and G. S. Sell, *Clemson University, Clemson, SC.*

The objective of this study was to determine the percentages of forage-fed bulls passing a breeding soundness exam (BSE) at two different ages (14 and 20 mo). Thirty-six bulls representing 5 breeds completed the 168 d Clemson University Edisto Forage Bull Test and were consigned for sale 332 d from the start of test. The bulls consigned fell into senior (Sr) and junior (Jr) divisions based on birth date and were developed on forage without any type of supplementation. Bulls were weighed, scrotal circumference measured, and semen collected at 13.6 ± 0.5 and 14.8 ± 0.6 mo of age (BSE 1) and at 19.4 ± 0.5 and 20.9 ± 0.6 mo of age (BSE 2) for Jr and Sr bulls, respectively. Percent motile sperm and sperm morphology were assessed, with the number of normal sperm and sperm with cytoplasmic droplets, mid-piece or tail, or head abnormalities recorded. Statistical analyses were conducted using LS mean procedures (SAS Institute, Cary, NC), with division, age at BSE, and their interaction as main effects. Means were compared using Student *t*-test. Chi square analysis was used to evaluate significance for the percentage of bulls passing at BSE 1 or 2. Scrotal circumference was lower at BSE 1 compared to the BSE 2 (33.8 ± 0.4 and 37.6 ± 0.4 cm, respectively; $P = 0.0001$); however, no difference in SC was observed for bull division or division by age at BSE interaction. There was a significant division by age at BSE interaction for the percentage motile sperm, with the highest motility observed for the Jr bulls at BSE 1 compared to all other observations ($P = 0.04$). Age at BSE significantly impacted sperm morphology, as the number of normal heads increased (77 ± 2.1 compared to 83.6 ± 2.1% for BSE 1 and 2, respectively; $P = 0.03$) and the number of cytoplasmic droplets decreased (10.9 ± 1.7 and 2.7 ± 1.7%, for BSE 1 and 2, respectively; $P = 0.001$) at BSE 2. A numerically higher number of bulls failed a BSE at BSE 1 than BSE 2 (83 versus 94%, respectively; $P = 0.13$). These data show that the numerically higher number of bulls at BSE 1 failed due to the poor semen quality and not SC. These data also show semen quality improves with age, and developing bulls on forage did not appear to negatively impact breeding potential as evaluated by BSE.

Key Words: breeding soundness exam, bull, forage bull test
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BREEDING AND GENETICS

161 Population structure in a Thai multibreed dairy cattle population.

T. Laodim[1], M. A. Elzo*[1], S. Koonawootrittriron[2], and T. Suwanasopee[2], *[1]University of Florida, Gainesville, [2]Kasetsart University, Bangkok, Thailand.*

Accounting for population structure is important to help identify SNP associated with production traits in domestic animals, particularly in multibreed populations. Models used to identify relevant SNP in multibreed populations utilize genetic groups usually constructed based on expected breed fractions. However, these groups may not appropriately account for structural differences due to SNP allelic frequencies. Thus, the objectives of this study were to construct genetic groups using SNP marker information, obtain genetic distances between genetic groups, and determine the correspondence between SNP-based and breed-fraction-based genetic groups. The study included 2,661 cattle (89 bulls and 2,572 cows) from 304 farms located in Central, Northern, Northeastern, and Southern regions of Thailand, with complete pedigree that had been genotyped with GeneSeek Genomic Profiler 9K. Only SNP with minor allele frequency higher than 0.01, call rate larger than 90%, *P*-value of Hardy-Weinberg equilibrium lower than 0.0001, and r^2 value of linkage disequilibrium lower than 0.2 were included in this study (n = 5,005). A principal component analysis was used to obtain eigenvectors that were subsequently utilized to assign animals to genetic groups using a k-means clustering algorithm. Computations were performed using the discriminant analysis of principal component (DAPC) program of R-package adegenet. The optimum number of genetic groups in this population based on the lowest Bayesian Information Criterion (BIC) value was 28. Genetic distances among these SNP-based genetic groups were estimated using Nei's genetic distance. The DAPC scatterplot of the first and second principal components showed four genetic groups clearly separated, and 24 genetic groups were very close to each other forming a "super cluster." Conversely, Nei's genetic distances among the 28 groups revealed 3 clusters, one containing group 23, a second one including groups 1, 2, 12, 20, 21, 25, and 27, and a third cluster with the remaining groups. There was almost no correspondence (r = 0.00025) between breed composition of animals and their allocation to SNP-based genetic groups. In fact, SNP-based genetic groups contained animals of a wide range of Holstein fractions, and animals with Holstein fractions above 90% were represented in all SNP-based genetic groups. Thus, the DAPC algorithm was effective at identifying structural differences among animals based on gene frequencies regardless of their breed origin. However, genetic distances between these groups showed a different clustering pattern compared to the one obtained with the DAPC scatterplot of the first and second principal components.

Key Words: dairy cattle, genomic, population structure
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162 Comparison of genomic-polygenic evaluations using random regression models with Legendre polynomials and splines for milk yield and fat percentage in Thai multibreed dairy cattle.

D. Jattawa[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville.*

The objective of this research was to compare random regression models with third-order Legendre polynomials (RRLP) and linear splines of four knots (RRSP4) for milk yield (MY) and fat percentage (FP) genomic-polygenic evaluations in a Thai multibreed dairy cattle population. Models were compared using estimates of variance components, genetic parameters, model-fit criteria, accuracy of genomic EBV, and animal rankings. The dataset contained pedigree and first-lactation monthly test-day records (69,029 for MY; 29,878 for FP) of 7,206 cows from 761 farms. Genotypic information included 74,144 actual and imputed SNP markers from 2,661 animals. Variance components and genetic parameters for MY and FP were estimated using REML procedures. The single-step random regression genomic-polygenic models included contemporary group (herd-year-season), calving age, heterozygosity, and population lactation curve regression coefficients as fixed effects. Random effects were animal additive genetic random regression coefficients, permanent environment random regression coefficients, and residual. The effects of population lactation curve, animal additive genetic, and permanent environment were fitted using regression coefficients of third-order Legendre polynomials for RRLP and splines of four knots for RRSP4. Results showed estimates of 305-day additive genetic variances and heritabilities for MY and FP to be higher for RRLP (additive genetic variances: 279,893.2 kg^2 for MY, $0.10\%^2$ for FP; heritabilities: 0.27 for MY, 0.16 for FP) than for RRSP4 (additive genetic: 260,178.1 kg^2 for MY, $0.08\%^2$ for FP; heritabilities: 0.19 for MY, 0.11 for FP). Similarly, RRLP yielded a better model-fit and higher prediction accuracies than RRSP4. The RRLP had lower values of −2 log-likelihood (−2logL; 293,813), Akaike's information criteria (AIC; 293,855), and Bayesian information criteria (BIC; 293,915) as well as higher prediction accuracies (49.25% for MY; 38.63% for FP) than RRSP4 (−2logL = 362,738; AIC = 362,888; BIC = 363,101; prediction accuracies: 47.23% for MY, 37.76% for FP). However, rank correlations between genomic EBV from RRLP and RRSP4 were high for MY (0.94) and FP (0.90). Results indicated that genomic EBV from RRLP should be preferred to those from RRSP4 to help

increase selection responses for MY and FP in the Thai multibreed dairy cattle population.

Key Words: dairy cattle, genomic evaluation, random regression
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163 Population structure and genetic diversity of Russian native cattle breeds.

A. V. Dotsev[1], A. A. Sermyagin[1], E. A. Gladyr’[1], T. Deniskova*[1], K. Wimmers[2], H. Reyer[2], G. Brem[1,3], and N. A. Zinovieva[1], *[1]L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [3]Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.*

Conservation of native cattle populations’ biodiversity is a crucial element in breeding selection programs. Reduction of local and improved livestock gene pool leads to the loss of valuable alleles for adaptation to specific environments. In our work, we investigated the genetic structure of the most essential native cattle breeds in Russia. Using Illumina Bovine 50K BeadChip, we genotyped nine breeds: Bestuzhev (BEST, n = 26), Black and White (BLWT, n = 21), Kalmyk (KALM, n = 14), Kholmogor (KHLM, n = 25), Kostroma (KSTR, n = 20), Red Gorbatov (RGBT, n = 23), Suksun (SKSN, n = 20), Yakut (YAKT, n = 25), and Yaroslavl (YRSL, n = 21). Statistical analysis was performed with PLINK 1.07, Admixture 1.3 software, and R packages “diveRsity” and “adegenet.” Multi-dimensional scaling (MDS) analysis showed that all of the breeds formed their own clusters. The YAKT cluster was completely separated on the first component (C1) and was most distant from all other populations. KALM also separated on C1 but was much closer to the other clusters. Both of these breeds are of Asian origin. The other seven breeds, which are of European origin, separated from one another mostly on the second component (C2). Admixture analysis showed that the most probable number of populations (K) was 8. At K = 2, YAKT was separated from the other populations. Considerable admixture of YAKT was only found in the KALM cluster (from K = 2 to K = 8). At K = 8, all of the breeds but KALM formed their own clusters. KALM was combined from the seven other breed fragments (all but SKSN). Pairwise genetic distances (F_{ST}) values were higher for YAKT (from 0.126 with KALM to 0.187 with RGBT). Fst values between the other breeds ranged from 0.036 (BLWT and SKSN) to 0.103 (KSTR and RGBT). The lowest rarified allelic richness value was observed for YAKT (1.781 ± 0.002). For all of the other breeds, it ranged from 1.919 ± 0.001 for KSTR to 1.958 ± 0.001 for KALM. Expected heterozygosity was the lowest in YAKT (0.273 ± 0.001) while in all of the other breeds it ranged from 0.329 ± 0.001 in KSTR and RGBT to 0.352 ± 0.001 in BEST. Inbreeding coefficient (F_{IS}) values in all of the breeds were close to zero (from −0.05 to 0.01). Our study revealed that all of the evaluated Russian breeds were structured, and only KALM had a more complex admixture. The most diverged, indigenous YAKT breed had a lower genetic diversity than all of the other breeds. The study was supported by the Russian Science Foundation within Project no.14–36–00039.

Key Words: genetic diversity, native cattle breeds, SNP
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164 Single nucleotide variants and indels identified from whole-genome resequencing of Gyr, Girolando, and Holstein cattle breeds.

N. B. Stafuzza*[1], A. Zerlotini[2], F. P. Lobo[2], M. E. B. Yamagishi[2], T. C. S. Chud[1], A. R. Caetano[3], D. P. Munari[1], D. J. Garrick[4], J. B. Cole[5], M. A. Machado[6], M. F. Martins[6], M. R. Carvalho[7], and M. V. G. B. da Silva[6], *[1]Departamento de Ciências Exatas, Universidade Estadual Paulista, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, [2]Embrapa Informática Agropecuária, Campinas, Brazil, [3]Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brazil, [4]Department of Animal Science, Iowa State University, Ames, [5]Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, [6]Embrapa Gado de Leite, Juiz de Fora, Brazil, [7]Departamento de Biologia Geral, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.*

Whole-genome resequencing, alignment, and annotation analyses were undertaken for ten sires representing Gyr, Girolando, and Holstein cattle breeds to detect and make publicly available genome-wide single nucleotide variations (SNVs) and insertions/deletions (InDels). A total of approximately 3.5 billion reads from an Illumina HiSeq 2000 sequencer generated for each animal 10.7 to 16.4-fold genome coverage. Sequencing reads were mapped to the UMD 3.1 bovine genome assembly using the Burrows-Wheeler Aligner tool (v. 0.7.10-r789) with default parameters. Picard tools (v. 1.54) were used to eliminate PCR duplicates, and the variant calling was conducted with FreeBayes. The resulting variant lists obtained for each animal were filtered by vcffilter in order to remove variants with quality scores lower than 30 or coverage lower than 7. A total of 23,743,970 SNVs and 3,171,711 InDels were detected in the samples, of which approximately 2,224,013 SNVs and 798,8910 **[Editor: Please check number.]** InDels were novel. The high number of genetic variants identified for each animal within the same breed shows the importance of resequencing to identify novel variants for monitoring genetic diversity in the cattle breeds and for developing strategies to prevent some eventual loss of genetic variability. The submission of these genetic variants to the dbSNP database significantly increased the number of known variants, particularly for the indicine genome. The concordance rate between genotypes obtained using the Bovine HD BeadChip array and the same variants identified by sequencing was about 99.05%. The annotation of variants identified numerous nonsynonymous SNVs and frameshift InDels, which could affect phenotypic variation. Functional enrichment analysis was performed by the David (v. 6.8) tool and revealed that variants in the olfactory transduction pathway were overrepresented in all three cattle breeds, while the ECM-receptor interaction pathway was overrepresented only in the Girolando breed, the ABC transporters pathway was overrepresented only in the Holstein breed, and the metabolic pathways were overrepresented only in the Gyr breed. Therefore, the genetic variants discovered in this study provide a rich resource to help identify potential genomic markers and their associated molecular mechanisms that impact economically important traits for Gyr, Girolando, and Holstein breeding programs.

Key Words: composite breed, deletion, insertion
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165 Genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing.

N. B. Stafuzza*[1], A. Zerlotini[2], F. P. Lobo[2], M. E. B. Yamagishi[2], M. E. Buzanskas[3], T. C. S. Chud[1], A. R. Caetano[4], D. P. Munari[1], D. J. Garrick[5], M. A. Machado[6], M. F. Martins[6], M. R. Carvalho[7], J. B. Cole[8], and M. V. G. B. da Silva[6], *[1]Departamento de Ciências Exatas, Universidade Estadual Paulista, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, [2]Embrapa Informática Agropecuária, Campinas, Brazil, [3]Departamento de Zootecnia, Universidade Federal da Paraíba, Areia, Brazil, [4]Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brazil, [5]Department of Animal Science, Iowa State University, Ames, [6]Embrapa Gado de Leite, Juiz de Fora, Brazil, [7]Departamento de Biologia Geral, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [8]Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD.*

The aim of this study was to detect, by whole-genome resequencing, SNVs (single nucleotide variants) and indels (insertion/deletions) and annotate them into functional categories in order to identify functionally relevant variants in three important cattle breeds in Brazil: Gyr and Girolando (dairy production) and Guzerat (dual-purpose). A total of approximately 2.7 billion reads from an Illumina HiSeq 2000 sequencer generated for each animal 10.9- to 16.4-fold genome coverage. Sequencing reads were mapped to the UMD 3.1 bovine genome assembly using the Burrows-Wheeler Aligner tool (v.0.7.10-r789). Picard tools (v.1.54) were used to eliminate PCR duplicates, and the variant calling was conducted with FreeBayes. The resulting variant lists were filtered by vcffilter in order to remove SNVs and indels with quality scores lower than 30 or coverage lower than 7. A total of 25,020,024 SNVs (16,743,392 from Guzerat, 15,941,804 from Gyr, and 13,286,669 from Girolando) and 3,249,148 indels (1,975,563 from Guzerat, 1,833,387 from Gyr, and 1,413,047 from Girolando) were detected in the DNA samples. A total of 13,253, 13,817, and 12,480 genes showed genetic variation in Guzerat, Gyr, and Girolando, respectively, of which 64.84% of genes with SNVs and 31.29% of genes with indels were shared among all breeds. The functional enrichment analysis by the DAVID (v.6.8) tool revealed 24, 27, and 28 enriched KEGG pathways (FDR < 10%) in Guzerat, Gyr, and Girolando, respectively, of which 14 pathways were common to all breeds, three pathways were significantly overrepresented only in Guzerat (arachidonic acid metabolism, Fc gamma R-mediated phagocytosis, and aldosterone-regulated sodium reabsorption), six pathways only in Gyr (alanine, aspartate and glutamate metabolism, inflammatory mediator regulation of TRP channels, thyroid hormone synthesis, pancreatic secretion, central carbon metabolism in cancer, and choline metabolism in cancer), and eight pathways only in Girolando (amino sugar and nucleotide sugar metabolism, inositol phosphate metabolism, vascular smooth muscle contraction, tight junction, regulation of actin cytoskeleton, amoebiasis, small cell lung cancer, and dilated cardiomyopathy). Although the genetic variants identified were distributed throughout the genomes, a large number of novel variants were clustered in specific genes. A total of 61 genes were identified with novel variants common in all breeds, while 349, 404, and 206 genes were identified as enriched with novel variants exclusively in the Guzerat, Gyr, and Girolando breeds, respectively. These genes are related to many biological processes, providing valuable information about genomic variants that may be responsible for variation in economically important traits among these breeds.

Key Words: indels, pathways, single nucleotide variants
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166 Effects of genetic and non-genetic factors on bovine milk cholesterol content.

D. N. Do[1,2], F. S. Schenkel[3], F. Miglior[3,4], X. Zhao[2], and E. M. Ibeagha-Awemu*[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada, [2]McGill University, Department of Animal Science, Ste-Anne-de-Bellevue, QC, Canada, [3]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [4]Canadian Dairy Network, Guelph, ON, Canada.*

Dairy products are rich in cholesterol (CHL); therefore, monitoring CHL levels in cow milk may become an important factor. This study aimed to (a) determine the factors that influence milk CHL content, (b) estimate (co) variances and heritability for milk cholesterol, and (c) estimate genetic correlations between milk CHL and other production traits. Milk samples were collected from 2,907 cows from 38 commercial herds in Quebec. Milk CHL content was determined by gas chromatography and expressed as mg of CHL in 100 g of total fat (CHL_fat) or in 100 mg of milk (CHL_milk). Test-day milk (Milk), fat (Fat) and protein (Prot) yields, fat (Fat%) and protein (Prot%) percentages, and somatic cell counts (SCC) were also determined. A total of 2,418 cows were retained for analysis after editing for registration status, cow, sire/dam identification, breed, age at calving, and stage of lactation. Linear mixed models with fixed effects of test date, parity, age at calving, and stage of lactation and random effects of herd-year-season of calving and residual were run to test the significance of fixed effects on CHL. Univariate models were used to estimate (co) variances and heritability; meanwhile bivariate models were used to compute phenotypic and genetic correlations. The mean values of CHL_fat and CHL_milk were 274.60 ± 74.66 mg and 11.27 ± 0.74 mg, respectively. Cholesterol content was significantly affected by stage of lactation but not by parity and age at calving, regardless of the scale of expression ($P <$ 0.05). Heritability estimates for CHL_fat and CHL_milk were 0.09 ± 0.04 and 0.18 ± 0.05, respectively. Phenotypic and genetic correlations between CHL_fat and CHL_milk were 0.85 ± 0.01 and 0.33 ± 0.17, respectively. CHL_fat had no significant genetic correlations with Milk, Fat, and Prot% (−0.17 to −0.37) and close to zero genetic correlation with Prot and Fat%. CHL_milk also had low nonsignificant genetic correlations with Fat (0.33) and Prot (−0.39) but moderate and significant genetic correlations with Milk (0.58) and Prot% (0.47) and high genetic correlation with Fat% (0.81). CHL_fat and CHL_milk also had no significant genetic correlations with SCC. This is the first study to estimate genetic parameters for milk CHL content. Further studies on response to selection and genomics are required to assess the possibility of genetically selecting cows with desired CHL content.

Key Words: Canadian Holstein cows, cholesterol, genetic parameters, heritability, milk
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167 Genetic and genomic estimation for somatic cell score in relation with milk production traits of Russian Holstein dairy cattle.

A. A. Sermyagin*[1], E. A. Gladyr'[1], A. A. Kharzhau[1], K. V. Plemyashov[2], E. N. Tyurenkova[3], H. Reyer[4], K. Wimmers[4], G. Brem[1,5], and N. A. Zinovieva[1], *[1]L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Russian Research Institute of Farm Animal Genetics and Breeding, St. Petersburg–Pushkin, Russian Federation, [3]RC Plinor, St.Petersburg–Pushkin, Russian Federation, [4]Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [5]Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.*

Monitoring of udder health status is an important element in herd management and selection success for complex fitness traits. Identification of metabolic pathways and QTL responsible for the synthesis of amino acids and fatty acids in milk allows identification of missense mutations that are also associated with high fat, protein content, and somatic cell count. The aim of our research was to evaluate genetic correlations between milk production traits and somatic cell score in relation to assessing crucial SNPs. The calculation of variance and covariance components was performed by REML. Breeding value estimates for average daily milk yield (MY), fat (FP) and protein percentage (PP), fat (FY) and protein yield (PY), somatic cell count (SCC), and somatic cell score (SCS) were based on multiple-trait mixed model using BLUPF90 family programs. The genomic relationship matrix was calculated by the GBLUP approach. GWAS analysis was carried out using Plink 1.07. The total number of genotyped Holstein bulls (Illumina Bovine SNP50) with DGV values was 466, from which 247 had 8,935 daughters' records. Genomic values were used for GWAS as pseudo phenotype data. Genetic parameters for milk production traits were calculated based on records of 845 sires with 21,540 daughters. Heritability coefficients were 0.152, 0.213, 0.204, 0.101, 0.127, 0.050, and 0.055 for MY, FP, PP, FY, PY, SCC, and SCS, respectively. Genetic correlations between SCS and MY, FP, PP were −0.059, 0.024, and 0.197, respectively. GWAS analysis performed for FP showed the strong association of SNPs localized on BTA14 while the highest value of the additive variability was observed for *DGAT1* mutation (ARS-BFGL-NGS-4939, $P = 1.1\text{E}\times10^{-11}$, $R^2 = 9.5\%$). In total, we identified 52 SNPs associated with SCS at P-values of more than 1.24×10^{-6}. The coefficient of determination ranged from 5.9 to 9.2%. The greatest number of SNPs were found on BTA1, 4, 5, 8, and 17. Some of them were localized in the following key genes: rs110754403 (*STXBP6*, $P = 2.5\text{E}\times10^{-11}$), rs43072965 (*KCNMB4*, *PTPRB*, *TRNAC-GCA*, $P = 2.3\text{E}\times10^{-9}$), rs42600512 and rs42600489 (*CNOT2*, $P = 3.0\text{E}\times10^{-9}$), rs29019947 (117.6 to 117.9 Mb, *MED12L*, *P2RY12*, *P2RY13*, *P2RY14*, *IGSF10*, *LOC104971001*, *GPR87*, *GPR171*, $P = 5.3\text{E}\times10^{-8}..7.4\text{E}\times10^{-9}$), rs29020595

(*CALD1*, $P = 1.2E\times10^{-7}$). Our findings will be the basis for the development of the genomic evaluation concept for udder health and milk quality traits for the Russian Holstein and Black-and-White cattle population. Supported by the Russian Scientific Foundation, project number 15-16-00020.

Key Words: GWAS, Holstein cattle, somatic cell score
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168 The distribution for LoF mutations in the FANCI, APAF1, SMC2, GART, and APOB genes of the Russian Holstein cattle population.

O. S. Romanenkova, V. V. Volkova, O. V. Kostyunina, E. A. Gladyr', E. N. Naryshkina, A. A. Sermyagin*, and N. A. Zinovieva, *L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation.*

LoF (loss-of-function) mutations causing hereditary abnormalities and embryonic mortality are one of the reasons for a decline in fertility of cows. Currently, more than fifteen LoF mutations are known in Holsteins. In our work, we studied the frequency of LoF mutations in *FANCI*, *APAF1*, *SMC2*, *GART*, and *APOB* genes that are associated with fertility haplotypes HH0, HH1, HH3, HH4, and HCD in the Russian Holstein cattle population. We analyzed the estimated breeding values (EBVs) for daughters' milk production and reproduction traits in sires carrying LoF mutations compared to non-carrier sires using the BLUE approach. Genotyping LoF mutations was performed by PCR, PCR-RFLP or allele-specific PCR. In total, 1,521, 636, 880, 690, and 574 bulls and 896, 630, 773, 482, and 727 cows were genotyped for LoF mutations in *FANCI*, *APAF1*, *SMC2*, *GART*, and *APOB* genes, respectively. The ratio of carriers among bulls and cows was, respectively, 2.89 and 4.13% for *FANCI*, 2.04 and 1.83% for *APAF1*, 1.14 and 2.98% for *SMC2*, 1.30 and 1.04% for *GART*, and 5.57 and 2.06% for *APOB*. Generally, the sires carrying LoF mutations had higher EBVs for milk production traits. The greatest effect was observed for *SMC2* genotype: +236 kg for 305-days milk yield, 9.0 kg for fat yield, and 7.6 kg for protein yield. The bulls carrying LoF mutations in the *SMC2* and *GART* genes were characterized by the higher number semen doses per insemination (0.02 to 0.24 units) compared with the non-carrier bulls. The higher EBVs for the number of days open (from 12.6 ($P < 0.001$) to 7.2 days ($P < 0.05$)) and calving interval (from 9.0 ($P < 0.001$) to 10.5 days ($P < 0.01$)) were observed in bulls, which were carriers of LoF mutations in *SMC2* and *GART* genes. The group of sires with the mutation in the *FANCI* gene had the smallest length of calving interval (−6.0 days, $P < 0,001$). Analysis of the best linear unbiased estimates showed that for insemination of offspring from bull carriers of HH3 haplotype spent +0.026 units semen than for bulls with other mutations. The longest interval from calving to the first insemination and days open by +1.9 to 3.9 days were daughters of bulls with the *GART* gene (HH4). Given the dissemination of LoF mutations among the breeding sires and cows, with the aim of reducing genetically caused embryonic losses, matings of carriers bulls with mutations to cows whose fathers are hidden carriers of LoF mutations in the *FANCI*, *APAF1*, *SMC2*, *GART*, and *APOB* gene must be excluded.

Key Words: fertility, haplotype, LoF mutations
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169 A dairy calf DNA biobank for the discovery of new recessive genetic disorders.

J. B. Cole*, *Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD.*

This abstract describes the establishment of a new DNA biobank to support the discovery of new recessive genetic disorders in the U.S. dairy cattle population. High-density single-nucleotide polymorphism genotypes have recently been used to identify a number of novel recessive mutations that adversely affect fertility in dairy cattle, but the lack of consistent procedures for collecting DNA samples and supporting information for those projects underscores the need for a standardized process. The new Dairy Calf DNA BioBank in Beltsville, MD, is a repository for the collection and storage of samples. It complements the automated process of searching for new haplotypes that is part of the national dairy genetic evaluation system. The goal is to collect whole blood from calves that are born dead or that die shortly after birth, particularly if the calf appears to suffer from a congenital defect, as well as DNA from its dam and a sibling in the herd. Kits that include all sampling materials, a pre-paid return shipping label, a material transfer agreement, and a protocol for sample collection are shipped upon receipt of a request through the website. DNA providers are also able to provide substantial descriptive information about the calves for which they're providing blood, including digital photographs. When the samples are received in Beltsville, the DNA is extracted and stored for future analysis. The material transfer agreement ensures that a clear chain of permissions is available for every sample. If a pattern emerges to suggest that there is a new recessive genetic disorder in the population, the DNA is available for sequencing and causal variant discovery. Standardized protocols for DNA extraction and whole-genome sequencing will help ensure that data are of high quality. Information on carrier status for new recessives will be distributed through the Council on Dairy Cattle Breeding (Bowie, MD). The URL for the BioBank website is: http://aipl.arsusda.gov/BioBank/.

Key Words: dairy cattle, DNA bank, recessive disorders
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170 Genetic parameters of incidence and timing of respiratory disease in cattle.

T. M. Goncalves*[1], P. J. Pinedo[2], J. E. P. Santos[3], G. M. Schuenemann[4], G. J. M. Rosa[5], R. O. Gilbert[6], R. C. Bicalho[6], R. Chebel[3], K. N. Galvao[3], C. M. Seabury[7], J. Fetrow[8], W. W. Thatcher[3], and S. L. Rodriguez Zas[1], *[1]University of Illinois, Urbana-Champaign, [2]Colorado State University, Fort Collins, [3]University of Florida, Gainesville, [4]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [5]University of Wisconsin-Madison, Madison, [6]Cornell University, Ithaca, NY, [7]Department of Veterinary Pathobiology, College of Veterinary Medicine & Biomedical Sciences, Texas A&M University System, College Station, [8]University of Minnesota, St. Paul.*

Respiratory disease is a complex phenotype and the diagnostic can be attributed to multiple causes including viral infection (e.g., respiratory coronavirus, bovine respiratory syncytial virus), bacterial infection (e.g., pneumonic spp.; lungworm), and vena caval thrombosis. Moreover, the impact of respiratory disease in cows varies with the stage of lactation when the disease is detected. In general, intense management practices facilitate the detection of respiratory disorders in dairy cattle herds relative to beef cattle herds. Thus, we propose that study of respiratory disease incidence in a large dairy cattle data set as paradigm to advance the knowledge on the factors influencing the incidence of this disease across cattle types. Respiratory disease information on 6,283 Holstein cows across four U.S. states and nine herds were evaluated. Two descriptors of respiratory disease were evaluated: days in milk to respiratory disease detection and the binary detection of respiratory disease. Survival analysis was used to study the days in milk-to-disease. The binary variable respiratory disease detection was analyzed using a binary logistic model. Lactation number, season, region, farm, body condition score, and milk yield level (3 levels) were included in the model as fixed explanatory effects whereas sire was considered a random effect. Incidence of respiratory disease was lower in summer relative to winter, and there was a nonsignificant trend on lactation number. Body condition score had a significant effect, with higher body condition score associated with lower incidence of respiratory disease. Farm, body condition score, and milk yield level had significant effect on the time when respiratory disease was identified. The heritability estimate for incidence of respiratory disease was 0.4, suggesting that despite the high number of potential causative agents, selection for less susceptible cattle can be an effective strategy to reduce the impact of this disease. The heritability estimate of the days in milk-to-disease was 0.13, showing that non-genetic components may play an important role on the stage of the lactation when the disease is detected. These findings contribute to an animal health project (USDA-NIFA-ILLU-538909) and a multistate project database (USDA-NIFA-AFRI-003542) for direct measures of health and fertility in cattle.

Key Words: cattle, heritability, survival analysis
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171 Molecular breeding value prediction of pregnancy rate in Holstein dairy cows managed in a heat-stressed environment using candidate gene SNP.

R. Zamorano-Algandar*[1], J. C. Leyva-Corona[1], R. I. Luna-Ramirez[1], G. Luna-Nevarez[1], G. Rincon[2], J. F. Medrano[3], A. I. Hernandez[4], M. A. Sánchez-Castro[4], R. M. Enns[4], S. E. Speidel[4], M. G. Thomas[4], and P. Luna-Nevarez[1], *[1]Instituto Tecnologico de Sonora, Ciudad Obregon Sonora, Mexico, [2]Zoetis Inc., Kalamazoo, MI, [3]Department of Animal Science, University of California, Davis, [4]Department of Animal Sciences, Colorado State University, Fort Collins.*

Reproductive performance in Holstein dairy cattle managed during summer in southern Sonora is a challenge because of high ambient temperature and relative humidity. Both of these factors contribute to heat stress, which influences cow behavior. The physiological response of cows to heat stress is one component of a system-wide gene network. Within this environment, a superior cow's ability to get pregnant early during postpartum is favorable as to reduce the trait days open and to increase productive life. Recently, many reproductive specialists have recommended using pregnancy rate as a measure of reproductive success, after converting this trait into a quantitative value using a linear formula. In comparison to the traditional measure of days open, pregnancy rate calculation includes more easily cows that do not become pregnant; furthermore, the output variable indicates that larger values are more desirable, and therefore, more understandable by dairy producers. The objective herein was to predict pregnancy rate in lactating Holstein cows using molecular markers associated with fertility in Holstein cows under a heat-stressed environment. This study included 500 cows from three dairy herds located in the Yaqui Valley of Sonora. A blood sample was collected from every cow and spotted onto FTA cards. The DNA was extracted from each card and used to genotype 179 tag SNP within 43 genes in the prolactin and GH-IGF1 pathways. Five SNP within the genes IGFBP7, IGFBP2, PAPPA1, SSTR2, and STAT6 were associated with pregnancy rate using a mixed effects model. The genotype term was later included in this model to calculate allele substitution effects. Molecular breeding values of the individual cows were calculated by summing the additive genotype effect for each SNP that showed a significant independent association with pregnancy rate, and the average MBV was 0.46 ± 0.01%. Two statistical regression models were used to predict the variable pregnancy rate: a full model that included effects of days and number of lactations, contemporary group (e.g., farm management

group), health status, and MBV and a reduced model that only included MBV. Coefficients of determination were 37.61% and 3.07% for full and reduced models, respectively ($P < 0.01$). These results indicate that five SNP explained only a small proportion of the additive genetic variance for pregnancy rate. Additional research is needed to understand if these results are due to low heritability/repeatability of a fertility and (or) if these results are also influenced by heat stress.

Key Words: candidate gene, heat stress, pregnancy rate
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172 Comparison of genomic-enhanced EPD systems using an external phenotypic database.

L. A. Kuehn*[1], S. P. Miller[2], K. J. Retallick[2], and D. W. Moser[2], [1]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE,* [2]*Angus Genetics Inc., St. Joseph, MO.*

The American Angus Association (AAA) is currently evaluating two methods to incorporate genomic information into their genetic evaluation program: (1) multi-trait incorporation of an externally produced molecular breeding value as an indicator trait (MT) and (2) single-step evaluation with an unweighted G matrix (SS). Our objective was to quantify bias and accuracy of genomic predictions using these two approaches. Because phenotypic data was limited for actual carcass measures from genotyped bulls in the AAA database, we tested bias and accuracy using data from the germplasm evaluation program (GPE) at the U.S. Meat Animal Research Center. Traits evaluated included birth, weaning, and yearling weight, maternal weaning weight, carcass weight, marbling score, ribeye area, and backfat thickness. The GPE has sampled 197 AAA bulls over 45 years and has typically characterized weight and carcass data on 8 to 15 progeny from each bull. Of these 197 bulls, 128 had been genotyped using high density arrays. From the AAA database, EPDs were derived using MT, SS, and non-genomic (NG) animal model methods. To detect differences in accuracy, these EPD were correlated to multi-breed EPD derived from GPE. These correlations were restricted to bulls that had high-density genotypes. In addition, to quantify bias, breed-specific EPD regression coefficients were derived from GPE. Independent variables for regression analysis were derived by dropping the EPD from sampled bulls proportionally through the pedigree (1/2 reduction in each generation). These EPD regression coefficients were expected to be one if GPE conditions were similar to conditions in breed association databases. Regression coefficients were obtained for GPE progeny born after 1998, as bulls that produced these progeny were generally genotyped. The NG EPD were used as a benchmark for regression comparison, as any bias observed without genomic data was expected to persist with the addition of genomic information. Resulting correlations were very similar for all three methods for weight traits as correlations among MT, SS, and NG EPD were greater than 0.99. For carcass traits, SS and NG EPD were correlated to each other at 0.97 or more while correlations of each with MT were less than 0.93. For all traits, SS correlations were highest with GPE EPD. In regard to bias, SS regressions were always similar to NG regression while MT regressions were always lower. Data from outside sources, such as GPE, can be useful for evaluating alternative genetic prediction models.

Key Words: beef cattle, genetic evaluation, genomically enhanced EPD
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173 SNP discovery for QTL associated with grazing distribution in Angus cattle using RNA-Seq.

C. F. Pierce*[1], M. M. Dias[2], D. W. Bailey[3], J. F. Medrano[4], A. Canovas[5], S. E. Speidel[1], S. J. Coleman[1], R. M. Enns[1], and M. G. Thomas[1], [1]*Department of Animal Sciences, Colorado State University, Fort Collins,* [2]*Department of Animal Science, Sao Paulo State University (UNESP), Jaboticabal, Brazil,* [3]*Department of Animal and Range Sciences, New Mexico State University, Las Cruces,* [4]*Department of Animal Science, University of California, Davis,* [5]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

Grazing distribution is important for pasture management in beef cattle production systems. In mountainous terrain, abiotic factors such as steep slope and high elevation often yield concentrated grazing near riparian areas and limited livestock use in uplands. While management practices (fencing, water development, and herding) are effective in improving grazing distribution, these practices are costly and labor intensive. Previous research suggests that the traits used in indices to quantify grazing distribution are moderately heritable; therefore, genomic selection could be used to improve grazing distribution. Five QTL and underlying candidate genes (*ACN9*, *FAM48A*, *GRM5*, *MAML3*, and *RUSC2*) have been determined to be associated with grazing distribution traits in cattle. The objective of this study was to further examine these candidate genes and identify SNP that may then be incorporated into a previously developed 50-SNP panel used for genotype associations with grazing distribution phenotypes. Sequencing of RNA (RNA-Seq) yielded 30 million reads (single-read) per sample from 6 tissues (aorta, LM muscle, lung, pulmonary artery, and right and left ventricle) collected as part of an altitude tolerance study of Angus cattle. These tissues were from 10 steers with outlying pulmonary arterial pressure observations and unique sires. Sequences were assembled to the annotated bovine reference genome (UMD3.1; release annotation 87) and analyzed using CLC Genomics Workbench (version 8.0). Variant detection was performed using two methods: (1) individual samples and (2) a pool of all samples. No variants were detected in *GRM5*, *MAML3*, and *RUSC2*; however, individual sample analysis identified 30 SNP within

ACN9 and *FAM48A*, and pooled sample analysis identified 184 SNP within *ACN9* and *FAM48A.* Twenty-one SNP were identified in both approaches. The Ensemble Variant Effect Predictor was used to determine the functional consequence of each SNP. Of the 21 SNP, 16 were intronic, four were exonic, and one was reported to be a downstream variant and a splice acceptor variant. The SNP discovered using RNA-Seq technology were compared to the exonic SNP in dbSNP within the 5 candidate genes. There were 1,663 exonic SNP in dbSNP in these genes. One synonymous SNP, located within *ACN9* (rs382949979), was observed in both data from RNA-Seq and dbSNP. In summary, 21 SNP were discovered in two of the five candidate genes underlying QTL associated with grazing distribution. These SNP will be incorporated in a new genotyping panel to examine associations with the grazing distribution phenotypes.

Key Words: Angus, grazing distribution, SNP
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174 Multivariate analysis of beef cattle pulmonary arterial pressures measured at differing elevations.

M. M. Culbertson*[1], M. G. Thomas[1], L. L. Leachman[2], R. M. Enns[1], and S. E. Speidel[1], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]Leachman Cattle of Colorado, Fort Collins.*

Cattle living at altitudes greater than 1,500 m are susceptible to the development of high altitude disease (HAD) and a higher risk of death. Pulmonary arterial pressure (PAP) is used as an indicator of an animal's susceptibility to HAD. Measurements of PAP on cattle at lower elevations are generally considered less reliable indicators of HAD when compared to measurements taken at higher elevations, yet little evidence has been published evaluating this relationship. Therefore, the objective of this study was to evaluate PAP measurements from high and low elevations using a multivariate approach. We hypothesized that PAP measurements from lower elevations have a less than perfect relationship to PAP measurements from high elevations. Data collected from 2009 to 2017 was obtained from a multi-breed seedstock database that included PAP measurements and associated information (i.e., PAP testing date and elevation). The average PAP measurement was 44.08 ± 10.75 mmHg, with minimum and maximum observations of 32 and 149 mmHg, respectively. The age when PAP measurements were taken ranged from 9 to 21 months with an average age of 15.9 ± 2.8 months. Elevation ranged from 1,555 m to 2,407 m with a bimodal distribution. Therefore, animals with PAP measurements from elevations above 2,000 m were classified as high elevation (HPAP; n = 1,369) and animals with PAP measurements below 2,000 m were considered low elevation (LPAP; n = 1,243). A two-trait animal model was used to estimate genetic parameters and EBV for both LPAP and HPAP traits. The model contained the fixed effects of degree of outcross, breed percent, and PAP age as covariates, and sex and contemporary group (PAP date and yearling management combined) categories. Breed effects were included as covariates of breed percentages for Angus, Charolais, South Devon, Gelbvieh, Simmental, and "Other" breeds. Animal was included as a random effect and a 3-generation pedigree consisting of 11,573 animals was used. Heritability for LPAP and HPAP were 0.26 ± 0.08 and 0.37 ± 0.10, respectively, with a genetic correlation of 0.79 ± 0.23. Sire EBV for HPAP were regressed on corresponding sire EBV for LPAP, resulting in a regression coefficient of 0.705 ± 0.002 ($P < 0.0001$). These results suggest that a strong relationship exists between LPAP and HPAP, but the relationship is not perfect. The high genetic correlation between the traits suggest that measurements taken at lower elevations can still serve as an indicator of PAP measurements collected at higher elevations.

Key Words: cattle, elevation, pulmonary arterial pressure
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175 Construction of an association weight matrix to identify SNP that play a role in performance of Angus cattle at higher elevations.

K. J. Jennings*[1], X. Zeng[1], A. Reverter[2], T. N. Holt[3], S. J. Coleman[1], R. M. Enns[1], S. E. Speidel[1], and M. G. Thomas[1], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]CSIRO Agriculture, Brisbane, Australia, [3]College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins.*

High altitude disease (HAD) is of low incidence but occurs in cattle at altitudes of >1,500 m. Histopathologically, this condition is characterized by pulmonary arterial vasoconstriction resulting in reduced diameter of arterioles, subsequently causing pulmonary hypertension and right heart failure. Mean pulmonary arterial pressure (mPAP) is commonly used as an indicator trait of pulmonary hypertension leading to HAD. Animals with mPAP measurements of <41 mmHg are considered to be of low risk for the development of HAD. Because mPAP is a trait difficult to measure, studies have identified SNP that may be of interest in selecting cattle more tolerant of higher altitudes. These SNP, if evaluated in polygenic models, could elucidate ways to implement genomic selection by establishing genetic pathways that will identify cattle better suited for high altitudes. In previous genome-wide association studies (GWAS), SNP were associated with mPAP as well as traits of birth weight, milking ability, weaning weight, post-weaning gain, and yearling weight. The objective of this study was to identify relationships among previously identified SNP by means of an association weight matrix (AWM) with mPAP as the primary trait of interest. Significant SNP from six GWAS were included in the AWM if they accounted for >0.001% of the genetic variance for mPAP. Based on that

criterion, 954 SNP were identified for the AWM. Those SNP specifically associated with mPAP were then utilized to calculate the average number of phenotypes (A_p) a SNP should be associated in order to be included in the AWM. By averaging the number of additional phenotypes that SNP related to mPAP were associated with, an A_p of 0.266 was obtained, which was then rounded to one. All SNP that were significant at a genetic variance of >0.001% and associated with at least one phenotype were included in the AWM. Results indicated that significant SNP for the AWM spanned all 29 autosomal chromosomes as well as the X chromosome. Of the 262 SNP associated with mPAP, 17, 19, and 11 were associated with birth, weaning, and yearling weights, respectively. This supports previous studies indicating that the genetic correlations between mPAP and performance traits were weak to moderate $r_g < 0.27$. Results from this study can be utilized to construct gene networks of SNP that are associated with mPAP as an effort to develop multi-trait genomic selection tools for high altitude beef production systems.

Key Words: association weight matrix, cattle, elevation
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176 Genotyping a SNP in the endothelial PAS domain-containing protein 1 (EPAS1) gene: is it associated with mean pulmonary arterial pressures in yearling Angus cattle?

N. F. Crawford*[1], S. J. Coleman[1], T. N. Holt[2], S. E. Speidel[1], R. M. Enns[1], J. H. Newman[3], R. Hamid[4], 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,* [3]*Department of Medicine, Division of Allergy, Pulmonary and Critical Care, Vanderbilt University School of Medicine, Nashville, TN,* [4]*Department of Pediatrics, Division of Medical Genetics and Genomic Medicine, Vanderbilt University School of Medicine, Nashville, TN.*

At altitudes of >1,800 m, measurements of mean pulmonary arterial pressures (mPAP) have been used as an indicator trait of pulmonary hypertension and risk of right-sided heart failure in cattle. Genotypes from a G/A SNP (rs208684340) in the oxygen-dependent domain of the endothelial PAS domain protein 1 (EPAS1) gene were determined for yearling Angus cattle classified into mPAP risk categories (low, moderate, high) of heart failure. The A allele of this SNP was hypothesized to be associated with high altitude-induced hypoxemia. The initial objective of this study was to survey genotypic frequencies in Angus cattle at high altitude ranches in the Rocky Mountain west (elevation 1,850 to 2,800 m) and at low altitude ranches (elevation 91 to 1,192 m) in several states. For the latter, a random sampling (n = 118) of 1,275 Angus cattle from low altitude beef production systems in California, Missouri, Iowa, Texas, and New Mexico were genotyped. The mPAP phenotype was not collected for cattle residing at these altitudes. The percentages of cattle with genotypes G/G, G/A, and A/A were 64.4, 33.9, and 1.7%, respectively, with a MAF of 18.6%. Also, bulls, steers, and heifers (n = 690 progeny of 99 sires) from 4 Angus seedstock herds managed at high elevation were genotyped. The percentages of these cattle with genotypes G/G, G/A, and A/A were 48.7, 34.3, and 17.0%, respectively. The overall minor allele frequency (MAF; A allele) was 34.1% and mPAP averaged 40.6 ± 8.8 mmHg with a range of 28 to 126 mmHg. The MAF for the low, moderate, and high-risk categories were 35.4, 31.0, and 36.3%, respectively. No differences were observed for MAF between mPAP risk categories ($P > 0.05$). A second objective of this research was to evaluate the genotype to phenotype association of this SNP with mPAP phenotypes in the Colorado State University Beef Improvement Center (CSU-BIC; elevation 2,150 m) Angus herd. Genotypes from 496 Angus cattle were utilized in the association between this SNP and mPAP. Hardy-Weinberg equilibrium ($P = 0.07$) was not violated. A linear mixed model analysis with fixed effects of genotype, mPAP date, age, and a random effect of sire suggested genotype was not a predictor ($P = 0.5$) of mPAP and explained only 0.02% of the variation in mPAP. These results do not support the hypothesis that the A allele of this SNP (rs208684340) in the EPAS1 gene was associated with altitude-induced hypoxemia in cattle.

Key Words: Angus, pulmonary arterial pressure, SNP
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177 Genetic structure of Angus and Salers in relation to SNP associated with pulmonary arterial pressure.

B. C. Krehbiel*[1,2], M. G. Thomas[1], S. E. Speidel[1], R. M. Enns[1], and H. D. Blackburn[2], [1]*Department of Animal Sciences, Colorado State University, Fort Collins,* [2]*National Animal Germplasm Program, National Laboratory for Genetic Resources Preservation, ARS, USDA, Fort Collins, CO.*

Cattle living in the Rocky Mountains (elevations of >1,500 m) are often at risk of contracting high altitude disease. Low atmospheric pressure at high altitudes causes pulmonary hypertension and potentially right heart failure. Pulmonary arterial pressure (PAP) is an indicator for pulmonary hypertension. PAP measurements of <41 mmHg are categorized as low risk for the development of pulmonary hypertension at high altitudes. Genetic resilience to the disease is possible and can be achieved through breed or within breed selection. Here, we explored differences between Angus raised at 2,150 m divided into low (<41 mmHg; n = 24) and high PAP (>41 mmHg; n = 41) groups and Salers (n = 24) at loci associated with PAP. The Salers sampled, a French mountainous breed (<4,800 m elevation), were all full blood. The mean Angus PAP score was 49 ± 2.1 mmHg (range 35 to 115). To determine the population structure between the two breeds, 121,756 SNP pruned from the 777,972 SNP on BovineHD BeadChip were evaluated using

Admixture to infer ancestral populations. Previously identified SNP (n = 40) associated with PAP in Angus cattle through genome-wide association studies were used to assess the genetic diversity of both breeds. Chi-square tests were performed to identify statistical differences among the allele frequencies and breed groups. We used TreeSelect to identify allele frequency divergence from a central node due to selection. Admixture revealed by the lowest cross validation error that two distinct populations existed. Chi-square tests of SNP genotypic frequencies among the groups revealed that 23 of the 40 SNP differed ($P < 0.025$). Sixteen SNP differed between both low and high PAP Angus groups versus Salers. Also these results show the high PAP Angus genotypic frequencies differentiated themselves from the low PAP Angus genotypic frequencies. However, both high and low PAP Angus group allele frequencies showed evidence of approaching the frequencies observed in Salers. TreeSelect identified four SNP under selection. Of those SNP, three allele frequencies were similar between low PAP Angus and Salers, suggesting natural or artificial selection for both populations. These results indicate that genetic diversity exists between Angus and Salers cattle, which can be used to increase resilience to high altitude disease. Therefore, cattle breeders may choose to address such a problem through breed choice, selection within a breed, or both.

Key Words: cattle, pulmonary hypertension, SNP
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178 Black Hereford genetic parameters and predictions for calf traits with alternate modelling strategies.

J. S. Delgadillo*[1], D. G. Riley[1], J. M. Langdon, II[1], L. L. Hulsman Hanna[2], and A. D. Herring[1], *[1]Department of Animal Science, Texas A&M University, College Station, [2]Department of Animal Sciences, North Dakota State University, Fargo.*

Large breed databases allow use of multi-trait models for genetic parameter estimations (GE), genetic predictions (GR), and increased estimation accuracy. However, large databases are not always available to apply more complex models than single trait models. The objective of this study was to assess the potential of different variance structures (VS) to make GE and GR using multi-trait models with a small but rapidly growing database. Birth weight (BW), weaning weight (WW), and yearling weight (YW) records were obtained from the American Black Hereford Association. Single, bivariate, and trivariate models were evaluated using a mixed model approach for each trait, and final models were selected through likelihood ratio test. Random components for BW (n = 6,821) and WW (n = 5,348) were direct genetic (DG) and maternal genetic (MG), covariance between direct and maternal additive genetic components, and permanent environment (PE), while for YW (n = 2667) only DG was included. The set of VS tested in the multi-trait models included results from the single model analyses, covariance fixations to zero, and definition or not of residual structure. Heritability estimates for DG ranged from 0.30 to 0.32 (BW), 0.19 to 0.27 (WW), and 0.28 to 0.31 (YW); for MG ranged from 0.07 to 0.11 (BW) and 0.02 to 0.03 (WW); and for PE ranged from 0.05 to 0.06 (BW) and 0.09 to 0.16 (WW). EPD rank correlations between each pair of models for BW, WW, YW, birth weight maternal (BWM), milk (MK), and total maternal (TM) are presented in Table 178. These results show similar estimates to other breeds and that, despite low record numbers, heritability estimates by different models were fairly similar by trait. EPD rank correlations had high values for almost every trait, where BW had the higher values and MK the lower and more inconsistent correlations. Finally, a correct definition of VS makes it possible to employ a trivariate analysis to assess traits with a low number of records without detrimental effects on estimations and accuracy of estimation.

Table 178. EPD rank correlations between model pairs

Models/ traits	BW	BWM	WW	MK	YW	TM
1vs2	1.00	0.98	0.98	0.47		0.89
1vs3	0.99	0.94			0.93	
1vs4			0.96	0.62	0.84	0.88
1vs5	1.00	0.90	0.96	0.47	0.84	0.91
2vs3	0.99	0.93				
2vs4			0.95	0.33		0.80
2vs5	1.00	0.91	0.97	0.92		0.94
3vs4					0.81	
3vs5	1.00	0.96			0.89	
4vs5			0.99	0.52	0.96	0.94

Models nomenclature: 1, single model; 2, BW-WW; 3, BW-YW; 4, WW-YW; 5, BW-WW-YW.

Key Words: genetic prediction, heritability, multi-trait model
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179 Expected progeny differences for stayability in Angus cattle using a random regression model.

M. A. Sánchez-Castro*, R. J. Boldt, M. G. Thomas, R. M. Enns, and S. E. Speidel, *Department of Animal Sciences, Colorado State University, Fort Collins.*

Stayability (STAY) is a measure of whether or not a female remains productive in the herd until a specified point in time, with that point traditionally being 6 years of age. Waiting 6 years before an observation is generated represents a limitation to obtaining accurate Expected Progeny Difference (EPD) values for STAY at the age of 6 (STAY6). Random regression models (RRM) have been suggested for use in national cattle evaluations to improve the prediction of STAY6 by including observations from earlier ages into the analysis. Therefore, the objective of this study was to compare EPD for STAY at consecutive ages using traditional methods with EPD for STAY obtained with RRM in Angus cattle. Calving performance data consisting of 1,233 females (progeny of 215 sires and 791 dams) collected from 1993 to 2012 at the Colorado

State University Beef Improvement Center (CSU-BIC) was used for the study. Four STAY endpoints defined as whether a cow calved at age 3, 4, 5, and 6 given she calved as a 2-yr-old were assigned observations (0, unsuccessful; 1, successful). These observations were used to calculate EPD for each of the STAY endpoints. Traditional STAY was evaluated for each endpoint (STAY3 through STAY6) using a univariate BLUP threshold animal model along with a probit link function to convert binary observations to an underlying normal distribution. Effects in the models included contemporary group (dam birth year and calf birth year) as a fixed effect and animal as random effect. Additionally, all STAY endpoints were evaluated using a linear RRM with Legendre polynomials as the base function. For the RRM, contemporary group and a linear fixed regression were included as fixed effects. The RRM predicted the genetic merit of the presence of a weaned calf at each particular age endpoint; therefore, EPD were summed to obtain the individual's genetic merit for the presence of a calf at 3, 4, 5, and 6 years of age. Pearson correlation coefficients between EPD at each endpoint and the corresponding RRM EPD were 0.59, 0.83, 0.82, and 0.77 for STAY3, STAY4, STAY5, and STAY6, respectively. Regressions of predictions obtained from the RRM on traditional EPD were 1.76, 3.65, 4.76, and 5.05 for each of the consecutive endpoints. These results suggest that while both models are predicting similar genetic merit for individuals, the traditional method is under-predicting the genetic merit of individual animals when compared to that obtained with the RRM.

Key Words: beef cattle, random regression model, stayability
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180 Genetic parameters for carcass traits and stayability in Red Angus cattle.

R. J. Boldt*[1], S. E. Speidel[1], M. G. Thomas[1], and L. D. Keenan[2], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]Red Angus Association of America, Denton, TX.*

In Red Angus cattle, the stayability (STAY) EPD predicts the probability of a female producing five consecutive calves by 6 years of age. A fundamental issue that arises with genetic prediction for STAY is animal's accuracy values tend to improve later in life. An opportunity to overcome this is to use phenotypes recorded at younger ages to increase accuracy of STAY EPD earlier in an animal's life. Therefore, the objective of this study was to estimate genetic relationships between STAY and HCW, ribeye area (REA), back fat (BF), and marbling score (MARB), as well as their indicator traits, ultrasound ribeye area (UREA), ultrasound back fat (UBF), and ultrasound intramuscular fat percentage (UIMF). Data for the analyses were obtained from the Red Angus Association of America. Following data editing procedures, 1,676, 1,717, 1,459, 1,721, 29,406, 29,477, 29,269, and 43,328 phenotypic records were used for the analysis of REA, BF, MARB, HCW, UREA, UBF, UIMF, and STAY, respectively. (Co)Variances between traits were estimated using multiple two-trait animal models and the software package ASReml. These parameters were then used to calculate heritability and genetic correlations between each of the two trait pairs. The fixed effect of contemporary group was included for all traits. For all carcass and ultrasound traits, fixed effects also included sex (bull, heifer, and steer) and the linear covariate of age of measurement. A random effect of animal was included in each analysis to estimate additive genetic effects. Heritability estimates were 0.26 ± 0.08, 0.24 ± 0.07, 0.30 ± 0.08, 0.26 ± 0.07, 0.38 ± 0.02, 0.40 ± 0.02, 0.39 ± 0.02, and 0.10 for REA, BF, MARB, HCW, UREA, UBF, UIMF, and STAY (averaged across all analyses), respectively. Results of the analysis indicated that genetic relationships were strongest in magnitude between STAY and BF (0.53 ± 0.20), MARB (0.40 ± 0.20), UBF (0.37 ± 0.07), and UREA (0.19 ± 0.07), whereas genetic correlations between STAY and REA (0.01 ± 0.21), HCW (0.14 ± 0.21), and UIMF (−0.01 ± 0.07) suggested minimal, if not zero, relationship between the traits. Results show favorable genetic relationships are present between the carcass traits MARB and UREA and STAY and unfavorable relationships are estimated between BF, UBF, and STAY. In addition, the trait UBF could be introduced into a multiple trait model to improve accuracy of STAY genetic predictions due to the magnitude of the correlation and availability of data.

Key Words: beef cattle, carcass, stayability
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181 Supplementation with n-3 PUFA and post-insemination plane of nutrition alters global gene expression patterns in bovine uterine endometrial tissue.

C. Surlis, S. M. Waters, J. Evans, P. Cormican, D. Doyle, and D. A. Kenny*, *Teagasc Animal and Bioscience Department, Dunsany, Co Meath, Ireland.*

Early embryonic loss, occurring just prior to implantation is a significant cause of reproductive wastage in cattle. Dietary supplementation with n-3 polyunsaturated fatty acids (n-3 PUFA) has long been postulated to have a positive effect on fertility and reproductive success. The objective of the study was to examine (i) the effect of dietary supplementation with n-3 PUFA and level of post-insemination plane of nutrition on the uterine endometrial transcriptome and (ii) to identify alterations in key genes and pathways that may affect pregnancy outcome. A total of 60 estrous synchronized crossbred beef heifers were fed a high energy diet on an ad libitum basis and randomly assigned to one of two groups where the concentrate portion of the diet was either supplemented with a partially rumen protected source of n-3 PUFA (n = 32) or was unsupplemented (Control; n = 28) for 30 days prior to insemination. Immediately following insemination, animals were further allocated one of two post insemination diets, either remaining on the high plane of nutrition (High; n = 31)

or were offered 60% of estimated maintenance energy requirements (Low; n = 29). Heifers were maintained on their respective diets until slaughter and embryo recovery on Day 16 post insemination or pregnancy diagnosis by ultrasonic scanning on Day 30. Uterine endometrial tissue was collected from slaughtered heifers at Day 16, RNA isolated, and gene expression analysis conducted by RNAseq. There was no effect of either supplementation with n-3 PUFA or post-insemination plane of nutrition on pregnancy rate at either Day 16 or 30. Comparison of transcript abundance across groups, however, highlighted a statistically significant effect of diet on uterine endometrial transcript levels, with a notable effect of n-3 PUFA supplementation on a number of differentially expressed genes (DEG). Of particular interest, the comparison of n-3 PUFA supplemented and unsupplemented pregnant heifers on the low plane of post-insemination nutrition resulted in 561 DEG, including the increased expression of genes previously demonstrated to be involved in early pregnancy, such as *UPK3BL* and *CTSV*, and in reproductively important pathways, including an embryonic development pathway and mTOR signaling pathway enriched in PUFA supplemented heifers, important to establishing pregnancy. Results indicate that despite no effect on pregnancy outcome, supplementation with n-3 PUFA positively altered a number of key fertility related genes and pathways involved in early pregnancy, which may have roles in the maintenance of pregnancy.

Key Words: cattle, PUFA, reproduction
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182 Genetic markers associated with susceptibility to bovine respiratory disease.

R. M. Enns*[1], T. G. McDaneld[2], J. W. Keele[2], R. J. Boldt[1], T. P. Smith[2], and L. A. Kuehn[2], [1]*Department of Animal Sciences, Colorado State University, Fort Collins*, [2]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Bovine respiratory disease complex (BRDC) is the most expensive disease afflicting the U.S. beef industry. Efforts to reduce the effects of this disease have had modest success likely due to the multi-factorial nature of the disease with environmental and managerial factors interacting with associated bacterial and viral agents. Previous work suggests a genetic component to animal susceptibility to BRDC; therefore, the objective of this study was to identify DNA markers associated with incidence of BRDC in commercial feedlot cattle. Using a case/control strategy, DNA samples from 3,648 commercial feedlot animals were collected with half (n = 1,824) having shown clinical signs of BRDC (i.e., cases) and the other half non-symptomatic controls sampled from the corresponding feedlot pen. A DNA pooling approach was used in the genome-wide association study. After extraction, a high density bovine marker array was run on 19 case and 19 control DNA pools of approximately 96 animals each. There were ~770,000 SNP with sufficient data quality for all 38 pools. Twelve SNP achieved a false discovery rate (FDR) of 5% or less in the genome-wide association analysis. There were 3 significant SNP on BTA11, 2 on BTAX, and 1 each on BTA 1, 9, 18, 22, 24, 27, and 29. Three significant SNP were located in intergenic regions, and 9 occurred within introns or exons of genes. Significant SNP resided within the introns of LOC100847501, HPCAL1, RSAD2, DNAAF3, CCD1798, and ATP7A and exons of LOC510798 (missense) and LOC519208 (synonymous). The potential role of some of these genes in BRDC is suggested by literature. For instance, the RSAD2 transcript response to bacterial lipopolysaccharides has been reported to decrease in the presence of bovine viral diarrhea virus. In humans, mutations in DNAAF3 cause primary ciliary dyskinesia resulting in ineffective airway mucociliary clearance and frequent respiratory infections in human infants. The ATP7A gene has been suggested to influence bactericidal activity in macrophages through its role in copper homeostasis. The results of this study indicate a genetic component to susceptibility to BRDC and encourage the development of DNA marker tests to aid in selection of animals less susceptible to BRDC.

Key Words: beef cattle, bovine respiratory disease, genomic marker
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183 Optimum selection of core animals in the efficient inversion of the genomic relationship matrix.

H. L. Bradford*, I. Pocrnic, B. O. Fragomeni, D. A. L. Lourenco, and I. Misztal, *University of Georgia, Athens.*

The objective was to determine the effect of using core animals from different generations in single-step genomic BLUP with the Algorithm for Proven and Young (APY). Effective population size and number of independent chromosome segments (ICS) are limited in livestock populations, indicating limited dimensionality of genomic information. The APY takes advantage of this dimensionality and assumes that breeding vales (BV) for noncore animals are functions of the BV for core animals. The core animals represent the same information as the ICS. Simulations comprised a moderately heritable trait for 95,010 animals and 50,000 genotypes for animals across 5 generations. Genotypes consisted of 25,500 SNP distributed across 15 chromosomes. Core animals were defined based on individual generations, equal representation across generations, and at random. For a sufficiently large core size, core definitions had the same accuracies ($r^2 = 0.90 \pm 0.01$) and biases ($\beta_1 = 1.02 \pm 0.01$) for young animals, even if the core animals had imperfect genotypes because of imputation. Using the youngest generations as core caused an increase in the number of rounds to convergence indicating some numerical instability with these core definitions. When 80% of genotyped animals had unknown parents, accuracy and bias were significantly better ($P \leq 0.05$) for random and across-generation core definitions ($r^2 = 0.71 \pm 0.01$; $\beta = 0.75 \pm 0.01$) than for single-generation core definitions ($r^2 = 0.61 \pm 0.01$; $\beta = 0.53 \pm 0.01$). This difference could result from improved relationship estimates between animals in different generations because all generations were represented in the core partition that was directly inverted in APY. Thus, any subset of genotyped animals can be used to approximate the ICS when pedigrees are complete, but core animals should represent all generations when pedigrees are incomplete.

Key Words: APY, genomic selection, single-step genomic BLUP
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184 Impact of SNP selection on genomic prediction for different reference population sizes.

D. A. L. Lourenco*[1], B. O. Fragomeni[1], H. L. Bradford[1], I. Menezes[2], S. Tsuruta[1], and I. Misztal[1], [1]*University of Georgia, Athens,* [2]*FZEA, University of Sao Paulo, Pirassununga, Brazil.*

Methods for SNP selection can improve prediction accuracy over genomic BLUP, but in practice, the improvement is trait and population specific. This study investigates the importance of SNP selection in populations with 2,000 to 25,000 genotyped animals. Populations were simulated with effective population sizes (Ne) of 20 or 100 and assuming that 10, 50, or 500 QTL were affecting a trait with heritability of 0.3. Pedigree information was available for 6 generations; phenotypes were recorded for the 4 middle generations. Animals from the last 3 generations were genotyped for 45,000 SNP. Single-step genomic BLUP (ssGBLUP) and weighted ssGBLUP (WssGBLUP) were used to estimate genomic EBV (GEBV). For WssGBLUP, 2 iterations of weights were calculated and were used to derive SNP variances and to construct a weighted genomic relationship matrix (G). Improved prediction accuracies are expected in WssGBLUP because more weight is placed on important SNP. Prediction accuracies were calculated for 1,000 genotyped animals in the last generation. Reference populations included 2,000, 5,000, and 25,000 genotyped animals. The latter genotyped set was used to assess the dimensionality of genomic information (number of effective SNP or effective chromosome segments - Me). This was calculated as the number of the largest eigenvalues explaining 98% of the variation in the genomic relationship matrix with and without the weights. For the data sets with Ne = 20 and 10 QTL, the accuracy gain from WssGBLUP was 12, 9, and 4 points for 2,000, 5,000, and 25,000 genotyped animals, respectively. With Ne = 100, this gain was 8, 10, and 7 points, respectively. For both an Ne of 20 and 100, the gain assuming 50 QTL was halved, and no gain was observed assuming 500 QTL. The number of effective SNP was about 4-fold less in weighted G (~1,512) than in unweighted G (~5,790), explaining the greater gain in accuracy with fewer genotyped animals. The impact of SNP selection decreases with increasing size of the reference population and number of QTL. In large populations, the detection of chromosome segments is more difficult, requiring more genotyped animals.

Key Words: accuracy, variable selection, weighted ssGBLUP
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185 Increasing accuracy of genomic selection in presence of high density marker panels through the prioritization of relevant polymorphisms.

L. Y. Chang*[1], S. Toghiani[1], S. E. Aggrey[2,3], and R. Rekaya[1,3,4], [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,* [4]*Department of Statistics, University of Georgia, Athens.*

An increase in the density of marker panels did not result in a significant increase in the accuracy of genomic selection (GS) using either regression (RM) or variance component (VC) approaches. Increasing the number of variants using a RM approach will increase collinearity and reduce the effects of associated variants, which will hamper the ability to prioritize relevant polymorphisms. Using the VC approach, increasing marker density, after a certain threshold, will not improve and could adversely affect the quality of (G) as the relative number of shared polymorphisms between any two individuals decreases. One way to increase the quality of G in the presence of HD panels is to prioritize the variants. The fixation index (F_{ST}), as a measure of allele frequency variation among subpopulations, could be used as a score to prioritize candidate SNPs. In this study, we evaluated the impact of SNP prioritization using F_{ST} scores on the genetic similarity between individuals and on the accuracy of GS. A trait with heritability of 0.4 was simulated, and the phenotypic distribution was divided into three subpopulations (bottom 5%, middle 90%, top 5%). Genomic data consisted of 400K SNP markers distributed on 10 chromosomes to mimic a 1.2 million SNP marker panel in bovine. Using different quantiles of the F_{ST} distribution, 500 to 80,000 SNPs were selected. Similar numbers of SNPs were selected randomly for comparison. The matrix G was calculated for each set of selected SNPs based on their F_{ST} score and randomly selected counterpart. Using all 400K SNPs, 46% of the off-diagonal elements (ODE) were between −0.01 and 0.01, whereas only 16% of ODE were within that range when 20K SNPs were selected based on their F_{ST} scores for computing G. When 20K SNPs were selected at random, around 33% of the ODE fell within the same range. The number of ODE greater than 0.05 was significantly greater (27%) when G was constructed using F_{ST}-selected SNPs compared to 5 and 10% when G was calculated using all or randomly selected SNPs. Maximum accuracy (0.82) was achieved when 5 to 10K SNPs are selected based on F_{ST} scores compared to an accuracy of 0.71 and 0.54 using all or randomly selected SNPs. Accuracy could be improved by maximizing the genomic similarity between individuals by prioritizing relevant markers. A balance between the number of SNPs and the portion of the genetic variance explained is needed to achieve higher accuracy.

Key Words: accuracy, high density, SNP prioritizing
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186 A hybrid of prioritized SNP and polygenetic effect method for implementation of genomic selection.

S. Toghiani*[1], L. Y. Chang[1], S. E. Aggrey[2,3], and R. Rekaya[1,3,4], [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,* [4]*Department of Statistics, University of Georgia, Athens.*

Genomic selection (GS) is rapidly becoming the method of choice for genetic evaluation. GS is implemented using either a linear regression or mixed effect models. The continuous enhancement of the density of marker panels and the number of genotyped animals are creating major theoretical and implementation problems to both approaches. Furthermore, little to no improvement in accuracy of GS was achieved using this high density (HD) genomic data. This lack of improvement in accuracy is not due to the lack of informativeness of the HD data, rather because of the inability of existing methods to harness additional information. This is the case due to lack of statistical power using linear regression models and the limited improvement of the genomic relationship matrix (G) for the mixed linear model approach. The later suffers additionally from the increase in the number of genotyped animals, which complicates substantially the inversion of G. Thus, it is reasonable to assume both problems could be solved or at least attenuated if SNP markers are prioritized not based on their estimates effects (i.e., BayesB) but rather on some other criteria that are not affected by the limited statistical power. Only the "prioritized" SNPs will be included in the association model and a polygenic term will be added to account for the remainder of the genetic merit. This hybrid method is a compromise between both existing approaches. In this study, fixation index (F_{ST}) scores were used as criteria to prioritize SNPs. To evaluate hybrid method, a simulation was carried out for 15k genotyped animal with 50k SNP panel. The heritability of a trait (0.4) was totally explained by 200 QTLs, which 12%, 33%, and 66% of them explain at least 1%, 0.5%, and 0.3% of the total genetic variance (GV), respectively. No polygenic component was simulated. By using the 97.5 quantile of the distribution of F_{ST} scores to prioritize SNPs, the proposed method resulted is a more accurate estimate of heritability (0.36) compared to BayesB (0.32). Although both methods have similar estimates of the portion of GV explained by the genomic information, the proposed method induces a reduction in the residual variance due to a non-zero estimate of the polygenic variance (0.10). Accuracy was similar between hybrid and BayesB methods (0.48 vs. 0.49). However, the new approach does not require the inversion of G and is able to handle genotyped and non-genotyped animals with a limited increase in computational cost.

Key Words: F_{ST}, genomic selection, hybrid model
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187 Analysis of misclassified categorical responses.

A. Ling*[1], P. Sumreddee[1], E. H. A. Hay[2], R. Rekaya[1,3,4], and S. E. Aggrey[3,5], [1]*Department of Animal and Dairy Science, University of Georgia, Athens,* [2]*USDA/ARS/LARRL, Miles City, MT,* [3]*Institute of Bioinformatics, University of Georgia, Athens,* [4]*Department of Statistics, University of Georgia, Athens,* [5]*NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens.*

Misclassification in categorical outcome variables is a common and difficult issue that results in biased inference. Several traits of economic and welfare importance in animal improvement programs are discrete in nature. The recording of these traits is prone to misclassification for several reasons, including subjectivity of measurement, improper recordkeeping, or simply changes in the definition of the traits over time. Although several methods have been proposed to deal with misclassification in binary outcome variables, to the best of our knowledge, there is no methodology that has been applied to the analysis of multinomial responses subject to misclassification. In this study, we proposed a method for analysis of misclassified ordered categorical responses through the extension of our previous work on dealing with noisy binary data. The proposed method identifies potentially misclassified observations, adjusts their status, and conducts the analysis with the corrected data. To evaluate the effectiveness of the proposed method, a simulation study was carried out. Two data sets of 10K and 1.5K records were simulated. The latter was simulated following the structure of an existing beef cattle calving ease data set. For both data sets, a discrete response with three classes (70%, 20%, and 10% incidence rate) and a heritability of 0.1 was simulated. A misclassification rate of 5% was randomly introduced to the data set by switching the true response to the two alternative outcomes with equal probability. True and misclassified data sets were analyzed by two approaches: a classical threshold model that does not account for misclassification (M1) and by our proposed model that contemplates potential misclassification (M2). Each simulation scenario was replicated 10 times. For all scenarios, when the true data sets were analyzed, the true parameters were estimated without bias, although the estimates using the small data set had large posterior standard deviation, as expected.

When the misclassified data was analyzed with M1, a 20.5% and 11.8% bias was observed in the estimation of the heritability for the large and small data sets, respectively. Using M2, bias was removed. In fact, estimates of heritability were almost identical to those obtained using the real data (0.106 vs. 0.106 and 0.097 vs 0.098 for 10K and 1.5K data sets, respectively). Furthermore, the proposed method was able to detect true misclassified records with high probability. These results clearly indicate the effectiveness of the proposed method in reducing bias in the analysis of discrete data subject to misclassification.

Key Words: calving ease, misclassification, multinomial responses
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188 Ability to genotype differing variants with arrays vs. whole genome sequencing.

P. M. VanRaden*[1], G. L. Spangler[1], C. P. VanTassell[1], J. Jiang[2], L. Ma[2], J. R. O'Connell[3], S. Smith[4], and S. K. DeNise[4], *[1]Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, [2]University of Maryland, College Park, [3]University of Maryland-Baltimore, Baltimore, [4]Zoetis Inc., Kalamazoo, MI.*

Whole genome sequencing has identified millions of new variants, but many (about 35% in our experience) of the single nucleotide polymorphisms (SNPs) may not produce high quality genotypes from microarrays. Properties of SNPs can help predict which will pass or fail when designing arrays, such as the customized version of Illumina's Bovine LD chip examined here. Genotypes for 26,970 reference bulls were imputed using 440 sequenced Holsteins from run 5 of the 1000 Bull Genomes Project, and 4,821 SNPs with largest effects for net merit were selected. When adding those to the Zoetis LD chip (version 5), the success rate was 96% for 3,220 SNPs from the Bovine HD chip, but only 64% for 1,601 new sequence SNPs not previously on any chip. To determine why SNPs failed, a pass/fail (1/0) indicator of sequence SNP conversion success was correlated with (1) Illumina design scores, (2) estimated heritabilities of the genotypes for 3,000 randomly selected bulls, and (3) the base distance that the SNP was inside a repetitive DNA segment as determined by RepeatMasker, using a minimum distance of 0 if outside a repeat and maximum of 50 bases if inside. The correlations were 0.51 for design scores, 0.14 for estimated heritabilities, and −0.15 for repeat distance. All three were highly significant ($P < 0.0001$), but repeat distance was less significant ($P = 0.04$) after fitting design score and heritability in multiple regression. Three other factors (minor allele frequency, SNP position with genes, and the reference/alternate allele combination pattern) were not associated with conversion success. In a reverse test, 56,815 SNPs from the Bovine 50K version 1 chip were matched with 38 million sequence SNPs. Previously 15,772 of the 50K SNPs had been declared not usable, and 11,969 (87%) of those were also either not identified or removed by sequence edits. However, 3,803 (9%) of the 43,053 currently used SNPs that produce high quality genotypes on the 50K chip were absent from the sequence data, and the absence was not associated with minor allele frequency or allele combination. If the goal is to select the best SNP subset for a chip, design scores could be pre-computed and examined before rather than after estimating SNP effects, allowing selection of other linked SNPs expected to perform better. Eventually, targeted sequencing could provide genotypes for important SNPs that fail to convert because many SNPs from sequence data are difficult to genotype using arrays.

Key Words: design scores, genotyping arrays, single nucleotide polymorphisms
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189 Genomic relatedness strengthens genetic connectedness across management units.

H. Yu*, M. L. Spangler, R. M. Lewis, and G. Morota, *University of Nebraska-Lincoln, Lincoln.*

Genetic connectedness refers to a measure of genetic relatedness across management units (e.g., herds and flocks) in animal breeding. Connectedness has shown to be an important measure of reliability when comparing genetic values derived from pedigree-based best linear unbiased prediction (BLUP) among management units. With the presence of high genetic connectedness in management units, BLUP is known to provide less biased comparisons between genetic values. Genetic connectedness has been applied successfully to pedigree-based BLUP; however, relatively little attention has been paid to using genomic information, such as single nucleotide polymorphisms, to estimate genetic connectedness. Thus, it remains unclear whether and to what extent genome-based information enhances connectedness. In this study, we assessed genome-based genetic connectedness across management units by applying prediction error variance of difference (PEVD), coefficient of determination (CD), and prediction error correlation (r) to a combination of computer simulation and real data (mice and cattle). Relationship matrices were constructed from three different sources: pedigree (A), genomics (G), and a hybrid of these two. We found that genomic information increased the estimate of connectedness among individuals from different management units compared to that of pedigree, and a disconnected design benefited the greatest. In the well-structured mice data (full-sib families), regardless of heritability (0.2 vs. 0.8), all 3 statistics inferred increased connectedness across-units when using G- rather than A-based relationships. With the cattle data, genomic relationships decreased PEVD across-units suggesting stronger connectedness. With r once scaling G to values between 0 and 2, which is intrinsic to A, connectedness also increased with genomic information. However, PEVD often increased and r often decreased when obtained using the alternative form of G, instead suggesting less connectedness. Such inconsistencies were not found with CD. Caution should be exercised

when interpreting connectedness measures derived using genomic data, as the underlying assumption is that relationships are built based on alleles being identical by state and not necessarily being identical by descent. We contend that genomic relatedness strengthens estimates of genetic connectedness across management units and has a potential to aid genomic evaluation of livestock species.

Key Words: genomic connectedness, prediction error variance, relatedness
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190 Single nucleotide polymorphisms in the signal transducer and regulator of transcription (STAT) genes are associated with milk production, milk composition, and fertility traits in Holstein Friesian cattle.

L. Ratcliffe*[1], M. Mullen[1], M. C. McClure[2], J. McClure[2], and F. Kearney[2], [1]*Bioscience Research Institute, Athlone, Ireland,* [2]*Irish Cattle Breeding Federation, Bandon, Ireland.*

Signal transducer and activator of transcription (STAT) genes encode for a family of proteins that are involved in pre- and post-natal growth and development. In cattle, variants in these genes have been associated with economically important traits including milk production and embryonic survival. The objective of this study was to estimate the effects of polymorphisms in the *STAT1*, *STAT3*, and *STAT5* genes on milk production, composition, and fertility traits in Holstein Friesian dairy cattle. *STAT* genotypes (n = 8) on 10,707 dairy cattle were obtained through the Irish Cattle Breeding Federation (ICBF). The phenotypes (n = 16) for milk production, milk composition, and fertility traits also were obtained from the ICBF and expressed as predicted transmitting abilities (PTAs). The association between each SNP and deregressed PTA was analyzed in ASREML using a weighted mixed animal model. The association analysis included n = 6,876 for milk yield and composition traits. The analysis for fertility traits included n = 1,193, 264, 4,566, 8,564, 152, and 2,380 cows for calving interval, survival, calving difficulty, gestation length, calf mortality, and maternal calving difficulty, respectively. In the analysis of the *STAT* variants with milk traits (milk protein concentration, milk fat concentration, milk yield, milk fat yield, milk protein yield), a significant association ($P < 0.05$) was observed between *STAT3* (25042) and *STAT5* variants (12195, 13244, 13319, 13516) and milk protein percentage. *STAT3* variants (19069, 25042) were associated ($P < 0.001$) with milk fat percentage; additionally *STAT5* variants (13244, 13516) were also found to be associated ($P < 0.05$) with this trait. The G allele of *STAT3* (25042) was also associated with increased milk yield (17.01 kg, s.e. 6.708, $P < 0.05$). No associations were observed between *STAT1* and the remaining polymorphisms analyzed in either *STAT3* or *STAT5* with the milk production and milk composition traits examined. Associations were observed between *STAT3* (19069) and gestation length (0.11 days, s.e. 0.056, $P < 0.05$) and *STAT5* (12195) with calf mortality (2.04, s.e. 1.017, $P < 0.05$). None of the six remaining polymorphisms considered in this study within the *STAT* genes were associated with any of the aforementioned fertility traits. These results support a multifaceted role of the *STAT* family in milk production, composition, and fertility which warrants further functional analysis and consideration for incorporation into genetic evaluation programs for maximizing the rate of genetic gain.

Key Words: fertility traits, milk traits, signal transducer and regulator of transcription
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191 Genetic relationship between wool shedding in ewe-lambs and ewes.

N. Vargas Jurado*[1], K. A. Leymaster[2], L. A. Kuehn[2], and R. M. Lewis[1], [1]*University of Nebraska-Lincoln, Lincoln,* [2]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Interest in reducing labor costs related to shearing has led to the development of breeds that naturally shed their wool annually. This goal has been achieved by introducing hair-sheep genetics. These developments are relatively recent and thus the genetic underpinnings of wool shedding (WS) are not entirely known. Moreover, in many instances, it is desirable to select and cull progeny at young ages based on performance. However, if performance at an early age is not a good predictor of performance at later ages, erroneous selection decisions could be made. The goal of this study was to determine the accuracy of predicting wool shedding in ewes (EWS) using information from the same individuals as lambs (LWS) by estimating the genetic correlation between EWS and LWS. Data from a flock composed of Katahdin, Dorper, and Romanov crosses were available. A total of 1,368 records for each trait (LWS and EWS) were used for the analyses. Model selection was performed by initially fitting a cumulative probit link model including age of dam (AOD) and contemporary group (CG; genetic line by year of record) as fixed effects and weaning weight (WW) as a covariate for LWS and age of record (AGE), contemporary group (CG), and number of lambs born and reared (NBR) as fixed effects for EWS. For both traits, a random sire effect with pedigree relationships was also included. Variance components were estimated by fitting a bivariate threshold animal model, which contained the factors found to have an important effect ($P < 0.001$) on each trait. Only AGE and CG were included in the analysis of EWS and only CG for LWS. Additive variances (on the liability scale) were 0.053 ± 0.008 and 0.168 ± 0.027 for EWS and LWS, respectively, while residual variances (also on liability scale) were 0.058 ± 0.005 and 0.209 ± 0.019 for EWS and LWS, respectively. Both traits were found to be moderately heritable and genetically correlated. Heritability of liability was 0.477 ± 0.056 for EWS and 0.444 ± 0.059 for LWS. In addition, the genetic correlation

between EWS and LWS was 0.649 ± 0.063, while the phenotypic correlation was 0.450. Based on these genetic parameters, selection to increase shedding can be achieved fairly quickly. In addition, given that the correlation between EWS and LWS is moderately strong, selecting and culling young animals based on their first WS performance may be successfully used as indirect selection on EWS.

Key Words: genetic correlation, sheep, wool shedding
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192 Single nucleotide polymorphisms of candidate genes associated with growth performance and meat quality traits in Tau Vang chicken.

D. Vo Anh Khoa*[1], D. Bo[2], N. Shunlin[3], N. Hoai An[4], N. Thi Dieu Thuy[5], N. Thi Kim Khang[1], N. Van Truyen[6], and N. Thanh Phi Long[1], *[1]Can Tho University, Can Tho, Vietnam, [2]Menon Production and Trade Co., Ltd., Ho Chi Minh, Vietnam, [3]Thien Bang Animal Feed Co., Ltd, Vietnam Branch, Long An, Vietnam, [4]Hoang Long Agriculture Co., Ltd., Dong Nai, Vietnam, [5]Institute of Biotechnology, Ha Noi, Vietnam, [6]Greenfeed Vietnam Joint Stock Company, Long An, Vietnam.*

Tau Vang, one of the locally-recognized chicken breeds in southern Vietnam has been known for its quality meat satisfying Vietnamese customers, but its biological growth is slow. Recently, Marker Assisted Selection (MAS), which could be based on single nucleotide polymorphisms (SNPs) of candidate genes to support selection of animals with important traits, has been developed and applied to a range of animal breeding. However, in Vietnam, MAS for local animal breeds has not been applied yet. Therefore, in this study, SNPs in some genes, such as IGFBP2, GH, Insulin, TSH-β, leptin, GHSR, GHR, and IGF1, were detected by using PCR-RFLP in a population of 648 Tau Vang broilers, which were raised in private cages in the duration of 5 to 13 weeks old. After that, all of the broilers were slaughtered to measure parameters of carcass, chemical compositions, and quality of breast and thigh meat. A General Linear Model containing factors of line, sex, genotype, as well as interaction of line*genotype and of sex*genotype was statistically established to analyze genetic association of SNPs with observed traits. As a result, genotypic and allelic frequencies at some loci (i.e., C352T of leptin, C3199T of GH, A565G of GHR) were not found in a Hardy-Weinberg equilibrium test. Many SNPs significantly associated with economic traits, such as body weight, breast, thigh, and body length; average daily gain, feed conversion ratio, breast depth, and abdominal fat; dry matter, ether extract, crude protein, calcium, and ash concentration of meat; as well as pH, driploss, and water holding capacity of meat after slaughtering were found ($P \leq 0.05$). These provided great evidence to design MAS in efforts of improving growth performance and meat quality in Tau Vang chicken as well as other local chicken breeds in Vietnam.

Key Words: carcass and meat quality, single nuleotide polymorphism, Tau Vang broilers
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193 Including causative variants into single step genomic BLUP.

B. D. Fragomeni*[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 purpose of this study was determining, by simulation, whether (single-step) GBLUP is useful for genomic analyses when some or all causative Quantitative Trait Nucleotides (QTNs) are known. Simulations included 180,000 animals in 11 generations. Single phenotypes were available for all animals in generations 6 to 10. Genotypes were available for 24,000 parents in generations 6 to 10 and 5,000 randomly chosen animals in generation 11. Genotypes included 60,000 SNP (called regular SNP) in 10 chromosomes, with genetic variance fully accounted for by 100 or 1,000 biallelic QTNs. Raw genomic relationship matrices were computed from (a) unweighted regular SNP, (b) unweighted regular SNP and causative QTN, (c) regular SNP with variances from GWA, (d) unweighted regular SNP and causative QTN with known variances, (e) as before but only using 10% of the largest causative SNPs, and (f) using only causative SNPs with known variances. Accuracies for the 11th generation were computed by BLUP and single-step GBLUP. To ensure full rank, raw genomic relationship matrices (GRM) were blended with 1% or 5% of numerator relationship matrix or 1% of the identity matrix. Inverses of GRM were computed directly or using APY; the APY algorithm exploits limited dimensionality of the GRM for fewer computations and sparse inverse. Rank of GRM with 100 QTN as determined by the number of largest eigenvalues explaining 90% variation in GRM was 8,497 for raw unweighted GRM, increased to 9,553 after blending, decreased to 4,054 with weighted GRM and 10% QTNs included, and was 76 when only causative QTNs were used to create the GRM. The accuracy for the last genotyped generation with BLUP was 0.32. For ssGBLUP with the dense inverse, that accuracy increased to 0.49 with a regular GRM, to 0.53 after adding unweighted QTN markers, to 0.63 when QTN variances were estimated, and to 0.89 when QTN variances were assumed known. When GRM was constructed from QTN markers only, the accuracy was 0.95 with 5% blending raising to 0.99 with 1% blending. Accuracies assuming 1,000 QTNs were generally lower, with a similar trend. Accuracies using the APY inverse were equal or higher than those with a regular inverse. The rank of weighted GRM is between the rank of unweighted GRM and that computed with QTNs only. Single-step GBLUP can account for causative

SNP with nearly optimum accuracy when variances of causative QTN are known.

Key Words: genomic prediction, genomic relationship matrix, quantitative trait nucleotide
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194 Multibreed Angus-Brahman genetic parameters and predictions for nine ultrasound and carcass traits using three genomic-polygenic models and one polygenic model.

M. A. Elzo*, R. G. Mateescu, D. D. Johnson, T. L. Scheffler, J. M. Scheffler, C. Carr, D. O. Rae, J. D. Wasdin, M. D. Driver, and J. D. Driver, *University of Florida, Gainesville.*

The objectives of this study were to estimate variance components, genetic parameters, EBV, accuracies, and rankings for nine ultrasound and carcass traits in a multibreed Angus-Brahman population using three genomic-polygenic models and one polygenic model (PM). The genomic-polygenic models used the complete GeneSeek GPF250k SNP set (GPM), top 5% SNP (GPMR1), and 5% SNP evenly spread across the genome (GPMR2). Yearling ultrasound traits were weight (UW), ribeye area (UREA), backfat (UFAT), and percent intramuscular fat (UPIMF). Carcass traits were slaughter age (SLA), hot carcass weight (HCW), ribeye area (REA), backfat thickness (FAT), and marbling score (MAR). The 9-trait GPM, GPMR1, GPMR2, and PM contained fixed contemporary group, age of calf (ultrasound traits only), sex of calf, and direct heterosis effects, and random animal and residual effects. Variance components and genetic parameters were computed using AIREMLF90. Comparable heritabilities were obtained with GPM and PM for UW (GPM: 0.54 ± 0.05; PM: 0.51 ± 0.05), UREA (GPM: 0.36 ± 0.03; PM: 0.34 ± 0.03), UFAT (GPM: 0.12 ± 0.02; PM: 0.11 ± 0.02), UMPIMF (GPM: 0.34 ± 0.03; PM: 0.30 ± 0.03), SLA (GPM: 0.59 ± 0.07; PM: 0.61 ± 0.06), HCW (GPM: 0.58 ± 0.06; PM: 0.52 ± 0.07), REA (GPM: 0.48 ± 0.04; PM: 0.45 ± 0.05), FAT (GPM: 0.41 ± 0.05; PM: 0.30 ± 0.05), and MAR (GPM: 0.56 ± 0.07; PM: 0.51 ± 0.08). Additive genetic correlations between pairs of ultrasound and carcass traits were all between −0.31 and 0.81. The highest positive additive genetic correlations were between UW and UREA, UW and HCW, UW and REA, UREA and HCW, UREA and REA, UFAT and FAT, and between HCW and REA. The largest negative additive genetic correlations were between UREA and UPIMF, UFAT and SLA, UFAT and HCW, UPIMF and REA, and between REA and MAR. High similarity existed among predicted EBV and accuracies from GPM, GPMR1, and GPMR2 as well as high-rank correlations for sires, dams, and progenies. This indicated that the two reduced genotype sets were appropriate alternatives to the complete GPF250k set for genomic-polygenic evaluation and selection in this multibreed Angus-Brahman population. High EBV variability existed among animals of all Angus and Brahman percentages, and no specific breed composition was overwhelmingly better or worse for any of the nine traits. This indicated that optimization of genetic progress through selection in multibreed Angus-Brahman populations should be based solely on genetic merit regardless of breed composition.

Key Words: beef, carcass, genomic
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195 Genome-wide association study of heifer pregnancy in Red Angus cattle.

B. A. Buckley[1], S. E. Speidel*[2], R. J. Boldt[2], R. M. Enns[2], X. Zeng[2], M. L. Spangler[3], J. Lee[3], and M. G. Thomas[2], [1]*University of Hawaii - Manoa, Honolulu,* [2]*Department of Animal Sciences, Colorado State University, Fort Collins,* [3]*University of Nebraska - Lincoln, Lincoln.*

Reproductive performance in cattle herds is one of the most critical factors influencing the economic viability of beef enterprises. Heifers that become pregnant as yearlings will have more calves over their lifetime and allow for greater recovery of heifer development costs. However, genetic improvement of the trait heifer pregnancy (HPG) under traditional genetic approaches is difficult due to low heritability and accuracy of selection. An approach to address this dilemma is to identify QTL that could be used to improve HPG. The objective of this study was to identify QTL associated with HPG in Red Angus cattle. A genome-wide association study (GWAS) was performed using deregressed HPG EBV, estimated using a single trait animal model and three generation pedigree formed from animals in the data used for national cattle evaluation performed during December 2014 for the Red Angus Association of America. Initially, animals were genotyped using various Illumina SNP chip-platforms ranging in density from 32,186 to 140,114 SNP. Genotype data were then imputed with FImpute so each animal (n = 9,380) possessed 74,659 SNP genotypes. Individual animals that contained a reported breed percent of >50 percent Red Angus with a deregressed EBV reliability greater than 0.05 were merged with the genotype file and marker quality control was performed yielding 567 animals. Criteria for sifting genotypes consisted of removing those markers where the average call rate was <0.85, minor allele frequency <0.01, those not in Hardy-Weinberg equilibrium ($P < 0.0001$), or those SNP in extreme LD ($r^2 > 0.99$). These criteria left 64,010 SNP available for GWAS. Genomic windows of approximately 1 Mb (25.12 ± 8.31 SNP) in size were determined to significantly influence HPG if the size of their effect explained greater than 0.75% of the genetic variance in the trait. Bayes B in the software GenSel was used in GWAS. Two marker windows were associated with HPG. One QTL was located on bovine chromosome 28 and accounted for nearly 2% of the genetic variance, while the second on chromosome 11 accounted for 1.6% of the variance. These QTL results differ from other reports and suggest that QTL for HPG are not in concordance with GWAS results involving breeds such as Brangus and Simmental. Discovery of these

QTL are encouraging for genetic improvement programs in Red Angus cattle. Continued genotyping and increased reporting across family lines within the Red Angus breed would serve to enhance these results.

Key Words: genome-wide association study, heifer pregnancy, QTL
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196 Genome-wide association study for stayability in Red Angus cattle.

S. E. Speidel*[1], B. A. Buckley[2], R. J. Boldt[1], R. M. Enns[1], X. Zeng[1], J. Lee[3], M. Spangler[4], and M. G. Thomas[1], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]University of Hawaii - Manoa, Honolulu, [3]University of Nebraska Lincoln, Lincoln, [4]University of Nebraska, Lincoln.*

Beef female stayability (STAY), as defined by the Red Angus Association of America (RAAA), is the ability of a female to produce five consecutive calves by six years of age given she produced as a heifer. Stayability has been described as an economically relevant trait, and the magnitude of the value placed on STAY in various commercially available general purpose economic selection indices indicates its value to producers is greater than any other trait included in those indices. Given the importance of STAY to the profitability of commercial beef operations, the objective of this study was to identify QTL associated with STAY in Red Angus cattle. A genome-wide association study (GWAS) was performed using deregressed STAY EBV, calculated using a single trait animal model and three generation pedigree formed using data for the national cattle evaluation in December 2014 for the RAAA. Initially, animals were genotyped using various Illumina SNP chip-platforms ranging in density from 32,186 to 140,114 SNP. Genotypes were then imputed with FImpute so each animal possessed 74,659 SNP genotypes. Individual animals whose breed percent was >50 percent Red Angus with a deregressed EBV reliability of >0.05 were merged with the genotype file and marker quality control was performed. Criteria for sifting genotypes consisted of removing those markers where the average call rate was <0.85, minor allele frequency <0.01, those not in Hardy-Weinberg equilibrium ($P < 0.0001$), and those SNP in extreme LD ($r^2 > 0.99$). These criteria resulted in 2,664 animals with 62,807 SNP available for GWAS. Genomic windows of approximately 1 Mb (25.12 ± 8.31 SNP) in size were determined to significantly influence stayability if the size of their effect explained greater than 0.75% of the genetic variance in the trait. Association studies were performed using Bayes B methodology in the software package GenSel. Twelve marker windows were identified as QTL associated with STAY. These windows were located on BTA 2, 5, 6, 9, 12, 15, and 16. On two chromosomes, 9 and 15, multiple windows were identified (3 and 4, respectively). Although these are the first set of markers reported to be associated with STAY in *Bos taurus* beef cattle, similar chromosomes were identified in GWAS involving Nellore-Angus crossbred cows (BTA4, 5, 15, 19) for STAY, as well as for calving interval (BTA 5) and productive lifespan (BTA 15) in dairy cattle.

Key Words: beef cattle, genome-wide association study, stayability
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197 Functional SNP associated with birth weight in independent populations identified with a permutation step added to GBLUP-GWAS.

W. M. Snelling*[1], S. D. Kachman[2], G. L. Bennett[1], M. L. Spangler[2], L. A. Kuehn[1], and R. M. Thallman[1], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska - Lincoln, Lincoln.*

This study was conducted as an initial assessment of a newly available genotyping assay containing about 34,000 common SNP included on previous SNP chips, and 199,000 sequence variants predicted to affect gene function. Objectives were to identify functional variants associated with birth weight in the Germplasm Evaluation (GPE) project, a crossbred population representing 18 breeds having U.S. national cattle evaluations, and to evaluate variants identified from GPE in other populations also genotyped with the functional variant assay. Genotypes available for GPE included 1,109 sires, 506 dams, and 237 non-parents, and were imputed to 13,286 animals having genotypes from the moderate-density assays. Independent populations with functional genotypes included 2,500 animals from 4 selection populations at the U.S. Meat Animal Research Center and 1,500 animals from two breeds in seedstock herds cooperating in a project to evaluate genomic predictions. Genome-wide association studies (GWAS) of birth weight were conducted in GPE using genomic BLUP (GBLUP) then solving variant effect estimates from the GBLUP animal solutions. A permutation step was implemented to determine if variant effect estimates might be systematically biased. Animal solutions were randomly reordered 10,000 times, and variant effects were solved for each permutation. The reordered vectors of animal effects were not correlated (mean $r^2 < 0.0001$; max $r^2 = 0.002$), but variant effects solved from the reordered vectors were correlated (mean $r^2 = 0.21$; max $r^2 = 0.94$), indicating a systematic influence which appears to be related to linkage disequilibrium (r^2) among variants. Variants having at least moderate r^2 (>0.25) with several other variants tended to have smaller effect estimates and permutation variances than variants having only weak r^2 with others. Testing the estimated effect of each variant against its permutation variance revealed 293 variants with significantly (Bonferroni-corrected $P < 0.05$) larger effects than expected from permutation. These variants explained 36% of phenotypic variation in GPE birth weights, and molecular breeding values trained using GPE effects had genetic correlations with birth weight in other populations ranging from 0.25 to 0.44. Similar correlations were obtained from an 11 variant panel identified by repeating permutation on two successively smaller sets. Genetic correlations between birth weight and genotypes for the single most significant variant in GPE, a non-synonymous SNP in NCAPG, were between 0.17 and 0.34 in the independent populations.

Key Words: beef cattle, birth weight, genetic markers
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198 Meta-analysis of RNA-Seq data across cohorts in a multi-season feed efficiency study of crossbred beef steers accounts for biological and technical variability within season.

B. N. Keel*, C. M. Zarek, J. W. Keele, L. A. Kuehn, W. M. Snelling, W. T. Oliver, H. C. Freetly, and A. K. Lindholm-Perry, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

High-throughput sequencing is often used for studies of the transcriptome, particularly for comparisons between experimental conditions. Due to sequencing costs, a limited number of biological replicates are typically considered in such experiments, leading to low detection power for differential expression. Moreover, validation of transcriptomic data is likely to suffer from poor reproducibility from study to study due to the large amount of variation from sources, such as breed and season. The major aim of this study was to identify genes differentially expressed in the muscle of beef cattle associated with gain and feed intake that will be robust across a large segment of the cattle industry, regardless of breed of origin, season, or year of study. To avoid differences in gene expression due to environment and breed of origin, crossbred steers representing 19 different breeds were selected from fall and spring seasons over 3 years. RNA sequencing (RNA-Seq) was performed on longissimus dorsi muscles from 80 steers (5 cohorts, each with 16 animals) selected with the greatest distance from the bivariate means of gain and feed intake within season. Initial analysis of the data, using a generalized linear model with gain, feed intake, and season as explanatory variables, from all 80 steers identified a strong seasonal effect in differentially expressed genes (DEG). Although selection of animals in each season was performed using the same procedure, there was a clear segregation of gain and intake phenotypes between seasons. In order to estimate the overall difference in expression between phenotypes, differential expression analysis was performed independently for each season, and a *P*-value combination technique was employed to identify robust DEGs across the seasons. We identified a total of 148 DEGs for the main effect of gain, 1,738 DEGs for feed intake, and 59 DEGs for the gain × intake interaction. Moreover, nine of the genes associated with gain and twelve of the genes associated with intake shared the same gene expression directionality across all five groups of steers. The integration of data from multiple experiments (seasons) may enable extraction of deeper biological insights compared to what is achieved through analyzing a single experiment by allowing efficient elimination of false-positive findings pertaining to experimental and design conditions.

Key Words: feed efficiency, meta-analysis, RNA-Seq
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199 Genetic correlation between body weights and frame size measures in Hanwoo.

A. Mahboob, T. Choi, B. Park, M. N. Park, and Y. H. Choy*, *National Institute of Animal Science, Chonan, Republic of (South) Korea.*

The objective of this study was to estimate the genetic correlation between body weight traits and frame size measurement traits of three different types of age adjustment in Hanwoo bulls and steers raised at a test station in South Korea. Body weights and ten frame size measurement records on 6,832 bulls and 5,916 steers born between 1996 and 2013 and raised at Hanwoo test station from six months of age were collected. Body weights were linearly adjusted to 365 days (YW), 548 days (BW18), and 730 days (BW24) of age. Multi-trait animal models included test batch as a fixed contemporary group effect and animal's genetic effect as random. Variance components were estimated using REMLF90. Body weight reached 52% at yearling compared to the body weight at 24 months of age while frame size measures reached 75 to 87% at yearling depending on measurement position. Heritability estimates of body weights were moderate: YW 0.34 to 0.41, BW18 0.35 to 0.38, and BW24 0.35 to 0.38. Heritability estimates of stature (wither height or hip height) were somewhat higher (0.36 to 0.49) than those of chest volume (chest girth, depth, and width of chest), body length or rump volume (rump or pelvic widths, rump length, or hip bone width) measurement traits were moderate: 0.26 to 0.55 at yearling, 0.24 to 0.38 at 18 mo of age, and 0.24 to 0.49 at 24 mo of age. Genetic correlation between body weight traits and frame size traits were high. Genetic correlation between body weight traits and stature traits were rather stable over the ages: 0.45 to 0.70. However, the genetic relationships of the other frame size traits with body weight traits became higher as animals grew. Chest or rump volume traits except chest girth measured at yearling were moderately correlated genetically with BW18 (0.33 to 0.54) or with BW24 (0.30 to 0.51). Chest or rump volume size traits except chest girth measured at 18 or 24 mo of ages were highly correlated genetically with BW18 (0.48 to 0.75) or with BW24 (0.45 to 0.74). Chest girth measured at three age groups had high genetic correlations with body weight traits (0.61 to 0.85). To conclude, overall skeletal size traits - wither height, hip height, and body length are moderately to highly correlated genetically with body weight traits without great differences over ages. Chest or rump volume size traits measured later than yearling age reflect the individual differences

in the degree of fattening, thus changing the genetic relationships with body weight traits.

Key Words: frame size, genetic correlation, Hanwoo
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200 Genetic correlation between yearling body size traits and carcass traits in Hanwoo steers.

Y. H. Choy*, A. Mahboob, T. Choi, B. Park, and M. N. Park, *National Institute of Animal Science, Chonan, Republic of (South) Korea.*

The objective of this study was to estimate genetic correlation between yearling body size measurement traits and carcass traits in Hanwoo steers on a progeny test station in South Korea. Body weights and ten frame size measurement records on 6,832 bulls and 5,916 steer progeny of the bulls born between 1996 and 2013 and raised at Hanwoo test station from six months of age were collected. Body weights (YW, kg) and frame size measurements (cm) were all adjusted linearly to 365 days of age from measures at six months of age. Steer progeny were slaughtered at 24 months of age, and carcass evaluations of cold carcass weight (CWT, kg), backfat thickness (BFT, mm), eye muscle area (EMA, cm^2), and marbling score (MS, 1 to 9 score; 1 as emaciated to 9 as abundant) were used for analyses. Animal models for live body measurement traits included test batch as a fixed contemporary group effect and a random animal genetic effect. Animal models for carcass traits included date of slaughter as a fixed contemporary group effect and age in days at slaughter as a covariate with a random animal genetic effect. The REMLF90 program was used for variance component estimation for these genetic models. Heritability estimates of live body size measurements were in intermediate range, 0.16 to 0.32 (0.19 for YW, 0.32 for hip height). Heritability estimates of carcass traits were medial to high: 0.36 for CWT, 0.45 for EMA, 0.49 for BFT, and 0.60 for MS. YW was highly correlated genetically with frame size traits (0.43 for chest width to 0.73 for hip height, body length, and rump length). Genetic correlation of YW with CWT was 0.80, with EMA was 0.40, with BFT was 0.02, and with MS was 0.10. Frame size traits were highly correlated genetically with CWT (0.41 to 0.70). Genetic correlations between body size traits and EMA were moderate and positive, 0.17 to 0.40. Those between body size traits and MS were now to null, −0.04 to 0.29. Genetic correlations between body size traits and BFT were low but negative, −0.01 to −0.28. In conclusion, live body size traits are moderately heritable while carcass traits are highly heritable. The genetic correlations of live body size traits with CWT are high and positive, but those with carcass component traits were low to be effectively used for indirect selection early in life.

Key Words: carcass trait, genetic correlation, Hanwoo
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201 Genotype × nutritional environment interaction in a composite beef cattle breed.

E. H. A. Hay*[1] and A. J. Roberts[2], [1]*USDA/ARS/LARRL, Miles City, MT,* [2]*USDA, ARS, Ft. Keogh LARRL, Miles City, MT.*

Environmental effects have been shown to influence several economically important traits in beef cattle. In this study, genetic × nutritional environment interaction was evaluated in a composite beef cattle breed (50% Red Angus, 25% Charolais, 25% Tarentaise). Cows were randomly assigned to be fed levels of harvested supplemental feed from December to March of each year that were expected to result in adequate (ADEQ) or marginal (MARG; ~61% of the supplemental feed provided to ADEQ) levels of protein based on average quality and availability of winter forage. At weaning, daughters from these cows were randomly assigned to either ad libitum (CONTROL) or restricted (RESTRICTED; 80% of control at a common body weight basis) access to feeding for 140 d development post weaning. Similar nutritional treatments were applied to the male offspring. This design resulted in offspring exposed to 1 of 2 prenatal and 1 of 2 postweaning nutritional treatments resulting in four different environments: MARG-CONTROL, MARG-RESTRICTED, ADEQ-CONTROL, and ADEQ-RESTRICTED. Genetic parameters of average daily gain during the 140-d post wean trial (ADG), yearling weight (YW), and ultrasound measurement of fat depth over the rib (FAT) and intramuscular fat (IMF) of 3,020 individuals in the four environments were estimated. The heritabilities estimated using a single trait mixed linear model were: ADG, 0.21, 0.23, 0.19, and 0.21; YW, 0.27, 0.33, 0.20, and 0.26; FAT, 0.30, 0.29, 0.29, and 0.55; IMF, 0.45, 0.51, 0.33, and 0.53 for MARG-RESTRICTED, MARG-CONTROL, ADEQ-RESTRICTED, and ADEQ-CONTROL, respectively. The genetic correlations were also estimated using a multi-trait model; ADG and IMF traits showed correlations less than 0.80 between the four different environments, providing evidence of genetic by environment interaction. The genetic correlation for ADG of MARG-CONTROL and MARG-RESTRICTED was 0.73 and 0.65 of ADEQ-RESTRICTED and MARG-RESTRICTED. The present study demonstrated the existence of genetic by nutritional environment interaction for growth and carcass traits in beef cattle.

Key Words: genetic correlation, genotype × environment, heritability
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202 Residual feed intake is not associated with muscle, fat, or liver expression of growth hormone receptor, insulin-like growth factor i, or beta-adrenergic receptor mRNA in Angus steers.

W. Zheng[1,2], X. Leng[2], M. Vinsky[3], C. Li[3,4], and H. Jiang*[2], [1]*College of Animal Sciences, Nanjing Agricultural University, Nanjing, China,* [2]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg,* [3]*Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Lacombe, AB, Canada,* [4]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The genetic and physiological basis of feed efficiency in beef cattle is unclear. The objective of this study was to test the hypothesis that more efficient cattle might have greater expression of growth hormone receptor (GHR) or beta-adrenergic receptor (ADRB) mRNA in skeletal muscle, fat, or liver, the major target tissues of GH and beta-adrenergic agonists. This hypothesis was based on the fact that both GH and beta-adrenergic agonists can improve feed efficiency in animals. Skeletal muscle, subcutaneous fat, and liver samples were collected at slaughter from top 10 high-residual feed intake (RFI) (1.03 ± 0.12) and top 10 low-RFI (−0.69 ± 0.02) steers selected from a population of 75 Angus steers (422 ± 14 days old). Abundances of GHR, insulin-like growth factor I (IGF1), IGF1 receptor (IGF1R), beta-1 adrenergic receptor (ADRB1), ADRB2, and ADRB3 mRNAs were quantified by real-time RT-PCR using validated primers. As expected, RFI was positively correlated with dry matter intake (DMI) ($R = 0.63$, $P = 0.003$) and feed conversion ratio (FCR) ($R = 0.74$, $P = 0.0002$) but not correlated ($P > 0.05$) with average daily gain (AVG); FCR was negatively correlated with ADG ($R = 0.69$, $P = 0.0008$) but not correlated with DMI ($P > 0.05$). Expression levels of GHR, IGF1, IGF1R, ADRB1, ADRB2, and ADRB3 mRNAs in muscle, fat, and liver were neither different ($P > 0.05$) between high- and low-RFI steers nor correlated ($P > 0.05$) with RFI. Expression levels of GHR and IGF1R mRNAs in muscle and liver and expression levels of IGF1, ADRB1, ADRB2, and ADRB3 mRNAs in muscle, fat, and liver were not correlated ($P > 0.05$) with FCR. However, expression levels of both GHR mRNA ($R = 0.48$, $P = 0.009$) and IGF1R mRNA ($R = 0.47$, $P = 0.002$) in fat were negatively correlated with FCR. Expression levels of GHR, IGF1, and GF1R mRNAs in muscle and fat were positively correlated with ADG ($R = 0.52$ to 0.65, $P = 0.002$ to 0.02), whereas expression levels of GHR mRNA ($R = 0.50$, $P = 0.03$) and IGF1 mRNA ($R = 0.47$, $P = 0.04$) in liver were negatively correlated with ADG. These results suggest expression of GHR, IGF1R, or ADRB mRNA in muscle, fat, or liver does not influence RFI in Angus steers. However, greater GHR and IGF1R mRNA expression in fat may improve feed efficiency, and increased GH and IGF-I in muscle and fat may stimulate body growth in beef cattle.

Key Words: beta agonist, growth hormone, residual feed intake
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203 Genetic parameter estimation for foot structure in American Angus cattle.

L. Wang*, S. P. Miller, K. J. Retallick, and D. W. Moser*, Angus Genetics Inc., St. Joseph, MO.*

To enable breeders to select for correct foot and leg structure to increase productive life of beef cattle, the American Angus Association is developing genetic selection tools for these important traits. The Association accepts categorical 1 to 9 scores, with 5 being ideal, from its members for two traits, foot angle and claw set. Objectives were to explore alternative genetic evaluation approaches for these traits and estimate genetic parameters using 5,722 records collected on Angus bulls and heifers ranging from 320 to 460 days of age. Frequency of observations in the 1 to 9 categories, respectively, were 0, 1, 6, 197, 3,845, 1,468, 166, 34, and 5 for foot angle and 0, 0, 5, 263, 3,251, 1,883, 270, 45, and 5 for claw set. All traits were analyzed using a linear animal model with ASREML 3.0. In addition to a model fitting all phenotypes (1 to 9), each of the traits was also analyzed as two independent traits depending on the score to investigate if foot angles 1 to 5 (steep) were different from 5 to 9 (weak) and claw sets 1 to 5 (spread) were different from 5 to 9 (scissor), with 5 being ideal for each trait. A two-trait model for foot angle and claw set (1 to 9) was used to investigate the genetic correlation. All models included contemporary group (customer, scoring date, sex, and diet type) and weaning creep type as fixed effects, age at measurement as a covariate, animal, and error as random effects. Heritability estimates were 0.34, 0.21, 0.16, 0.25, 0.22, and 0.37, respectively, for foot angle, claw set, spread, scissors, steep, and weak, with a low genetic correlation between claw set and foot angle (0.22) determined with the bivariate model. The moderate heritability estimates for these foot score traits indicate that genetic evaluations are warranted. The traits of scissor and weak (5 to 9) appear to have a slightly higher heritability than the respective overall (1 to 9) traits, but it is not clear if splitting the traits is warranted for genetic evaluation. These genetic parameters will play an important role in the American Angus Associations development of genetic evaluations for foot structure.

Key Words: beef cattle, foot score, heritability
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204 Genomic study for beef tenderness in a polled Nelore cattle population. R. M. O. Silva*[1], L. Mendes de Castro[2], E. Peripolli[3], F. B. Lopes[2], A. S. C. Pereira[4], F. Baldi[1], G. J. M. Rosa[5], L. C. A. Regitano[6], R. D. Sainz[7], and C. Ulhôa Magnabosco[8], *[1]School of Agricultural and Veterinarian Sciences, Sao Paulo State University - FCAV/UNESP, Jaboticabal, Brazil, [2]Embrapa Cerrados, Brasília, Brazil, [3]Sao Paulo State University (UNESP), School of Agricultural and Veterinarian Sciences (FCAV), Department of Animal Science, Jaboticabal, Brazil, [4]State University of São Paulo, Jaboticabal, Brazil, [5]University of Wisconsin-Madison, Madison, [6]Embrapa Southeast Livestock, Sao Carlos, Brazil, [7]University of California, Davis, [8]Brazilian Agricultural Research Corporation (EMBRAPA), Brasília, Brazil.*

This study was carried out to identify genomic regions associated with beef tenderness (Warner-Bratzler shear force, WBSF) and to evaluate the prediction ability using preselected markers based on the genome-wide association study (GWAS) results in an experimental Nelore cattle population. The dataset was provided by Guaporé Agropecuária S/A – OB Ranch, located in Mato Grosso State, Brazil and by the Brazilian Agriculture Research Corporation (EMBRAPA-Cerrados), located in Goiás State, Brazil. The animals, born from 2002 to 2010, were slaughtered at 25 months of age. Twenty-four hours after the slaughter, 436 samples with 2.5 cm of longissimus dorsi muscle, from the 10th to 13th rib of the left half-carcass were obtained to measure WBSF. Part of the studied animals (61) were genotyped using a high-density SNP panel (BovineHD BeadChip assay 777k, Illumina Inc., San Diego, CA) and part (548) were genotyped with a lower-density 80k BeadChip (GeneSeek Genomic Profiler HD BeadChip) and then imputed for a 777k chip through FImpute v. 2.215 software using pedigree and genomic information. After genomic data quality control, there were available 375,678 SNP and 599 genotyped animals. The single-step GWAS was used to identify genomic regions associated with the phenotypes. The traditional genetic evaluation and the single-step genomic BLUP were run using a single-trait animal model that included the fixed effect of sex, slaughter control number, and the linear effect of age of slaughter and the random effect of animal. Confirming the polygenic nature of WBSF, 17 windows (located in 9 different chromosomes) were found to be associated with WBSF. Several genes that have their functions related to energy metabolism and fat and calcium ion were found in the associated windows. As meat quality is a multidimensional concept and fat enriches tenderness, it is important to highlight these genes that act on energy metabolism and fat. Also, the associated window that explained more than 12% of the additive genetic variance is very close to the region where the CAST gene is located. The inclusion of genomic information into the traditional genetic evaluation increased 8.11% the accuracy of the evaluation. In addition, using only the preselected markers (5k) increased 21.62% and 74% of the ability to predict EBV and phenotype, respectively, compared to using high density markers. The results showed that using genomic information could help to better understand the genetic architecture of beef tenderness and increase the prediction ability of genetic evaluation.

Key Words: beef quality, *Bos indicus*, GWAS
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205 Estimates of genetic parameter for tick count and infection level of *Babesia Bovis* traits in Braford and Hereford cattle. L. Cavani*[1,2], F. F. Cardoso[3], C. G. Gomes[3], A. R. Caetano[4], R. Giglioti[2], M. C. D. S. Oliveira[5], and H. N. Oliveira[2], *[1]Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil, [2]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, [3]Embrapa Southern Region Animal Husbandry, Bage, Brazil, [4]Embrapa Genetic Resources and Biotechnology, Brasilia, Brazil, [5]Embrapa Southeast Livestock, São Carlos, Brazil.*

Tick and tick-borne diseases, including babesiosis (*B. bovis*), constitute 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. This study aimed to estimate genetic parameters for tick counts (TC) and infection level of *Babesia bovis* (IB) using Bayesian inference. Tick counts on one side of each animal were obtained from 717 Braford and 43 Hereford cattle in farms located at Rio Grande do Sul State, Brazil. The tick counts were collected when average individual infestation exceeded 20 engorged tick females with at least 4.5 mm in length. Blood samples were collected in tubes containing EDTA for DNA extraction. *B. bovis* quantification was performed using both the qPCR technique from genomic DNA of each animal with specific primers for this protozoan and the absolute quantification method. The TC and IB records were transformed in log base 10 (x + 1), and the means were 1.334 and 1.511 for TC and IB, respectively. The model included fixed effects, random effects that represented additive genetic direct effects of each animal, and residuals. The fixed effects were composed by contemporary group (same farm, sex, year and season of birth, management, and tick count date). Also, the effects of Nelore breed proportion, heterozygosity, recombination loss, and linear and quadratic coefficients for animal age at counting in days (358 to 697) were included in the model as covariates. Contemporary groups with less than 4 individuals were excluded from analyzes. The Gibbs sampler in a bivariate animal model analysis using GIBBSF90 software was run for 500,000 iterations (burn-in period of 50,000). Moreover, the convergence of the Markov chains was checked based on tests by using the coda package of R software. The mean additive genetic variances were 0.018 and 0.080 for TC and IB, respectively. The mean residual variances were 0.144 and 0.356 for TC and IB, respectively. The mean h^2 were 0.109 and 0.182 for TC and IB, respectively. The genetic correlation was 0.38 between TC and IB. The selection response of Braford and Hereford cattle for IB trait will have greater magnitude than for TC, and moderate correlated response between these two traits would be expected.

Key Words: genetic correlation, heritability, qPCR
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206 Impact of multiple sire mating system on the accuracy of genomic breeding value prediction in a beef cattle population under selection.

R. L. Tonussi*[1], R. M. O. Silva[2], A. F. B. Magalhães[2], E. Peripolli[1], B. F. Olivieri[1], F. L. B. Feitosa[1], A. S. C. Pereira[3], R. B. Lôbo[4], C. U. Magnabosco[5], I. Aguilar[6], and F. Baldi[1], *[1]Sao Paulo State University (UNESP), School of Agricultural and Veterinarian Sciences (FCAV), Department of Animal Science, Jaboticabal, Brazil, [2]Sao Paulo State University - FCAV/UNESP, Jaboticabal, Brazil, [3]University of Sao Paulo (USP), School of Veterinary Medicine and Animal Science (FMVZ), Department of Animal Science (VNP), Pirassununga, Brazil, [4]National Association of Breeders and Researchers - ANCP, Ribeirão Preto, Brazil, [5]Brazilian Agricultural Research Corporation - EMBRAPA, Brasília, Brazil, [6]Instituto Nacional de Investigación Agropecuaria - INIA, Las Brujas, Uruguay.*

The objective of this study was to investigate the application of BLUP and ssGBLUP in different scenarios of uncertain paternity using data from a Nellore cattle population. The analyzed data set was provided by the National Association of Farmers and Researchers (ANCP). The data set contained information from 18 Nellore herds located in the southeast and mid-west regions of Brazil, which participate in the ANCP breeding program. A total of 60,325 records for weight adjusted at 450 days (W450) were used. The mean value ± standard deviation was 290.20 ± 50.26 kg, and the contemporary groups (CG) were defined as farm, year of birth, season of birth, sex and management group. Records with values above or below the range of 3.5 standard deviations from the CG mean were excluded, as well as CGs with less than five animals. The variance components were estimated using BLUP and ssGBLUP methods. The relationship matrix (A) was created with different proportions of animals with unknown sires (0, 25, 50, 75, and 100% of multiple sires). All models included contemporary groups as fixed effects. The breeding value (EBV/GEBV) accuracy was calculated according to BIF and evaluated in each scenario with eight groups of animals: ALL = all animals in the population, BULL = only bulls with ten or more progenies, GEN = genotyped animals, GENwithPHEN = genotyped animals with phenotypes, GENwithoutPHEN = genotyped animals without phenotypes, YOUNG = male and female young animals without phenotypes, YwithoutGEN = young animals without phenotypes and genotypes, and YwithGEN = young animals without phenotypes and with genotypes. The additive genetic variance decreases as the proportion of multiple sire increased in the population for both methods. Prediction accuracies ranged from 0.02 to 0.46 and from 0.12 to 0.48 for BLUP and ssGBLUP, respectively. In general, for all scenarios, the EBV/GEBV prediction accuracy decreased as the proportion of MS in the population increased; however, the decrease of EBV accuracy was more intense compared to GEBV accuracy, which was of 8.8%, 4.3%, 46.2%, 27.3%, 82.4%, 25.0%, 18.8%, and 87.5% for ALL, BULL, GEN, GENwithPHE, GENwithoutPHE, YOUNG, YwithoutGEN, and YwithGEN groups, respectively. The breeding values for W450 were influenced by presence of the paternity uncertainly in the pedigree. The presence of paternity uncertainly affects more intensively the breeding value of young animals. The genotyped young animals were benefited from the application of ssGBLUP, particularly in situations with missing pedigree.

Key Words: genetic evaluation, missing pedigree, uncertain paternity
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207 Genome-wide association study for beef fatty acid profile using haplotypes in Nellore cattle.

F. L. B. Feitosa*[1], C. U. Braz[1], M. V. A. D. Lemos[1], M. P. Berton[1], R. M. D. O. Silva[1], R. L. Tonussi[1], E. Peripolli[1], B. F. Olivieri[1], A. M. Ferrinho[2], L. F. Mueller[2], J. D. J. M. Furlan[3], A. S. C. Pereira[3], L. G. de Albuquerque[1], F. S. Schenkel[4], and F. Baldi[1], *[1]Sao Paulo State University (UNESP), School of Agricultural and Veterinarian Sciences (FCAV), Department of Animal Science, Jaboticabal, Brazil, [2]University of Sao Paulo (USP), School of Animal Science and Food Engineering (FZEA), Department of Animal Science (ZAZ), Pirassununga, Brazil, [3]University of Sao Paulo (USP), School of Veterinary Medicine and Animal Science (FMVZ), Department of Animal Science (VNP), Pirassununga, Brazil, [4]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

The aim of this study was to identify genomic regions associated with the total amount of saturated (SFA), monounsaturated (MUFA), and polyunsaturated (PUFA) fatty acids in the beef of Nellore cattle. The investigated dataset contained records from 963 Nellore bulls, about two years old, finished in feedlot (90 days). Meat samples of Longissimus dorsi muscle, between the 12th and 13th ribs of the left half-carcasses, were taken to measure the fatty acids (FAs). FAs were quantified by gas chromatography (GC-2010 Plus - Shimadzu AOC 20i autoinjector) using SP-2560 capillary column (100 m × 0.25 mm diameter with 0.02 mm thickness; Supelco, Bellefonte, PA). The animals were genotyped using the high-density SNP panel (BovineHD BeadChip assay 777k, Illumina Inc., San Diego, CA). Those SNP markers with minor allele frequency less than 0.05, call rate less than 90%, monomorphic, located on sex chromosomes, and those with unknown position were removed from the analysis. After genomic quality control, 470,007 SNPs and 868 animals were available for the analyses. Missing genotypes were imputed using FImpute software. Genotypes were phased to haplotypes using fastPHASE software and then haplotype blocks were defined based on linkage disequilibrium using HaploView software. Genome-wide association analyses were performed considering one haplotype at a time. The model included fixed effects of contemporary group (92 levels), haplotype (linear regression on number of copies), and age at slaughter as a linear covariate. Bonferroni correction was applied at 5% significance to adjust for multiple tests. A total of 83,883 haplotypes were included in the genome-wide association analyses. From those haplotypes, 292, 17, and 31 were significantly associated ($P < 0.05$) with SFA, MUFA, and PUFA, respectively. Most associations were found on BTA17, BTA3, BTA1, BTA8, BTA25, and BTA2. These significant regions harbor genes such as GALNT12, SLC6A7, CAMK2A, SYTL3, EPAS1, PRKCB, EPHA6, MPZL1, UHMK1, KIRREL, FYN, LTBP1, PRKCE, SIK2, TOM1L1, NF1, DNAJA3, SH2B2, AFAP1L2, and AGAP1. These genes are involved in lipid metabolism, reproductive hormone receptors, transport and use of fatty acids and cholesterol, phospholipid and membrane hydrolysis and biosynthesis, energy metabolism, and protein kinase synthesis. Thus, the identification of these associated haplotypes may contribute to further studies to validate these regions and prospect candidate genes that would be useful for breeding programs to improve the beef quality of Nellore cattle.

Key Words: *Bos indicus*, genetic markers, meat quality
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208 Fillet yield and quality traits as selection criteria for Nile tilapia (*Oreochromis niloticus*) breeding.

A. L. Garcia*[1], C. Sary[2], H. M. Karin[2], R. P. Ribeiro[2], D. A. L. Lourenco[1], S. Tsuruta[1], and C. A. Oliveira[2], *[1]University of Georgia, Athens, [2]Universidade Estadual de Maringa, Maringa, Brazil.*

Nile Tilapia breeding programs have been focused on growth improvement by selecting for either body weight (BW) or daily weight gain (DWG). Along with growth traits, yield and quality traits are also of great importance in livestock breeding. Our objective was to evaluate the feasibility of including fillet yield and quality traits as selection criteria for improving performance in Nile tilapia. The fish used in this study came from a population of 3 generations undergoing selection (Aqua America Company, Brazil). Pedigree information was available for 5,263 fish. Phenotypes for body weight at 290 days (BW290) and daily weight gain (DWG) were measured on 2,585 males and females, fillet weight (FW) and fillet yield (FY) were measured on 1,198 males, and fillet fat content (FAT) was measured on 1,136 males. Variance components were estimated in single and two-trait models using GIBBS1f90, and the post-analyses were carried out using POSTGIBBSF90, both from the BLUPF90 family of programs. For all analyses, spawning was considered as a random common environmental effect; harvest weight, weight at tagging, and age were used as covariables for DWG and BW; body weight at slaughter was used as a covariable for FW, FY, and FAT; floating cage and sex were included as fixed effects for all traits and for BW290 and DWG, respectively. Heritability estimates for DWG, BW, and FW were close to 0.23, whereas FY had the highest heritability (0.32) and FAT had the lowest (0.20). Genetic correlations of DWG with FY and FAT were −0.09 and −0.4, respectively; BW290 with FY and FAT were −0.1 and −0.32, respectively. The only positive correlation was between FY and FAT (0.6). Negative correlations between growth and fillet traits indicate an increase in guts and carcass weight in bigger fish, which is not desirable. Based on the estimated heritabilities, the genetic improvement of fillet yield and quality traits can be effective and should be included in the selection criteria. These results are particularly important for FW and FY since there is a market interest on increasing fillet yield. In addition, fillet quality traits such as FAT are also of interest to enhance meat quality.

Key Words: genetic correlations, meat quality, tilapia breeding
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209 Prospecting genomic regions associated with columnaris disease in two rainbow trout breeding populations.

R. M. O. Silva*[1,2], R. L. Vallejo[1], J. P. Evenhuis[1], T. D. Leeds[1], G. Gao[1], J. E. Parsons[3], K. E. Martin[3], D. A. L. Lourenco[2], and Y. Palti[1], *[1]National Center for Cool and Cold Water Aquaculture, Agricultural Research Service, United States Department of Agriculture, Kearneysville, WV, [2]University of Georgia, Athens, [3]Troutlogde, Inc., Sumner, WA.*

Flavobacterium Columnare, the causative agent of columnaris disease (CD), is distributed around the world in fresh water sources, infecting freshwater finfish species. Recently, it has been identified as an emerging problem for the rainbow trout aquaculture industry in the U.S. Two live-attenuated vaccines have been commercialized, but their efficacy in rainbow trout is still not clear. The purpose of this study was to prospect genomic regions that explain large portion of the additive genetic variance of CD resistance in rainbow trout. Two important aquaculture populations were investigated: The National Center for Cool and Cold Water Aquaculture (NCCCWA) odd-year line, with resistance to bacterial cold water disease (BCWD), and the Troutlodge, Inc., May odd-year (TLUM) nucleus breeding population, which provided 54,350 and 36,265 pedigree records, in which 8,453 and 3,986 fish had CD resistance phenotype records, respectively. Fish that survived to 21 days post immersion challenge were recorded as resistant (phenotype = 2), and those that did not were rated as susceptible (phenotype = 1). Genotypes for 57k SNP (Affymetrix Axiom®) were available for 1,185 and 1,137 fish from NCCCWA and TLUM, respectively. The SNP effects and variances were estimated using the weighted single-step genomic BLUP approach for genome-wide association (WssGBLUP), which uses pedigree, genotypes, and phenotypes from genotyped and ungenotyped animals. The weighting strategy accounted for 1 Mb moving SNP-windows. Genomic regions that explained more than 1% of the additive genetic variance were considered associated with CD resistance. A total of 13 windows located on six chromosomes were found to be associated with CD resistance in the NCCCWA population: two windows, located at 59 to 60 Mb and 61 to 62 Mb on chromosome Omy17, explained 12% and 11.33% of the genetic variance for CD resistance, respectively. In the TLUM population, a total of 16 windows located on nine chromosomes were detected. Only three similar windows (located on two chromosomes) were detected in both populations. The results suggest that CD resistance has an oligogenic architecture, and the SNP windows found to be associated with CD are not informative enough for selection decisions across populations. A moderate positive genetic correlation has been previously shown between CD and BCWD resistance in the NCCCWA population. One factor that might have contributed to detecting different QTL for CD resistance in the two populations is the five generations of selective breeding for BCWD resistance applied to the NCCCWA population in contrast to no selection pressure for disease resistance in the TLUM population.

Key Words: columnaris disease resistance, GWAS, rainbow trout
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210 Genetic analysis of production traits in different parities using multiple trait animal models in a Thai Landrace-Yorkshire swine population.

U. Noppibool[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

Number of piglets born alive (NBA) and litter birth weight (LTBW) in different parities of 2,124 Landrace (L), 724 Yorkshire (Y), 2,650 Landrace × Yorkshire (LY), and 4,332 Yorkshire × Landrace (YL) sows were analyzed using multiple trait animal models (MTM). All sows farrowed from 1989 to 2013 in a commercial swine population, and all of them had four parities. The MTM contained the fixed effects of farrowing year-season, additive genetic group of the sow, heterosis of the sow, heterosis of the litter, and age at first farrowing and the random effects of sow, boar, and residual. A MTM that considered each trait in each parity as a separate trait (MTM-PAR) was compared with a MTM that considered each trait measured in the first, second, and the sum from the third to the last parity (MTM-SPAR) as three separate traits. The estimates of heritability from MTM-PAR ranged from 0.04 ± 0.01 (second parity) to 0.09 ± 0.02 (fourth parity) for NBA and 0.07 ± 0.02 (second parity) to 0.16 ± 0.02 (third parity) for LTBW. Estimates of heritabilities for MTM-SPAR were low for all traits, ranging from 0.04 ± 0.01 (first and second parity) to 0.09 ± 0.02 (third to last parity) for NBA and 0.06 ± 0.02 (second parity) to 0.08 ± 0.02 (third to last parity) for LTBW. Estimates of genetic correlations in MTM-PAR were high for NBA (0.50 ± 0.18 to 0.96 ± 0.02) and LTBW (0.72 ± 0.1 to 0.93 ± 0.07), except between NBA in the first parity with the second (0.29 ± 0.24) and in the fourth parity (0.50 ± 0.18). Estimates of genetic correlations for MTM-SPAR were low to moderate for NBA (0.11 ± 0.19 to 0.54 ± 0.21) and LTBW (0.12 ± 0.17 to 0.23 ± 0.18) but high between LTBW in the first and the second parities (0.83 ± 0.11). Genetic correlations for NBA and LTBW were higher for MTM-PAR than for MTM-SPAR. Results suggested that the MTM that treated each parity as a different trait should be used for genetic evaluation and selection for NBA and LTBW in this swine herd.

Key Words: genetic parameters, multiple trait model, swine
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211 Joint genome-wide association analysis of continuous and discrete traits.

P. Sumreddee*[1], S. Toghiani[1], S. E. Aggrey[2,3], and R. Rekaya[1,3,4,5], [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,* [4]*Department of Animal and Dairy Science, The University of Georgia, Athens,* [5]*Department of Statistics, University of Georgia, Athens.*

Genome-wide association studies (GWAS) are becoming a standard tool for the genetic dissection of complex traits and for the estimation of genomically enhanced breeding values. Although linear regression models for implementation of association studies were used to analyze continuous and discrete responses, their implementation was always in a univariate context. Arguably, the joint analysis of continuous and discrete traits in GWAS will be advantageous because of a better use of available information and the existing correlation structure among traits. However, a joint association analysis for multiple continuous and discrete traits presents several theoretical and implementation complexities. In the presence of binary traits in the analysis, the residual (co)variance matrix is not completely random due to the fixation of some diagonal elements, which complicates substantially the sampling process. The residual updating algorithm often used to solve the system of equations in GWAS analyses requires some changes to accommodate the changing liabilities of discrete responses each round of the sampling process. Missing traits, more frequently for discrete responses, add another layer of implementation complexity. In order to investigate the advantages of a joint analysis of continuous and discrete responses, a real data based simulation was carried out. Two continuous, one binary, and one multinomial trait with heritability of 0.3, 0.4, 0.1, and 0.1, respectively, and varying covariance structure were simulated. Traits were generated following a linear model that included three systematic effects, 100 QTLs, and error terms. The data consisted of 1,365 animals genotyped for 41,694 SNPs. A random missing rate of 10% was assumed for the discrete responses. Each of the four traits was analyzed separately using either a linear (for continuous responses) or a threshold (for discrete responses) model. The four traits were also analyzed jointly using a linear-threshold model. For the univariate and multivariate analyses, a BayesA-like approach was implemented. For all analyses, a 5-fold cross validation was carried out. Using the univariate analyses, the accuracy (correlation between true and estimated breeding values) was 0.48, 0.62, 0.31, and 0.28 for the continuous, binary, and categorical traits, respectively. Multivariate analyses resulted in a 4 to 17% increase in the accuracy of discrete traits dependent of the covariance structure. However, for the continuous responses, the accuracy increased only when the correlations between traits exceeded 0.1. For moderate to high correlations, the accuracy of all continuous traits increased by 2 to 6%. Joint analyses resulted in substantial increase in computational costs.

Key Words: genome-wide association studies (GWAS), joint analysis, regression models
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212 Abstract withdrawn.

213 Association of microsatellite profile with phenotypic traits of semi-domesticated reindeer.

V. R. Kharzinova*[1], T. V. Karpushkina[1], A. V. Dotsev[1], A. D. Solovieva[1], T. M. Romanenko[2], G. Brem[1,3], and N. A. Zinovieva[1], *[1]L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Narjan-Mar Agricultural Experimental Station, Narjan-Mar, Russian Federation, [3]Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.*

Reindeer herding is the historical branch of animal husbandry in the northern regions of the Russian Federation. There are four reindeer breeds, the most numerous of which is Nenets (with over 800,000 reindeer). For further development of the reindeer herding, in addition to traditional breeding methods, it is necessary to apply modern technologies, such as genetic analysis. The aim of the current work was to identify the possible association between microsatellites loci and phenotypic traits of the Nenets reindeer breed. DNA was extracted from tissue samples of 43 female individuals using Nextech column (Agrobiogen Biotechnologie GmbH, Munich, Germany) according to the manufacturer's recommendations. Fourteen microsatellite loci (NVHRT21, NVHRT24, NVHRT76, RT1, RT6, RT7, RT9, RT27, RT30, RT25, RT13, NVHRT03, RT5, and NVHRT73) were selected to examine the associations between marker genotypes and eight phenotypic traits: height at the withers (HaW), chest depth (CD), chest width (CW), chest girth (CG), wrist girth (WG), body length (BL), head length (HL), and body weight (BW). Associations between the genotypes and the traits were evaluated using the one-way ANOVA model. Results were considered statistically significant if the P-value was less than 0.05. All of the microsatellites loci were polymorphic, and the number of alleles ranged from three (NVHRT03) to six (RT25 and NVHRT73). The RT6 marker was associated with four traits: BW ($P < 0.001$), CG ($P < 0.05$) BL ($P < 0.01$), HL ($P < 0.01$), whereas the RT27 marker was linked to three traits: HaW ($P < 0.05$), BW ($P < 0.05$), and HL ($P < 0.01$). The variability of the HL trait was also associated with two loci: RT25 ($P < 0.05$) and NV 24 ($P < 0.001$). The RT30 marker was only significantly associated with height at the withers ($P < 0.05$). Thus, our study revealed that five microsatellite loci were significantly associated with five phenotypically important traits (HaW, HL, BW, CG, and BL), and these markers could be potentially used for the improvement of the reindeer herding breeding program. This research was funded by Russian scientific foundation project No. 16-16-10068.

Key Words: microsatellite, phenotypic traits, semi-domesticated reindeer
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214 The leptin R84Q mutation is present in Charollais sheep, increasing fat deposition of carrier crossbred lambs.

J. A. Martínez-Quintana*, D. E. Briones, F. A. Rodríguez-Almeida, M. E. Burrola-Barraza, and I. A. García-Galicia, *Universidad Autónoma de Chihuahua, Chihuahua, Mexico.*

This study investigated the presence of single nucleotide polymorphisms (SNPs) in exon 3 of the ovine leptin gene (*oLEP*) in Mexican sheep and their potential phenotypic effects. For that purpose, PCR-SSCP analyses and sequencing of genomic DNA were performed for a set of experimental crossbred lambs. A G251A SNP was detected, which results in a R84Q change in the deduced protein sequence. The G251A mutation was then investigated through real-time PCR allelic discrimination analyses. The results showed that the genotype frequencies (n = 45) for wild type (WT), heterozygous, and mutant homozygotes were 95.6, 4.4, and 0%, respectively. The presence of the G251A SNP in another set of F_1 lambs sired by Suffolk, Hampshire, Charollais, Texel, and Dorper rams was determined. Among other phenotypes, average daily feed intake (FI56d) and average daily weight gain (ADG56d) on the first 56 d of a performance test were quantified. In addition, back fat thickness (BFT), kidney fat (KF), and percentage of carcass fat tissue (CFT) at slaughter (target BW of 40 and 42 kg for females and males, respectively) were assessed. Five out of 64 lambs were carriers; interestingly, all of them were sired by Charollais rams and represented 20.8% (n = 24) of that breed group. Even though no differences ($P > 0.05$) were observed between levels of sex or genotype for FI56d and KF, heterozygous males were located between the 85 and 95 percentiles for FI56d. The ADG56d was higher ($P < 0.01$) for males (0.303 ± 0.01 kg) than for females (0.253 ± 0.01 kg), but no differences ($P > 0.05$) were found by genotype, although the data for heterozygous lambs were in the lower half of the percentiles. In females, BFT (4.66 ± 0.88 and 3.55 ± 0.24 mm) and CFT (32.0 ± 1.96 and 23.7 ± 2.35%) were higher ($P < 0.05$) in carriers than in WT animals. Finally, 172 registered full blood Charollais from four different flocks in Mexico were genotyped for the G251A SNP. The frequency of carriers was only 1.2%. We concluded that the R84Q mutation in exon 3 of the *oLEP* gene in Charollais is related to fat deposition in feeder lambs; however, its frequency is low.

Key Words: fat deposition, ovine leptin gene, R84Q mutation
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215 Effect of breed (local, imported, and crossbreed) on turkey egg measurements.

O. T. Abanikannda[1], O. A. Oyeleke[2], O. N. Ottun[3], F. H. Abanikannda[3], and A. O. Giwa*[1], [1]*Lagos State University, Ojo-Lagos, Nigeria,* [2]*La Trobe University, Melbourne, Australia,* [3]*University of Lagos, Akoka-Lagos, Nigeria.*

The egg, a biological structure intended by nature for reproduction, protects and provides a complete diet for the developing embryo and serves as the principal source of food for the first few days of the chick's life. This study aims to assess the quality of eggs used for incubation, which to a very large extent determines fertility and hatchability recorded in hatchery operations. An initial total of 2000 eggs from three different breeds (local, imported, and their cross) of turkey hens, all between the ages of 51 and 60 weeks, were collected over a period of thirty days. Hens were raised on a litter floor and pen-mated using commercially accepted management practices. The eggs were tagged at the sharp end indicating breed and egg number. All eggs were measured soon after lay and stored prior to incubation. Measurements included egg weight, egg length, egg width, and vertical and horizontal circumferences. The weight loss at the 25th day of incubation and shape index of each egg were also computed. All statistical analyses (exploratory, descriptive, general linear model (GLM), and Tukey honestly significant difference post hoc comparisons) were done with Minitab 17® Statistical Software. Data were scrutinized for normality, and outlier values for all variables across the three breeds were eliminated, resulting in only 1930 eggs included in the final analyses. With the exception of horizontal circumference, breed had significant ($P < 0.05$) influence on all other variables studied. The imported breed consistently had higher values on all variables except incubation weight loss and shape index (Table 215). However, the performance of the crossbreed was below expectation as it did not reflect any improvement on the values obtained in the local breed and was mostly less than the mid-parental average. This study revealed that crossbreeding the imported with the local breed did not yield any significant improvement in the performance of the crossbreed. Thus, selecting higher performing local birds for breeding purposes will lead to faster genetic gain than crossbreeding the local with the imported breed.

Key Words: crossbreeding, egg, turkey
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Table 215. Descriptive Statistics of Variables Studied

Breed	N	Egg Weight (g)	Egg Length (mm)	Egg Width (mm)	Vertical Circumference (mm)	Horizontal Circumference (mm)	Weight Difference (g)	Shape Index (%)
Local	780	67.27±0.61^b	63.06±0.32^a	44.80±0.12^b	170.10±0.66^a	139.54±0.41	8.72±0.23^a	71.14±0.31^b
Imported	670	69.18±0.70^a	63.78±0.32^a	45.32±0.14^a	171.18±0.70^a	140.49±0.40	8.45±0.28^{ab}	71.14±0.31^b
Crossbred	480	66.97±0.65^b	61.29±0.31^b	45.05±0.13^{ab}	166.50±0.73^b	139.63±0.51	7.75±0.30^b	73.57±0.32^a
Combined	1930	67.86±0.39	62.87±0.20	45.04±0.08	169.58±0.42	139.89±0.25	8.38±0.15	71.75±0.20

Means with different superscripts within the same column differ significantly ($P < 0.05$).

216 Genomic regions and pathways associated with resistance to gastrointestinal parasites in tropical sheep breed.

M. P. Berton*[1], R. M. D. O. Silva[1], E. Peripolli[1], N. B. Stafuzza[2], J. Fernández[3], M. Saura[3], B. Villanueva[3], M. A. Toro[4], G. Banchero[5], P. S. Oliveira[6], J. P. Eler[7], F. Baldi[1], and J. B. S. Ferraz[7], *[1]Department of Animal Science, School of Agricultural and Veterinarian Sciences, Sao Paulo State University, Jaboticabal, Brazil, [2]Departamento de Ciências Exatas, Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista, Jaboticabal, Brazil, [3]Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain, [4]Animal Production Department, Universidad Politecnica de Madrid, Madrid, Spain, [5]INIA, Colonia, Uruguay, [6]University of Sao Paulo, Pirassununga, Brazil, [7]NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil.*

The aim of this study was to estimate variance components and to identify genomic regions and pathways associated with resistance to gastrointestinal parasites, particularly *Haemonchus contortus,* in Santa Inês sheep, a Brazilian breed adapted to tropical climate. The degree of anemia assessed by the FAMACHA card (FAM) and the egg counts per gram of feces (EPG) were evaluated to verify the resistance to gastrointestinal parasites. A total of 576 animals were genotyped using 12,785 SNPs of the Ovine SNP12k BeadChip (Illumina, Inc.). The variance components were estimated using a single trait model by single step genomic BLUP (ssGBLUP) procedure. The overall LD mean between marker pairs measured by r^2 was 0.23. Heritability estimates were low for EPG (0.11) and high for FAM (0.35). A total of 22 and 21 important windows for EPG and FAM traits were identified. The results of the enriched genes and functional grouping analyses showed that genes associated with FAM and OPG are involved in functions related to the body's immune and defense response. The *CCL28* gene located in OAR16 identified both for EPG and FAM acts as a chemotactic for CD4 and CD8 inactive T cells. The metabolic pathway involved in the *CCL28* gene and in other genes associated with EPG and FAM, which are related to immunoglobulin synthesis in the intestine. The high heritability observed for FAM suggests that good genetic progress should be possible in selective breeding programs for Santa Inês sheep besides the fact that the FAM is the most precise method to identify an infection by *Haemonchus* when compared to EPG. This study reported for the first time estimates of linkage disequilibrium between markers and genetic parameters for traits related to gastrointestinal parasite resistance in the Santa Inês sheep breed.

Key Words: GWAS, linkage disequilibrium, parasite resistance
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COMPANION ANIMALS

217 Outdated perceptions influence the acquisition of pet dogs in the United States and quietly reshape the dog market place.

P. Strand*[1], J. New[2], F. O. Smith[3], and B. Reichman[4], *[1]National Animal Interest Alliance, Portland, OR, [2]University of Tennessee, Knoxville, [3]Orthopedic Foundation for Animals, Burnsville, MN, [4]National Animal Interest Alliance, Port Murray, NJ.*

Introduction: As of 2015, 44% of American households had at least one dog, with recent surveys indicating 70–80 million in U.S. homes and nearly 7 million dogs needed annually just to replace the ones that die each year.[1,2] Given the popularity of dogs in the U.S. and the economic activity surrounding their acquisition, it is surprising how little notice has been paid to the changing sources of dogs available to the public today. The objective of this study was to examine consumer perceptions and preferences regarding U.S. dog acquisition and to consider how current trends and perceptions impact the availability, type, and quality of pet dogs in the future. Methods: An online survey was administered to 1000 respondents. The survey asked questions about current dog ownership, future pet dog acquisition plans, consumer dog preferences (e.g. size, breed), and consumer beliefs regarding dog overpopulation. Results: About half (49.3%) of respondents currently owned at least one dog and 38% of respondents anticipated acquiring a new dog within the next 5 years. The two most important characteristics impacting this decision were the dog's predictable size (42.8%) and purebred status (41.2%). When asked whether the U.S. had a surplus of dogs based on their perception of the number of dogs entering animal shelters, 63.7% of respondents believed there was a surplus, and of these, 58.8% thought that the domestic surplus of dogs was getting worse. Most respondents (66.6%) were not aware that some animal shelters import dogs from other states or countries. While 43.7% of respondents were supportive of importation of dogs from other states, only 16% were supportive of importing dogs from other countries. Discussion: The study confirmed high levels of dog ownership and support for future dog acquisitions and identified consumer preferences for specific types of dogs. The study also revealed that prospective dog owners were uncertain about the type of dogs available in animal shelters as well as the perception of continued U.S. dog overpopulation. The degree to which these perceptions affect the marketplace is a major concern. While there will always be overseas street dogs available for importation into the U.S., one concern of the study regards the shrinkage of purebred dog segment in response to a belief in domestic overpopulation. References: [1]APPA National Pet Owners Survey, 2015-2016, p. 64–65. [2]U.S. Pet Ownership & Demographics Sourcebook (2012), www.avma.org/KB/Resources/Statistics/

Pages/Market-research-statistics-US-pet-ownership.aspx.

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Key Words: overpopulation, ownership, purebred
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218 Soybean hulls as a sustainable dietary fiber source in canine diets.

K. B. Detweiler*[1], G. M. Davenport[2], and M. Cattai de Godoy[1], *[1]Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, [2]Archer Daniels Midland Company, Decatur, IL.*

Soybean hulls (SBH) are a fiber-rich co-product of the soybean oil extraction process that corresponds to 8% of the soybean seed. Despite being readily available and priced competitively, SBH are underutilized in monogastric nutrition. Thus, the objective of this study was to evaluate the use of SBH as a dietary fiber in canine diets. Four diets were formulated with either SBH, beet pulp (BP), or cellulose (CL) as the main source of dietary fiber (15% total dietary fiber), with the last diet formulated with no supplemental fiber (NF). All animal procedures were approved by the University of Illinois Institutional Animal Care and Use Committee. Eight adult female beagles (mean age = 4.6 ± 0.6 r; mean BW = 12.8 kg ± 1.7 kg) were used in a replicated 4 × 4 Latin square design. Each period consisted of 14 d, with 10 d of diet adaptation followed by 4 d of total fecal and urine collections. At the end of each period, a blood sample was collected and analyzed for serum chemistry. Food was offered twice daily and fed to maintain body weight. The data were analyzed using mixed model procedure of SAS, and $P < 0.05$ was considered statistically significant. Food intake (g/d) on a dry matter basis (DMB) did not differ among treatments. Fecal score was lower ($P < 0.05$) in dogs fed CL in contrast to other dietary treatments, 2.0 vs. 2.3, respectively, using a 5-point scale. As-is and DM fecal outputs did not differ in dogs fed BP, CL, or SBH and were approximately 50% lower ($P < 0.05$) in dogs fed NF. Apparent total tract (ATT) dry matter, organic matter, and gross energy digestibilities were greater ($P < 0.05$) in dogs fed NF when compared to dogs fed BP, CL, or SBH. Dogs fed CL had greater ($P < 0.05$) ATT fat digestibility (94%) among all treatments (avg. 91%). Dogs fed CL and NF had greater ($P < 0.05$) ATT crude protein digestibility, 87% and 86%, respectively, while dogs fed SBH were intermediate (83%) and dogs fed BP were lowest (79%). Serum metabolites were within reference ranges, and animals remained healthy throughout the study. In conclusion, SBH resulted in similar ATT macronutrient digestibility when compared to BP and CL, fiber sources widely used in commercial pet foods. In general, moderate inclusion of dietary fiber sources decreased ATT macronutrient digestibility in dogs in contrast to NF.

Key Words: digestibility, dog, fiber
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219 Effect of fiber type on extruded dog and cat foods.

R. A. Donadelli* and C. G. Aldrich, *Kansas State University, Manhattan.*

To assist weight management, some pet foods are produced with higher fiber content to increase bulking and dilute the energy content of the diet. *Miscanthus* grass (M) is a novel fibrous ingredient that might have similar functionality to standard fibers used by the pet food industry like cellulose (C) and beet pulp (B). The objective of this study was to determine the effects of dried ground M, relative to C, and B on extrusion processing of dog and cat foods. Both dog and cat diets were made with 10% of each M, C, or B and 90% basal ration. Each diet was split into 3 batches and mixed separately prior to production in a commercial scale single screw extruder (E525, ExtruTech, Sabetha, KS). During production, preconditioner water (PW) and steam (PS) and extruder water (EW) and steam (ES) injections and SME were recorded every 20 minutes. At each time point, 5 kibbles were randomly sampled for diameter and length out of the extruder and exiting the dryer. From the kibble and die diameters, sectional expansion ratio index (SEI) was calculated (kD^2/dD^2). Data were analyzed using the GLIMIX procedure of SAS (v. 9.4), and means were separated by significant alpha (5%). For both dog and cat foods, extruder parameters were similar among treatments (cat diets: PW 39.0 $kg*h^{-1}$, PS 28.6 $kg*h^{-1}$, EW 0 $kg*h^{-1}$, ES 18.8 $kg*h^{-1}$, SME 96.2 $W*kg^{-1}$; dog diets: PW 37.7 $kg*h^{-1}$, PS 65.6 $kg*h^{-1}$, EW 0.03 $kg*h^{-1}$, ES 0.8 $kg*h^{-1}$, SME 110.1 $W*kg^{-1}$; averages of all treatments). Kibble characteristics (length, diameter, SEI, weight, volume, and density) were similar among all the cat diets. However, dog diets with B had larger ($P < 0.05$) diameter and SEI than M and C. Diets with B tended ($P > 0.10$) to have slightly greater volume than M and greater density than C. These results indicate that M behaved similar to C during extrusion of cat and dog diets and was consistent with the fiber profile between these two ingredients. The small differences that were observed can be adjusted with modest process modifications. In conclusion, the extrusion parameters were not affected by fiber source, and small differences in kibble characteristics can be corrected with modest process adjustments.

Key Words: cat, dog, extruded diet, *Miscanthus* grass
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220 Crude fiber and total dietary fiber concentrations of popular, premium, and clinical canine diets fed to client-owned osteoarthritic dogs.

Z. T. Traughber*[1], K. B. Detweiler[1], A. K. Price[1], K. E. Knap[2], T. A. Harper[2], K. S. Swanson[1,2], and M. R. C. de Godoy[1], [1]*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana,* [2]*Department of Veterinary Clinical Medicine, University of Illinois at Urbana-Champaign, Urbana.*

Dietary fiber has been used as a nutritional strategy in the management of osteoarthritis (OA) in companion animals. The non-enzymatically digestible quality of dietary fiber has been shown to aid in weight loss through lowering caloric density of pet foods. Crude fiber (CF) is the officially required fiber method in the pet food industry. However, it only measures portions of insoluble fractions of the total dietary fiber (TDF) content. With clinical cases in which weight management is an important outcome, accurate determination of the dietary fiber content is crucial, and the correlation between CF and TDF measurements must be questioned. The objective of this study was to compare the analyzed concentrations of CF and TDF of commercial diets fed to a cohort of client-owned osteoarthritic dogs. These data were derived from a larger study evaluating multiple parameters of the lifestyle, medical, and dietary history of dogs with osteoarthritis. As part of this study, samples of food from client-owned dogs were evaluated for macronutrient composition, and labels of the diets were provided by the dog owners. A total of 51 different diets were collected and subsequently characterized into three main categories: Popular (n = 11), Premium (n = 32), and Clinical (n = 8). Our hypothesis was that the correlation between the analyzed concentrations of CF and TDF would be low due to the extreme variability and the inaccuracy of the CF assay. All diets were analyzed for dry matter and ash (AOAC, 2006), CF (AOAC, 2006), and TDF (Prosky et al., 1988). A linear regression was performed to analyze the correlation between CF and TDF measurements. The correlation between CF and TDF measurements was statistically significant ($P < 0.001$; r = 0.7086). With the exception of one sample, TDF values were greater than CF values. On average (mean ± SD), TDF values were 5.24 ± 2.53 percentage units greater than CF values, with a range of 65% to 332% of the analyzed CF content. These results suggest that CF analysis leads to an incomplete and inaccurate measurement of dietary fiber content and for this reason should not be utilized as a predictor of dietary fiber content.

Key Words: crude fiber, fiber, total dietary fiber
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221 Effects of dietary yeast culture product supplementation on fecal microbial communities of adult healthy dogs.

K. de Melo Santos[1], C. Y. Lin[2], M. A. Brunetto[1], and M. R. C. de Godoy*[2,3], [1]*School of Veterinary Medicine, University of São Paulo, Pirassununga, Brazil,* [2]*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana,* [3]*University of Illinois at Urbana-Champaign, Urbana.*

Prebiotics, defined as dietary fibers that can benefit the host by selectively stimulating the growth and activity of beneficial intestinal bacteria, have gained increased attention in companion animal nutrition. However, limited information is available on prebiotic supplementation and canine GI microbiota using high-throughput molecular techniques. Thus, the aim of this study was to evaluate the effects of increasing dietary concentrations of a yeast culture product (YCP) on fecal microbiota of adult healthy dogs. Eighteen dogs (15.8 ± 7.37 kg mean BW; 3.7 ± 1.62 yr mean age) were randomly assigned to 1 of 3 treatments: control diet (CO), CO supplemented 0.3% YCP (YCP-0.3), and CO supplemented 0.6% YCP (YCP-0.6). The experimental period consisted of 21 d of diet adaptation, followed by 3 d of fresh fecal collection. Three fecal samples were collected from each dog within 15 minutes of defecation and stored at -80°C. Fecal genomic DNA was extracted using Mo-Bio PowerSoil kits. The V4 region of the 16S rRNA gene was amplified and sequenced using Fluidigm specific primers and MiSeq (v3 reagents). High quality sequences were analyzed using QIIME 1.9.1 and mixed procedure of SAS, with $P \leq 0.05$ considered as statistically significant, whereas a $P \leq 0.10$ was considered as a trend. A total of 917,433 reads were obtained. An even sampling depth of sequences per sample (16,300 reads) was used for assessing alpha- and beta-diversity. YCP supplementation did not affect fecal microbial alpha- and beta-diversities. Firmicutes and Fusobacteria made up about 85–88% of bacterial sequences, with Bacteroidetes, Proteobacteria, Actinobacteria, and Deferribacteres contributing to only about 8–12%, 1–3%, 0.1–2%, and <0.02% of sequences, respectively. The predominant fecal bacterial genera were *Clostridium* (18–15%)*, Fusobacterium* (16–25%), and *Blautia* (7–11%). Supplementation of YCP-0.6 tended to increase the relative abundance of *Collinsella* and *Slackia* but tended to decrease ($P < 0.10$) fecal *Coprobacillus*. In conclusion, supplementation of 0.6% of YCP resulted in modest changes in fecal microbial communities of healthy adult dogs. Further studies should evaluate higher doses of YCP supplementation and its effects on fecal microbiota and gut health of dogs suffering from gastrointestinal disorders.

Key Words: canine, microbiota, prebiotic
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222 Avocado meal: A novel dietary fiber source in feline diets.

A. N. Dainton[*] and M. R. C. de Godoy, *University of Illinois at Urbana-Champaign, Urbana.*

As the pet population continues to rise with the growing human population, the need to find new ingredients is more immediate. Oil and pulp of avocados are consumed by humans, but there has been limited use of the peel and avocados that are not fit for human consumption. This experiment tested avocado meal, the processed remainders of avocado processing for oils and human consumption, as a novel and sustainable dietary fiber source in extruded diets for felines. Three diets containing either avocado meal (AM), beet pulp (BP), or cellulose (C) were formulated to meet the AAFCO (2016) nutritional requirements for adult cats. Dietary treatments were formulated to have similar nutrient concentrations. Eight neutered male cats (mean age = 10.8 ± 0.8 years, mean BW = 5.31 ± 1.7 kg, and mean BCS = 5.13 ± 0.4) were randomly assigned to 1 of the 3 dietary treatments using an incomplete replicated 3 × 3 Latin square design. Each period was 3 weeks long with 17 days of diet adaption, followed by 4 days of fecal and urine collection period. All animal procedures were approved by the University of Illinois Institutional Animal Care and Use Committee. Food intake and fecal and urine output were measured and sampled for macronutrient analysis and digestibility calculations. Each fecal sample was scored on a 5-point scale (1 = dry, hard feces, 5 = diarrhea). Blood samples were collected at the end of each period for serum chemistry and complete blood count. The data were analyzed using MIXED procedure, SAS, version 9.4. There was no dietary treatment effect ($P > 0.05$) on total fecal output or daily fecal output. Daily food intake (dry matter basis) did not differ ($P > 0.05$) among dietary treatments. Similarly, apparent total tract digestibilities of dry matter and organic matter were not affected ($P > 0.05$) by diet. Apparent total tract digestibility of crude protein differed ($P < 0.05$) across all diets, with diet C having the greatest digestibility (87.35%), followed by BP (82.82%) and AM (78.00%) diets. Fecal scores for BP (2.48) and C (2.18) were significantly different ($P < 0.05$), whereas AM (2.44) did not differ ($P < 0.05$) from BP or C diets. Blood work results were not impacted by the dietary treatments. In conclusion, AM diet appears to be an acceptable dietary fiber source for feline extruded diets.

Key Words: avocado, cat, digestibility
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223 Comparison of four digestibility markers to estimate fecal output of dogs.

I. C. Alvarenga[*1], C. G. Aldrich[1], and Z. Ou[2], [1]*Kansas State University, Manhattan,* [2]*Department of Statistics, Kansas State University, Manhattan.*

The use of chromic oxide is the standard marker for determining digestibility of dog diets. However, this method is not without issue regarding safety and repeatability. Therefore, it was our objective to determine the effect of using alternative markers to estimate fecal output and calculate diet digestibility. Four dietary treatments were produced from sorghum fractions (WSD, whole sorghum diet; FLD, sorghum flour diet; MFD; sorghum mill-feed diet) and rice, corn, wheat 1:1:1 (CON, control) as starch sources and fed to twelve Beagle dogs in a 4 × 4 replicated Latin square design. Fecal output was estimated using external markers Cr_2O_3 (0.25%) and TiO_2 (0.40%) mixed with the diet prior to extrusion and acid insoluble ash (AIA) as an internal marker and by total fecal collection (TFC). Fecal output of OM, DM, CP, GE, crude fiber, and crude fat by the 4 different methods was analyzed and compared using Pearson partial correlation coefficients from the Error SSCP Matrix. Correlations (R^2) were considered significant at $P < 0.05$. The TiO_2 and Cr_2O_3 were highly ($P < 0.05$) correlated for estimates of fecal output of all nutrients: 0.93, 0.91, 0.91, 0.91, 0.99, and 0.93 for OM, DM, CP, crude fat, crude fiber and GE, respectively. The TiO_2 also had significant correlations ($P < 0.05$) to TFC (0.59, 0.55, 0.61, 0.61, 0.82, and 0.60 for OM, DM, CP, crude fat, crude fiber, and GE, respectively) and AIA (0.84, 0.82, 0.82, 0.82, 0.84, and 0.86 for OM, DM, CP, crude fat, crude fiber, and GE, respectively). The Cr_2O_3 was also correlated ($P < 0.05$) to TFC (0.56, 0.50, 0.57, 0.57, 0.81, and 0.56 for OM, DM, CP, crude fat, crude fiber, and GE, respectively) and AIA (0.75, 0.71, 0.73, 0.73, 0.79, and 0.78 for OM, DM, CP, crude fat, crude fiber, and GE, respectively). The TFC and AIA methods had the poorest correlation among estimates of fecal outputs of OM, DM, CP, crude fat, crude fiber, and GE (0.29, 0.22, 0.33, 0.33, 0.54, and 0.33, respectively). Within these nutrients, only TFC and AIA for crude fiber fecal output correlated ($P < 0.05$). The study suggests that TiO_2 may be a better marker to estimate fecal output in dogs than Cr_2O_3. TiO_2 is considered GRAS and is a common colorant in pet foods. The use of the AIA technique needs to be further studied since it represents a potential option for evaluating diets that are difficult to incorporate external markers.

Key Words: AIA, chromic oxide, fecal marker, titanium dioxide
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224 Evaluation of faba beans (*Vicia faba* L.) as a dietary ingredient in dog diets.

I. C. Alvarenga[*1], C. G. Aldrich[1], L. M. Molnar[1], M. E. Morts[1], and L. Schole[2], [1]*Kansas State University, Manhattan,* [2]*3D Corporate Solutions, Monett, MO.*

Legumes are increasingly popular in pet foods. Dehulled faba beans (FB) are a legume well researched in human diets but not pet foods. Therefore, the objective of this work was to evaluate the effect of graded levels of FB in dog diets. Four experimental diets were extruded in a single-screw extruder (Model 525; ExtruTech, Inc., Sabetha, KS) in which FB were included at 0% (FB0), 10% (FB10), 20% (FB20), and 30%

(FB30) in exchange for rice. The FB and experimental diets were analyzed for proximate constituents. Diets were then fed to twelve Beagle dogs in a replicated 4 × 4 Latin square design. Dogs were adapted to food for 9 days, and feces were collected for 5 days, then (d14) blood was collected by brachial venipuncture into vacuum tubes. Feces were scored on a scale from 1 to 5 (1 = runny; 5 = very hard feces). Fecal output was estimated using chromic oxide to determine digestibility. Blood was analyzed for complete blood count (CBC) and chemistry profile. The experiment was approved by the KSU IACUC. Means were separated by multivariate analysis of variance (MANOVA) by the GLM procedure (SAS, v 9.4). There were no differences among treatments for dietary intake, fecal output, and stool score. Apparent total tract digestibility (ATTD) of DM was highest ($P < 0.05$) for FB0 (89.3%), intermediate for FB20 (88.9%), and slightly lower for dogs fed FB10 and FB30 (average 88.1%). Organic matter ATTD differed ($P < 0.05$) for each treatment: with FB0 > FB20 > FB10 > FB30 (92.7, 92.2, 91.7, and 91.4%, respectively). Gross energy ATTD was greater ($P < 0.05$) for FB0, FB10, and FB20 (average 83.4%) than FB30 treatment (82.6%). Crude protein ATTD was greater ($P < 0.05$) for FB0 and FB20 (average 90.7%) than for dogs fed FB10 and FB30 (average 89.8%). Crude fat ATTD was greater ($P < 0.05$) for FB20 (95.2%) and intermediate for FB0 and FB30 (average 94.0%), and for dogs fed FB10 it was lowest and similar to FB30 (93.5%). No differences were noted among treatments for CBC or chemistry profile, and all values were within normal range for adult medium sized dogs. Palatability was slightly lower for total volume, intake ratio, and first choice for dogs fed the FB10 and FB30 relative to control. However, palatability measures for dogs fed the FB20 did not differ from that of dogs fed the control. This study suggests that FB is an effective ingredient for use in a commercial dog diet.

Key Words: digestibility, dog, faba beans
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225 Fecal microbiota and metabolites of adult dogs fed extruded, mildly cooked, and raw diets.

K. M. Algya*[1], T. W. L. Cross[2], A. H. Lee[1], L. Lye[3], M. R. C. de Godoy[1], and K. S. Swanson[1],
[1]*University of Illinois at Urbana-Champaign, Department of Animal Sciences,* [2]*University of Illinois at Urbana-Champaign, Division of Nutritional Sciences,* [3]*Chewy, Dania Beach.*

The pet food market continues to produce diets with novel formats and unique processing methods. Although extruded and canned diets are still the most popular diet choice, lightly cooked and raw diets are other options. Unfortunately, there is little research on these diets and how they may alter fecal characteristics. The objective of this study was to determine fecal microbiota and metabolite concentrations of adult dogs fed the following commercial dog diets: 1) Freshpet Vital Balanced Complete Nutrition (CO); 2) Freshpet Roasted Meals (RM); 3) Freshpet Vital Raw (VR); and 4) Purina Dog Chow (DC). Eight dogs (mean age = 3.6; mean BW = 12.9 kg) were used in a replicated 4 × 4 Latin square design. Each period consisted of 28 d, with a 21-d adaptation phase followed by a total and fresh fecal collection phase. All samples were scored based on a 5 point scale (1 = hard, dry pellets; 5 = watery liquid). A fresh fecal sample was collected for pH, moisture, microbiota, and metabolite measurements. Microbiota was assessed using 16S rRNA-based amplicon sequencing using Illumina, QIIME, and linear discriminant analysis effect size (LEfSe). Dogs fed CO had a higher ($P < 0.05$) fecal pH than dogs fed VR, with dogs fed RM and DC being intermediate. Dogs fed DC, CO, or RM had lower ($P < 0.05$) fecal moisture than dogs fed VR, but fecal scores were not affected. Dogs fed VR had a higher ($P < 0.05$) fecal acetate concentration than dogs fed RM, with dogs fed CO and DC being intermediate. Dogs fed RM had a higher ($P < 0.05$) fecal indole and total phenol:indole ratio than dogs fed CO, VR, and DC. Dogs fed VR had a higher ($P < 0.05$) fecal ammonia concentration than dogs fed RM, CO, and DC. Dogs fed RM had a higher ($P < 0.05$) ammonia concentration than dogs fed DC, with dogs fed CO being intermediate. All other fecal metabolites were not affected by treatment. Dogs fed CO or VR had a lower ($P < 0.05$) alpha diversity of fecal microbes than dogs fed DC. Dogs fed CO or VR also shifted from dogs fed DC when unweighted and weighted beta diversity was evaluated. LEfSe demonstrated that each diet tended to be enriched in different microbial taxa: DC (Firmicutes; Actinobacteria), CO (Proteobacteria), VR (Bacteroides; Pediococcus), and RM (Fusobacteria). All diets were well tolerated, and dogs remained healthy throughout the study. Diet-induced differences in fecal microbiota and metabolites should be further studied.

Key Words: diets, dogs, microbiota
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226 Retention of thiamine and other water soluble vitamins in a wet pet food application.

L. M. Molnar*, R. A. Donadelli, and C. G. Aldrich,
Kansas State University, Manhattan.

Since 2008, there have been several recalls due to insufficient thiamine levels in canned cat food. Cats have a high requirement of thiamine, and deficiencies can lead to death within a month if not treated. Limited studies have been published regarding the impact of processing on thiamine loss. Therefore, it was our objective to determine the effect of container size and type on thiamine retention during processing of cat food. A model canned cat food was produced and placed in two container sizes (small: 89–104 mL vs medium: 163–207 mL) and three container types (can, pouch, and tray). Within each replicate batch (64 containers per replicate, two replicates), thermocouple probes were inserted into 14 separate containers. The retort time was determined by thermocouple heat penetration to meet $F_o = 8$ min at 121°C and 21 psi. The three sampling points for vitamin analysis were 1) batter without vitamins, 2) batter with vitamins, and 3) post retort loaf product. Samples from 1 and 2 were stored in the freezer (-20°C) and from 3 were stored at room temperature. Composite samples were analyzed for proximates (moisture, crude protein, crude fat, ash), pH, and B vitamin (thiamine, riboflavin, niacin, pyridoxine, pantothenic acid, biotin, folic acid, cobalamin) concentrations. Results were analyzed using the GLM procedure in SAS (v. 9.4) with means and interactions separated using Fischer LSD method by significant F values and an α of 5%. The proximate composition and pH were similar ($P > 0.10$) among treatments. Neither container size nor container type had an effect on riboflavin, pyridoxine, or cobalamin concentrations (average 87.0, 179.0, 0.41 mg/kg, respectively). Small containers retained more ($P < 0.05$) thiamine than medium (3,209 and 2,513 mg/kg), niacin (909 and 861 mg/kg), and folic acid (22 vs 15 mg/kg), while pantothenic acid retention in small containers was lower ($P < 0.05$) than medium (273 and 324 mg/kg, respectively). The main effect means for container type only influenced thiamine concentration, wherein retention was greater for pouches than for trays with cans intermediate to both (2,540, 2,359, and 2,274 mg/kg). This work suggests that thermal processing of B vitamins can be influenced by container size and type, which likely relate to the controls over the heating and cooling cycle.

Key Words: B vitamins, thermal process, thiamine
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227 Apparent and true digestibility of minerals in animal and vegetable ingredient based adult maintenance dog food.

C. L. Cargo-Froom*, A. K. Shoveller, and M. Z. Fan, *University of Guelph, Guelph, ON, Canada.*

Minerals are essential in the diet of dogs throughout all life stages. There is a dearth of knowledge with regards to mineral digestibility in canines, and current knowledge focuses on the digestibility of supplemented minerals, not of endogenous mineral bioavailability of ingredients or formulated diets. The objective of this study was to determine the apparent digestibility and true digestibility of macro and trace minerals in canines fed either animal or vegetable based adult maintenance diets. We hypothesized that dogs fed the animal ingredient based diet would have higher mineral digestibility as compared to dogs fed the vegetable ingredient based diet. This study was designed as a 4 × 4 replicated Latin square. Eight purpose bred Beagles (2 intact males, 6 spayed females) of similar age (2.12 ± 0.35 years) were pair housed but fed individually based on individual energy requirements. Four diets (animal ingredient based diet, vegetable ingredient based diet, animal ingredient based diet diluted to 50% α-D-glucose, and vegetable ingredient based diet diluted to 50% with α-D-glucose) were fed to dogs with titanium dioxide included in the diet at 0.3% to enable calculation of digestibility. Kennel numbers were randomly assigned to each pair of dogs with all 8 dogs cycling through the 4 trial diets in random order. Each diet was fed for 10 d, and fecal samples were collected from d 6 to 10. Data were analyzed using a mixed model through SAS (version. 9.4, SAS Institute) with treatment, period, and kennel as a fixed effect and dog as the random effect. There was no difference in apparent digestibility of calcium between dogs fed vegetable vs. animal diets; however, dogs fed the vegetable based diet had greater true digestibility of calcium ($P = 0.0143$) as compared to dogs fed the animal based diet. The apparent and true digestibility phosphorus and iron were greater in dogs fed the vegetable based diets as compared to animal based diets ($P < 0.001$). There were no differences in apparent or true digestibility of potassium, copper, and zinc between dogs fed the animal and vegetable based diets ($P > 0.05$). These results suggest that apparent and true digestibility do not result in similar conclusions, and digestibility of endogenous minerals are similar or greater in dogs fed diets that are largely vegetable based.

Key Words: canine, digestibility, mineral
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228 Chemical composition, nutrient digestibility, and true metabolizable energy of differentially processed chicken-based pet food ingredients using the precision-fed cecectomized rooster assay.

K. S. Swanson*[1,2,3], P. L. Utterback[4], and C. M. Parsons[4], [1]*Department of Veterinary Clinical Medicine, University of Illinois at Urbana-Champaign, Urbana,* [2]*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana,* [3]*Division of Nutritional Sciences, Urbana, IL,* [4]*University of Illinois, Urbana.*

In addition to the nutrient composition of raw ingredients, processing conditions may greatly affect the quality and digestibility of protein-based ingredients used in pet food products. Testing the quality of protein sources undergoing different processing conditions provides important information to pet food producers. Therefore, the objective of this study was to determine the chemical composition, nutrient digestibility, and nitrogen-corrected true metabolizable energy (TMEn) of chicken-based ingredients that had undergone different processing conditions using the precision-fed cecectomized rooster assay. Chicken meal was compared to raw (no processing; frozen), steamed (cooked to 200°F and held for 10 min at 200°F, cooled, and frozen), and retorted (retorted at 250°F for 30 min, cooled, and frozen) chicken ingredients. Chicken meal had higher ash [16.3% of dry matter (DM)] and crude protein (CP; 67.4% of DM) but lower acid-hydrolyzed fat (AHF; 15.7% of DM) and gross energy (GE; 5.09 kcal/g of DM) than raw chicken (5.8% ash; 41.7% CP; 52.4% AHF; 6.98 kcal/g), steamed chicken (6.7% ash; 53.0% CP; 44.8%

AHF; 6.59 kcal/g), and retorted chicken (7.6% ash; 55.6% CP; 41.8% AHF; 6.68 kcal/g). Chicken meal had lower digestibility of DM (60.0%) and organic matter (OM; 65.9%) but higher AHF digestibility (90.3%) than the raw (DM: 75.9%; OM: 80.5%; AHF: 88.3%), steamed (DM: 76.5%; OM: 80.6%; AHF: 86.5%), and retorted (DM: 73.5%; OM: 77.8%; AHF: 83.5%) ingredients. For all essential and non-essential amino acids, steamed chicken had the highest digestibilities. For all essential amino acids and all but one non-essential amino acid (proline), raw and retorted chicken digestibilities were similar to one another and greater than that of chicken meal. For proline, steamed and retorted chicken had a similar digestibility that was greater than that of raw chicken and chicken meal, which were similar to one another. TMEn was lower for chicken meal (3.43 kcal/g) than raw (5.37 kcal/g), steamed (4.88 kcal/g), and retorted (4.99 kcal/g) ingredients. This study demonstrates how greatly processing method may affect the chemical composition, nutrient digestibility, and energy content of protein-based ingredients intended for use in dog and cat foods. Based on our results, the use of slightly cooked ingredients can be expected to deliver a higher quality protein to pets than that provided by rendered meals.

Key Words: nutrient digestibility, pet food, processing
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229 Bioprocessed soy protein influences the fecal microbiota of healthy adult dogs.

A. H. Lee*, *Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana.*

Plant-based proteins such as soy protein have a more consistent nutrient profile than animal proteins but contain anti-nutritional factors such as trypsin inhibitors and oligosaccharides that can negatively affect digestion, increase flatulence, and decrease fecal quality. Bioprocessed soy protein (BSP) is a high-quality protein with lower anti-nutritional factor concentrations that has been shown to alleviate some of the negative effects of soy. A previous study revealed that BSP increased fecal short-chain fatty acid (SCFA) concentrations and decreased fecal putrefactive compounds, suggesting active and beneficial fermentative action in the colon. However, little is known about the effects of BSP on the composition of canine fecal microbiota. The objective of this study was to evaluate the effects of increasing dietary BSP concentration on fecal microbiota of healthy adult dogs. Forty-eight healthy adult Beagle dogs (20 females and 28 males; 3.4 yr mean age; 10.0 kg mean BW) were randomly allotted to one of 6 dietary treatments containing 0 (control), 4, 8, 12, 24, or 48% BSP. The experiment consisted of a 7 d adaptation phase followed by a 14 d treatment period (first 10 d were an adaptation period; last 4 d were used for fecal collections). Extraction of DNA from fresh fecal samples was followed by amplification of the V4 region of the 16S rRNA gene using barcoded primers. High quality sequence data were analyzed using QIIME 1.9.1 and Statistical Analyses of Metagenomic Profiles (STAMP) software 2.1.3. Correlations between microbial taxa and fecal metabolites were assessed using Pearson correlation coefficients. Principal coordinates analysis (PCoA) of weighted UniFrac distances revealed that samples with high dietary inclusion of BSP (24 and 48%) clustered separately from samples with lower dietary inclusion. Alpha diversity measures revealed lower ($P < 0.05$) species richness in dogs fed the control diet compared to those fed 24% BSP. Higher inclusion of BSP (24 and 48%) led to greater ($P < 0.05$) relative abundance of *Veillonellaceae*. A lower ($P < 0.05$) relative abundance of *Clostridium* was observed in dogs fed 48% BSP compared to those fed 0, 4, and 8%. A positive correlation ($P < 0.001$) was identified between *Clostridium* and fecal branched-chain fatty acid concentrations. Relative abundance of *Megamonas*, a known SCFA producer, was greater ($P < 0.05$) in dogs fed 48% BSP. In conclusion, BSP was shown to significantly shift the fecal microbial communities of healthy adult dogs. Further research is needed to understand the diet-microbe-metabolite relationships identified in this study and apply them to canine health.

Key Words: bioprocessed soy protein, canine health, fecal microbiota
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230 Gastrointestinal mucosal microbiota of young adult and geriatric dogs fed animal- or plant-based diets.

C. Y. Lin*[1], T. W. L. Cross[2], and K. S. Swanson[1,3,4], *[1]Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, [2]University of Illinois at Urbana-Champaign, Urbana, [3]Department of Veterinary Clinical Medicine, University of Illinois at Urbana-Champaign, Urbana, [4]Division of Nutritional Sciences, Urbana, IL.*

The gastrointestinal microbiota is known to be important for host health and disease, but most studies rely on fecal samples that may not be an accurate indicator of populations in the gastrointestinal tract and/or those adhering to the mucosa and important for disease. Therefore, the objective of this study was to characterize the phylogeny and predicted functional capacity of microbiota residing on the gut mucosa of healthy young adult and geriatric dogs fed different diets. Twelve weanling (8 wk old) and 12 senior (11.1 yr old) beagles were randomly assigned to an animal product-based diet (APB) or plant product-based diet (PPB) and fed for 12 mo. After 12 mo, mucosal samples from the stomach, duodenum, jejunum, ileum, and mid-colon were collected. DNA was extracted, and the V4 region of the bacterial 16S rRNA gene was amplified for Illumina MiSeq sequencing. Data were analyzed using QIIME 1.9.1. and Statistical Analyses of Metagenomic Profiles (STAMP) software 2.1.3. Gene predictions were made using Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt). Taxonomic assessment revealed that the mid-colon had a greater ($P < 0.05$) species richness compared to other segments. Principal coordinates analysis (PCoA) of weighted and unweighted UniFrac distances demonstrated that mid-colon samples clustered together and away from other segments that were more variable. Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria, and Fusobacteria were the predominant phyla in all five segments, but the abundances of each were unique. The stomach had the greatest ($P < 0.05$) relative abundance of Proteobacteria, followed by the jejunum, duodenum, mid-colon, and ileum. The duodenum had a greater ($P < 0.05$) relative abundance of Bacteroidetes than the stomach or ileum. The ileum and mid-colon had greater relative abundance of Firmicutes than the other segments. The mid-colon had a greater ($P < 0.05$) relative abundance of Fusobacteria than other segments. Within the mid-colon, PCoA of unweighted UniFrac distances demonstrated separate clustering of young adult and geriatric dogs as well as dogs fed APB vs. PPB. Unlike the taxonomic analyses, PICRUST prediction suggested that the functional capacity of microbiota present in the stomach was different from those present in the other segments. In conclusion, the mucosal microbiota were distinct among gastrointestinal segments. In addition to segment effects, age and diet also affected the mucosal microbiota communities, especially in the mid-colon.

Key Words: canine, microbiota, nutrition
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231 *Saccharomyces cerevisiae* fermentation product increases volatile fatty acid production and reduces *Salmonella* growth in an in vitro rabbit intestinal model.

J. M. Butler*, *Diamond V, Cedar Rapids, IA.*

A study was conducted to evaluate the effect of *Saccharomyces cerevisiae* fermentation product (SCFP, Diamond V Original XPC™) on in vitro volatile fatty acid (VFA) production and *Salmonella typhimurium* growth, using an in vitro rabbit fecal inoculated intestinal model. Gas tight culture tubes (50 ml) containing 0.3 g pre-digested commercial rabbit feed and 0.15 g treatment (Control [ground grain], SCFP, or inulin) were inoculated with an anaerobic buffered homogenate of fresh rabbit manure and incubated for 24 h at 39°C. Data represent the summary of two independent trials N = 5 for a total of N = 10 data points per each treatment. Data were analyzed using the GLM model of JMP. Significance was defined as $P \leq 0.05$. Treatment with SCFP significantly increased acetate, propionate, butyrate, and total VFA concentrations (Table 231; $P < 0.05$). In addition, SCFP reduced *Salmonella* growth by 1.27 log cfu/ml compared to Control ($P < 0.05$). Inulin yielded the greatest increase in acetate, propionate, and total volatile fatty concentration compared to control and SCFP ($P < 0.05$). The inulin treatment also significantly reduced pH ($P < 0.05$); however, it did not affect *Salmonella* growth. Compared to inulin, SCFP significantly increased butyrate and reduced *Salmonella* growth ($P < 0.05$). SCFP and inulin can be used to increase volatile fatty acid production; however, only SCFP was able to increase endogenous butyrate levels and reduce *Salmonella* growth.

Table 231. Effect of treatment on VFA (mM), pH and *Salmonella* (log cfu/ml)

Item	Control	Original XPC	Inulin	SEM
Acetate, mM	13.48^a	15.42^b	27.41^c	0.24
Propionate, mM	6.87^a	7.73^b	19.12^c	0.15
Butyrate, mM	0.03^a	0.11^b	0.03^a	0.004
Total VFA*, mM	20.65^a	23.60^b	46.89^c	0.37
pH	7.26^a	7.24^b	6.73^c	0.005
Salmonella, log cfu/ml	7.34^a	6.07^b	7.40^a	0.43

^{abc}Means within a row without a common superscript letter differ by $P < 0.05$.

*Total VFA is the sum of acetate, propionate, butyrate, isobutyrate, isovalerate and valerate.

Key Words: rabbit, *Salmonella*, XPC
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232 Relationship between velocity and step parameters for the stepping gait of leash led large-breed dogs.

K. Cotton[1], M. C. Nicodemus*[1], and K. Slater[2], [1]*Mississippi State University, Mississippi State,* [2]*Banfield Pet Hospital, Magnolia, TX.*

Canine lameness evaluation in the clinical setting consists of visually assessing the gait of the dog as the owner walks the dog on a leash. Nevertheless, research has shown that different handlers and handler position can influence walking gait mechanics in small dog breeds, but further research specific to the leash led gait as it relates to large dog breeds is limited. The objective of this study was to determine the relationship between velocity and step parameters of large-breed dogs being led at a stepping gait. Six dogs classified as large dog breeds (weight: 29 ± 4 kg) that were determined to be clinically sound according to veterinary evaluation were led by the same handler positioned on the same side of the dog at a slow (s = 1.3–1.5 m/s) and fast (f = 1.8–2.0 m/s) stepping gait. Gait inclusion required a stride phase free of suspension, gait consistency with velocity maintained at ranges comparable to a large-breed trot, and noticeable paw placement and lift-off. Step parameters determined by frame-by-frame analysis with video frames of paw placement and lift-off were documented. Step parameters were given as a % of stride. Means (SD) were determined for step parameters, and t-tests ($P < 0.05$) were performed between velocities. Although both stepping gaits demonstrated a lateral footfall sequence, stride duration decreased with increasing velocity (s = 0.54 ± 0.05 msec, f = 0.40 ± 0.02 msec; $P < 0.05$) as stride length remained consistent (s = 0.79 ± 0.04 m, f = 0.81 ± 0.07 m; $P > 0.05$). Both gaits alternated between bipedal and tripedal support phases (s = 11 ± 1%, f = 15 ± 3%; $P > 0.05$). Nevertheless, as velocity increased, the primary support phase transitioned from a lateral bipedal (s = 63 ± 4%, f = 35 ± 3%; $P < 0.05$) to a diagonal bipedal (s = 26 ± 2%, f = 50 ± 5%; $P < 0.05$) support phase. The majority of stride was spent in the stance phase for both velocities (s = fore-50 ± 1%, hind-61 ± 3%; f = fore-58 ± 2%, hind-58 ± 4%), but the slower velocity demonstrated a significant difference between the fore and hind stance durations ($P < 0.05$). Typically, with increasing velocity a dog will add a period of suspension to conserve energy and increase distance covered, but when this addition is restricted by the handler, as performed in this study, the large-breed dog utilizes changes in stride and stance durations along with limb support to achieve the faster velocity. The lack of influence on stride length to increase velocity as seen in this study may be restricted by the stride length of the handler, particularly in a large-breed dog, and thus, this may need to be a consideration when selecting handlers for gait assessment.

Key Words: large-breed dogs, step parameters, velocity
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233 Variation in macronutrient composition of popular, premium, and clinical canine diets fed to client-owned osteoarthritic dogs.

K. B. Detweiler*[1], Z. T. Traughber[1], A. K. Price[1], K. E. Knap[2], T. A. Harper[2], K. S. Swanson[1], and M. Cattai de Godoy[1], [1]*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana,* [2]*Department of Veterinary Clinical Medicine, University of Illinois at Urbana-Champaign, Urbana.*

The objective of this study was to compare the guaranteed analysis (GA) and analyzed proximate analysis measurements of commercial diets fed to a cohort of client-owned osteoarthritic dogs. These data were derived from a larger study designed to evaluate the demographics, dietary and medical history, and exercise regimen of dogs with osteoarthritis. Owners also were asked to provide a sample and label of the diet fed to their dog. A total of 51 different diets were collected and subsequently categorized into three main categories: Popular (n = 11), Premium (n = 32), and Clinical (n = 8). Our hypothesis was that the difference between GA and analyzed values would be greatest in the 'Popular' brand category due to the larger variability in ingredient sources based on minimum-cost formulations. All diets were analyzed for dry matter (DM) and ash (AOAC, 2006), crude fiber (AOAC, 2002), acid-hydrolyzed fat (AACC, 1983 and Budde, 1952). Crude protein (CP) was calculated from Leco total nitrogen values (AOAC, 2006). Analyzed DM concentrations conformed to the GA for all 51 diets. That is, the average difference (mean ± SD) between analyzed and GA values was below the maximum guaranteed on the labels: Popular dry (-3.34% ± 1.20) and wet (-5.35% ± 0.82), Premium dry (-3.77% ± 1.36) and wet (-2.70%), and Clinical (-2.45% ± 1.13). With the exception of one Popular diet (-0.72% less than GA), CP value differences (DM basis) of Popular (4.26 ± 2.03), Premium (4.08 ± 2.28), and Clinical (3.84 ± 1.74) diets all conformed to the guaranteed minimum values. Crude fiber differences on a DM basis were the most variable, with 9%, 44%, and 75% of Popular, Premium, and Clinical diets, respectively, failing to conform to the guaranteed maximum values. Similarly, differences between analyzed acid hydrolyzed fat and crude fat GA on a DM basis were also highly variable, with 18%, 31%, and 25% of Popular, Premium, and Clinical diets, respectively, failing to conform to the guaranteed minimum values. From this information, it cannot be concluded that 'Popular' brand diets have the greatest overall deviations from the GA; however, it can be concluded that measurements for crude fiber are the most variable macronutrient profile. The results of this study indicate that crude fiber is too variable of a measurement to be used as the industry standard for pet food diets.

Key Words: commercial diets, guaranteed analysis, macronutrient
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234 Paws for a Cause: Stress relief using therapy dogs.

M. J. Anderson*, K. Franks, M. M. Beverly, S. F. Kelley, and K. J. Stutts, *Sam Houston State University, Huntsville, TX.*

Therapy dogs have commonly been used to relieve a number of different types of stress in people ranging from PTSD to the more simple stresses of daily life. On a university campus, two of the most stressful times for a student are during midterm and final examinations. The objective of this study was to quantify the effectiveness of therapy dogs to relieve stress and/or anxiety during major exam time periods. To accomplish this, therapy dogs were made available for students to interact with during the week of midterms and finals. Students voluntarily completed a short survey after their visit with the therapy dogs. On the survey, students (n = 168) recorded demographic information and assessed their stress level before and after interacting with the dogs on a 15 cm line scale where greater numerical values indicated a greater level of stress. Across all participants, stress levels were greater ($P < 0.01$) prior to interacting with a therapy dog (10.4) than afterwards (4.4). This suggests that, regardless of gender, interacting with a therapy dog is highly effective in reducing stress as noted by the almost 60% reduction in stress level observed in the current study. When investigating differences between genders, females indicated greater stress levels ($P = 0.02$) compared to males before interacting with a therapy dog; however, no difference was detected between genders ($P = 0.94$) in stress level following their interaction with a therapy dog. These data suggest that females may perceive a greater level of stress about midterm and final exams than males, but the therapy dogs were effective in reducing stress to a similar level in both genders. While interacting with a therapy dog may not completely remove the

stresses in one's life, it may help deal with those stressors by bringing the stress level down to a manageable level.

Key Words: dogs, stress, therapy
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235 An evaluation of the protein quality of various protein sources from chicken, whey, and soy concentrates commonly used in pet diets and select human performance foods.

M. E. Morts*, G. Aldrich, C. K. Jones, and S. Beyer, *Kansas State University, Manhattan.*

The objective of this experiment was to evaluate protein utilization and nutrient composition of various animal and vegetable proteins used in pet food manufacturing. All protein sources were analyzed for proximate, amino acid, and mineral composition. Experimental protein sources included spray dried egg (SDEG), and 4 spray dried chicken samples varying by process conditions (SDLF, SDLF1, SDLF2, and PDC), low temp and pressure fluid bed dried chicken (LTPC), powdered chicken broth (PCB), pea protein concentrate (PPCO), pea protein isolate (PPIS), soy protein concentrate (SPCO), soy protein isolate (SPIS), 2 whey protein concentrates (WPCO and WPCOA from previous experiment), and 2 whey protein isolates (WPIS and WPISA from previous experiment) were added to a nitrogen free basal diet to contribute 10% crude protein. The nitrogen free basal diet was used as a negative control while the SDEG was the positive control. Day old male broiler chicks (Cobb*Cobb) were allowed a 7-day acclimation period and fed a starter diet and water ad libitum. The experimental unit was pen, containing 5 broiler chicks each. Experimental diets were fed for 10 days with weights and feed intake recorded. The experiment was approved by the KSU IACUC. Differences in treatment were analyzed using the GLIMMIX procedure in SAS (v9.4). Protein efficiency ratio (PER) was calculated as weight gain per unit of protein intake. The PER of SDEG was 4.50 and was similar to SDLF, SDLF1, SDLF2, and PDC, which were 4.04, 3.96, 4.22, and 4.56, respectively. The PCB, PPCO, PPIS, SPCO, SPIS, WPCO, WPCOA, WPIS, and WPISA had much lower ($P < 0.0001$) PER values of -1.82, -1.06, -0.32, 2.19, 1.65, -1.47, -2.55, -4.38, and -6.98, respectively. The negative PER values indicate that the birds lost weight when fed these protein sources due to critical limitations of one or more amino acids. Overall, this work suggests that broiler chicks, as a model, work well when evaluating processing differences among protein sources of poultry origin but severely penalize plant and dairy protein sources and might not be the appropriate model when exploring process modifications in these non-poultry ingredients for use in pet food applications.

Key Words: PER, pet, processing
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236 Effect of *Miscanthus* grass as a dietary method to aid hairball control in cats.

R. A. Donadelli* and C. G. Aldrich, *Kansas State University, Manhattan.*

Feline grooming habits can lead to accumulation in the stomach and formation of masses (trichobezoars), hairballs, that are regurgitated. Some pet food companies have created diets intended to force the concretion into the intestines, primarily by supplementing large quantities of insoluble fiber like cellulose. *Miscanthus* grass (M) possesses a similar content of insoluble fiber and may be an alternative for this purpose. Therefore, the objectives of this study were to determine the effects of M on hairball passage in cats. Experimental diets were composed of 90% basal ration and 10% of either M or rice flour (C). Cats (12 American Shorthair) were individually fed one of the two extruded diets for 16 days of adaptation; then feces were collected for 5 days. Hair masses were washed from feces and counted, and total hair weight and fecal dry weight were quantified. Hair masses were sorted by their length and diameter (extra small: <10.0 mm × <5.0 mm, small: 10.0–20.0 mm × 3.5–6.5 mm, medium: 20.0–30.0 mm × 4.0–7.0 mm, large: 30.0–40.0 mm × 4.5–8.5 mm, and extra-large >40.0 mm × >5.0 mm). Treatments were fed as a switchback design, and data were analyzed using the GLM procedure in SAS (v. 9.4) with means separated by significant alpha (5%). Total dry fecal weight was greater for cats fed M than C ($P < 0.0001$; 112.99 vs. 66.71, respectively). There was a tendency for less total fecal hair mass per gram of dry feces ($P = 0.0712$) and fewer fecal hairball counts per gram of dry feces ($P = 0.1082$) for cats fed M. However, hairball size ($P = 0.2431$) total fecal hairball weight ($P = 0.2541$), and total fecal hair weight ($P = 0.3027$) did not differ between treatments. The addition of M lead to some improvement in gastrointestinal management of hair in short-hair cats not otherwise predisposed to hairball. Use of predisposed animals, long-hair cats, a larger number of animals, and (or) larger fiber particle size may increase differences among the treatments. In conclusion, M decreased hairball size and total fecal hair mass per gram of feces, which could be an indication of increased ability of cats to eliminate hair masses through fecal excretion and reduce their regurgitation in a home setting.

Key Words: cat food, hairball, *Miscanthus* grass
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237 Development of a preference ranking test with dogs.

S. C. Smith*, *Kansas State University, Manhattan.*

One of the key drivers pet owners use to select the ideal food for their companion animal is liking. However, there is a scarcity of tests to quantify liking. Therefore, the objective of this study was to develop a test that might provide insight into liking. The underlying hypothesis was that dogs would work to solve a puzzle for foods they liked. Twelve Beagle dogs were presented with a puzzle-test to determine the multi-choice ranking of various treats. Each dog was presented with five options to which a different flavor and (or) aroma compound had been applied to baked treats prepared in our laboratory. The treats were placed inside a numbered rubber puzzle toy (Kong®), from which the dog had to extract the treat before consuming it. Once chosen the puzzle toy was removed with four choices remaining, then three, two, and a final choice. Each of the five phases lasted 5 days. The phases included (1) an adaptation or learning period and (2–4) ingredients tests: (2) fats: fish oil, butter, vegetable shortening, chicken fat and lard, (3) proteins: liver, chicken, fish, tofu, and beef, and (4) starches: corn, wheat, tapioca, potato, and chickpea. Phase 5 tested commercial foods that were labeled as “Fish and Potato” (F/P), “Chicken and Rice” (C/R), “Lamb and Oatmeal” (L/O), “Turkey and Chickpea” (T/C), and “Chicken and Pea” (C/P). The order of selection and extraction was recorded, and the data were analyzed accordingly as a Friedman analysis of variance. The dogs ranked fish oil and butter above ($P < 0.05$) lard, with vegetable shortening and chicken fat intermediate. Chicken liver was ranked higher ($P < 0.05$) than beef, with chicken, fish, and tofu intermediate. Corn was ranked higher ($P < 0.05$) than tapioca, potato, and chickpea, with wheat intermediate. The F/P was ranked higher than all other treatments. The study confirmed the hypothesis that dogs will work for foods they like. This test provides insight into methods for understanding dog liking when presented with options.

Key Words: dogs, palatability, preference
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238 The effect of container size and type on lethality values during production of thermally processed wet pet foods.

L. M. Molnar*, R. A. Donadelli, and C. G. Aldrich, *Kansas State University, Manhattan.*

Wet pet foods make up 18% of the market. Most studies report thermal inactivation of pathogens, but data reporting the heat penetration in containers other than cans are scarce. Therefore, the objective of this work was to determine heat penetration in various container types and sizes of pet food. The experiment was conducted as a 2 × 3 factorial arrangement of treatments with two general container sizes (small: 89–104 mL vs medium; 163–207 mL) and three container types (can, pouch, and tray). A model cat formula was produced for all six experimental treatments, and each was produced in duplicate over six days in commercial scale equipment. The containers were cooked in a retort (cans: SJ Reid Retort, Bellingham, WA; trays and pouches: FMC retort, Madera, CA) with thermocouples attached to the center of representative cans, pouches, or trays (n = 14) in each batch. Software (Calsoft Systems, v. 5.0.5) was used to record the internal temperatures and lethality during processing. Cumulative lethality values were determined for both the cooking and cooling processes. Data were analyzed using the GLM procedure of SAS (v. 9.4), and main effect means and interactions were separated by significant F test. There was an interaction ($P < 0.05$) between container size and type for time to reach the $F_0$8, wherein the medium can and tray had the longest time (45.5 and 46.3 min, respectively), the small can and tray and medium pouch were intermediate (35.4, 36.0, and 32.0 min, respectively), and the small pouch had the shortest time (36.0 min). There was no difference for either main effect of container type or size on heating lethality values (each main effect average $F_o = 10.3$). Container size did not affect cooling lethality values (average $F_o = 4.6$), but pouches and trays had a higher ($P < 0.05$) cooling lethality than cans ($F_o = 4.5$, 5.9 vs 3.3, respectively). Total lethality values were not affected by container size (average $F_o = 14.9$), but there was a trend ($P = 0.0569$) for pouches and trays to have a higher total lethality than cans. These heating differences may have an impact on the retention of heat labile nutrients like thiamine.

Key Words: heat penetration, thermal process, wet cat food
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239 Effect of diets containing sorghum fractions on antioxidant capacity of dogs and phenolic acids of both food and plasma measured by high performance liquid chromatography (HPLC).

I. C. Alvarenga* and C. G. Aldrich, *Kansas State University, Manhattan.*

Sorghum pericarp is abundant in antioxidant phenolics that might benefit companion animal diets. Key among these are ferulic (FA) and p-coumaric (PCA) acids. The objective of this study was to determine the effects of diets containing sorghum fractions rich in phenolic acids on antioxidant activity in dog plasma. Four nutritionally similar diets were extruded containing whole sorghum (WSD), sorghum flour (FLD), sorghum mill-feed (MFD), or a combination of corn, wheat, and rice (ratio 1:1:1; CON) and fed to twelve Beagle dogs in a replicated 4 × 4 Latin square design experiment. At the end of each period blood was collected, and plasma was separated and stored (-80°C) until analyses. The experiment was approved by the KSU Institutional Animal Care and Use Committee. Antioxidant activities in dog plasma were measured using an Oxygen Radical Absorbance Capacity (ORAC) kit (Cell Biolabs, Inc., San Diego, CA) and phenolic acids (following extraction) by HPLC using a Spherisorb S5 ODS2 C18 reversed-phase column. Means of plasma phenolics and ORAC were separated using multivariate analysis of variance (MANOVA) with the GLM procedure of the statistical analysis software (SAS, v 9.4). Dietary phenolic acid means were separated with analysis of variance using the GLM procedure (SAS, v 9.4). Unexpectedly, whole corn had the greatest ($P < 0.05$) PCA and FA (410 and 2711 ppm, respectively), followed by sorghum mill-feed (372 and 1311 ppm, respectively). Rice and sorghum flour had the lowest

($P < 0.05$) FA (average 236 ppm, respectively), and rice, sorghum, and wheat flour had the lowest PCA (average 30.8 ppm). Wheat flour and whole sorghum had similar and intermediate FA concentrations (average 525 ppm). P-coumaric concentration was not different among CON, WSD, or FLD (average 128 ppm) but was higher ($P < 0.05$) for MFD (298 ppm). Ferulic acid was lowest ($P < 0.05$) in WSD and FLD (average 649 ppm), intermediate in CON (1028 ppm), and highest in MFD (1380 ppm). However, plasma FA and PCA did not differ across treatments (averages 0.143 and 0.095 ppm, respectively). Yet the ORAC of MFD was more than 2-fold ($P < 0.05$) the value of the other treatments (20,482 vs average 8,923 µM TE/L). The study suggests that the FA and PCA concentrations in plasma or the diet were not related to the antioxidant capacity of dogs fed the dietary treatments.

Key Words: ferulic acid, HPLC, p-coumaric acid
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CSAS GRADUATE STUDENT ORAL COMPETITION

240 Sire verification in multi-sire breeding systems.

S. J. Domolewski[*1], K. Larson[2], J. Campbell[3], F. C. Buchanan[4], and H. Lardner[2], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada, [3]Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK, Canada, [4]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The objective of this study was to evaluate the use of DNA parentage testing on commercial cow-calf operations using multi-sire breeding pastures and to determine associations between phenotypic and spermatological traits of bulls and number of calves sired. Seven breeding pastures located within 4 commercial Saskatchewan ranches cooperated in this study. Calves and bulls were DNA parentage tested to determine sires. Data were analyzed using Chi square procedures. Bulls sired a significantly different ($P < 0.01$) number of calves compared to expected in 5 of the breeding pastures. Bull age was found to significantly ($P < 0.01$) affect bull prolificacy. All bulls were required to pass a breeding soundness exam (BSE) before entering a breeding pasture, so no association was found between either scrotal circumference ($R^2 = 0.04$) or percent normal sperm ($R^2 = 0.13$). Economic models were developed to evaluate the value of adopting this technology on farm. One model showed that bulls who sired more calves had a lower cost per calf sired. Another model showed that using parentage testing to identify bulls causing dystocia, by testing calves from difficult births and then culling the responsible bull, can provide an economic return on investment to the farm. Results also show that a producer could reduce testing costs by up to 70% by only testing calves born in week 3 and still obtain results that correctly identify low and high prolificacy sires. Only testing a sample of the calf crop also ensures lab results are obtained in time to make changes to the bull battery ahead of the next breeding season. Real value from parentage testing comes from being able to couple sire parentage with other basic production records. There is potential to increase overall bull prolificacy in a herd and increase other economically important traits by using DNA parentage to aid in sire selection.

Key Words: bull prolificacy, DNA parentage, sire verification
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241 Effects of low vs. high dietary lipid and source of lipid on performance of gestating beef cows and subsequent effects on progeny.

F. Añez-Osuna[*1], G. B. Penner[1], J. Campbell[2], C. F. Fitzsimmons[3,4], M. E. R. Dugan[5], P. G. Jefferson[6], H. A. Lardner[1,6], and J. J. McKinnon[1], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, [2]Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK, Canada, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [4]Agriculture and Agri-Food Canada, Edmonton, AB, Canada, [5]Agriculture and Agri-Food Canada, Lacombe, AB, Canada, [6]Western Beef Development Centre, Humboldt, SK, Canada.*

A two-year study was conducted to evaluate the effects of dietary lipid inclusion and source of lipid on performance of gestating beef cows and subsequent effects on progeny. Each year, 75 multiparous (≥3 calving) pregnant Angus cows were stratified by BW and BCS (Scottish System: 1 to 5) and randomly assigned to 15 pens (5 cows/pen). Subsequently, each pen was randomly assigned to one of three ($n = 5$) treatments: a low-lipid diet (LL; 1.4 ± 0.03% EE) consisting of grass hay, barley straw, and barley grain and two high-lipid diets (HL) where barley grain was substituted with a canola seed (CAN; 3.3 ± 0.02% EE) or a flaxseed (FLX; 3.3 ± 0.05% EE) based pelleted feed. Diets were formulated to meet the requirements of pregnant beef cows during the last two trimesters of gestation (184 ± 0.9 d) and adjusted for changes in environmental conditions and to be iso-caloric (DE: 2.6 ± 0.02 Mcal/kg) and iso-nitrogenous (CP: 10.5 ± 0.09%). Data were analyzed as a randomized complete block design with contrasts to separate the effects of lipid (LL vs. HL) and source of lipid (CAN vs. FLX). At the start of trial, all treatments had similar ($P = 0.37$) corrected (for conceptus) BW (659 ± 3.8 kg) and similar ($P \geq 0.33$) proportion of thin (0.7 ± 0.69%), optimal (95.2 ± 3.04%), and over conditioned (4.1 ± 2.80%) cows. After 160 d on trial (24 ± 0.9 d pre-calving), corrected BW of LL cows

(711 ± 2.2 kg) and proportion of fat cows (15.2 ± 8.8%) were greater ($P \le 0.04$) than those fed HL, with no difference ($P \ge 0.47$) between CAN and FLX for corrected BW (698 ± 4.6 vs. 702 ± 4.4 kg) and proportion of over conditioned cows (3.7 ± 3.3 vs. 5.6 ± 4.3%). From calving to weaning, no differences ($P \ge 0.22$) were observed in ADG, BW, BCS, milk yield, and milk composition of cows. Birth weight of bull-calves from LL cows (41 ± 0.5 kg) was lower ($P < 0.01$) than those from HL cows, while no difference ($P = 0.70$) was observed between bull-calves from CAN (45 ± 0.7 kg) and FLX (45 ± 1.2 kg) cows. At weaning, ADG and BW of steer-calves from LL cows (1.17 ± 0.02 kg/d and 251 ± 3.7 kg) were similar ($P \ge 0.74$) to those from HL, while steer-calves from CAN cows had greater ($P \le 0.04$) ADG (1.20 ± 0.03 vs. 1.11 ± 0.04 kg/d) and BW (261 ± 5.4 and 245 ± 6.9 kg) than those from FLX cows. In conclusion, differences observed in corrected BW and BCS between cows fed low vs. high-lipid diets before calving and the difference between their bull-calves at birth suggest a differential partitioning of ME by gestating beef cows which is dependent on the form of dietary energy.

Key Words: dietary lipids, energy partitioning,
gestating beef cows
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242 Performance response of piglets to acid-preserved high moisture wheat or barley as an alternative to in-feed acidification.

D. Sotto Jr.* and D. Beaulieu,
University of Saskatchewan, Saskatoon, SK, Canada.

Two experiments were conducted to compare the effectiveness of acidified high moisture wheat or barley in the diet of weanling pigs as an alternative to in-feed acidification. Wheat and barley were stored for 34 and 38 days, respectively, following reconstitution to 20% moisture and the addition of the appropriate acid (propionic acid or a commercial acidifier with 30–50% phosphoric acid). Weight loss of galvanized and carbon steel coupons, embedded in the acidified grain, was used to estimate corrosion rate. Trial 1 (wheat) and trial 2 (barley) used 160 and 90 pigs, respectively (weaned at 21 ± 2 days, 6.50 to 6.70 kg BW, housed 4 pigs/pen). Pigs were fed stage 1 and 2 treatment diets from day 0 to 7 and 8 to 21, respectively, and a common commercial diet from day 22 to 35. The treatments in trial 1, arranged as a 2 × 2 factorial, were type of acid (propionic or phosphoric) and application method (wheat preservation or diet supplementation) plus a negative control (5 treatments). The 3 treatments in trial 2 were phosphoric acid applied either as barley preservation or diet supplementation, plus a negative control. Mold was observed on phosphoric acid-preserved wheat and barley (7,000 and 820,000 cfu/gram, respectively); however, mycotoxin levels were below acceptable limits. During storage, the pH of phosphoric acid-preserved wheat and barley increased from 4.27 to 5.72 and 4.60 to 5.47, respectively, while the pH of propionic acid-preserved wheat increased from 4.56 to 4.85. In trial 1, treatment had no effect on ADG or ADFI ($P > 0.05$), but G:F (0.78 negative control vs 0.84 propionic acid) was improved in stage 2 in pigs fed diets with propionic acid, regardless of application method ($P < 0.05$). Treatment had no effect on ADG, ADFI, or G:F in trial 2 ($P > 0.05$). Corrosion rate was higher with propionic than phosphoric acid on carbon steel but not galvanized steel (acid × coupon interaction, $P < 0.05$). Regardless of acid, a higher corrosion rate was observed on galvanized steel than carbon steel ($P < 0.05$). In conclusion, propionic acid addition to weanling pig diets improved G:F, and wheat preserved with propionic acid provided comparable feed efficiency benefits to diet supplementation with the acid. Phosphoric acid in wheat or barley-based diets did not affect piglet performance and requires further investigation as a grain preservative. Furthermore, a higher corrosion rate can be expected if propionic acid preserved grains are stored in bins made of galvanized steel.

Key Words: acids, high-moisture grain,
weaned pig performance
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243 The effect of binding feed enzymes to spores of *Bacillus subtilis* (var. *natto*) on in vivo digestibility and in situ disappearance.

C. L. Rosser[*1,2], L. Jin[1], K. A. Beauchemin[1], M. Oba[2], and T. W. Alexander[1],
[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.

The objective of this study was to determine whether binding a commercial xylanase feed enzyme to the surface of *Bacillus subtilis* spores would improve feed digestibility compared to free enzyme. An *in vivo* study was conducted using 4 treatments: control (CON; no enzyme), *B. subtilis* spores (SPR; 1.0×10^{10} spores/kg DMI), free enzyme (ENZY; 2.5 ml of commercial xylanase enzyme/kg DMI), and spore-bound enzyme (SBE; 2.5 ml of commercial xylanase enzyme bound to 1.0×10^{10} spores/kg DMI) applied to alfalfa grass hay. The treatments were fed to 4 ruminally and duodenally cannulated heifers in a 4 × 4 Latin square design, with 21 d experimental periods and a 7 d washout between periods. Ruminal in situ disappearance was determined on d 13 to 18, where triplicate polyester bags containing alfalfa grass hay (5 g) were removed after 0, 4, 8, 12, 24, 36, 48, 72, 96, and 120 h of incubation. Total collection of feces and feed refusals occurred on d 19 to 21 to measure total tract digestibility. Rumen and fecal samples were collected and processed for 16S rRNA gene sequencing to analyze bacterial microbiota. There were no differences in ruminal in situ rates of disappearance of DM, OM, NDF, or ADF ($P \ge 0.086$). Effective rumen degradability of DM and OM was greater for ENZY, SBE, and SPR compared to CON ($P \le 0.048$), but there was no difference between ENZY and

SBE (contrast $P \geq 0.146$). Total tract and ruminal DM and OM digestibilities were not affected by treatment ($P \geq 0.067$); however, intestinal DM and OM digestibilities were increased for SBE (SBE vs ALL, $P \leq 0.043$). There was also an increase in total tract digestibility of NDF and ADF for SBE (SBE vs ALL, $P \leq 0.048$). Rumen microbiota diversity was affected by treatment, with differences observed between CON and SPR ($P = 0.050$), CON and SBE ($P = 0.033$), and SPR and SBE ($P = 0.009$). There was no difference in fecal microbiota diversity between CON and SPR ($P = 0.113$) or SPR and SBE ($P = 0.406$), but fecal microbiota was different between CON and SBE ($P = 0.009$) as well as ENZY and SBE ($P < 0.001$). These results suggest that spore-bound enzymes are more stable than free enzyme, increasing total tract digestibility of NDF and ADF. The effects likely resulted from enhanced postruminal digestion and alteration of the gastrointestinal microbiota.

Key Words: *B. subtilis* spores, digestibility, enzymes
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244 Kinetic characterization of a porcine intestinal alkaline phosphatase isomer over-expressed in the *E. coli* BL21 (λDE3).

X. Yin*[1], W. Wang[1], N. Burello[1], M. Li[2], T. Archbold[1], and M. Z. Fan[1], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Henan University of Animal Husbandry and Economy, Zhengzhou, China.*

Intestinal alkaline phosphatases (IAP), one group of the most abundant apical membrane-bound enzymes in the gut, play a pivotal role in protecting intestinal health and preserving mutually beneficial host-microbial relationships against pathogenic bacterial toxins by reducing their toxicity through dephosphorylation of the endotoxin lipopolysaccharides (LPS) lipid moiety and other emblematic members of pathogen-associated-molecular patterns (PAMPs) such as ATP, therefore preventing gut dysbiosis and enteric diseases. There are 6 alkaline phosphatase genes identified in the porcine genome with possible 4 IAP and 1 tissue-non-specific alkaline phosphatase isomers that are all likely expressed in the small intestine. To elucidate roles of post-translational glycosylation on IAP isomer affinity, this study was conducted to characterize a porcine IAP isomer (protein product ID: XP_003133777.1-X1) that had been over-expressed in the prekaryotic *E. Coli* BL21 (λDE3) without glycosylation. Both negative and X1-IAP over-expressed *E. coli* BL21 (λDE3) cell samples were sonicated to be homogenous and diluted for further enzyme kinetic analyses. The kinetic experiments were carried out by using the chromogenic synthetic substrate *p*-nitrophenyl phosphate (PNPP) with 16 gradient concentrations of PNPP, ranging 0–6 mM in incubation media in 4 replicates at pH 7.4 and 37°C for 30 minutes. The kinetics (parameter estimates ± SE, $P < 0.05$, $R^2 = 0.91–0.94$, n = 64) of the X1-IAP isomer specific and the intrinsic *E. coli* BL21 (λDE3) alkaline phosphatase activities were obtained, including Vmax values of 11.59 ± 1.58 vs. 19.02 ± 3.39 nmol/(mg protein·min) and K_m values of 4.72 ± 1.16 vs. 7.56 ± 2.09 mM. The X1-IAP isomer Km value measured at 4.72 ± 1.16 mM in this study is substantially higher than the range of the IAP Km values (0.1–0.3 mM) determined in the weanling porcine jejunum under the same conditions (using PNPP at pH 7.4 and 37°C) from our previous studies. It is known that alkaline phosphatase isomers expressed in vivo in the porcine gut would be highly glycosylated. Results of this study show that the porcine X1-IAP isomer over-expressed in the *E. coli* BL21 (λDE3) without glycosylation was associated with a very low enzyme affinity. Therefore, factors affecting post-translational glycosylation of the alkaline phosphatase isomers in the porcine gut would greatly influence their enzyme affinity towards detoxifying relatively low levels of pathogenic bacterial LPS and other emblematic PAMPs members in the gut lumen for protecting gut health.

Key Words: enzyme affinity, glycosylation, porcine gut alkaline phosphatase
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245 Standardizing infrared thermography (IRT) and micro-behavioral biometrics for estrus detection in dairy cows.

H. Perez*, *University of Alberta, Edmonton, AB, Canada.*

Most Canadian dairy herds operate in tie-stall housing (61%) where estrus detection rates may be lower than 35%. Infrared thermography (IRT) is a non-invasive technology which can predict ovulation by measuring radiated heat. Complementary behavioral biometric algorithms may improve accuracy (>40%) and specificity (>6.7%). The objective of this study was to standardize infrared thermography and micro-behavioral biometrics for estrus detection in dairy cows. Thirty-six cows were divided into 2 treatments with 18 pregnant (CON) and 18 open (OPEN) cows. Open cows were synchronized with GnRH and CIDR protocol on (-14 d) and 2 injections of PGF2α 12 hours apart on (-7 d). Pregnant cows received a sham injection and CIDR on the same schedule and frequency as OPEN cows on the synchronization protocol. Cows were monitored via visual cameras (Swann DVR) 5 minutes before, during, and after milking to establish the frequency of treading, drinking, neighbor interactions, tail movements, and laying and shifting behaviors. Radiated heat and physiological changes were monitored relative to estrus using an infrared camera (FLIR T450s). Infrared measurements were adjusted by recording environmental and relative humidity before and after thermogram collection. Infrared images were recorded for the eye, muzzle, cheeks, neck, front feet, round, heart girth, vulva surround, tail head, and withers and analyzed using FLIR Tools software. Data were analyzed using the Glimmix procedure in SAS (v9.4) with cow as the experimental unit. All results are reported as LSmeans ± SEM. Thermal biometrics differed by imaging location in CON versus OPEN cows (e.g., vulva: CON 34.8°C ± 0.047; $P < 0.0001$, OPEN 35.32°C ± 0.047; $P < 0.0001$; muzzle: CON 32.51°C ± 0.09;

$P < 0.0001$, OPEN 33.45°C ± 0.091; $P < 0.0001$, and cheeks: CON 32.30°C ± 0.084; $P < 0.0001$, OPEN 31.22°C ± 0.083; $P < 0.0001$). Thermograms found OPEN cows cooled at the tail head and heart girth as ovulation approached (tail head: -3 d 33.2°C ± 0.2 vs. 0 d 32.7°C ± 0.23; $P < 0.0367$; heart girth: -3 d 33.21°C ± 0.19 vs. 0 d 32.66°C ± 0.22; $P < 0.0097$). Treading behavior was significantly higher in CON (20.84 ± 0.39; $P < 0.0001$) and OPEN (16.35 ± 0.34; $P < 0.0001$) cows. Tail movements increased 72 hours before ovulation (-3 d 9.95 ± 1.18) compared with ovulation day (0 d 5.1 ± 1.03; $P < 0.0001$). Results indicate there is variation in temperature and micro-behaviors in the days leading up to ovulation as well as between CON and OPEN cows.

Key Words: behavior, dairy, infrared thermography
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246 Over-feeding metabolizable protein supply in late gestation beef cattle: Effects on colostrum composition, milk and milk component yield, and pre-weaning growth of calves.

K. S. Hare[*1], K. M. Wood[2], C. Fitzsimmons[3,4], and G. B. Penner[1], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, [2]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [3]Agriculture and Agri-Food Canada, Edmonton, AB, Canada, [4]Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

The objective was to determine the effect of oversupplying metabolizable protein (MP) pre-partum on colostrum composition, milk and component yield, blood metabolites, and pre-weaning growth of calves. Twenty-four primiparous crossbred Hereford cows were assigned to either a high protein (HP; 140% of predicted MP requirement, n = 12) or control (CON; 100% of predicted MP requirement, n = 12) treatment. Cows were individually fed their treatment diet from d -56 until parturition and then were switched to a common diet post-partum. Colostrum samples were collected, via hand stripping, immediately after calving. The 24-h milk yield was estimated by measuring a 2-quarter 12-h milk yield (MY) on d 7, 13, 28, 33, 70, and 112. Milk and colostrum samples were analyzed for fat, CP, lactose, urea-N (MUN), and somatic cell count (SCC). Blood samples were collected from cows via jugular venipuncture on d -35, -17, 7, and 28 and analyzed for plasma glucose and serum NEFA. Calf BW and frame measurements were conducted at birth and on d 7, 28, 57, 82, and 112. Data were analyzed as a completely randomized block design using the MIXED procedure of SAS. Fixed effects included treatment, time, and the two-way interaction, and the random effects were cow and block. Day was analyzed as a repeated measure. Heifers consuming the HP diet pre-partum had less fat in colostrum (3.63 vs. 7.01%; $P < 0.01$) compared to the CON, but CP, lactose, and MUN were not affected. There was no effect of pre-partum treatment on MY or composition. Day relative to parturition affected MY (kg/d) with a progressive decrease from 6.91 on d 7 to 5.06 kg on d 112 ($P < 0.01$). Milk fat decreased from d 7 (3.59%) to d 28 (3.43%) and then gradually increased to d 112 (3.85%, $P = 0.01$). Milk CP ($P < 0.01$) and MUN ($P < 0.01$) followed a similar pattern as reported for fat. Lactose concentration increased from d 7 (4.55%) to d 28 (4.80%) and then decreased to d 112 (4.51%, $P < 0.01$). Plasma glucose and serum NEFA did not differ by treatment or week. There was no effect of pre-partum treatment on calf BW or frame measurements. Oversupplying MP pre-partum may decrease colostrum fat without affecting MY, milk composition, and calf growth.

Key Words: beef cow, calf performance, lactation
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247 Effect of 3- vs. 9-d whole-plant corn allocation with or without fiber supplementation on cow performance, grazing preference, and ruminal fermentation.

B. Anderson[*1], G. B. Penner[1], K. Larson[2], J. J. McKinnon[1], and H. Lardner[1,2], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

Grazing whole-plant corn is becoming increasingly common on western Canadian beef farms as a winter feeding method. This 2-yr study evaluated the impact of provision of 3- or 9-d (3D or 9D, respectively) whole-plant corn allocation (*Zea mays,* P7332R; yr 1, TDN = 69.5%, CP = 8.6% [DM basis]) with or without fiber (FIB or NFIB, respectively) supplementation on cow performance, grazing preference, and ruminal fermentation. Supplemental fiber (hay, TDN = 60.2%, CP = 12.9% [DM basis]) was provided at 15% of DMI in 3DFIB and 9DFIB systems. Ninety-six Angus cows (BW = 664.4 kg ± 20.05), including 16 ruminally cannulated cows, were allocated to 1 of 4 replicated (n = 2/yr) systems for 84 and 88 d in yr 1 and 2, respectively. Cow BCS and BW were recorded at the start and end of the study, and grazing preference and ruminal fermentation data were collected at the start, middle, and end of the grazing allocation. Grazing preference was determined based on plant part (stem, husk, leaf, and cob) disappearance. Data were analyzed as a completely randomized design with a 2 × 2 factorial arrangement using the mixed model of SAS. Year was included as a random effect and time within an allocation as a repeated measure. Cow BCS and ADG were not affected ($P > 0.05$). As grazing progressed within an allocation, the proportion of cob, husk, and leaf decreased ($P < 0.01$), while the stem increased ($P < 0.01$). For 3D cows, ruminal NH_3-N concentration did not differ within an allocation, whereas NH_3-N increased for 9D cows (allocation × timing, $P < 0.05$). Total short chain fatty acid concentration was greater (95.2 vs. 85.6 m*M*, $P < 0.05$) and acetate was greater (62.2 vs. 55.1 m*M*, $P < 0.05$) for FIB than

NFIB. Butyrate concentration decreased from 13.8 to 6.5 m*M* from the start until the end of the 9D grazing allocation, but concentrations did not differ for 3D (allocation × timing, $P < 0.05$). Minimum pH increased during the grazing allocation, but the magnitude of the increase was greater for 9D than 3D (allocation × timing, $P < 0.05$). The duration that ruminal pH was <5.8 was not affected by allocation or provision of FIB but decreased ($P < 0.01$) from 143 min/d at the start of grazing allocation to 0 min/d at the end. The provision of fiber alters ruminal fermentation, and extending the duration of the grazing allocation increases the selection of plant structures and differences in ruminal pH within a grazing allocation.

Key Words: grazing behavior, ruminal fermentation, winter grazing
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248 Validating the stage of maturity at harvest for barley, oat, and triticale for swath grazing.

C. L. O'Keefe*[1], K. Larson[2], G. B. Penner[1], J. J. McKinnon[1], and H. Lardner[1,2], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Western Beef Development Centre, Humboldt, SK, Canada.*

The objective was to determine the effect of harvest maturity (SOM) for barley, oat, and triticale on grazing days, nutrient composition, DMI, cow rib and rump fat, and production costs. Three 16-ha fields were seeded to either barley (*Hordeum vulgare*; cv. CDC Maverick), oat (*Avena sativa*; cv. CDC SO1), or triticale (*Triticosecale*; cv. Taza). Each forage was cut at an early (EAL; late milk for oat and soft dough for barley and triticale) and late (LAT; hard dough) SOM. One hundred twenty Angus cows (640 kg ± 1.13 kg) were randomly allocated to 1 of the 6 replicated (n = 3) treatments and allowed to graze the paddock (3-d forage allocations) until all forage had been allocated. Cow BW (conceptus adjusted) and rib and rump fat were measured at the start and end of the study. Forage DM yield was determined using randomly sampled 0.25-m^2 quadrats of pre-swath biomass and regrowth biomass. Data were analyzed as a completely randomized design with a 3 × 2 factorial arrangement, using the mixed model of SAS. Forage yield for EAL and LAT oat, barley, and triticale were (kg/ha) 7,634, 8,240, 8,242, 7,372, 8,773, and 11,080, respectively. Grazing days increased from 50 to 89 d for LMO to HDO; however, there were no effects of SOM for barley or triticale (crop type × SOM interaction, $P < 0.01$). Crude protein differed by crop type with barley (12.1%) having greater ($P < 0.01$) CP than oat (11.0%) and triticale (11.4%). Harvesting at more advanced maturity decreased CP (12.1 vs. 11.0%, $P < 0.01$) and TDN (58 vs. 51%, $P < 0.01$). Crop type ($P = 0.19$) and maturity ($P = 0.36$) did not affect BW change. However, the change in rib fat (mm) was greater ($P < 0.01$) for oat (0.43 mm) than barley (-0.27) and triticale (-0.15). Cows fed EAL oat increased rump fat while LAT oat decreased: no change in rump fat was observed for other crops (crop × maturity, $P = 0.01$). Cows fed LAT oat had greater DMI than EAL oat (13.0 vs. 6.0 kg/d), but intake did not differ among the other treatments, averaging 9.5 kg/d (crop × maturity, $P = 0.01$). Cost ranged from $1.16/cow/d for LAT triticale to $2.43/cow/d for EAL oat. The results of this study suggest that harvesting whole crop annuals at a later SOM may improve yield and reduce costs without negative effects on animal performance.

Key Words: annual cereals, stage of maturity, swath grazing
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249 Antimicrobial activities of commercial essential oils against the bovine respiratory pathogen *Mannheimia haemolytica* and analysis of their chemical composition and cytotoxicity on bovine turbinate cells.

S. Amat*[1,2], D. Baines[3], and T. W. Alexander[2], [1]*Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Recent studies have shown the emergence of bacterial pathogens associated with bovine respiratory disease (BRD) that are resistant to all classes of antibiotics used to treat BRD. Therefore, there is an impetus to develop alternatives to antibiotics for use in the beef industry. Essential oils (EO) may offer a potential mitigation strategy against BRD bacterial pathogens through direct inhibition and also attenuation of resistance to antibiotics. The purpose of this study was to determine the chemical composition of commercial EOs (N = 16) and their in vitro antimicrobial activities against the model BRD pathogen *Mannheimia haemolytica,* as well as any cytotoxicity in bovine turbinate (BT) upper respiratory cells. The EO chemical composition was determined using gas chromatography-mass spectrometry. Minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of the 16 EOs against *M. haemolytica* serotype 1 were determined using the broth dilution method with serial dilutions ranging from 0.2% to 0.006% (v/v). Based on MIC and MBC, the most inhibitory EOs (N = 7; ajowan, cinnamon leaf, citronella, fennel, ginger grass, lavender, and thyme) were further characterized by evaluating their vapor-phase antimicrobial activities against *M. haemolytica*, impact on *M. haemolytica* morphology, and cytotoxicity against BT cells at concentrations between 0.0125% and 0.4% (v/v). A variety of volatile compounds were detected from the EOs, with some containing thymol and eugenol, which are known to have antibacterial activities. Thymol was most abundant in ajowan and thyme EOs (>46% of EO content), and eugenol was most predominant in cinnamon leaf EO (84% of EO content). The MIC ranged between 0.025% and 0.2%. The lowest MIC (0.025%)

was observed with ajowan, fennel, and thyme EOs. Cinnamon leaf and citronella EOs showed MIC value of 0.05%. All MIC values were the same as MBC for all EOs. Ajowan, thyme, and cinnamon leaf EOs completely or moderately inhibited *M. haemolytica* in their vapor-phase. Scanning electron microscopy revealed noticeable changes in cell structure between EO treated and non-treated cells. The cells treated with ajowan and thyme EOs displayed the greatest morphological cell damage compared to other EOs. None of the selected EOs exhibited noticeable cytotoxicity on BT cells within the tested concentrations. Our results indicate that ajowan, thyme, and cinnamon leaf EOs may have potential to be used as antibiotic alternatives to control BRD bacterial pathogens.

Key Words: antimicrobial activity, bovine respiratory pathogens, essential oil
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250 Muscle amino acid composition of pigs is influenced by the feeding system and amino acid intake.

A. Remus*[1,2,3], M. P. Létourneau Montminy[2], L. Hauschild[4], and C. Pomar[3], *[1]Universidade Estadual Paulista, Jaboticabal, Brazil, [2]Département des sciences animales, Université Laval, Québec, QC, Canada, [3]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [4]Sao Paulo State University, Jaboticabal, Brazil.*

Pigs fed individually with daily tailored diets (PF: precision feeding) may respond differently to amino acid (AA) supply compared to pigs fed under conventional group-phase feeding (GF) systems. The response of growing pigs in PF and GF systems fed with different levels of threonine (70%, 85%, 100%, 115%, and 130% of the ideal threonine-to-lysine ratio of 0.65) was studied in a 21-d experiment. A total of 110 pigs of 25 (±0.8) kg BW were housed in the same pen and fed using electronic feeders. Individual pigs were the experimental unit. Five out of eleven pigs per treatment were slaughtered to obtain organs and muscle composition. The chemical composition of the longissimus dorsi and the pool of other carcass muscles were estimated by near-infrared transmittance, and AA were analyzed by gas chromatography. Data were analyzed by SAS mixed model procedures in a 2 × 5 factorial arrangement. Threonine intake increased linearly ($P < 0.05$) with increasing dietary Thr levels for PF (6.28 to 11.76 g/d) and GF pigs (6.85 to 11.01 g/d). Lysine intake was similar (12.5 g/d) across treatments. Dietary Thr supply did not affect longissimus dorsi CP concentration but increased Thr concentration (g/100 g of CP) in a quadratic manner in PF pigs without effect on GF pigs (interaction $P < 0.05$). Threonine concentrations in the muscle pool presented an interaction between feeding system and Thr level as it changed in a cubic manner (4.56 to 4.38 g; $P < 0.05$) in PF and GF pigs. Muscle pool CP concentration was greater for GF than PF pigs (18.06% vs. 17.79%; $P = 0.05$) and tended ($P < 0.10$) to increase linearly with increasing Thr levels in both systems. Threonine concentrations (g/100 g of CP) in the small intestine (4.62 g) and liver (4.41 g) were similar across dietary Thr levels, confirming that these organs have priority over muscles under Thr restriction. However, Thr liver concentration tended ($P < 0.10$) to be greater in PF than GF pigs (4.44 vs. 4.39 g), showing that AA retention in organs may be more efficient in PF than GF pigs. Threonine restriction can, therefore, modify longissimus dorsi AA composition based on the AA intake. However, muscles respond differently to dietary Thr supply, and, under restriction, organs seem to be prioritized over muscles. These results indicate that feeding systems can affect the way pigs use Thr.

Key Words: ideal protein profile, precision feeding, threonine
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251 Net energy content of camelina cake fed to growing pigs and additivity of energy in mixed diets.

J. W. Kim* and C. M. Nyachoti, *University of Manitoba, Winnipeg, MB, Canada.*

This experiment was conducted to determine the DE, ME, and NE content of camelina cake (CC) and to test the hypothesis that dietary glucosinolates originating from CC will affect the additivity of energy in mixed diets containing different inclusion levels of corn, soybean meal (SBM), and CC. A total of 30 growing barrows [(Yorkshire × Landrace) × Duroc] with an average body weight (BW) of 16.8 ± 1.4 kg (mean ± SD) were randomly allotted to 1 of 5 treatments with 6 replicates per treatment. Pigs were fed experimental diets for 16 d, including 10 d for adaptation and 6 d for total collection of feces and urine. The 5 experimental diets consisted of 3 corn-based diets to determine the DE, ME, and NE of the 3 ingredients (corn, SBM, and CC) and 2 mixed diets to test the additivity of DE, ME, and NE. The corn diet contained 97.52% corn, the SBM diet contained 67.52% corn and 30.0% SBM, the CC diet contained 67.52% corn and 30.0% CC, the Mixed1 diet contained 67.52% corn, 20.0% SBM, and 10.0% CC, and the Mixed2 diet contained 67.25% corn, 10.0% SBM, and 20.0% CC. Vitamins and minerals were included in the diets to meet or exceed the requirements for growing pigs (NRC, 2012). Pigs were fed their assigned diets at 550 kcal ME/kg $BW^{0.60}$ per day on the basis of BW on d 1, 5, and 10, which was close to ad libitum intake. Pigs had free access to water. Determined DE, ME, and NE contents of corn and SBM were 3,348, 3,254, and 2,579 kcal/kg and 3,626, 3,405, and 2,129 kcal/kg, respectively, whereas, respective values for CC were 3,755, 3,465, and 2,383 kcal/kg. No differences between the predicted and determined DE, ME, and NE were observed in the two mixed diets. Differences between predicted and determined DE, ME, and NE values for the Mixed1 diet were 29, 13, and 20 kcal/kg, respectively. Respective values for the Mixed2 diet were 47, 38, and 38 kcal/kg (as-fed basis), respectively. In conclusion, the DE, ME, and NE of CC were 3,755, 3,465, and 2,383 kcal/kg, respectively. In addition, the observed additivity of energy values in the mixed diets indicates that the CC can be used to accurately formulate swine diets.

Key Words: camelina cake, net energy, pig
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CSAS GRADUATE STUDENT POSTER COMPETITION

252 Apparent ileal and total tract digestibility of corn DDGS steeped without or with fiber degrading enzymes and fed to growing pigs.

Y. Rho*, C. Zhu, E. Kiarie, and C. F. M. de Lange, *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

Corn dried distiller's grains with solubles (DDGS) are high in gross energy but their use in pig diets is limited due to high fiber concentration. Steeping fiber rich ingredients with fiber degrading enzymes (FDE) may improve their feeding value. We evaluated apparent ileal (AID) and total tract (ATTD) of CP, crude fat, and fiber in DDGS steeped without or with 2 commercially available FDE (A and B). FDE-A supplied 5,500 U of xylanase and 1,050 U of β-glucanase per kg of feed, and FDE-B supplied 1,200 U of xylanase, 150 U of β-glucanase, 500 U of cellulose, and 5,000 U of protease per kg of feed. A mixture of 350 g of DDGS, additives (none for control), and 1.5 l of water was placed in sterile containers and incubated at 40°C with agitation every 40 min for 24 h. For feeding, respective DGGS was mixed with a base at a ratio of 65:35 to provide 20% CP. The base contained corn starch, minerals, vitamins, and 0.2% TiO_2 as indigestible marker. Six ileal-cannulated pigs (20 kg BW) were fed the 3 diets in a replicated 3 × 3 Latin square design to give 6 replicates per diet. Pigs were fed at 2.8 × maintenance energy and had free access to water. In each period, pigs were adjusted to diets for 5 d followed by 2 d for grab fecal and 2 d, 8 h continuous collection of ileal digesta. Treatments had no effects ($P > 0.05$) on AID of CP, fiber, and crude fat (Table 252). DDGS steeped with FDE-A had lower ($P = 0.005$) ATTD of NDF than control but higher ($P = 0.001$) ATTD of crude fat compared to the control or DDGS steeped with FDE-B. In conclusion, under conditions of the study, steeping DDGS with fiber degrading enzymes had no effects on fiber (NDF and ADF) digestibility in growing pigs.

Key Words: fiber degrading enzymes, steeped corn DDGS, utilization of fiber in growing pigs
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Table 252. AID and ATTD (%) of components in corn DDGS steeped without or with FDE

	DM	CP	NDF	ADF	Crude fat
AID					
Control	59.0	59.9	26.5	17.4	66.1
FDE-A	58.9	59.4	24.7	19.2	66.2
FDE-B	60.5	56.4	28.9	21.4	67.1
SEM	2.22	2.69	5.85	6.69	2.47
P-value	0.794	0.450	0.847	0.900	0.945
ATTD					
Control	76.2	73.3	55.3a	59.3	46.8b
FDE-A	74.8	71.8	46.7b	54.5	56.4a
FDE-B	76.0	70.7	50.7ab	58.6	46.4b
SEM	1.14	2.15	1.94	2.56	2.44
P-value	0.109	0.109	0.005	0.065	0.001

253 Sire verification in multi-sire breeding systems.

S. J. Domolewski*[1], K. Larson[2], J. Campbell[3], F. C. Buchanan[4], and H. Lardner[2], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Western Beef Development Centre, Humboldt, SK, Canada,* [3]*Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK, Canada,* [4]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The objective of this study was to evaluate the use of DNA parentage testing on commercial cow-calf operations using multi-sire breeding pastures and to determine associations between phenotypic and spermatological traits of bulls and number of calves sired. Seven breeding pastures located within 4 commercial Saskatchewan ranches cooperated in this study. Calves and bulls were DNA parentage tested to determine sires. Data were analyzed using Chi square procedures. Bulls sired a significantly different ($P < 0.01$) number of calves compared to expected in 5 of the breeding pastures. Bull age was found to significantly ($P < 0.01$) affect bull prolificacy. All bulls were required to pass a breeding soundness exam (BSE) before entering a breeding pasture, so no association was found between either scrotal circumference ($R^2 = 0.04$) or percent normal sperm ($R^2 = 0.13$). Economic models were developed to evaluate the value of adopting this technology on farm. One model showed that bulls who sired more calves had a lower cost per calf sired. Another model showed that using parentage testing to identify bulls causing dystocia, by testing calves from difficult births and then culling the responsible bull, can provide an economic return on investment to the farm. Results also show that a producer could reduce testing costs by up to 70% by only testing calves born in week 3 and still obtain results that correctly identify low and high prolificacy sires. Only testing a sample of the calf crop also ensures lab results are obtained in time to make changes to the bull battery ahead of the next breeding season. Real value from parentage testing comes from being able to couple sire parentage with other basic production records. There is potential to increase overall bull prolificacy in a herd and increase other economically important traits by using DNA parentage to aid in sire selection. Study results indicated a large variation in number of calves sired by each bull in multi-sire breeding pastures. Although some phenotypic and spermatological factors can be correlated with bull prolificacy, the large variation in number of calves sired suggests that these traits alone cannot be relied on to predict bull prolificacy. If basic production records are kept on farm, there is an economic incentive to adopt this technology.

Key Words: bull prolificacy, DNA parentage, sire verification
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254 In vitro evaluation of short-season corn silage hybrids grown in central and southern Alberta, Canada, and harvested before or after frost: Nutrient content, degradability and enteric methane emission.

I. A. Aboagye*[1,2], V. Baron[3], M. Oba[1], and K. A. Beauchemin[2], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Lacombe, AB, Canada.*

The objective of this study was to characterize the nutritive value of short-season corn silage (CS) hybrids (rated at ≤2600 corn heat units (CHU) for grain maturity) and examine their in vitro rumen fermentation and CH_4 emission (batch culture; 2 runs, 3 replicates/run). Four CS hybrids were grown in 2 years in Central (Lacombe; hybrids: 39F44, 39M26, P7632HR, PS2262RR; 2000–2200 CHU rating) or Southern (Vauxhall; hybrids: P7632HR, P8210HR, P8622AM, P8673AM; 2200–2600 CHU rating) Alberta and harvested before or after slight frost to increase dry matter (DM) concentration. Hybrids grown at each location were selected based on having a CHU rating suitable for the location. Starch content was greater ($P < 0.05$) for hybrids grown in Southern compared with Central AB (27.8 vs. 22.0% DM) and for hybrids harvested after frost (26.4 vs. 23.4% DM). The NDF content did not differ between locations (mean 53.2%; $P > 0.05$) but was decreased after frost in Southern hybrids (50.4 vs. 55.0; location × harvest, $P = 0.04$). Similarly, DMD did not differ between locations (mean 58.7%; $P = 0.11$) but was increased after frost for Southern hybrids (59.9 vs. 56.5%; location × harvest, $P < 0.001$). The NDF degradability (NDFD) was greater for Central versus Southern hybrids (39.8 vs 37.5%, $P < 0.001$) but was increased after frost for Southern hybrids (40.0 vs. 36.0%; location × harvest, $P < 0.001$). Total VFA concentration in vitro was greater for Central than Southern hybrids (40.2 vs. 37.8 m*M*), and it increased after frost for Southern hybrids (39.7 vs. 35.9 m*M*; location × harvest, $P = 0.01$). The proportion of propionate (mol/100 mol) was greater ($P < 0.01$) for Southern hybrids (30.7 vs. 29.5) and those harvested after frost (31.0 vs. 29.3). Harvesting before frost tended (location × harvest, $P = 0.08$) to increase CH_4 (mL/g digested DM) for Central (28.2 vs. 27.0) but not Southern hybrids (mean 25.8). Methane production was inversely correlated with propionate proportion ($r = -0.64$; $P < 0.05$). Greater starch content of Southern versus Central hybrids corresponded to lower CH_4 emissions through its impact on propionate. DMD was not affected by location because Southern hybrids had higher starch content but Central hybrids had greater NDFD. Harvesting Southern hybrids after frost increased DMD and thus has the potential to improve animal performance while lowering CH_4 emissions. Although harvesting Central hybrids after frost had limited effects on degradability, it tended to reduce CH_4 emissions.

Key Words: methane, nutrient degradability, short-season corn silage hybrids
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255 Evaluation of canola meal versus soybean meal as a protein supplement on performance and carcass characteristics of growing and finishing beef cattle.

A. C. Good*[1], J. J. McKinnon[1], G. B. Penner[1], T. A. McAllister[2], and T. Mutsvangwa[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Two trials were conducted to evaluate the performance and carcass characteristics of backgrounding and finishing cattle fed canola meal (CM) versus soybean meal (SBM) as a protein supplement with or without wheat dried distillers' grains with solubles (WDDGS). Trial 1 was a 95-d backgrounding program in which 398 steer calves (288 ± 0.27 kg; mean ± SE) were assigned to one of 12 pens and fed one of four barley silage, barley grain-based diets formulated to 13.5% CP and 1.52 and 0.92 Mcal kg^{-1} NE_m and NE_g, respectively. The dietary treatments included CM (8.7% DM), SBM (7.0% DM), CM+WDDGS (4.6 & 4.8% DM), and SBM+WDDGS, (4.2 & 4.4% DM). Trial 2 utilized 300 head (306 ± 0.94 kg) assigned to 25 pens for a 61-d backgrounding and 147-d finishing program. Backgrounding diets were identical to Trial 1 with the addition of a fifth treatment (WDDGS, 9.5% DM). The basal finishing diet was barley grain-based and formulated to 13% CP and 1.95 and 1.30 Mcal kg^{-1} NE_m and NE_g, respectively. The five dietary treatments included CM (5.7% DM), SBM (4.3% DM), CM+WDDGS (3.0% & 3.1% DM), SBM+WDDGS (2.4% & 2.6% DM), and WDDGS (6.7% DM). Performance results for each trial were analyzed as a completely randomized design using the Mixed model procedure with pen as the experimental unit. Quality and yield grades were analyzed using GLIMMIX with a binomial error structure and logit data transformation. In trial 1, there were no differences between treatments for final BW (420.7 ± 1.8 kg; $P = 0.30$) or gain-to-feed (G:F) (0.16 ± 0.003; $P = 0.60$); however, ADG was greatest ($P < 0.05$) for cattle fed SBM relative to cattle fed SBM+WDDGS (1.45 ± 0.04 kg vs. 1.32 ± 0.03 kg). In trial 2, no treatment differences ($P > 0.22$) were detected for ADG (1.65 ± 0.01 kg), DMI (9.77 ± 0.07 kg), or G:F (0.17 ± 0.001). Cattle fed SBM+WDDGS had the least subcutaneous fat depth relative to cattle fed CM+WDDGS (1.17 ± 0.06 cm vs. 1.46 ± 0.05 cm; $P = 0.02$) and the poorest marbling score relative to cattle fed WDDGS (398.75 ± 15.19 vs. 440.10 ± 8.20; $P = 0.05$). There was a tendency ($P = 0.09$) for greater proportion of AAA carcasses with the WDDGS treatment (66.1 ± 6.2%) while SBM+WDDGS had the least (41.4 ± 6.5%). These results indicate that CM is equal to SBM as a protein supplement for backgrounding and finishing cattle and that provision of WDDGS as a source of rumen undegradable protein did not benefit performance. The combination of SBM+WDDGS negatively influenced energy partitioning to carcass fat deposition.

Key Words: feedlot performance, canola meal, soybean meal
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256 Effects of post-partum lipid supplementation and source of supplemental lipid on reproductive performance of lactating beef cows grazing cool-season grass pastures.

F. Añez-Osuna*[1], G. B. Penner[1], J. Campbell[2], D. Damiran[1,3], P. G. Jefferson[3], H. A. Lardner[1,3], and J. J. McKinnon[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK, Canada,* [3]*Western Beef Development Centre, Humboldt, SK, Canada.*

A three-year study was conducted to evaluate the effects of post-partum lipid supplementation and source of supplemental lipid on performance of lactating beef cows grazing cool-season grass (CSG) pastures. Each year, 36 second- and third-calving Angus cows with calves were stratified by BW, BCS (Scottish System: 1 to 5), and days post-partum (38 ± 1.5 d) and randomly assigned to 9 paddocks (4 cows/pen) of long-established CSG pastures. Subsequently, each paddock was randomly assigned to one of three replicated (n = 3) treatments: a non-supplemented control (CON) treatment and two supplemented (SUP) treatments where cows were offered either a canola seed (CAN; 9.1 ± 0.68% EE) or a flaxseed (FLX; 8.5 ± 0.38% EE) based pellet. Pelleted supplements were offered daily, and amounts were such that each paddock received 1.2 kg/d (300 g/cow/d) of lipids (EE) from supplement. Each year, the supplementation period was 42 d, after which all cows were managed in a single group and exposed to a 63 d breeding season (1:18 bull:cow). Data were analyzed as a randomized complete block design with contrasts for the effect of lipid supplementation (CON vs. SUP) and source of lipids (CAN vs. FLX). At the start of trial, no difference ($P \geq 0.42$) was observed among treatments for BW (554 ± 3.0 kg), BCS (95 ± 0.02% of optimal cows), proportion of cows cycling (39 ± 4.7%), and available CSG forage (1977 ± 105.7 kg/ha). Over the 42 d of supplementation period, no difference ($P \geq 0.56$) was observed among treatments for nutrient composition of CSG pastures (12.5 ± 0.24% CP and 41.5 ± 0.45% ADF). However, CON had lower ($P = 0.04$) residual forage (806 ± 118.8 kg/ha) and tended ($P = 0.06$) to have greater forage utilization (61 ± 4.3%) compared to SUP, while no difference ($P \geq 0.34$) was observed between CAN and FLX (904 ± 88.8 vs. 971 ± 88.8 kg/ha and 50 ± 3.6 vs. 52 ± 3.8%). At the end of trial, no difference ($P \geq 0.69$) was observed among treatments for BW (578 ± 7.6 kg), ADG (0.6 ± 0.12 kg/d), BCS (99 ± 0.01% of optimal cows), and proportion of cows cycling (88 ± 3.1%). Forty-five d after the end of breeding season, no difference ($P = 0.97$) was observed among treatments for conception rate (97 ± 1.6%). These results show that supplementing lipids to second- and third-calving beef cows prior to breeding has no effect on their reproductive performance. However, the lower forage utilization shown for supplemented cows suggests that this supplementation strategy might be suitable under limited forage and/or high stocking rates scenarios.

Key Words: grazing beef cows, lipid supplementation, reproductive performance
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257 Ruminal volatile fatty acid concentration and microbial populations as a proxy for of feed efficiency in beef steers.

P. B. A. I. K. Bulumulla*[1], M. M. Li[2], Y. Chen[1], F. Li[1], R. R. White[3], M. D. Hanigan[2], G. Plastow[1], and L. L. Guan[1], [1]*Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*Department of Dairy Science, Virginia Tech, Blacksburg,* [3]*Virginia Tech, Blacksburg.*

Breeding and management of animals to achieve improved feed efficiency is a significant priority for the beef industry. Feed conversion ratio (FCR) and residual feed intake (RFI) have become popular measurements for feed efficiency, although both have limitations and practical challenges. The identification of additional, cost-effective indicators of feed efficiency is needed to improve breeding programs. We hypothesized that volatile fatty acids (VFAs), the end products of rumen microbial fermentation and the primary energy source for ruminants, could potentially dictate feed utilization for growth and production. In this study, we tested whether residual VFA (rVFAs) could serve as a predictor of feed efficiency. Rumen content was collected from a total of 204 beef (Angus, Charolais, and Kinsella composite) steers raised under a Growsafe® system, and VFA concentrations (mol/L) were analyzed by gas chromatography. Microbial populations were estimated using total copy numbers of 16S rRNA genes for bacteria and archaea using quantitative PCR (qPCR). Animal phenotypic measures including body weight (BW), dry matter intake (DMI), average daily gain (ADG), feeding frequency, RFI, and carcass performances were collected. The feed was collected at the time of rumen sample collection, and its nutrient content was analyzed. VFA concentrations and production rates were predicted using the Molly mathematical model for each animal based on observed BW, DMI, and ration composition. Residual VFA concentrations were calculated as observed minus predicted VFA concentration. The relationships among digestion parameters and rVFA were tested using stepwise, backward linear regression, which was also used to test rVFA as a predictor of feed efficiency. Residual acetate (ResAc), propionate (ResPro), and total VFA concentrations were significantly correlated with BW, DMI, and breed. Residual butyrate (ResBu) was correlated only with DMI. Total bacterial copy number was negatively correlated with eating frequency ($P < 0.05$) and ResAc ($P < 0.01$) and positively associated with ResPro ($P < 0.01$) concentrations. Total archeal copy number was inversely related to ResPro. RFI was significantly affected by DMI ($P < 0.01$) and ResAc and showed a significant negative relationship with ResPr and ResBu ($P < 0.05$). Similarly, FCR was significantly affected by DMI, ADG, and breed. Both ResPr and ResBu had non-significant ($P < 0.1$), inverse relationships with FCR. Although the work needs to be independently evaluated, our preliminary results identified the potential of using rVFA concentrations to predict feed efficiency traits in beef steers.

Key Words: feed efficiency, ruminal microbial populations, volatile fatty acid
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EXTENSION EDUCATION

258 Effectiveness of a certification program to facilitate practice change in cattle handling and care.

K. D. Bullock*[1], B. R. Crites[1], W. R. Burris[2], J. Lehmkuhler[1], L. Anderson[1], M. Arnold[1], K. Laurent[1], B. Knight[2], B. Thompson[3], and P. Prater[4], [1]*University of Kentucky, Lexington,* [2]*University of Kentucky, Princeton,* [3]*Kentucky Beef Network, Lexington,* [4]*Morehead State University, Morehead, KY.*

Proper handling and care of cattle is important to the beef industry and beef producers as a whole. During a workshop of leading Kentucky beef cattle farmers held in 2012, proper handling and care were identified as one of the top five industry concerns. Based on this information an educational program on cattle handling and care was developed, and a certification process was implemented to acknowledge beef producers who successfully completed the program. The program centered on an educational video that covered the following topics: Genetic Influences, Proper Handling Techniques, Transportation, Proper Nutrition, Body Condition Scoring, Dystocia, Castration, Dehorning, Vaccinations, Eye Disorders, Disease, Lameness, Pasture/Housing, and Humane Euthanasia. Upon completion of the video, the participants were administered an exam and were required to correctly answer 30 out of 35 questions to be certified. Farmers completing certification received a barn sign for display, a laminated chute-side aid, and a trailer bumper sticker with weight limits. From summer 2014 through the end of 2016, 2026 farmers were Cattle Handling and Care Certified in Kentucky. In December 2016 and January 2017, a survey was sent to all certified farmers, one per household, who were certified prior to December 1, 2016, which totaled 1519 individuals. Four hundred ninety-two surveys were completed for a response rate of 32.4%. Demographics indicated the respondents were 88.8% male and 49.4% were over the age of 60 years. When asked if the video was an effective delivery tool, 98.4% responded positively, and 96.1% felt that becoming certified was an effective use of their time. Four hundred thirteen producers (84.6%) indicated they had made practice changes due to the program. Areas that showed the greatest change were improved handling facilities (68.4%), improved handling techniques (58.8%), improved cattle sorting techniques (56.2%), improved nutrition management (51.8%), improved herd health (51.2%), and improved genetics for calving ease (44.9%). When asked if the chute-side aid, bumper sticker, or barn sign were useful resources, the positives responses were 61.7%, 23.6%, and 56.0%, respectively. Of the respondents, 95.0% were either likely or very likely to recommend the program to other beef farmers. These results indicate that a cattle handling and care certification program can be successful in fostering practice change in beef cattle managers, and utilizing an educational video, along with other resources, is an effective tool in delivering the information.

Key Words: cattle, certification, welfare
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259 Relationships between beef bull sale prices and feeder calf price in Virginia.

A. R. Weaver*, J. Saville, and S. P. Greiner, *Virginia Polytechnic Institute and State University, Blacksburg.*

In recent years, fluctuations in beef cattle prices have resulted in uncertainty among beef producers regarding value of seedstock cattle. A relationship between feeder cattle prices and bull prices would allow producers to more accurately estimate the value of their breeding stock. Monthly averages from Virginia feeder calf sales between January 2006 and December 2016 were utilized. Feeder steer (FdSt) and heifer prices (FdHf, Med and Large 1, CWT) were reflective of 227–273 kg calves. Prices for 364–409 kg steers were utilized to represent backgrounded steer (BkSt) prices. Corresponding bull prices (per head) from annual Virginia Beef Cattle Improvement Association bull test sales held in March and December were obtained. Regression analysis (PROC REG) in SAS (SAS Institute Inc., Cary, NC) was utilized to determine relationships between calf prices and corresponding bull sale averages. FdSt prices were highly associated with FdHf ($r^2 = 0.99$, $P < 0.0001$) and BkSt prices ($r^2 = 0.96$, $P < 0.0001$). FdSt and bull value were highly correlated over the 11-yr period ($r^2 = 0.91$, $P < 0.0001$). Bulls were valued approximately 18 * (FdSt) or 3.27 * (FdSt per head). FdHf were valued less than FdSt and had a greater regression coefficient ($B_1 = 19.5$, 3.5 * (FdHf per head)) when compared to bull prices and remained highly correlated ($r^2 = 0.89$, $P < 0.0001$). Bulls were worth approximately 24 * (BkSt) or 2.8 * (BkSt per head), and there remained a strong relationship between these prices ($r^2 = 0.90$, $P < 0.0001$). Angus bull prices were more sensitive to changes in FdSt prices ($B_1 = 18.0$, $P < 0.0001$) compared to Simmental and Simmental hybrid prices ($B_1 = 15.7$, $P < 0.05$ and 17.5, $P < 0.001$, respectively). Compared to Simmental and Simmental hybrid prices, Angus bull value was more strongly associated with FdSt prices ($r^2 = 0.37$ and 0.61 vs. 0.91, respectively). Bulls that commanded prices in the top third of their respective sale had prices most volatile to changes in FdSt price ($B_1 = 24.5$, $P < 0.0001$). Correspondingly, bulls that sold in the lowest third were least volatile ($B_1 = 12.7$, $P < 0.0001$); those valued in the middle third were intermediate ($B_1 = 16.8$, $P < 0.0001$). Bull sale prices are highly correlated with feeder calf value. These models provide predictive opportunities for beef cattle producers to estimate seedstock value based on current feeder cattle market conditions.

Key Words: beef bull, market, price
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260 The induction and synchronization of estrus in sheep during the fall and late spring (season and out of season) using controlled internal drug release (CIDR) devices on Delmarva.

E. N. Escobar*[1], E. Kassa[1], D. O'Brien[2], and H. Taylor[1], [1]*University of Maryland Eastern Shore, Princess Anne,* [2]*Virginia State University, Petersburg.*

Changing U.S. demographics have increased lamb demand, which usually follows holidays, changing from year-to-year coinciding with traditions/festivals. In 2013, >80,000 t (metric tons) of lamb were imported to USA. A chief constraint to continuous year-round lamb supply is the influence of season on sheep reproduction. The purpose of this project was not to determine FDA approved CIDRs' (2009) efficacy in sheep but to resolve applicability and practicality of CIDR use in commercial flocks to condense lambing periods and target peak lamb demands. From 2012 to 2015, purebred and crossbred Katahdin ewes (n = 201) were separated into two groups, synchronized (CIDR) or not (CONTROL), for breeding in late Spring (anestrus-season) or Fall (natural-breeding-season). At each breeding event, CIDRs were inserted for 12 to 18 d, and at the time of CIDR removal, ewes were grouped for mating in single sire groups of no more than 6 ewes/group. The FDA approved protocol (12 to 18 d) was followed because pre-trials at this station gave inconsistent results following the label's CIDR insertion and removal time (5 d). At birth, lambs were tagged, weighed, and sexed, and litter size was recorded (LSZ) (lambs/ewe exposed). Data were analyzed using Chi-square and analysis of variance (SAS software package) for effect of synchronization and season on pregnancy rates (PR) (pregnant ewes/exposed ewes) and LSZ at birth. Overall PR did not differ from one year to the other in CIDR or CONTROL ewes. PR was higher ($P < 0.0001$) in CIDR ewes (63.4%) than in CONTROL ewes (34.3%) but was similar between breeding seasons (62.4% and 37.6% for CIDR and 52.8% and 47.2% for CONTROL in Fall and Spring, respectively). During Spring, PRs were higher ($P < 0.0001$) in CIDR ewes (71.4%) than in CONTROL ewes (17.6%). During Fall, PRs were similar (58.5% and 49.1% for CIDR and CONTROL, respectively). Overall, ewe LSZ was influenced by season bred and use of CIDRs, with CONTROL Spring-bred ewes having a lower ($P < 0.0001$) litter size (0.3 ± 0.1) compared to CONTROL-Fall, CIDR-Fall, and CIDR-Spring bred ewes (1.0 ± 0.1, 1.2 ± 0.1, and 1.3 ± 0.1, respectively). The results encourage using CIDRs in commercial sheep flocks to increase pregnancy rate and litter size. Additionally, CIDR synchronization in our station reduced a 60 to 90 d lambing period to 10 d, allowing operators to arrange facilities, labor, and supplies accordingly, enhancing lamb survival and ewe welfare. Project funded by Evans-Allen grant USDA/NIFA MDX-AS1012001.

Key Words: CIDR, litter size, pregnancy rate
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261 Relationships of production practices for producers participating in the UK Beef IRM Farm Program.

B. R. Crites*[1], G. Conway[1], E. S. Vanzant[1], K. D. Bullock[1], J. W. Lehmkuhler[1], W. R. Burris[2], and L. Anderson[1], [1]*University of Kentucky, Lexington,* [2]*University of Kentucky, Princeton.*

The University of Kentucky Beef IRM team has developed a project-based educational program (UK IRM Farm Program) designed to instigate long-term changes in adoption of production practices and examine its impact on productivity and profitability of cow-calf operations. Our current objective is to elucidate relationships among various production practices. Beef cattle producers (n = 72) from 27 counties in Kentucky were selected to participate in the program. Each participant completed a survey to obtain production data and assess production practices being implemented. Data were analyzed using Spearman's nonparametric correlations in JMP v11. Spearman's rho (sr) values of 0.10–0.249, 0.25–0.50, and 0.50 and greater were classified as low, moderate, and strong, respectively. Production practices (n = 67) were classified into five categories: general management (n = 13), reproduction (n = 7), nutrition (n = 19), genetics (n = 5), and health (n = 23). Production practices evaluated included identifying cows/calves, recording birth information, keeping performance testing records, pregnancy diagnosis, deworming cows/calves, and average weaning weight. Producers who identified (e.g., tags, tattoo, freeze brand) cows were more likely to record birth information (sr = 0.35, $P < 0.05$), have a controlled breeding season (sr = 0.40, $P < 0.05$), and have more complete reproduction and health programs (sr = 0.31 and 0.39, $P < 0.05$). Producers who dewormed cows/calves tended to have higher average calving and weaning percentages (sr = 0.22 and 0.23, respectively, $P = 0.07$). Recording birth information was associated with having controlled breeding seasons (sr = 0.43, $P < 0.05$) and also indicative of more complete reproduction (sr = 0.42, $P < 0.05$), health (sr = 0.32, $P < 0.05$), and genetics programs (sr = 0.39, $P < 0.05$). Similarly, producers keeping performance records had increased reproduction (sr = 0.45, $P < 0.05$), nutrition (sr = 0.34, $P < 0.05$), management (sr = 0.49, $P < 0.05$), and genetics program (sr = 0.38, $P < 0.05$). Those keeping performance records were also more inclined to have controlled breeding seasons (sr = 0.35, $P < 0.05$) and pregnancy diagnosis (sr = 0.38, $P < 0.05$). Logically, pregnancy diagnosis was associated with controlled breeding seasons (sr = 0.44, $P < 0.05$), breeding soundness examinations (sr = 0.34, $P < 0.05$), and more complete management and genetics programs (sr = 0.34 and 0.22, respectively, $P < 0.05$). Production practices that positively influenced average weaning weight included controlled breeding seasons (sr = 0.39, $P < 0.05$), managing thin cows separately (sr = 0.28, $P < 0.05$), and having the ability to weigh cattle (sr = 0.25, $P < 0.05$). Additionally, operations identifying cows and implementing more complete reproduction and nutrition programs tended to have increased average weaning weights (sr = 0.23, 0.23, and 0.25 respectively, $P = 0.07$). These producer survey results provide evidence suggesting that identifying cows/calves, recording birth information, keeping performance testing records, and pregnancy diagnosis are important management practices that are positively related to economically important responses.

Key Words: beef cattle, production practices, survey
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262 Comparison of production practices for producers participating in the UK Beef IRM Farm Program and USDA NAHMS survey data.

B. R. Crites[1], G. Conway*[1], E. S. Vanzant[1], K. D. Bullock[1], J. W. Lehmkuhler[1], W. R. Burris[2], and L. Anderson[1], *[1]University of Kentucky, Lexington, [2]University of Kentucky, Princeton.*

The University of Kentucky Beef IRM team has developed a project-based educational program (UK IRM Farm Program) designed to instigate long-term changes in adoption of production practices and examine its impact on productivity and profitability of cow-calf operations. Our current objective is to compare the UK IRM Farm Program survey responses to the data collected in the 2007–2008 United States Department of Agriculture National Animal Health Monitoring System (USDA NAHMS) Reference of Beef Cow-Calf Management Practices. The UK IRM Farm Program selected 72 producers from 27 counties in Kentucky to participate in the program, and each participant completed a survey to obtain production data and assess standard production practices being implemented. The 2007–2008 USDA NAHMS reference included 24 states and represented 28.6 million head of beef cows (87.8% of US beef cows) and 603,000 operations (79.6% of US beef operations). Producer herd size in the IRM Farm Program averaged 45 cows, slightly higher than the Kentucky herd size average (30.5 head) and similar to the national average in the USDA NAHMS report (42.3 head). More participants in the IRM Farm Program tagged cows (86%) and calves (77%) compared to the USDA NAHMS report (66% and 46.7% respectively). The average weaning weight (238 and 240 kg), calving percentage (90–95% and 91.5%), and proportion that retained heifers (87.5% and 83%) were similar between groups. In the IRM Farm Program, 39% of operations used some form of heat synchronization, 37% incorporated the use of artificial insemination, 41% had their cowherd diagnosed for pregnancy, and nearly half (49%) performed a breeding soundness examination on their bulls. In contrast, only 7.6% of operations utilized heat synchronization, 7.9% had used artificial insemination, and one-fifth of all operations had their cattle diagnosed for pregnancy (20.2%), while 26.8% had their bulls undergo a breeding soundness examination in the USDA NAHMS report. Also, 54.5% of all U.S. beef operations did not have a controlled breeding season, while 35% of those in the IRM Farm Program did not. While still having similar calving percentages and average weaning weights to the operations represented in the USDA NAHMS review, those involved in the UK IRM Farm Program had a larger percentage of participants utilize more common reproductive techniques and have a controlled breeding season.

Key Words: beef cattle, production practices, survey
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263 Effects of in-feed administration of a *Saccharomyces cerevisiae* fermentation product on the liver abscess microbiome and liver abscess rate in cattle reared to produce natural-branded beef.

K. L. Huebner*, J. N. Martin, M. D. Weinroth, K. H. Holzer, C. J. Weissend, Z. Abdo, J. L. Metcalf, I. Geornaras, J. K. Parker, P. S. Morley, and K. E. Belk, *Colorado State University, Fort Collins.*

Liver abscesses are the leading cause for liver condemnation in cattle. Liver abscess bacteriology has traditionally been evaluated using culture-based methods, with most commonly isolated organisms including *Trueperella pyogenes* and *Fusobacterium necrophorum*. Investigation into feed additive antibiotic alternatives, such as *Saccharomyces cerevisiae* fermentation products (SCFP), show potential to reduce abscess prevalence and fecal pathogen shedding. However, the effects of SCFP on the microbiome of abscesses are not well characterized. The primary objective of this study was to evaluate the effects of feeding SCFP on liver abscess rate and microbiome in natural-branded beef. The secondary objective was to characterize the liver abscess flora and diversity using 16S ribosomal RNA marker genes to determine operational taxonomic units (OTUs) and to compare these results to traditional cultural findings. In a controlled, randomized, triple-blinded trial, cattle were assigned to two dietary treatment groups and blocked by weight when placed in a Colorado feedlot in March 2016. Cattle were sorted into 14 pen blocks (28 pens total; 4325 head) and were reared similarly. Treated pens received SCFP (18 g/day) in their diet, and control pens were fed a base ration. At harvest, liver abscess rates were scored for individual animals. Five liver abscesses per pen were collected, and purulent material was saved. The content was cultured anaerobically, and isolates were saved for characterization and antimicrobial susceptibility testing. Additionally, DNA was isolated, and the bacterial community (microbiome) was characterized by 16S rRNA sequencing, where universal PCR primers amplify specific hyper-variable V4 regions within the 16S region. Paired-end reads were trimmed and filtered for quality. They were then assigned OTUs using open reference OTU picking in QIIME, rare OTUs were filtered, sequences were rarefied to 93243 reads, and beta diversity was estimated using unweighted Unifrac distances. The mean total abscess prevalence at harvest across 28 pens was 38.5% (95% CI 37.0 to 39.9%). Cattle with severe abscesses represented 15.7% of all abscesses (95% CI 14.6 to 16.8%). From blinded analysis of data from 13 pens, taxa belonging to the phyla Fusobacterium and Bacteroides and unassigned taxa were most abundantly represented. Actinobacteria (including *Trueperella*) had lower relative abundance across samples. There was a correlation between pen and differences in the microbiota accounting for 55% of variation in the PCoA plot. OTU differences in the genus *Fusobacterium* are driving some of the differences in clustering by abscess rate and pen block.

Key Words: food safety, liver abscess, microbiome
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264 The effect of tylosin supplementation and tylosin alternative control treatments on fecal microbial populations, performance, and liver abscess prevalence in feedlot cattle.

C. J. Weissend*, K. H. Holzer, K. L. Huebner, J. L. Metcalf, I. Geornaras, J. K. Parker, K. E. Belk, P. S. Morley, and J. N. Martin, *Colorado State University, Fort Collins.*

Currently, there is significant public and private pressure to reduce and find alternatives for antibiotics used in animal production. Tylosin phosphate, a macrolide commonly used to reduce and prevent liver abscesses in feedlot cattle, has come under intense scrutiny for its widespread use in cattle feeding. The potential removal of tylosin from cattle feeding could have a marked impact on the beef industry. Thus, investigating tylosin alternatives is imperative. In light of this, a blinded, randomized, controlled field trial was conducted to evaluate the effect of tylosin and two alternative treatments on fecal microbial populations, feedlot performance, and the prevalence of liver abscesses in feedlot cattle. Commercial steers and heifers (n = 5,481 hd) from similar sources were placed on feed at a commercial feedyard in Texas. Ten 4-pen blocks (40 pens) were assembled beginning in March 2016. At placement, cattle were randomly assigned to one of four treatment groups: 1) finishing ration with tylosin (90 mg/hd/d) fed until harvest (Tyl), 2) finishing ration without tylosin or other treatments (NTyl), 3) finishing ration without tylosin, but with an essential oil fed until harvest (EsOil), or 4) finishing ration without tylosin but with a yeast fermentation by-product (18 g/hd/d) fed until harvest (SCP). A composite fecal sample was obtained from each pen floor within four weeks of placement and again two to four d prior to harvest in order to evaluate fecal microbial populations and obtain isolates of *Salmonella enterica, Enterococcus,* and non-type-specific *Escherichia coli* for further characterization. At the conclusion of the finishing period, cattle were harvested at a commercial processing facility. Livers were evaluated for abscess prevalence and severity scoring at harvest. Additionally, a subset of livers from each pen (n = 5/pen) were collected for analysis of the microbial population using traditional culture-based techniques in addition to 16S rRNA gene sequencing to evaluate the microbiome. Although previous data and results from the current study highlight the utility of Tylosin inclusion on the reduction of liver abscesses, investigating alternatives is a necessity for the beef cattle industry. Furthermore, understanding the influence of these alternatives of microbial populations will not only aid in improving their efficacy but also assuring the safety of the beef food chain. This understanding will be

imperative for the future implementation of strategies aimed to mitigate liver abscesses and maintain the safety and economical production of beef.

Key Words: food safety, liver abscess, tylosin
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265 Genomic and metagenomic analysis of antibiotic resistance in dairy animals.

B. J. Haley*, S. W. Kim, H. Cao, J. S. Karns, and J. A. S. Van Kessel, *USDA-ARS, Beltsville, MD.*

The extent to which carriage of antibiotic resistant bacteria in food animals is responsible for the burden of antibiotic resistance in human infections is currently not well known. Thus, there is a need to further evaluate the genomic diversity of multidrug resistant (MDR) bacteria and the microbial communities in which they are found within these animals. To further evaluate the prevalence of antibiotic resistance in the feces of dairy animals, we sequenced the genomes of 160 antibiotic resistant *Escherichia coli* and 28 fecal metagenomes isolated from adult dairy cows, veal calves, and pre-weaned calves. *E. coli* isolates were collected from composite fecal samples and fecal grab samples taken directly from the animal. Isolates were screened for susceptibility to a panel of 14 antibiotics, and 150 showing resistance to at least one antibiotic and 10 antibiotic-susceptible isolates were selected for whole genome shotgun sequencing using a paired-end sequencing approach on an Illumina NextSeq 500. Twenty-eight fecal grab samples collected from animals shedding variable levels of antibiotic resistant *E. coli* were selected for shotgun metagenomics sequencing. Phylogenetic relationships among the *E. coli* genomes were inferred using a maximum likelihood approach in RAxML, and sequence types were determined in silico. At least four *E. coli* isolates from each of the major phylogroups were detected. The most frequently detected sequence types were ST88 (10% of all isolates), ST10 (9%), and ST117 (6%). Within these sequence types, isolates from different animals on the same farm and isolates from different farms were closely related, indicating that some strains of antibiotic resistant *E. coli* may be circulating among dairy herds within the same region. Interestingly, several MDR ST117 isolates were closely related to human ExPEC isolates and isolates recovered from chickens with colibacillosis. Metagenomic analyses indicated that for all samples tetracycline resistance genes were the most frequently identified resistance genes (61% of all resistance genes), followed by aminoglycoside (20%), macrolide (8%), beta-lactam (3%), sulfonamide (0.8%), and trimethoprim (0.6%) resistance genes. In veal calf fecal samples trimethoprim and fluoroquinolone resistance genes were more frequently detected than in pre-weaned dairy calf samples. Future work will identify genomic features that may confer persistence of high frequency antibiotic resistant *E. coli* strains and sequence types in the dairy cow hindgut and factors that influence the presence of antibiotic resistance in pre-weaned calves.

Key Words: antibiotic resistance, dairy, *Escherichia coli*
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266 Prevalence and risk factors for antimicrobial resistance on U.S. dairy operations.

H. Cao*[1], A. K. Pradhan[2], J. S. Karns[1], D. R. Wolfgang[3], E. Hovingh[4], B. T. Vinyard[1], and J. A. S. Van Kessel[1], *[1]USDA-ARS, Beltsville, MD, [2]University of Maryland, Department of Nutrition and Food Science, College Park, [3]Pennsylvania State University, Veterinary and Biomedical Sciences, University Park, [4]Pennsylvania State University, University Park.*

Antimicrobial resistance has become a major public health concern, and animal agriculture is often implicated as a source of resistant bacteria. The primary objective of this study was to determine prevalence of antimicrobial resistance in *Salmonella* and *E. coli* from healthy animals on dairy farms in Pennsylvania. Confidence intervals (CI) of farm prevalence were calculated for resistance, and the comparisons between different animal groups were adjusted for within-farm clustering. The secondary objective was to identify potential risk factors associated with antimicrobial resistance. In particular, we investigated the correlations between previous antimicrobial use and current resistance in *E. coli* using multiple logistic regression models. A total of 444 composite manure samples were collected from 80 herds in Pennsylvania. Four age and production groups were included: pre-weaned calves, post-weaned calves, dry cows, and lactating cows. *E. coli* (n = 2370) and *Salmonella* (n = 1095), when isolated from the manure composite samples (n = 444), were screened for resistance on antimicrobial supplemented agar. Isolates of interest were further assayed against 14 antimicrobials using a broth microdilution method. *Salmonella* was isolated from at least one composite manure sample from 51 (67%) farms, with 99% being pan-susceptible, and was detected more frequently in lactating cows and dry cows than pre- and post-weaned calves. The most prevalent *Salmonella* serogroups were K, C1, and C2. Among the *E. coli* isolates, resistance was more frequently detected in pre-weaned and post-weaned calves than in dry and lactating cows for all 14 antimicrobials tested ($P < 0.05$). Multi-drug resistance (resistant to ≥3 antimicrobial classes) in *E. coli* was detected in 66 farms (83%) and was detected more often in pre-weaned calves ($P < 0.05$). The $bla_{\text{CTX-M}}$ and bla_{CMY} genes were found in cephalosporin-resistant *E. coli* from 5% and 35% of the farms surveyed, respectively. A number of risk factors, including antimicrobial use, were found to be associated with an increased likelihood of resistance in *E. coli*, and these associations were not limited to the same antimicrobial classes. The results of this study showed dairy farms, especially pre-weaned calves and their environment, are significant reservoirs for antimicrobial resistance, and antimicrobial use may aggravate the resistance problem.

Key Words: antimicrobial resistance, dairy, risk factors
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267 Inspection for fecal contamination on chicken carcass using handheld imaging device.

M. Oh*[1,2], S. Moon[2], and M. S. Kim[1], [1]*USDA-ARS, Beltsville, MD,* [2]*Konkuk University, Chungju, Korea.*

Current inspection regulations for screening of chicken carcasses for fecal contamination require a human inspector to directly inspect the carcasses by naked eye. The chicken processing inspection environment may be illuminated at an intensity of up to 200 foot-candles. A portable fluorescence imaging device was developed to aid the human inspectors during chicken inspection. The device enhances the observable detection of chicken fecal material by using 405 nm excitation light to cause fecal fluorescence emissions near 636 and 680 nm. The objective of this study was to assess the usefulness of the recently developed portable fluorescence imaging device to detect fecal contamination of chicken carcasses under various luminous intensities. Fresh whole chickens were purchased from a local supermarket. Fresh fecal material was extracted from four sections (duodenum, small intestine, ceca, and colon) of the digestive tracts of 4-week-old broilers grown on corn and soybean meal in USDA farm facilities in Beltsville, MD. The fecal material was applied to the skin of the supermarket chickens to create visible and invisible areas of contamination, and detection of the contamination was tested using the portable device under five ambient lighting intensities (0, 10, 30, 50, and 70 foot-candles). The portable device with 680 nm optical filter was able to definitively distinguish both visible and invisible contamination of all four types from the normal chicken skin under all tested lighting conditions in real time. The results demonstrate that this portable fluorescence imaging device can be used to assist human inspectors in detecting fecal contamination during poultry carcass inspection.

Key Words: chicken, fecal contamination, fluorescence
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FORAGES AND PASTURES

142 Effect of pre and postpartum herbage allowances of grasslands on reproductive parameters of primiparous beef cows.

A. L. Astessiano Dickson*[1], M. Claramunt[2], A. Casal[1], M. Carriquiry[1], and P. Soca[3], [1]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay,* [2]*Centro Universitario de la Región Este, Universidad de la República, Treinta y Tres, Uruguay,* [3]*Facultad de Agronomia. Universidad de la Republica, Paysandu, Uruguay.*

The aim of this study was to evaluate the effect of the herbage allowance of grasslands during pre (PRE) and postpartum (POST) on beef cow productive and reproductive performance. Fifty pregnant Hereford heifers (5.6 ± 0.4 of BCS) were used in a randomized block design with a factorial arrangement of PRE (fall; high vs. low, H vs. L) and POST (spring to summer, high vs. low, H vs. L) herbage allowance (4 vs. 2.5 kgDM/kgBW of annual mean for high vs. low), determining four treatments (HH, HL, LH, LL). Progesterone (P4) was measured weekly from 80 to 160 days postpartum (DPP; mating period) to confirm commencement of luteal phase (CLA; plasma P4 $\geq$ 1 ng/mL), and early (first month of mating period) and final pregnancy were recorded. Calf weight was recorded at birth and weaning. Data were analyzed as repeated measures with a mixed model that included PRE and POST within PRE as fixed effects and block as a random effect. Means were considered to differ when P was <0.05. During the prepartum phase, all cows lost BW and BCS, but calving BCS was not affected by PRE and averaged 3.9 ± 0.1 units. However, at the initiation of the mating period, BCS was greater for LH cows than for the other three groups (4.1, 4.0, 4.5, and 4.0 ± 0.1 for HH, HL, LH, and LL, respectively). The CLA was not different between treatments and averaged 133 ± 5 days, but it was affected by BCS at mating as it decreased 25 days for every unit of BCS. However, plasma P4 during mating was greater for LH than HL cows, as it was intermediate for HH and LL cows (4.6, 2.4, 5.6, and 3.1 ± 1.0 ng/mL for HH, HL, LH, and LL, respectively). Early pregnancy was not affected by treatment and averaged 56%, but it also increased with BCS at mating. Final pregnancy was greater ($P = 0.051$) for LH than HL and intermediate for the other two groups (88.68, 80.0, 100.0, and 90.1% for HH, HL, LH, and LL, respectively). Calf birth weight did not differ due to PRE, but weaning weight tended to be greater ($P = 0.08$) in HH and LH than HL and LL cows as calf average daily gain was greater ($P < 0.01$) in the former than latter cow groups (1.05, 0.88, 1.08, and 0.95 ± 0.05 kg/d for HH, HL, LH, and LL, respectively). High POST improved calf performance independently of PRE herbage allowance;

Table 268.

	Trial 1					Trial 3				
Items	BFT	CMV	MB	SEM	P-Value	ALF	SAN	SML	SEM	P-Value
Treatments (Cows)										
BUN (mg/dL)	6.9^{a}	16.5^{b}	10.0^{a}	1.6	0.0033	18.7^{a}	13.4^{b}	4.2^{c}	1.8	0.0003
UUN (g/day)	81.7^{ac}	228.7^{b}	82.9^{c}	19.9	0.0043	216.8	98.6^{a}	24.4^{b}	26.6	0.0084
CH4 (L/day)	46.29^{a}	44.84^{a}	55.12^{a}	5.97	0.51	52.79^{a}	51.37^{a}	28.72^{b}	5.79	0.048
Intake (g intake/kg BW)	15.5^{a}	15.19^{a}	12.27^{a}	1.94	0.45	15.92^{ab}	12.82^{a}	18.29^{b}	1.44	0.062
	Trial 2					Trial 4				
Items	ALF	MB	SAN	SEM	P-Value	BFT	CMV	SML	SEM	P-Value
Treatments (Heifers)										
BUN (mg/dL)	27.9^{a}	10.9^{b}	14.9^{b}	16.1	0.0007	14.8^{a}	19.2^{a}	4.5^{b}	27.7	0.023
UUN (mg/day)	238.7^{a}	32.8^{b}	44.1^{b}	17.5	0.0003	119.6^{a}	183.9^{b}	23.8^{c}	8.2	<.0001
CH4 (L/day)	54.11^{a}	52.58^{a}	37.09^{a}	7.57	0.26	37.25^{a}	39.08^{a}	36.11^{a}	5.15	0.91
Intake (g intake/kg BW)	24.42^{a}	16.95^{b}	19.86^{ab}	0.95	0.0043	23.0^{a}	19.78^{b}	16.96^{c}	0.68	0.0021

Means in a row with different superscripts differ ($P < 0.1$).

however, it improved cow reproductive performance only when cows grazed low PRE.

Key Words: grazing, heifers, reproductive performance
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268 Environmental impacts from cattle consuming tannin-containing hays.

E. K. Stewart*[1], K. A. Beauchemin[2], J. W. MacAdam[3], and J. J. Villalba[1], [1]*Utah State University, Logan,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Department of Plants, Soils, and Climate, Utah State University, Logan.*

The cow-calf phase accounts for approximately 80% of total greenhouse gas emissions attributed to beef production systems. There is potential for tannin-containing hays to reduce these environmental impacts. Fifteen mature beef brood cows and 9 yearling beef heifers were blocked by weight and randomly assigned to 3 groups of 5 cows or 3 heifers and fed tannin-containing (bird's-foot trefoil-BFT, sainfoin-SAN, small burnet-SML) or non-tannin-containing (alfalfa-ALF, cicer milkvetch-CMV, meadow bromegrass-MB) hays in 4 trials. Groups of cows were fed BFT, CMV, or MB in Trial 1 and ALF, SAN, or SML in Trial 3. Groups of heifers were fed ALF, MB, or SAN in Trial 2 and BFT, CMV, or SML in Trial 4. Each trial used a completely randomized block design with repeated measures during 5 days following a 14-d adjustment period. Nine cows and 9 heifers were selected for total collection of enteric methane using the SF6 methodology, feces, and urine while intake was measured for all animals. Methane emission from cows was lower for SML than ALF ($P = 0.04$) or SAN ($P = 0.03$; Table 268). Additionally, cows and heifers fed tannin-containing hays had lower urine urea nitrogen (UUN) and blood urea nitrogen (BUN) than animals fed non-tannin-containing hays (Table 268), suggesting a shift in nitrogen excretion from urine to feces. In conclusion, tannin-containing legumes consumed as hays have the potential to reduce environmental impacts attributed to cattle fed in confinement.

Key Words: legumes, methane emissions, urinary urea
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269 Effect of oilseed source on ruminal fermentation and methane production of a grass-legume diet in continuous culture.

A. I. Roca-Fernandez*[1,2], S. L. Dillard[1], C. J. Dell[1], J. W. MacAdam[3], and K. J. Soder[1], [1]*USDA-Agricultural Research Service, University Park, PA,* [2]*Universidad de Santiago de Compostela, Lugo, Spain,* [3]*Department of Plants, Soils, and Climate, Utah State University, Logan.*

Addition of oilseeds to pasture-based ruminant diets has been shown to decrease enteric CH_4 emissions. However, little research has directly compared the effect of oilseed source on ruminal fermentation and CH_4 production. A 4-unit continuous culture fermentor system was used to test 4 oilseeds supplemented to a 45% orchardgrass (*Dactylis glomerata* L.) + 45% sericea lespedeza (*Lespedeza cuneata* Don. cv. Auburn Grazer) diet. Oilseeds (supplemented at 10% of total DM fed) were soybean (SOY), sunflower (SUN), canola (CAN), and a mixture of equal proportions of SOY, SUN, and CAN (MIX). Diets were randomly assigned to fermentors in a 4 × 4 Latin square design. Feeding occurred 4 times daily throughout four 10-d periods using 7 d for adaptation and 3 d for collection. Effluent samples were analyzed for pH, VFA, and DM, OM, ADF, and NDF digestibilities. Gas samples were recorded using a photoacoustic gas analyzer for total daily CH_4 production. Data were analyzed using the GLIMMIX procedure of SAS with treatment as a fixed effect and fermentor and period as random effects. No differences ($P > 0.10$) were found for pH (7.10) among oilseeds. Total VFA concentration was greatest ($P < 0.01$) in SOY (46.0 mmol/L), with no differences ($P > 0.05$) among other oilseeds (38.2 mmol/L). There were no differences ($P > 0.05$) among oilseeds in molar proportions of acetate, propionate, isobutyrate, butyrate, isovalerate, and valerate. No differences ($P > 0.10$) were found for apparent and true DM and OM digestibilities or apparent ADF and NDF digestibilities. Total daily CH_4 production and total CH_4 production per gram of nutrients fed or per gram of digestible nutrients fed were greatest ($P < 0.001$) in SOY. The SOY produced daily 68, 81, and 85% greater ($P < 0.001$) amounts of CH_4 (80.1 mg/d) compared to SUN, CAN, and MIX, respectively. No differences ($P > 0.05$) were found between SUN, CAN, and MIX for total daily CH_4 production or total CH_4 production per gram of DM, OM, ADF, and NDF fed or per gram of digestible OM fed. The SOY produced greater ($P < 0.001$) amounts of CH_4 per gram of digestible DM fed or per gram of digestible ADF and NDF fed than MIX, with SUN and CAN showing intermediate levels. Addition of oilseeds such as SUN and CAN to a grass-legume diet is a potentially environmentally friendly feeding strategy to reduce enteric CH_4 emissions without negatively impacting ruminal fermentation.

Key Words: methane, oilseeds, ruminal fermentation
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270 Monensin effects on beef heifers grazing bahiagrass pastures and receiving molasses supplementation.

J. Vendramini*, P. Moriel, C. Carnelos, M. Piccolo, and H. M. da Silva, *UF/IFAS Range Cattle Research and Education Center, Ona, FL.*

The objective of this study was to evaluate the effects of monensin on forage characteristic and performance of beef heifers. The experiment was conducted in Ona, FL, from August to November 2016. Treatments were the addition of monensin (200 mg/animal/d) in the supplement or control (no monensin) distributed in a complete randomized design with five replicates. Heifers received 2.3 kg/heifer/d of liquid sugarcane (*Saccharum officinarum*) molasses (11% CP, 76% TDN) supplement. The daily supplement level was multiplied by 7 d and divided by 3 feeding events/wk (Mondays, Wednesdays, and Fridays). Ten pastures (experimental units; 1.2 ha) of bahiagrass (*Paspalum notatum*) were used with a fixed and continuous stocking rate. Three Brangus heifers with initial BW of 389 ± 36 kg were allocated per experimental unit. Herbage mass (HM) and nutritive value were estimated every 14 d, and the heifers were weighed every 28 d. There was no effect of the treatments on HM ($P = 0.11$, SE = 200, mean = 3100 kg/ha), CP ($P = 0.37$, SE = 0.6, mean = 8.1%), and in vitro digestible organic matter ($P = 0.72$, SE = 1.0, mean = 50.9%). Molasses disappearance 34 h after feeding was greater for control than monensin (98 vs. 93%, $P = 0.01$, SE = 0.2); however, there was no difference in heifers ADG ($P = 0.58$, SE = 0.07, mean = 0 kg/d), final BW ($P = 0.87$, SE = 18, mean = 385 kg), and BCS ($P = 0.51$, SE = 0.27, mean = 6.2). Heifers receiving monensin tended to have less blood glucose (86 vs. 94 mg/dL, $P = 0.07$, SE = 2.8) and greater BUN concentrations (12.0 vs. 9.4 mg/dL, $P = 0.06$, SE = 1.3), but there was no difference in blood IGF – 1 ($P = 0.76$, SE = 4.2, mean = 72 ng/mL). The addition of monensin in molasses supplement may decrease the rate of consumption of the supplement but the magnitude of the decrease may not be sufficient to affect ADG of heifers grazing warm-season grasses with limited nutritive value.

Key Words: beef cattle, monensin, supplementation
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271 Effect of enhanced management on behavior of calves grazing tall fescue of varied toxicity levels.

J. Diaz*[1], S. Gadberry[2], J. T. Richeson[3], P. A. Beck[4], D. Hufstedler[5], D. S. Hubbell III[6], J. D. Tucker[6], and T. Hess[6], [1]*University of Arkansas Department of Animal Science, Fayetteville,* [2]*University of Arkansas Division of Agriculture Coop. Ext. Serv., Little Rock,* [3]*West Texas A&M University, Canyon,* [4]*University of Arkansas Division of Agriculture SWREC, Hope,* [5]*Elanco Animal Health, Guthrie, OK,* [6]*University of Arkansas Division of Agriculture Livestock and Forestry Research Station, Batesville.*

The experimental objective was to evaluate the behavior of steers grazing tall fescue (*Festuca arundicea*) with low to high toxicity levels at different levels of growth promotion management (MGMT) using accelerometers. Steers ($n = 80$; 116.93 ± 4.9 kg BW) grazed pastures ($n = 16$; 1.2-ha pastures) during the spring grazing season from 22 March to 14 June for 84 d in 2016 at a stocking rate of 4.1 steers/ha. Accelerometers were placed on 3 steers in 15 pastures from 21 April to 17 May (Period 1) and from 17 May to 12 June (Period 2). Steers on 8 pastures were fed a control mineral (MIN) with no additional growth promotion. Steers on 7 pastures were managed with cumulative growth promotion management (CM), which included a growth promoting implant (TE-G with Tylan; Elanco Animal Health, Greenfield, IL) and 1% of BW of a 50:50 corn gluten feed:soybean hull pellet containing monensin at 150 mg per calf (Rumensin; Elanco Animal Health) fed daily. Ergovaline (EV) concentrations were analyzed in each pasture resulting in a range of EV from 90 to 2,180 ppb. Data were analyzed using management (MIN vs. CM), EV concentration, period, and the 2- and 3-way interactions. Reduced models were applied in case of nonsignificant interactions in the full models. Motion index decreased ($P = 0.04$) with EV but increased ($P < 0.01$) with CM compared with MIN. Total steps increased ($P < 0.01$) for CM compared with MIN, whereas total steps decreased with increasing EV ($P < 0.01$). Total standing minutes were less ($P < 0.01$) for CM than for MIN during Period 2. Lying bouts were not affected ($P \geq 0.22$) by EV or MGMT during Period 1. Lying bouts were greater ($P < 0.01$) for CM than for MIN in Period 2 and increased with increasing ($P = 0.02$) EV during Period 2. An

EV × MGMT interaction ($P = 0.02$) during Period 2 indicates that with CM, lying bouts decreased ($P = 0.02$) with increasing EV, but increasing EV increased ($P = 0.02$) lying bouts in MIN. The changes in behavior between periods indicate that EV concentration decreases total steps taken but will change behavior from standing to lying with higher environmental temperatures. Feeding high supplementation rates with the CM treatment increased minutes spent standing during Period 1 and decreased lying bouts in Period 2; this increased activity with CM occurred regardless of environmental temperatures.

Key Words: beef cattle, behavior, tall fescue
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272 Impact of adding *Saccharomyces cerevisiae* and *Lactobacillus buchneri* on fermentation, aerobic stability, nutritive value, and microbial communities in corn silage.

S. Xu*[1], J. Yang[2], M. Qi[3], B. Smiley[3], W. Rutherford[3], Y. Wang[1], and T. A. McAllister[1], [1]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Department of Animal Science, Inner Mongolia Agricultural University, Hohhot, P.R. China,* [3]*DuPont Pioneer, Johnston, IA.*

The objective of this study was to assess the impact of additives of *Lactobacillus buchneri* in combination with *Saccharomyces cerevisiae* on the fermentation characteristics, aerobic stability, nutritive value, and microbial communities of ensiled corn silage. Whole crop corn (391 g/kg DM) was either uninoculated (Control) or inoculated with *S. cerevisiae* and *L. buchneri* at the following concentrations: *S. cerevisiae* at 10^4 cfu/g fresh forage, *S. cerevisiae* at 10^5 cfu/g, *S. cerevisiae* at 10^4 cfu/g + *L. buchneri* at 10^5 cfu/g (Y4L5), and *S. cerevisiae* at 10^5 cfu/g + *L. buchneri* at 10^4 cfu/g; then, it was ensiled in mini-silos for 118 d followed by 7 d of aerobic exposure. Changes in fermentation characteristics and nutritive value were assessed in terminal silages. Quantitative PCR (qPCR) was used to quantify the inoculants *S. cerevisiae* and *L. buchneri* and total yeast, fungal, and bacterial communities in silage. The composition of bacterial and fungal communities during ensiling and aerobic exposure was characterized using 16S ribosomal DNA and internal transcribed spacer sequencing, respectively. The concentration of lactic acid rapidly increased ($P < 0.05$) in all treatment silages during the first 7 d, with pH declining to 4.0 and remaining at a similar level until the end of ensiling. Although Y4L5 contained a higher ($P < 0.05$) concentration of acetic acid compared with the Control, fermentation characteristics of silage were similar among all the treatments after 118 d ensiling. Inoculation with *S. cerevisiae* had no detrimental effect on the aerobic stability of silage, whereas addition of *L. buchneri* did not prevent the silage spoilage, with the pH across all treatments increasing to an average of 8.0 after 7 d of aerobic exposure. Total yeast, bacterial, and fungal communities as quantified by qPCR were not altered by the inoculants after ensiling or the aerobic exposure process. Sequencing results showed temporal shifts of bacterial and fungal populations during ensiling and the aerobic exposure stage. Concentrations of *S. cerevisiae* and *L. buchneri* in all inoculated treatments remained higher ($P < 0.05$) than those in the Control after ensiling, with numbers of *S. cerevisiae* increasing after 7 d of aerobic exposure. However, inoculation of *S. cerevisiae* and *L. buchneri* did not alter the overall composition of bacterial and fungal communities in silage, as indicated by principal coordinate analysis. Our findings suggest that the abundance of the beneficial yeast inoculants can increase or remain the same in silage during the aerobic exposure stage prior to feeding to animals.

Key Words: corn silage, ensiling, microbial communities
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273 Comparison of in vitro long digestion methods and digestion rates for diverse forages.

M. Valentine*, *Cornell University, Ithaca, NY.*

Long-term in vitro digestions of forages provide digestion rate estimates of NDF and undigested NDF (uNDF) at some time point short of infinity. The indigestible portion is required for an accurate estimate of the feed's potentially digestible fraction. Depending on the filtration system, potentially digestible particles could remain trapped or indigestible particles could mistakenly dislodge. Unreliable measures of uNDF can impact animal nutrition and performance when balancing diets based on flawed forage quality estimates. Two common techniques for in vitro digestion are the conventional flask method and the ANKOM filtration bag procedure. Small indigestible particles might escape the ANKOM F57 filter bag in long-term digestions because of its 25-µm pore size. An ANKOM filter bag has been developed (F58) with an 8- to 10-µm pore size, decreasing the chance of losing indigestible particles during NDF procedure, but it has not been evaluated for use with in vitro digestions. Our objective was to compare ANKOM F58 bags to F57 bags and the conventional flask method for in vitro long digestions. Analyses incorporated 24 forage samples representing a broad range of temperate and tropical grasses and legumes. Duplicate samples for both F57 and F58 filter bags digested for 30, 120 and 240 h. Cumberland Valley Analytical Services (CVAS) analyzed the same samples using the conventional flask procedure 3 times on separate days. Correlation between uNDF of F57 and F58 bags was 0.997, between the F57 bags and CVAS results was 0.964, and between F58 bags and CVAS results was 0.965. Correlation between digestion rate of F57 and F58 bags was 0.956, between F57 bags and CVAS results was 0.616, and between F58 bags and CVAS results was 0.546. All methods were relatively similar in terms of uNDF. Results of F57 and F58 bags were more related to one another than CVAS results for rates of digestion. Rates of digestion varied considerably between forages; however, they were consistent over procedures.

Key Words: forages, in vitro digestion, undigested neutral detergent fiber
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274 Growth stage at harvest influences forage quality and yield of brown midrib forage sorghum.

S. E. Lyons*, Q. M. Ketterings, D. J. R. Cherney, J. H. Cherney, G. S. Godwin, and T. F. Kilcer, *Cornell University, Ithaca, NY.*

Forage sorghum (*Sorghum bicolor* L.) can be a viable alternative to corn silage (*Zea mays*) in double-cropping rotations with winter cereals in the northeastern United States. Given a relatively short summer, a late September or early October harvest of sorghum is ideal for the rotation. Our objective was to determine the impact of harvest timing on quality and yield of forage sorghum. Sorghum was harvested weekly for 9 wk in 2015, from boot through hard dough, at 2 locations in central New York. In 2016, a rotation trial with forage sorghum and triticale (×*Triticosecale*) was initiated in Aurora, NY, to evaluate the impact of timing of sorghum harvest (2-wk interval; 4 timings) on quality and yield. Quality parameters that were measured included CP, RDP, ADF, NDF, lignin, ADL, starch, nonfiber carbohydrates (NFC), NDF digestibility (30 h; $NDFD_{30}$), and in vitro true 30-h digestibility ($IVTD_{30}$). Yields increased from 14.6 and 12.2 Mg DM/ha at flowering to 16.6 and 23.4 Mg DM/ha at milk stage (late September/early October) for 2015 and 2016, respectively, with no further yield gain beyond milk stage in either year. Between milk and soft dough in 2015, freshly dried samples decreased in CP, RDP, NDF, and $NDFD_{30}$ as plants matured whereas ADL, starch, and NFC increased. In the 2016 study, for freshly dried samples, NDF, ADF, $IVTD_{30}$, and $NDFD_{30}$ decreased with plant maturity whereas ADL increased. Ensiled samples in 2015 between milk and soft dough were higher in CP, RDP, ADL, and ADF and lower in starch, NDF, and $NDFD_{30}$ than the freshly dried samples. In 2016, the ensiled samples followed a pattern to that of the freshly dried samples; however, ADL and NDF were slightly lower at the soft dough stage. These data suggest that harvest of forage sorghum as early as milk stage optimizes yield and most forage quality parameters, enabling more timely planting of winter cereals. However, harvest at milk stage will result in lower starch and higher moisture content than forage harvested at soft dough. Additional work is ongoing to determine the feed quality of forage sorghum when harvested at milk stage.

Key Words: double cropping, forage quality, forage sorghum
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275 Assessment of *Eragrostis tef* (Zucc.) as a forage base for growing beef steers.

J. D. Sugg*, J. O. Sarturi, C. P. West, L. L. Baxter, and L. A. Pellarin, *Texas Tech University, Lubbock.*

A 2-yr study of animal gain performance and forage dynamics were evaluated over the course of a 63-d backgrounding period in which beef steers were supplemented while grazing *Eragrostis tef* (Zucc.). Paddocks ($n = 4$; 2.66 ha; experimental units) equipped with subsurface drip irrigation were seeded in 'Tiffany teff' grass (3.72 kg/ha) in both years, and each paddock was stocked with crossbred beef steers ($n = 4$, initial shrunk BW = 289 ± 30 kg in yr 1; $n = 5$, initial shrunk BW = 286 ± 22 kg in yr 2) using a randomized complete block design. Supplements were randomly assigned to paddock: cottonseed meal (0.45 kg/steer daily) or dried distiller's grains (DDG; 0.5% shrunk BW/steer daily). Steers were weighed on d 20, 41, and 62 (12-h fast). Weekly samples of whole plant (WP) and canopy (CNY) structures were obtained for DM, OM, and fiber concentrations. Biweekly, samples were analyzed for CP and IVTDMD. Data were analyzed with supplement, day, and their interactions as fixed effects. Gain did not differ by supplement from d 0 through 21 ($P = 0.13$). Observed ADG from d 0 through 42 and cumulative ADG was higher ($P \leq 0.03$) among steers offered DDG. Across the period, forage allowance was not affected by supplement or day ($P \leq 0.43$), and no supplement × day interaction ($P = 0.83$) was detected. Numerically, forage allowance was lowest on d 0 and greatest on d 28. A day × structure interaction resulted in measures of NDF greater ($P < 0.01$) in WP relative to CNY on d 35 and 49. A similar interaction in ADF concentration resulted in greater values ($P < 0.01$) in WP relative to CNY on d 49. Neither IVTDMD ($P = 0.63$) nor CP ($P = 0.54$) of forage were affected by cattle supplementation. A numerical 1.29% increase ($P = 0.18$) in IVTDMD was observed for CNY whereas CP of CNY was greater (1.59%; $P < 0.01$) than CP of WP. Concentration of CP tended to be greater at d 56 relative to d 28 ($P = 0.08$). Soil moisture was not affected by cattle supplementation ($P = 0.40$), with expected differences among soil depth ($P < 0.01$) and days through grazing period ($P < 0.01$) being observed. Supplementation with DDG increased weight assimilation in growing beef steers without negatively affecting pasture production or canopy structure. Teff grass may be well suited for backgrounding beef cattle with supplementation.

Key Words: digestibility, forage quality, teff
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276 Effects of feeding *Eragrostis tef* hay harvested at different stages of maturity on nutrient intake, ruminal fermentation, and nitrogen utilization in beef cattle.

J. R. Vinyard[*1], J. B. Hall[1,2], J. E. Sprinkle[1,2], and G. E. Chibisa[1], [1]*Department of Animal & Veterinary Sciences, University of Idaho, Moscow,* [2]*University of Idaho Nancy M. Cummings Research, Extension Education Center, Carmen.*

Eragrostis tef (‘Tiffany’ teff), a warm-season annual grass, could be an excellent forage for beef cattle. However, there is limited information on its nutritive value at different stages of maturity. Therefore, our objective was to determine the effect of feeding teff hay harvested at the boot (BT), early-heading (EH), or late-heading (LH) stages of maturity on nutrient intake, ruminal fermentation, and N utilization in beef cattle. Six ruminally cannulated beef heifers (476 kg [SD 32.6] initial BW) were used in a replicated 3 × 3 Latin square design with 28-d periods (18 d for adaptation and 10 d for measurements). Dietary treatments were BT, EH, or LH teff hay. Dry matter intake was measured daily, and indwelling pH loggers were used to continuously measure ruminal pH from d 21 to 28. Ruminal fluid for ammonia determination and spot urine samples for measurement of urine output, N, and urea N excretion were collected from d 26 to 28. Blood samples for plasma urea N (PUN) determination were collected 3 h after feeding on d 28. The NDF and ADF content were similar across diets. However, CP content was greater for the BT hay than for EH and LH hay (18.1, 14.1, and 11.5%, respectively, DM basis). Dry matter intake was higher ($P = 0.03$) for heifers fed the LH hay (11.6 kg/d) compared with heifers fed the BT hay (10.9 kg/d), whereas CP intake increased ($P = 0.03$) for heifers fed the EH hay (1.76 kg/d) compared with heifers fed the LH hay (1.65 kg/d). There was no diet effect ($P > 0.05$) on mean, minimum, and maximum pH and the duration and area pH < 6.2 and 5.8, but ruminal ammonia concentration was greater ($P < 0.05$) for heifers fed BT hay (14.04 mg/dL) than for heifers fed EH (8.82 mg/dL) and LH hay (5.01 mg/dL). Plasma urea N concentration also tended to be higher ($P = 0.08$) for BT hay compared with EH and LH hay (19.1, 15.9, and 14.1 mg/dL, respectively). Urine output increased ($P = 0.01$) in heifers fed the BT hay (15.2 kg/d) than in heifers fed the EH (11.5 kg/d) and LH hay (11.7 kg/d). Similarly, urine N and urea N excretion increased ($P < 0.01$) for heifers fed the BT hay compared with heifers fed the EH and LH hay. In conclusion, although there was no diet effect on ruminal pH, the decrease in CP content with advancing maturity resulted in a decrease in the ruminal ammonia and PUN concentrations and urine N and urea N excretion when teff hay was fed to beef cattle.

Key Words: beef cattle, nutritive value, teff hay
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277 Evaluation of average daily gain predictions by the integrated farm system model for forage-finished beef steers.

J. A. Dillon[*1], D. D. Harmon[2], C. A. Rotz[3], and D. W. Hancock[2], [1]*Department of Animal Science, Pennsylvania State University, University Park,* [2]*Department of Crop and Soil Sciences, University of Georgia, Athens,* [3]*USDA-ARS Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Representing the performance of cattle finished on an all forage diet in process-based whole-farm system models has presented a challenge. To address this challenge, a study was done to evaluate ADG predictions of the Integrated Farm System Model (IFSM) for steers consuming all-forage diets during the finishing period. Animal performance data from warm-season annual forage grazing trials conducted in 2014 and 2015 at the Eatonton Beef Research Unit were compared with model predictions. Treatments representing the highest (BMR14), average (BMR15), and lowest (PMCG15) forage yields were simulated. Forage quality for each treatment was provided to the model, and predicted forage yield was calibrated within 10% of observed values. With initial settings based upon recommended nutritional requirements, predicted ADG was 71, 12, and 44% lower than that observed for BMR14, BMR15, and PMCG15, respectively. These discrepancies may be related to assumptions about forage quality and intake or the animal’s nutrient requirements. The use of variable stocking rates to maintain forage quality in the grazing trial precluded the collection of intake data, which would have enabled a more conclusive evaluation of these differences. Two parameters representing feed efficiency (FE) and feed digestibility (FD) were explored for their impact on ADG predictions. Feed efficiency modified the amount of NE available per unit of feed consumed, whereas FD modified fiber digestibility, which essentially increased the rate of passage. A sensitivity analysis showed that ADG was highly sensitive to each of these model parameters. A 37% increase in FE or 39% increase in FD was required to predict ADG within 10% of observed values. Predicted forage intake decreased from 9.9 to 9.7 kg DM/d when FE was increased, and it increased to 15.4 kg DM/d when FD was increased to meet nutrient demands. No change in manure output was observed in either scenario, although manure N and P content decreased by 26 and 13% when FE was increased and by 35 and 7% when FD was increased. These values remain within biologically reasonable bounds and suggest that these parameters may be used to improve representation of finishing animals on all-forage diets. This improvement will enable use of IFSM in a life cycle assessment of forage-finished beef production systems.

Key Words: grass-finished beef, grazing, modeling
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278 Differences in digestive kinetics and methane production among rhizoma peanut (*Arachis glabrata* Benth.) cultivars.

A. B. Norris*[1], W. L. Crossland[1], J. L. Foster[2], J. P. Muir[3], and L. O. Tedeschi[1], [1]*Texas A&M University, College Station,* [2]*Texas A&M AgriLife Research, Beeville,* [3]*Texas A&M AgriLife Research, Stephenville.*

Our objective was to determine if fermentation dynamics of 8 rhizoma peanut (RP; *Arachis glabrata* Benth.) cultivars differed among themselves and alfalfa (*Medicago sativa* L.). Rhizoma peanut is a hardy subtropical legume of nutritive value comparable to alfalfa but produces polyphenol oxidase (PPO), which may potentially result in a protein sparing due to antimicrobial properties. Although alfalfa and RP demonstrate similar nutritive profiles, prior research indicates that decreased ruminal protein degradation rates of RP may improve N use efficiency relative to non-PPO producing forages. Polyphenol oxidase enzymes from RP and red clover (*Trifolium pretense* L.) decrease proteolysis during ensiling and within the rumen, decrease plant-facilitated lipolysis, reduce PUFA biohydrogenation, and lower CH_4 emissions. There is a large variation in nutritive value and PPO production among RP cultivars, signifying the need to screen. In our preliminary analysis, RP cultivars Arblick, Florigraze, UF Peace, Latitude 34, Arbrook, Ecoturf, UF Tito, and variety not specified (VNS) were hand collected late in the 2016 growing season from the Texas A&M AgriLife Research Center at Beeville, TX. Using an in vitro gas production technique, we determined 48-h fermentation dynamics of each RP cultivar and alfalfa. Measurements of CH_4 via gas chromatography, pH and redox potential, and digested residue were analyzed. Kinetic analysis of cumulative 48-h gas production was performed using GasFit. All cultivar kinetics fit the exponential model with discrete lag times. There were no differences ($P > 0.05$) among RP cultivars for total gas production, fermentation rate, lag time, total CH_4 grams per liter, or CH_4 grams per liter per gram of NDF digested. There were no differences between RP cultivars and alfalfa for total gas production, lag time, or total CH_4 (g/L). However, fractional rate of fermentation was slower for alfalfa vs. UF Peace (9.44 vs. 19.76%/h; $P = 0.03$) but not different from other cultivars (12.94, 17.62, 17.79, 14.62, 11.69, 17.89, and 16.53%/h for Arblick, Florigraze, Latitude 34, Arbrook, Ecoturf, VNS, and UF Tito, respectively) and marginal mean differences could not be determined using Tukey's honest significant difference. Further analyses of neutral detergent insoluble N and PPO are required to determine the impact of PPO on N metabolism. Based on these in vitro findings, RP may serve as a viable forage substitute, nutritionally and environmentally.

Key Words: fermentation dynamics, methane, perennial peanut
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279 Can potassium chloride mitigate nitrous oxide emissions from grassland soil?

A. S. Cardoso*[1], B. G. Quintana[1], E. R. Januschkiewicz[1], L. F. Brito[1], E. S. Morgado[2], R. A. Reis[1], and A. C. Ruggieri[1], [1]*São Paulo State University, Jaboticabal, Brazil,* [2]*Universidade Federal de Uberlandia, Uberlandia, Brazil.*

Nitrous oxide (N_2O) is the third most important greenhouse gas, with a global warming potential 300 times more than carbon dioxide. The main sources of N_2O in grassland soils are nitrogen fertilizers application and animal excretion. The objective of this research was to test the hypothesis that KCl can inhibit N_2O emissions from soil. The experimental design was completely randomized with 5 treatments and 4 replicates. The treatments were 4 concentrations of KCl diluted in cattle urine (0.0, 5.0, 10.0, and 20.0 g/L). The N_2O emissions from a tropical Ferralsol were evaluated in an incubation under controlled conditions. The N_2O emissions were evaluated using a static closed chamber and the gas concentration was determined by gas chromatography. Nitrous oxide emissions were integrated over time to calculate the cumulative emissions and the amount of N lost as N_2O and then the ANOVA was performed. To analyze the effect of KCl concentrations on N_2O emission, a polynomial orthogonal contrast was tested. The percent of applied N emitted as N_2O was 3.22 (±1.21), 4.44 (±0.65), 3.03 (±0.42), and 1.17 (±0.23) for the KCl concentrations of 0.0, 5.0, 10.0, and 20.0 g/L of urine, respectively. The KCl addition to the soil affected N_2O emissions ($P < 0.01$). The effect of KCl concentration was curvilinear ($P < 0.01$, $R^2 = 0.87$). A possible mechanism that explains the reduction of N_2O production when KCl concentration increases is that higher KCl concentration may inhibit the nitrification. The increase in the K^+ ions probably negatively affects the nitrification. The KCl addition to a grassland soil diminishes N_2O emissions and possibly can be used to mitigate N_2O production.

Key Words: climate change, nitrous oxide, tropical soil
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280 Isolation and identification of lactic acid bacteria that colonize tropical whole-plant corn silage during the fermentation process.

L. Silva[1], O. G. Pereira*[1], T. C. Silva[1], J. P. Roseira[1], M. C. N. Agarussi[1], V. P. Silva[1], R. A. Paula[1], R. M. Martins[1], and T. F. Bernardes[2], [1]*Federal University of Vicosa, Vicosa, Brazil,* [2]*Federal University of Lavras, Lavras, Brazil.*

The goals of the present study were to isolate and identify the lactic acid bacteria (LAB) that colonize tropical whole-plant corn silage during the fermentation process. The experiments were conducted and crops were grown at the Department of Animal Science of the Federal University of Vicosa, Minas Gerais, Brazil. Corn (*Zea mays*) plants were harvested when

kernels reached the hard dough stage. The mini-silos were stored at room temperature and opened after 0, 1, 3, 7, 14, 28 and 56 d of storage. The isolates were purified by streaking individual colonies. Preselected cells grown in 5 mL of MRS broth at 37°C for 18 h were used for 16S rRNA gene sequencing. The 16S rRNA gene sequences that show similarity greater than 97% were considered as belonging to the same operational taxonomic unit. One hundred fifty-one LAB strains were isolated. In the first 3 d of storage, the LAB species *Pediococcus pentosaceus*, *Lactobacillus plantarum*, and *Weissella cibaria* were the most identified. *Lactobacillus plantarum* was the predominant species until the 28th day of storage. At d 56 of storage, the predominant species were *Lactobacillus buchneri* followed by *Streptococcus salivarius* and *Lactobacillus casei*. The predominant species of tropical corn silage, considering isolates in MRS agar, for all the days of ensiling were *L. plantarum* (53.0%), *P. pentosaceus* (11.9%), *L. buchneri* (9.9%), *Lactobacillus pentosus* (5.3%), *W. cibaria* (4.6%), and *Lactobacillus brevis* (4.0%). The appearance of *L. buchneri* naturally occurs in the 56th day of ensiling corn under tropical conditions. Supported by Fapemig, CNPq CAPES, and INCT-CA.

Key Words: *Lactobacillus buchneri*, *Lactobacillus plantarum*, 16S rRNA
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281 Effect of *Lactobacillus buchneri* isolated from tropical corn silage on fermentation and aerobic stability.

L. Silva[1], O. G. Pereira*[1], S. A. Santos[2], K. G. Ribeiro[1], J. P. Roseira[1], M. C. N. Agarussi[1], V. P. Silva[1], F. Amaro[1], and R. M. Martins[1], *[1]Federal University of Vicosa, Vicosa, Brazil, [2]Universidade Federal da Bahia, Salvador, Brazil.*

The objectives of this study were to evaluate the *Lactobacillus buchneri* strains isolated from tropical whole-plant corn silage for use as a silage inoculant. The corn plants with kernels at hard dough stage of maturity were harvested. The isolated strains 56.22, 56.27, 56.28, and 56.29 were evaluated, and the theoretical application rate was 1.0×10^6 cfu/g of fresh weight. Approximately 7 kg of treated material was conditioned in plastic buckets (mini-silos), 25 cm in diameter and 25 cm in height, sealed with tight lids. The variance analysis and multiple comparisons of data were performed using PROC MIXED of SAS (SAS Inst. Inc., Cary, NC), and the means were separated by Tukey's test ($P \leq 0.05$). The *L. buchneri* strains did not affect the DM content, yeast and molds population, DM losses, water-soluble carbohydrates, lactic acid, propionic acid, butyric acid, and ethanol of corn silage after 90 d of ensiling ($P > 0.050$). The pH, lactic acid bacteria (LAB) population, and acetic acid were affected by inoculants ($P < 0.050$). The 56.27, 56.28, and 56.29 strains showed lower pH values than the control silage. The LAB number was greater for the silages containing the strains 56.22, and 56.27 in comparison with the control silage ($P = 0.003$). The *L. buchneri* strains 56.22, 56.28, and 56.29 decreased the concentration of acetic acid in comparison with the control silage ($P = 0.041$). After 7 d of air exposure, there was observed no improvement of inoculation with the *L. buchneri* strains in the aerobic stability of silage when compared with the control ($P = 0.289$). The overall mean for aerobic stability of corn silage was of 32.7 h. The treated and untreated silages showed high pH, high number of yeasts and molds, and low concentrations of water-soluble carbohydrates and organic acids. In conclusion, the isolated strains when applied in corn silage showed no beneficial effect. Supported by Fapemig, CNPq CAPES, and INCT-CA.

Key Words: acetic acid, lactic acid, *Zea mays*
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282 Effect of *Lactobacillus buchneri* isolated from tropical corn silage on fermentation and aerobic stability of sugarcane silage.

L. Silva, O. G. Pereira*, E. S. Leandro, J. P. Roseira, M. C. N. Agarussi, V. P. Silva, F. Amaro, and S. C. Valadares Filho, *Federal University of Vicosa, Vicosa, Brazil.*

The objective of this study was to evaluate the *Lactobacillus buchneri* strains isolated from tropical whole-plant corn silage for use as a silage inoculant in sugarcane. Sugar cane plants (approximately 16 mo old) were harvested and chopped to 25 mm. The isolated strains 56.1, 56.4, 56.9, and 56.26 and the commercial inoculant "Lalsil Cana" (*L. buchneri* NCIMB 40788) were evaluated. For all the treatments, the theoretical application rate was 1.0×10^6 cfu/g of fresh weight. Approximately 7 kg of treated material was conditioned in plastic buckets (mini-silos; 25 by 25 cm) sealed with tight lids. The mini-silos were opened after 90 d of storage. The variance analysis and multiple comparisons of data were performed using PROC MIXED of SAS, and means were separated by Tukey's test ($P \leq 0.05$). The silages inoculated with the isolated strains 56.1 and 56.4 and the commercial strain 40788 showed the highest DM content ($P = 0.004$). Silages inoculated with the isolated strains 56.1 and 56.9 and the commercial strain 40788 showed lower yeast and mold populations than the control silage ($P = 0.024$). Regarding the ethanol concentration, the silages inoculated with the strains 56.1, 56.4, and 40788 showed lower values than the silages inoculated with the strains 56.9 and 56.26, whereas the control silage showed intermediate values ($P = 0.016$). In addition, lower DM losses were observed for the isolated strains 56.1 and 56.4 and the commercial strain 40788 in comparison with the control silage ($P < 0.001$). However, there was no effect of the inoculation with the strains of *L. buchneri* on the aerobic stability ($P = 0.524$). Even so, the strains 56.1 and 56.4 are promising for use as an inoculant in sugarcane silages. Supported by Fapemig, CNPq CAPES, and INCT-CA.

Key Words: ethanol, lactic acid bacteria, *Saccharum* spp.
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283 Effects of condensed tannins on bacterial and fungal core microbiomes involved in the ensiling and aerobic spoilage of purple prairie clover (*Dalea purpurea* Vent.) silage.

K. Peng[1,2], Q. Huang[2,3], L. Jin[2], D. Niu[4], T. A. McAllister[2], H. Denis[5], H. E. Yang[2], S. Acharya[2], Z. Xu[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, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]College of Animal Science and Technology, Yangzhou University, Yangzhou, P.R. China, [4]Alberta Agriculture and Forestry, Lethbridge, AB, Canada, [5]European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, UK.*

Effects of condensed tannins (CT) on rumen microbes have been well documented, whereas little information exists about their effects on the microbial communities involved in ensiling. The objective of this study was to determine the effects of CT on the composition and diversity of bacterial and fungal core microbiomes associated with ensiling and aerobic spoilage of purple prairie clover (PPC). Purple prairie clover (*Dalea purpurea* Vent.; 60 g CT/kg DM) was harvested at full flower and ensiled in polyvinyl chloride laboratory silos with and without polyethylene glycol (PEG) for 76 d. Silage was then subjected to aerobic exposure for 14 d. Bacterial and fungal core microbiomes in the silage and in the aerobically exposed silage were examined using real-time qPCR and high-throughput sequencing. Real-time qPCR analysis revealed that PPC ensiled without PEG exhibited less ($P < 0.01$ to approximately 0.001) gene copy numbers of total bacteria, *Lactobacillus*, yeasts, and fungi than PEG-treated silage. This trend was also observed for d-7 aerobically exposed silage with the exception of *Lactobacillus*, which had greater ($P < 0.05$) gene copy numbers for non-PEG than for PEG-treated silage. Metagenome analyses generated a total of 4,273,668 bacterial sequences and 3,455,929 fungal sequences, which were assigned to 225 bacterial and 142 fungal genera, respectively. Addition of PEG increased ($P < 0.001$) the abundance of *Lactobacillus* and *Pediococcus* but decreased ($P < 0.01$) that of *Lactococcus*, *Leuconostoc*, *Agrobacterium*, *Erwinia*, *Methylobacterium*, *Pseudomonas*, and *Sphingomonas*. The abundance of the fungal genera *Colletotrichum*, *Xylogone*, *Galactomyces*, *Penicillium*, *Fusarium*, and *Cryptococcus* in silage were also increased ($P < 0.05$) by PEG. Diversity measurements of bacterial and fungal communities indicated that addition of PEG decreased ($P < 0.01$) the number of microbial core genome operational taxonomic units (OTU), ACE, Chao 1, and Shannon indexes. It did not affect the diversity of fungal communities. The PEG-treated silage had a higher ($P < 0.001$) abundance of *Pediococcus* but less ($P < 0.001$) *Lactococcus* and *Leuconostoc* than non-PEG silage after aerobic exposure. The PEG-treated silage also had a greater ($P < 0.05$ to approximately 0.01) abundance of *Colletotrichum*, *Penicillium*, and *Fusarium* at d 7 and greater ($P < 0.05$ to approximately 0.001) abundance of *Candida*, *Colletotrichum*, *Wickerhamomyces*, *Penicillium*, and *Pterula* after aerobic exposure. The observed bacterial and fungal OTU, ACE and Chao 1 were lower ($P < 0.05$) for PEG-treated than for non -PEG treated silage after aerobic exposure. The results indicated that CT decreased population of majority bacteria, fungus, and yeast but increased bacterial diversity during ensiling and aerobic deterioration but increased fungal diversity only after aerobic exposure.

Key Words: condensed tannin, metagenome analysis, purple prairie clover silage
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284 Characterization of condensed tannins from freeze-dried, silage, or hay purple prairie clover (*Dalea purpurea* Vent.): Structure composition, protein precipitation, and anti-*Escherichia coli* properties.

K. Peng[1,2], Q. Huang[2,3], Z. Xu[2], T. A. McAllister[2], S. Acharya[2], S. Wang[1], I. Mueller-Harvey[4], C. Drake[4], and Y. Wang*[2], [1]*College of Engineering, China Agricultural University, Beijing, P.R. China, [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]College of Animal Science and Technology, Yangzhou University, Yangzhou, P.R. China, [4]Chemistry and Biochemistry Laboratory, Food Production and Quality Division, School of Agriculture, Policy and Development, University of Reading, Reading, UK.*

Conservation methods have been shown to affect forage nutrient composition and value, but little information is available about the effect of forage conservation on plant condensed tannins (CT). The objective of this study was to assess the effects of conservation method on the concentration, chemical composition and biological activity of CT. Whole plant purple prairie clover (PPC; *Dalea purpurea* Vent.) was harvested at the full-flower stage and conserved as freeze-dried forage (FD), silage (SIL), or hay (HAY). Concentration of CT in conserved PPC was determined by the butanol HCl–acetone method. Structural composition, protein-precipitation capacity, and antibacterial activity of CT isolated from conserved forage were determined by in situ thiolytic degradation followed by liquid chromatography–mass spectrometry analysis, a protein precipitation assay using BSA and ribulose 1,5-disphosphate carboxylase as model proteins, and an *Escherichia coli* growth test, respectively. Conservation method had no effect on concentration of total CT, but ensiling decreased ($P < 0.001$) extractable CT and increased ($P < 0.001$) fiber-bound and protein-bound CT. In contrast, hay increased ($P < 0.01$) only protein-bound CT. Regardless of conservation method,

epigallocatechin (EGC), catechin, and epicatechin (EC) were the major flavan-3-ol subunits, and gallocatechin was absent from both terminal and extension units of PPC CT. The SIL CT had the lowest ($P < 0.001$) EGC but the highest ($P < 0.01$) EC in the extension units. Similarly, SIL CT exhibited a lower ($P < 0.001$) mean degree of polymerization but a higher ($P < 0.001$) procyanidin:prodelphinidin (PC:PD) ratio than FD or HAY CT. The protein-precipitating capacity of CT in conserved PPC ranked ($P < 0.001$) as FD > HAY > SIL. Growth of *E. coli* in M9 medium was inhibited by 25 to 100 µg/mL of CT isolated from FD, SIL, and HAY ($P < 0.05$), but preservation method had no effect on the ability of CT to inhibit bacterial growth. The results demonstrated that ensiling decreased the extractability and protein-precipitating capacity of CT by increasing the PC:PD ratio. Purple prairie clover conserved as hay retained more biologically active CT than if it was conserved as silage.

Key Words: condensed tannins, forage conservation, purple prairie clover
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285 Effects of isolated bacteria application on chemical composition and fermentation characteristic of rye silage.

Y. H. Joo[*1], H. J. Lee[1], S. S. Lee[1], O. K. Han[2], and S. C. Kim[1], [1]*Division of Applied Life Science (BK21Plus, Inst. of Agri. & Life Sci.), Gyeongsang National University, Jinju, Republic of Korea (South),* [2]*National Institute of Crop Science, Rural Development Administration, Suwon, Republic of Korea (South).*

This study was conducted to estimate the effect of 2 isolated bacteria on chemical composition and fermentation characteristics of rye silage harvested at 20 d after heading stage. Two microbes, which had confirmed the effect of antifungal activity (*Lactobacillus brevis* [LB]) or fibrinolysis ability (*Leuconostoc holzapfelii* [LH]), were selected from 832 dominant microbes by the tests of antimicrobial activities against fungi and fibrinolysis ability with 3 enzyme plate assay (cellulase, xylanase, and esterase). Rye forage was harvested at 20 d (27.3% DM) after heading stage, chopped into 3 to 5 cm lengths, and divided into 4 treatments: applications of 2 mL/kg of distilled water (CON), 1.2×10^5 cfu/g of LB, 1.0×10^5 cfu/g of LH, or combo of LB and LH at 1:1 ratio (MIX). The forages with applied bacterial additives were ensiled into 10-L mini-silo with 4 replications for 100 d. The bacterial additives were not affected on chemical composition and in vitro digestibility of rye forages. However, all silages with applied bacterial additives had lower NDF concentrations ($P < 0.05$; 67.1 vs. 69.0%) than CON silage whereas only AT silage had lower ADF concentrations ($P < 0.05$; 41.6 vs. 43.4%). The silages with LH alone and combo with LB applied had higher ($P < 0.05$; 67.5 vs. 63.2%) in vitro DM digestibility than the other silages, whereas bacterial additives were not affected on in vitro NDF digestibility. The pH was lowest ($P < 0.05$, 4.26 vs. 5.04) in LB and MIX silages but highest in CON silage. In contrast, lactate concentration was higher ($P < 0.05$; 5.36 vs. 0.50%) in all silages with bacterial additives applied than in CON silage. Silages with LB and MIX applied had higher acetate concentrations ($P < 0.05$; 5.43 vs. 2.82%) than the other silages, whereas silages with LH and MIX applied had lower propionate concentrations ($P < 0.05$; 0.35 vs. 0.66%) than CON silage. Lactic acid bacteria (6.75 vs. 5.13 $\log_{10}$ cfu/g) and yeast (6.56 vs. 5.42 log10 cfu/g) were more abundant ($P < 0.05$) in CON and LH silages than in LB and MIX silages, whereas mold was not detected in any silages. Therefore, it could be concluded that LB is more effective on antifungal activity by the results of lower pH and yeast but higher lactate and acetate concentrations. And again, LH is more effective on fibrinolysis ability by the results of lower NDF concentration but higher in vitro DM digestibility.

Key Words: *Lactobacillus brevis*, *Leuconostoc holzapfelii*, rye silage
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286 Structural composition and protein precipitation capacity of condensed tannins from purple prairie clover (*Dalea purpurea* Vent.).

Q. Huang[1,2], T. Hu[3], Z. Xu[2], L. Jin[2], T. A. McAllister[2], S. Acharya[2], W. Zeller[4], E. Hardcastle[4], C. Drake[5], I. Mueller-Harvey[5], and Y. Wang[*2], [1]*College of Animal Science and Technology, Yangzhou University, Yangzhou, P.R. China,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*College of Animal Science and Technology, Northwest A&F University, Yangling, P.R. China,* [4]*U.S. Dairy Forage Research Center, Madison, WI,* [5]*Chemistry and Biochemistry Laboratory, Food Production and Quality Division, School of Agriculture, Policy and Development, University of Reading, Reading, UK.*

Condensed tannins (CT) from purple prairie clover (PPC; *Dalea purpurea* Vent.) have shown anti-*Escherichia coli* O157:H7 activity in vitro and in vivo, but the composition and structure of these CT are unknown. The objectives of this study were to determine the concentration and composition of CT in different tissues of PPC at differing maturities and to determine their protein-precipitating capacity. Condensed tannins were extracted from leaf, stem, and flower tissues of PPC harvested at vegetative, early flowering (EF), and late flowering (LF) stages. The structural compositions of CT were elucidated by in situ thiolytic degradation and HPLC–mass spectrometry. The general composition of the CT in PPC obtained from thiolytic degradation was corroborated by ^{1}H-^{13}C heteronuclear single quantum coherence nuclear magnetic resonance spectroscopy. The protein-precipitating capacity of isolated CT was determined by their ability to precipitate BSA and ribulose 1,5-disphosphate carboxylase (RuBisCO).

Flowers contained the highest CT concentration followed by leaf and stem tissues. As the plant matured, CT concentration decreased in stem tissue but remained relatively constant in leaf and flower tissues. Regardless of plant tissue or maturity, PPC CT consisted mostly of epicatechin (EC; 70–80%) and epigallocatechin (EGC; 20–30%), with minor amounts of catechin and gallocatechin. Leaf CT consisted of more EC ($P < 0.01$) but less EGC units ($P < 0.01$) than CT from stem and flowers at both EF and LF stages. The procyanidin:prodelphinidin (PC:PD) ratio was greater ($P < 0.05$) for leaf CT than for stem and flower CT. The mean degree of polymerization (mDP) was highest for stem CT and lowest for leaf CT. The PC:PD ratio of stem CT decreased and the mDP increased as the plant matured. Leaf CT had higher BSA-precipitating capacity than stem and flower CT ($P < 0.001$), with EF leaf CT exhibiting the highest capacity ($P < 0.001$). Leaf and flower CT had a greater ability to precipitate RuBisCO protein than stem CT ($P < 0.05$). These results demonstrated that PPC CT were predominantly of the procyanidin type and that the concentration and chemical structure varied with different plant tissues and growth periods. Condensed tannins in PPC at the early flower stage exhibited the greatest protein-precipitation capacity.

Key Words: chemical structure, condensed tannins, purple prairie clover
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287 Comparison of diet selection by Raramuri Criollo and Angus crossbreeds in the Chihuahuan Desert.

S. Spiegal[1], S. Nyamurekung'e[2], R. Estell[*1], A. Cibils[2], M. McIntosh[2], A. Gonzalez[1], and D. James[1], [1]*Jornada Experimental Range, Las Cruces, NM,* [2]*New Mexico State University, Las Cruces.*

Raramuri Criollo (RC) is a cattle biotype that has undergone natural selection for the past 500 yr in northern Mexico. No information exists on diet selection for this biotype. The objective of this study was to compare diet selection of RC and Angus × Hereford crossbreeds (AH) typically found in the arid southwestern United States. We examined dietary composition of RC and AH cattle using DNA metabarcoding of fecal samples. Ten mature cows of each breed grazed 2 adjacent pastures (1,190 and 1,165 ha) for 28 d in July through August 2015 and January through February 2016 in a crossover design. Each breed grazed each pasture 14 d per period, and cows were then switched to the reciprocal pasture. Fecal samples were collected on d 14 in each pasture in both seasons. Dominant species present in fecal samples included black grama (*Bouteloua eriopoda*), tobosa (*Pleuraphis mutica*), plains bristlegrass (*Setaria leucopila*), hog potato (*Hoffmannseggia glauca*), and four-wing saltbush (*Atriplex canescens*). Black grama was present in higher concentration in AH than RC fecal samples ($P < 0.0001$) and was greater during winter dormancy than during the summer growing season ($P < 0.0001$). Hog potato was not affected by breed ($P = 0.137$) but was greater in fecal samples during the growing season than during winter dormancy ($P < 0.001$). Four-wing saltbush was marginally greater in AH than in RC fecal samples ($P = 0.053$) and greater during dormancy than in the growing season ($P < 0.0001$). These results suggest that RC cattle select diets that differ from AH cows and that differences are affected by plant growth phenology.

Key Words: diet selection, DNA metabarcoding, Raramuri Criollo cattle
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288 Winter supplementation of ground whole flaxseed impacts milk fatty acid composition on organic dairy farms in the Northeastern United States.

A. N. Hafla[1], K. J. Soder[*1], A. F. Brito[2], R. Kersbergen[3], F. Benson[4], H. Darby[5], M. D. Rubano[1], S. L. Dillard[1], J. Kraft[6], and S. F. Reis[2], [1]*USDA-Agricultural Research Service, University Park, PA,* [2]*University of New Hampshire, Durham,* [3]*University of Maine Cooperative Extension, Waldo,* [4]*Cornell University Extension, Cortland, NY,* [5]*The University of Vermont, Albans,* [6]*University of Vermont, Burlington.*

Fourteen organic dairy farms were used to 1) evaluate seasonal variation of bioactive fatty acids in milk and 2) evaluate supplementation of ground whole flaxseed to maintain levels of bioactive fatty acid concentrations during the nongrazing season. During year round farm visits (twice a month during the grazing season and once monthly during the nongrazing season) from April 2012 until April 2015, milk, feed, and pasture samples were collected and diet and milk production and composition were recorded. During the winters of 2013/14 and 2014/15, 9 farms supplemented ground whole flaxseed at 6% of diet DM to half of the cows within each herd ($n = 238$ cows/treatment). Milk samples were collected and pooled by treatment (flaxseed or control). Data were analyzed using the MIXED procedure of SAS. A month × year interaction ($P < 0.01$) for omega-3 fatty acid concentrations indicated an increase beginning in April of 2014 through the end of the study. Total milk CLA concentrations were seasonal, with the greatest ($P < 0.01$) concentrations (1.32% of total fatty acids) during the grazing season. Winter flaxseed supplementation did not impact concentrations of milk fat and milk protein or BCS. Compared with the control diet, flaxseed decreased total milk SFA concentrations ($P < 0.01$) by 3.1 percentage units, increased omega-3 fatty acid concentrations ($P < 0.01$) by 88%, and tended ($P = 0.13$) to increase total CLA concentrations ($P = 0.13$) by 9.0%. Although flaxseed supplementation increased milk omega-3 fatty acid concentrations, minimal impacts on SFA and total CLA concentrations indicated that a greater level of winter supplementation is required to maintain concentration of all beneficial fatty acids comparable to the grazing season.

Key Words: conjugated linoleic acid, flaxseed, grazing
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289 Evaluating cover crop cocktails for forage production in the Peace region of Alberta.

T. A. Omokanye*, *Peace Country Beef & Forage Association, Grande Prairie Regional College, Fairview, AB, Canada.*

Interest in the potential for a multispecies cover crop (CC) blend (cocktails) for silage, swath grazing, greenfeed, and pastures has been growing amongst beef cattle producers in the Peace Country region of Alberta, Canada. The idea of CC cocktails is new in the region, indicating that the concept of a CC cocktail mix is an area where local research for local producers is needed. The objective of this study was to test several cocktails to identify those with superior forage production (yield and nutritional value) for beef cattle production. Twelve cocktails (treatments) consisting of 2 to 9 cover crops and an oat (*Avena sativa*) monocrop as a check were arranged in a randomized complete block design in 3 replications in 2016 cropping season. The CC species used were from cereal grains/grasses, legumes, and brassicas. From forage DM yield and nutritional value obtained in this study for all cocktails and the check (CDC Haymaker oat), all cocktails generally had higher DM yield as well as better nutritional value than the check. Six of the 12 cocktails produced more DM yields (109–137%) than the check. Overall, cocktail number 1 (peas, oats, hairy vetch, tillage radish, purple top turnips, and crimson clover) produced the most forage DM yield (10 t/ha) than other cocktails and the check. The forage CP, TDN, and NEm significantly varied ($P < 0.05$) from 8.87 to 23.7%, from 60.1 to 70.1, and from 1.46 to 1.75 Mcal/kg, respectively, with the check recording the least values in each range. All cocktails were able to meet the protein requirements of mature beef cattle, and in most cases, cocktails were well within the CP requirements for growing and finishing beef calves. The cocktails in most cases had enough %TDN for mature beef cattle, whereas the check was able to meet the %CP and %TDN requirements of only a gestating beef cow. The benefits of cocktails were obvious, with higher forage macro- and trace minerals than the check. Four of the 12 cocktails seemed to have greater potential for forage production in the Peace Country region of Alberta. Field notes taken show that the following crops in the cocktails did not germinate and that where they did germinate, their growth was not impressive: Persian clover (*Trifolium resupinatum* L.), BMR hybrid sorghum (*Sorghum* spp.), berseem clover (*Trifolium alexandrinum*), and teff grass (*Eragrostis tef*).

Key Words: beef cattle, forage production, multispecies cover crop cocktails
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290 Effects of grazing diverse combinations of sainfoin, birdsfoot trefoil, and alfalfa on beef cow performance and environmental impacts.

S. Lagrange*[1,2], K. A. Beauchemin[3], J. W. MacAdam[4], and J. J. Villalba[2], *[1]INTA EEA, Bordenave, Argentina, [2]Utah State University, Logan, [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [4]Department of Plants, Soils, and Climate, Utah State University, Logan.*

Diverse combinations of forages with different nutrient profiles and plant secondary compounds may improve the efficiency of nutrient utilization by livestock. We tested the effects of grazing increasingly diverse combinations of the tannin-containing legumes sainfoin (SAIN) and birdsfoot trefoil (BFT) and the saponin-containing legume alfalfa (ALF) on cattle performance, digestible DM (DDM), blood urea nitrogen (BUN), and methane emissions. Twenty-one pairs of heifers grazed 3 replications of 7 treatments (single species, choice of all possible 2-way combinations, or a 3-way choice) in a completely randomized block design. Animals grazed during 2 periods of 28 d each, and composited forage and fecal samples were collected during 5 consecutive days at the end of each period to estimate apparent digestibility, using ADL as an internal marker. Methane emissions from ALF and SAIN were assessed using the sulfur hexafluoride technique during each 5-d collection period. Data were analyzed as a repeated measures design with cows (random effect) nested within treatments and period and day as the repeated measures. Average daily gain for the 3-way choice was 26 and 30% greater than for the 2-way choices and monocultures, respectively ($P < 0.05$). Gains of animals grazing tannin-containing legumes were 34 (BFT) and 17% (SAIN) greater than for those grazing ALF (Table 290). Methane emissions per unit of gain were greater for ALF than for SAIN, and DDM peaked for the ALF–SAIN combination and for the 3-way choice. Cattle grazing tannin-containing legumes as monocultures or in combinations showed lower BUN values than animals under ALF monocultures or legume combinations that had ALF, suggesting a shift in the site of N excretion from urine to feces. In conclusion, diverse combinations of legumes have the potential to enhance livestock performance over less diverse arrays of forages. Tannin-containing legumes in monocultures or in combinations

Table 290.

Item	Treatments							SEM	P-value
	ALF	SAIN	BFT	ALF–SAIN	ALF–BFT	SAIN–BFT	ALF–SAIN–BFT		
DM, %	26.1^{a}	26.7^{a}	22.3^{b}					0.63	0.002
CP, %	26.8^{a}	21.9^{c}	24.0^{b}					0.37	0.002
ADF, %	17.6^{b}	19.8^{a}	16.3^{c}					0.63	0.010
ADG, kg/d	0.82^{c}	0.96^{bc}	1.10^{ab}	0.97^{bc}	0.85^{c}	1.16^{ab}	1.25^{a}	0.09	0.022
DDM, %	71.8^{cd}	74.7^{abc}	72.4^{bcd}	76.1^{a}	71.0^{d}	70.3^{d}	75.6^{ab}	1.49	0.051
BUN, mg/dL	19.5^{a}	12.0^{d}	13.8^{cd}	16.2^{bc}	17.8^{ab}	14.5^{cd}	16.7^{abc}	1.24	0.013
Methane, g/kg ADG	336.6^{a}	253.7^{b}						36.56	0.097

$^{a–d}$Different superscript letters differ ($P < 0.1$).

may contribute to reducing methane emissions and urinary nitrogen excretion in grazing cattle.

Key Words: methane, nitrogen emissions, plant secondary compounds
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291 Starch or highly digestible fiber as energy supplement for replacement heifers grazing annual ryegrass.

G. Scaglia*, *LSU AgCenter Iberia Research Station, Jeanerette, LA.*

Animal response to concentrate supplementation on grazing systems depends on pasture and supplement characteristics. The objective was to evaluate the effect of level of ground corn and soybean hulls on performance of replacement heifer grazing annual ryegrass. In 3 consecutive grazing seasons, 90 crossbred beef heifers (269 ± 8.1 kg) were blocked by weight and genotype and assigned to 15 groups ($n = 6$) that were continuously stocked on 1.33-ha pastures of annual ryegrass. Groups were then allotted to 5 treatments (3 replicates): 1) control (CON), no supplement; 2) 0.5% BW ground corn (C05); 3) 0.5% BW soybean hulls (SBH05); 4) 1% BW ground corn (C1); and 5) 1% BW soybean hulls (SBH1). Forage mass, forage growth rate, forage nutritive value, and BW were determined on d 0 and every 15 d thereafter and the amount of supplement fed was adjusted accordingly. Annual ryegrass (var. 'Nelson') was no-tilled at a seeding rate of 45 kg/ha and fertilized with 120 units of N/ha (urea) split in 3 applications. The grazing period started in January of each year and lasted for 75 d. Data were analyzed using PROC GLM for treatment, year, and their interaction. There were no interactions on any variable, so main factors are discussed. No treatment effect ($P > 0.05$) was detected for ADG (1.19, 1.39, 1.29, 1.36, and 1.30 for CON, C05, SBH05, C1, and SBH1, respectively) and nutritive value parameters; however, forage mass (1,023, 1,401, 1,359, 1,991, and 2,020 kg DM/ha for CON, C05, SBH05, C1, and SBH1, respectively) and forage DMI (6.4, 5.7, 5.5, 4.6, and 4.2 kg DM/ha for CON, C05, SBH05, C1, and SBH1, respectively) were affected ($P = 0.002$ and $P = 0.03$, respectively). A year effect ($P = 0.004$) was observed for ADG (1.27, 1.49, and 1.16 kg for yr 1, 2, and 3, respectively), beef produced per hectare, and forage mass ($P = 0.04$; 1,621, 1,931, and 1,081 kg DM/ha for yr 1, 2, and 3, respectively). The amount of supplement fed in C1 and SBH1 (227 vs. 233 kg/animal, respectively) was different ($P = 0.02$). The efficiency of supplementation (kg supplement per kg gain over CON) was greater ($P = 0.002$) for C05 (7.8), intermediate for C1 (17.8) and SBH05 (15.5), and lowest for SBH1 (28.2). Both supplements reduced forage DMI with greater substitution effect at the 1% BW level. Larger yearly variation in forage production influenced animal performance more than level and type of supplement used.

Key Words: beef heifers, ryegrass, supplementation
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292 Study on the seasonal changes in average daily gain, feed value, forage productivity, and grazing intensity in native pasture grazed by Korean native goat (*Capra hircus coreanae*).

S. Moon*, *Konkuk University, Chungju, Republic of Korea (South).*

This study was conducted to determine grazing intensity of growing female Korean black goats (*Capra hircus coreanae*) on native pasture. It was carried out to obtain basic information for improvement of native pasture management and to establish a feeding system for these goats. The experiment was carried out using ten 4-mo-old female doelings with a mean BW was 14 ± 3.6 kg. The goats were fed supplementary diets containing different rates of concentrates (1.5% of BW) during grazing in native pasture. Supplementary feed and forage samples were dried in a forced-air oven at 65°C, ground to pass through a 1-mm screen, and stored for further analysis. These samples were analyzed for DM, ether extract, CP, ash, crude fiber (CF), ADF, and NDF (AOAC, 1990). The CP content of forage was the highest in July (18.2 ± 0.6%) and there were significant differences ($P < 0.05$). The CF content increased in August (31.5 ± 0.25%) at pasture ($P < 0.05$) and decreased in April (14.2 ± 0.17%). The forage productivity of the native pasture was highest in August (1,584.0 141.4 g/ha) and then decreased in September (666.7 g/ha). The highest ADG of 123.5 g/d occurred during June. Grazing intensity was calculated by forage productivity and DMI and was the highest in August (106 goats/ha). As shown in the results of this study, grazing intensity was suggested to average 68 goats/ha during the experiment period (from April to September). It is desirable to maintain adequate grazing intensity by adjusting supplement feed.

Key Words: black goat, daily gain, native pasture
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293 Nutritional evaluation of forage ephedra (*Ephedra nevadensis*) as an alternative forage using a dual-flow continuous culture system.

C. B. Sampaio[1], E. Marostegan de Paula[2], L. Galoro da Silva[2], V. Brandao[2], X. Dai[2], T. Shenkoru[2], B. Perryman[2], A. Faciola[*2], [1]*Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil,* [2]*University of Nevada, Reno.*

Forage ephedra (*Ephedra nevadensis*; ephedra) is well adapted and grazed by sheep and cattle in the Western United States; however, its nutritional value has not been well established. The objective of this study was to determine ruminal digestibility, ruminal microbial fermentation, and bacterial N synthesis of ephedra as compared with cheatgrass (*Bromus tectorum*; CG) and orchardgrass hay (*Dactylis glomerata* L.; OGH). Diets were randomly assigned to 6 fermenters in a dual-flow continuous culture system in a 3 × 3 Latin square design with three 10-d experimental periods consisted of 7 d for diet adaptation and 3 d for sample collection. Fermenters were fed a total of 72 g of DM/d equally divided into 2 portions per day. Diets were 1) 100% air-dried ephedra, 2) 100% air-dried CG, and 3) 100% air-dried OGH. Liquid and solid dilution rates were adjusted daily to 10 and 5%/h, respectively. A 500-mL sample was taken on 8, 9, and 10 d and analyzed for nutrient digestibility and microbial growth. Two 10-mL subsamples were filtered through 2 layers of cheesecloth and preserved with 0.2 mL of 50% sulfuric acid and 2 mL of metaphosphoric acid for subsequent ruminal NH_3–N and VFA analyses, respectively. Statistical analysis was performed using PROC GLIMMIX of SAS. Partial data are presented in Table 293. The NH_3–N concentration was greater for CG followed by ephedra and lowest for OGH ($P < 0.01$). Ruminal pH was greater for ephedra ($P < 0.01$), whereas total VFA was the lowest ($P < 0.01$). Ephedra had greater acetate molar proportion, which resulted in the greatest acetate:propionate ratio ($P < 0.01$). Ephedra also had the lowest propionate molar proportion. Results from this study indicate that ephedra should not be used as the main forage in cattle diets due to its poor fermentation as evidenced by the lowest total VFA and propionate molar proportion.

Table 293.

Item	Treatments			SEM	*P*-value
	Ephedra	CG	OGH		
pH	7.73^{a}	6.78^{b}	6.83^{b}	0.16	<0.01
NH_3–N mg/dL	8.59^{b}	18.09^{a}	3.47^{c}	0.93	<0.01
VFA, mmol	37.77^{c}	86.87^{a}	77.54^{b}	3.18	<0.01
Acetate, %	74.33^{a}	69.70^{b}	58.94^{b}	1. 50	<0.01
Propionate, %	17.10^{b}	20.82^{b}	24.54^{a}	1.31	<0.01
Butyrate, %	7.42^{b}	8.37^{b}	13.26^{a}	1.28	<0.01
Valerate, %	0.28	0.72	0.62	0.19	0.47
Acetate:propionate ratio	4.77^{a}	3.48^{ab}	2.25^{b}	0.42	<0.01

Key Words: grazing, in vitro fermentation, Western United States
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294 Productivity and carbon sequestration potential of reestablished native grassland in Canadian prairie following grazing.

A. W. Alemu[*1], A. D. Iwaasa[2], R. Kröbel[1], and B. McConkey[2], [1]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada.*

Canadian native grasslands are recognized for providing high-quality forage for grazing livestock and wildlife. The objective of the study was to determine changes in pasture productivity and soil organic carbon (SOC) level as affected by type of forage pasture mix and grazing management. In 2001, pasture was established on 32 ha of land (16 paddocks of 2.1 ha) that was cropped since the 1920s. Treatments consisted of a completely randomized experimental design with 2 replicates: 2 pasture mixes (simple and diverse, with 7 and 12 species, respectively) and 2 grazing systems (continuous and deferred rotational grazing). Between 2005 and 2014, pasture was stocked with commercial yearling Angus steers (*Bos taurus*; 354 ± 13 kg) to an average stocking rate of 0.8 and 1.9 animal unit/ha for continuous and deferred rotational grazing, respectively. All pastures were grazed to an average utilization rate of 50 to 60%. Body weight was measured at the beginning and end of the grazing season. Available pasture yield was estimated by taking 10 representative 0.25-m^2 quadrat samples. Soil samples (at 2 depths: 0–15 and 15–30 cm) were collected in the fall of 2000, 2004, 2008, 2011, and 2014. Data were analyzed using the mixed procedure of SAS and differences are discussed at $P \leq 0.05$. Aboveground biomass and available pasture yield between simple and diverse pastures showed no difference but varied among the experimental years ($P < 0.001$). Available pasture was greater ($P < 0.01$) for rotational grazing (1,328 kg/ha) relative to continuous grazing (855 kg/ha), which increased the number of grazing days per hectare by 9% over the continuous grazing system (57 d/ha; $P = 0.04$). Conversely, ADG was 18% higher ($P = 0.02$) for continuous grazing than for rotational grazing (0.88 kg/d), which was likely related to higher OM digestibility and DE of pasture under continuous grazing. Total live weight production per hectare was slightly higher for the diverse pasture mix. Over the 10 yr of production, average SOC level was 5 (0–30 cm) and 9% (0–15 cm) higher for complex pasture on continuous grazing than on deferred rotational grazing ($P < 0.01$). Furthermore, SOC level was affected by year ($P < 0.0001$), which was expected, with the different environmental conditions experienced among the different soil sampling years. Overall, our study indicated that pasture diversity with grazing management affected productivity and SOC level of grazing lands.

Key Words: grazing, reestablished pasture, soil carbon
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295 Feed processing affects palatability of ventenata-infested grass hay.

D. E. McCurdy*[1], C. J. Watts[1], G. E. Chibisa[2], T. S. Prather[1], and A. H. Laarman[1], *[1]University of Idaho, Moscow, [2]Department of Animal & Veterinary Sciences, University of Idaho, Moscow.*

Ventenata (*Ventenata dubia*) is an invasive grass species that infested rangelands in the inland Northwest, causing significant economic damage through declines in forage production. Despite its nutritional similarity to other forages such as cheatgrass in terms of CP content and NDF digestibility, its palatability for livestock is poor. The objective of this study was to investigate the role of texture and surface-bound microbes in determining palatability of ventenata-infested hay. Thirty-five weaned Charolais calves were separated into 5 treatments according to a taste-preference study that lasted for 7 d. Each animal had access to 2 feed bunks: one with a reference diet (mixed grass hay) and one with a treatment diet. The 5 treatments were the control, which was mixed grass hay used as the reference diet (CTRL); ventenata-infested hay (VENT); autoclaved mixed grass hay; autoclaved ventenata-infested hay; and pelleted ventenata-infested hay (PELT). Preference between mixed-grass hay and ventenata-infested hay was calculated such that 0% preference implies a total preference against the treatment diet, 50% preference implies an equal preference between mixed grass hay and ventenata-infested hay, and 100% preference implies a total preference for the treatment diet. Body weight gain was measured at the start and end of the experiment. Daily, intake of the reference diet and treatment diet were measured and percent preference was calculated. Among the 5 treatments, there was no difference in BW gain during the 7 d on treatment. The CTRL treatment showed no difference from 50% preference, indicating that our feed preference test worked. Calves on the VENT treatment had a preference of 19%, highlighting the poor palatability of ventenata-infested hay. Although autoclaving ventenata-infested hay made no difference to palatability, the PELT treatment increased preference to 50%, completely erasing the negative palatability of the ventenata-infested hay. Together, these results show the poor palatability of ventenata-infested hay may be due to texture of the hay and that ventenata's palatability can be improved through feed processing.

Key Words: grass hay, palatability, ventenata
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296 Black oat production in different oversowing modalities in an integrated crop–livestock system.

V. Zirondi Longhini*[1,2], C. Costa[3], P. R. L. Meirelles[3], C. M. Pariz[3], V. M. Protes[3], M. L. S. T. Piza[3], D. M. Souza[3], A. M. Castilhos[3], and F. de Oliveira Scarpino van Cleef[2], *[1]FAPESP, São Paulo, Brazil, [2]Sao Paulo State University, Jaboticabal, Brazil, [3]Sao Paulo State University, Botucatu, Brazil.*

The aim of this study was to evaluate the effects of corn (*Zea mays* L.) silage intercropped with palisade grass [*Urochloa brizantha* (Hochst. ex A. Rich.) R. Webster cv. Marandu] and pigeonpea [*Cajanus cajan* (L.) Millsp.] in summer/fall and oversowing modalities of black oat (*Avena strigosa* Schreb.) in winter/spring on forage mass of pasture. The experiment was conducted in a completely randomized design, with a 2 × 2 × 2 factorial treatment arrangement ($n = 48$/yr), combining 2 silage production systems (SPS; corn + palisade grass + pigeonpea [C+PG+PP] and corn + palisade grass [C+PG]), 2 black oat oversowing modalities (BO; in line [LI] and broadcasted [BR]), and 2 grazing cycles (GC). Grazing management used 12 crossbred male lambs (27.2 ± 0.6 and 24.0 ± 0.7 kg BW in the first and second growing season, respectively) by treatment. Animals spent the day grazing the black oat (fixed stocking rate and rotational grazing) and at night, they were herded into a barn. Prior to starting grazing, 16 height measurements, using a sward stick, were determined and forage mass of pasture (FM) was determined by cutting 2 representative samples (0.25 m^2 areas per plot at ground level). Forage samples were dried, weighed, and reported as kilograms of DM per hectare. Data were analyzed using PROC MIXED with SPS, BO, GC, and their interactions considered fixed effects and paddocks (SPS × BO × GC) as random effects. In the first growing season, FM was greater for C+PG+PP ($P = 0.04$; 814 vs. 665 kg of DM/ha), greater for black oat oversowing LI ($P = 0.05$; 813 vs. 667 kg of DM/ha), and greater in the first GC ($P < 0.001$; 884 vs. 635 kg of DM/ha). In the second growing season, there were interactions between SPS and BO. Greater FM was observed for C+PG+PP associated with LI oversowing of oat than BR ($P = 0.04$; 2,409 vs. 1,947 kg of DM/ha) in this season. However, for C+PG, the FM was not altered, regardless of oat oversowing, BR or LI ($P = 0.04$; 1,803 vs. 1,706 kg of DM/ha). For oversowing BR, the FM was not altered, regardless of silage production systems, C+PG+PP or C+PG ($P = 0.04$; 1,947 vs. 1,804 kg of DM/ha). For LI oversowing, the FM was greater for C+PG+PP ($P = 0.04$; 2,409 vs. 1,707 kg of DM/ha). In conclusion, corn intercropped with palisade grass and pigeonpea for silage in summer/fall increases the forage mass of pasture. In the winter/spring, in line oversowing of black oat presents greater forage mass than the broadcasted modality.

Key Words: corn silage, forage mass, pigeonpea
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297 Evaluation of neutral detergent fiber, acid detergent fiber, and acid detergent insoluble ash to predict forage selection among heifers grazing pastures containing a binary mixture of brassicas and grass.

B. R. Brunsvig*, A. J. Smart, and D. W. Brake, *South Dakota State University, Brookings.*

Diet selection is impacted by a myriad of factors among grazing cattle. A greater understanding of diet selection can allow improved estimates of performance, digestion, and nutrient balance. However, few data are available related to diet selection by cattle grazing cool-season annual forages. Often, estimates of diet selection among cattle grazing mixed pastures require complex laboratory analyses and can be variable. However, innate markers (e.g., NDF, ADF, acid detergent insoluble ash [ADIA]) may allow for prediction of diet selection in cattle grazing pastures that contain limited amounts of plant species. Diet samples were collected from ruminally cannulated heifers grazing a binary mixture of annual ryegrass (*Lolium perenne*) and brassica (*Raphinus sativus*, forage radish, and *Brassica rapa*, purple top turnip) at 3 stocking rates (1.7, 2.3, and 2.9 AUM/ha). Forage samples were clipped 11 d prior to grazing, and masticate was collected 2, 24, and 46 d after cattle began grazing pastures. Subsequently, forage samples and masticate were analyzed for NDF, ADF, and ADIA. Estimates of brassica or grass intake did not differ in response to increased stocking rate when intake was estimated with NDF ($P \geq 0.52$), ADF ($P \geq 0.48$), or ADIA ($P \geq 0.34$). However, intake predictions using NDF and ADIA resulted in differences in time (quadratic, $P < 0.01$) but ADF did not ($P \geq 0.61$). Interestingly, estimates of brassica and grass intake were 52% greater and 32% less when predicted using ADF in comparison with NDF. Similarly, estimates of brassica and grass intake using ADF were 35% greater and 38% less in comparison with ADIA. The overall pooled coefficient of variation for estimates of grass and brassica intake was 55, 60, and 65% for NDF, ADF, and ADIA, respectively. It seems logical that NDF may allow for improved estimates of brassica and grass intake because true fiber has no potential for contamination by endogenous sources. Improvement among nondestructive technologies that allow rapid analysis of samples (e.g., near-infrared reflectance spectroscopy) may allow further improvements in estimates of diet selection among cattle grazing binary mixtures of annual forages.

Key Words: cattle, diet selection, forage
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298 Greenhouse gas emissions from an intensive grassland: Key driving variables.

A. C. Ruggieri*[1,2], D. J. A. Santos[3], E. R. Janusckiewicz[3], L. F. Brito[3], E. S. Morgado[4], R. A. Reis[5], and A. S. Cardoso[3], *[1]University of Sao Paulo State, Jaboticabal, Brazil, [2]CNPq, Brasília, Brazil, [3]Sao Paulo State University, Jaboticabal, Brazil, [4]Universidade Federal de Uberlandia, Uberlandia, Brazil, [5]São Paulo State University (UNESP) School of Agricultural and Veterinarian Sciences, Jaboticabal, Brazil.*

Since the industrial revolution, the temperature of the Earth's atmosphere has been increasing, leading to observed global warming. Increases in the greenhouse gases (GHG) concentration in the atmosphere, such as carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O), are appointed to be responsible for these changes. In a livestock system based on grassland, a large amount of these gases can be emitted. A few quantifications of these GHG emissions and key drivers controlling their production were carried out. This research aimed to evaluate the key variables driving involved in the GHG emissions from a tropical soil cultivated with grass. The experiment was performed at São Paulo State University during 3 yr (2012–2014). The GHG emissions were measured using static closed chamber methodology and quantification by gas chromatography. To identify the key variables explaining the GHG fluxes, a principal component analysis was run. The variables analyzed were pasture height, precipitation, soil moisture, soil ammonium, soil nitrate, and the GHG fluxes. Two principal components, precipitation and pasture height, explained 44.74% of the cumulative variance. Within components for CO_2 fluxes, a significant correlation was found with pasture height (0.57; $P < 0.001$) and soil moisture (0.36; $P < 0.01$). For CH_4 emissions, a strong correlation was found with precipitation (−0.80; $P < 0.001$) followed with CO_2, whereas N_2O fluxes was correlated with precipitation (0.48; $P < 0.001$) and soil ammonium (0.36; $P < 0.05$). The GHG fluxes may have been explained by the moisture, which is an important issue for microorganism life and chemical reactions of the carbon and nitrogen cycles. Pasture height possibly explained the CO_2 fluxes because of the leaf area variation among the pastures, which influences the photosynthesis. Methane emissions could be associated with CO_2 fluxes because in certain conditions, this gas is oxidized and produces CH_4. The key driving variables involved in the GHG emissions were soil moisture and pasture height, precipitation and CO_2 fluxes, and precipitation and soil ammonium for CO_2, CH_4, and N_2O, respectively.

Key Words: carbon dioxide, methane, and nitrous oxide, climate change, tropical pasture
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299 Ingestive behavior of young grazing Nellore bulls supplemented with sources of nonprotein nitrogen during the dry season at two different times.

V. A. C. Mota*[1,2], R. M. Fernandes[3], C. F. Nascimento[3], H. A. S. Issa[4], V. B. Holder[5], J. E. Pettigrew[6], F. D. Resende[7], and G. R. Siqueira[7], *[1]São Paulo Research Foundation (FAPESP), São Paulo, Brazil, [2]UNESP/FCAV, Jaboticabal, Brazil, [3]UNESP – Univ. Estadual Paulista, Jaboticabal, Brazil, [4]UNIFEB, Barretos-SP, Barretos, Brazil, [5]Alltech Inc., Nicholasville, KY, [6]University of Illinois at Urbana-Champaign, Urbana, [7]Agência Paulista de Tecnologia dos Agronegócios – APTA, Colina, Brazil.*

Cattle in a hot climate have 2 peak grazing times, early morning and late afternoon, so feeding a supplement in early morning may interfere with pasture consumption. A controlled-release urea may synchronize ruminal ammonia and energy availability compared with urea. The objective of this study was to evaluate the ingestive behavior of grazing cattle in the dry season at a low latitude, receiving supplements containing urea or Optigen (a controlled-release urea) at 0700 or 1300 h. One hundred twenty young Nellore bulls with BW of 228 ± 39 kg and 12 mo old were used, 5 in each of 20 paddocks of 3 ha each. The pasture was *Brachiaria brizantha* cv. Marandu. The duration was 98 d, 14 d of adaptation and 3 periods of 28 d. The grazing time and the time at the supplement trough during daytime (0600 to 1750 h), nighttime (1800 to 0550 h), and total were evaluated by trained people at 10-min intervals on 1 d in each period. The 4 treatments were a factorial design of 2 feeding times × 2 urea sources, applied in a randomized complete block design. Statistical analysis was by the MIXED procedure of SAS, version 9.2 (SAS, 2008), considering block as a random variable. There was no influence of supplementation time, urea sources, or their interaction on the grazing time or the trough time during daytime, nighttime or total ($P > 0.10$). The grazing time was reduced by 92 min ($P < 0.01$) in the third period compared with the first 2 and the trough time was lower in the first period (33 min; $P = 0.03$) than in the second (50 min) and the third (65 min), but there were no interactions of period with treatment. These changes are presumably a response to increasing pasture growth as the seasonal rains began. In conclusion, under the conditions of this study, the time of supplementation and the urea sources do not alter the ingestive behavior of young bulls.

Table 299. Time spent daytime grazing (DG), nighttime grazing (NG), daytime trough (DT), and nighttime trough (NT) per 24 h

	Source (S)							
	Opitgen		Urea					
Item	Morning	After-noon	Morning	After-noon	SE	*P*-value		
	minutes							
DG	320	342	327	312	14.3	0.43	0.80	0.19
NG	199	191	195	180	20.2	0.63	0.46	0.81
DT	52.7	39.2	50.0	43.1	7.59	0.94	0.19	0.66
NT	3.33	3.44	4.78	1.36	1.72	0.84	0.32	0.29

Key Words: ammonia, grazing, ruminal degradation
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300 Contractile response of bovine lateral saphenous vein to ergotamine tartrate exposed to molecularly imprinted polymers – Physiological significance of in vitro studies.

M. B. Kudupoje*[1], E. S. Vanzant[2], A. Yiannikouris[3], K. A. Dawson[3], K. R. McLeod[2], and J. L. Klotz[4], *[1]Alltech-University of Kentucky Nutrition Research Alliance, Lexington, KY, [2]University of Kentucky, Lexington, [3]Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech Inc., Nicholasville, KY, [4]USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY.*

Previously, we have provided evidence from in vitro adsorption assays that specifically developed polymer adsorbents (molecularly imprinted [MIP] and nonimprinted [NIP]) can bind alkaloids. To aid in understanding the physiological significance, here we report on research using ex vivo models. The objective was to investigate the physiological significance of MIP and NIP application using ex vivo myography and to compare the impact of MIP and NIP on the ergot alkaloid bioavailability. Lateral saphenous veins were collected from 17 steers (2 veins/steer) for 4 independent studies: 1) dose response of ergotamine (ETA), 2) validation of adsorbent dose, 3) validation of incubation conditions, and 4) evaluation of MIP and NIP ($n = 10$, $n = 6$, $n = 6$, and $n = 12$, respectively). Products were also evaluated using in vitro isothermal adsorption (ETA [7.813×10^{-7} M] vs. increasing polymer). For Exp. 1, 2, and 4, 1-way ANOVA (GraphPad Prism) was used to analyze data within a CRD. Means were compared using Tukey's test. Percent contractile response normalized to norepinephrine, fitted with a 3-parameter nonlinear regression model ($R^2 = 0.95$) for ETA concentrations (9.8×10^{-8} to 5.0×10^{-5} M), exhibited a sigmoidal response with a maximum of 86.8 ± 7.3% and log EC_{50}(−log[ETA]) of 6.59 ± 0.26 M. Increasing polymer inclusion using a $\log_2$ scale (0.625 to 10 mg), as compared with a $\log_{10}$ scale (0.0001 to 1 mg), improved curve fits. Ergotamine added immediately upon thawing increased ($P < 0.05$) contractile response compared with addition after 1 h incubation at 39 or 20°C. Isothermal adsorption showed a maximum adsorption of approximately 96% (7.52×10^{-6} mol/10 mg) for both products, with an affinity coefficient (K_d; mg/10 mL) of 0.51 ± 0.10 ($R^2 = 0.92$) and 0.57 ± 0.19 ($R^2 = 0.83$) for MIP and NIP, respectively. At the maximum isothermal adsorption, a maximal reduction of 11.24 ± 2.25 and 9.30 ± 2.74% in contractile response was obtained for MIP and NIP, respectively. Imprinted polymer had better inhibitory response (IC_{50} = 0.28 ± 0.19 mg) than NIP (IC_{50} = 0.83 ± 0.26 mg). Comparing in vitro and ex vivo, the trend between the 2 products remained the same, and MIP had a better adsorption affinity (low K_d) to ETA and caused greater inhibition in contractile response (low IC_{50}). Percent contraction was predicted from the adsorption data using the equations $y = 0.98 \pm 0.06(x) + 0.15 \pm 2.07$ ($R^2 = 0.82$, $P < 0.01$) and $y = 0.92 \pm 0.05(x) - 1.35 \pm 1.74$ ($R^2 = 0.87$, $P < 0.01$) for MIP and NIP, respectively. These studies indicated that synthetic polymers are potentially effective adsorbents toward ergot alkaloids that could mitigate their impact, provided that they could be used in animals. Although earlier studies pointed towards an increased specificity of MIP towards alkaloids adsorption, no differences were observed between products. The ex vivo efficacy of both polymers was accurately predicted from in vitro adsorption data.

Key Words: ergot alkaloids, imprinted polymer, myograph
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301 Effect of nitrogen source on methane emissions from grassland soil.

A. S. Cardoso*[1], B. G. Quintana[1], E. R. Januskiewicz[1], L. F. Brito[1], E. S. Morgado[2], R. A. Reis[3], and A. C. Ruggieri[1], *[1]São Paulo State University, Jaboticabal, Brazil, [2]Universidade Federal de Uberlandia, Uberlandia, Brazil, [3]São Paulo State University (UNESP) School of Agricultural and Veterinarian Sciences, Jaboticabal, Brazil.*

Methane (CH_4) is an important greenhouse gas. Its global warming potential is approximately 32 times higher than that of carbon dioxide (CO_2). Animal feces is the main source of CH_4 in grassland sites. It has been speculated that methanogenic and methanotrophic microorganism activity can be affected by nitrogen source and, consequently, CH_4 fluxes. The aim of this study was to analyze the effect of different sources of nitrogen applied to a grassland soil on CH_4 fluxes. The experimental design was completely randomized with 3 treatments and 4 replicates. The treatments were 3 sources of nitrogen (ammonium, nitrate, and urea) applied to the soil using urea, potassium nitrate, and ammonium sulfate. An incubation under controlled conditions was carried out to quantify the CH_4 fluxes from a tropical Ferralsol. The CH_4 emissions were evaluated using a static closed chamber and the gas concentration was determined by gas chromatography. The ANOVA was performed using the cumulative CH_4 emissions that were obtained integrating the fluxes over time. The Tukey's test was run to distinguish differences among means. The cumulative CH_4 production was −1.19 (0.24), −1.26 (0.09), and 0.88 mg CH_4/m^2 (0.84) for ammonium, nitrate, and urea, respectively. The sources of nitrogen tended to influence the CH_4 emissions ($P < 0.1$). The treatment urea induced CH_4 emission, whereas for the sources ammonium and nitrate, CH_4 was oxidized. These differences can be attributed to the molecular composition of N sources. The CO_2 produced during urea hydrolysis can be converted to CH_4, and this probably explains the CH_4 emissions at approximately 2.4 times higher for urea compared with the ammonium sulfate and potassium nitrate. In a tropical grassland, CH_4 emission or oxidation vary according to the nitrogen source applied to the soil.

Key Words: greenhouse gas, methane oxidation, tropical soil
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302 Intake and digestibility of diets with different amounts of *Senna spectabilis* in hair lambs.

J. Pardo Guzmán*, D. Bonilla, D. Jaramillo, A. Velez, E. Sandoval, and R. Castaneda Serrano, *Universidad del Tolima, Ibagué, Colombia.*

The aim of this study was to determine the intake and digestibility of diets with different amounts of fruits of *Senna spectabilis*. The experiment was carried at Las Brisas Farm of the University of Tolima, Colombia. Twelve hair lambs (22 ± 2.5) were individually housed in digestion crates in 4 × 4 Latin square design. Each period consisted of 14 d of adaptation and 5 d of sample collection. The feeding treatments evaluated were based on hay from *Dichantium aristatum* with incremental amounts of *S. spectabilis*: 0, 15, 30, and 45%. The digestibility of the diets was determined through the total stool collection. Twelve crossbred male lambs were assessed, with an average weight of 22 kg (±4.49) housed for 14 d in a shed for adaptation to the experimental diets and 5 d in metabolic cages for the recollection and weighting of the food and feces of each experimental period. Data was analyzed using PROC REG of SAS version 9.1. The results (Table 302) show that the DMI was not influenced by the inclusions of *S. spectabilis*; however, CP intake did improve as fruit inclusion increased ($P < 0.0001$). The amount of *S. spectabilis* was

Table 302. In vivo digestibility of the DM, OM, and the RP in lambs fed with varying levels of fruits of *S. spectabilis*

		Treatments					*P*-value	
	Variable	T1 (0%)	T2 (15%)	T3 (30%)	T4 (45%)	Ether extract	Linear	Quadratic
DM	Intake, g/d	529.56	545.19	547.50	524.56	0.92	0.0005	0.002
	Dig, %	50.29	50.61	56.01	57.64	5.85	0.875	0.555
OM	Intake, g/d	492.83	508.49	513.01	491.92	8.14	0.980	0.539
	Dig, %	54.64	54.86	59.60	61.49	0.87	0.001	0.001
NDF	Intake, g/d	411.87	396.40	379.45	342.07	5.90	<0.0001	<0.0001
	Dig, %	50.86	51.52	54.91	52.36	0.94	0.342	0.477
CP	Intake, g/d	19.68	30.40	35.19	37.47	1.29	<0.0001	<0.0001
	Dig, %	44.36	56.80	58.39	65.94	1.69	<0.0001	<0.0001

directly correlated with the improvement in the digestibility of DM, OM, and CP ($P < 0.0001$). We conclude that the inclusion of the fruit *S. spectabilis* can improve consumption of CP and the in vivo digestibility of DM, OM, and CP in hair lambs.

Key Words: agroforestry, alternative forage, small ruminant
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GROWTH AND DEVELOPMENT

303 Poor maternal nutrition during gestation alters muscle gene expression in fetal offspring.

S. M. Pillai*[1], M. L. Hoffman[1], A. K. Jones[1], K. K. McFadden[1], J. R. Stevens[2], S. A. Zinn[1], S. A. Reed[1], and K. E. Govoni[1], [1]*Department of Animal Science, University of Connecticut, Storrs,* [2]*Department of Mathematics and Statistics, Utah State University, Logan.*

Fetal muscle development is a complex process that can be affected by maternal diet. However, the mechanisms by which this occurs are not well known. We hypothesized that fetal development would result in temporal changes of key myogenic regulatory factors and that under- and overfeeding ewes during gestation would alter the transcriptome profile of fetal muscle tissue. To test this hypothesis, pregnant Western White-faced ewes were individually housed and fed 100 (control fed, $n = 11$), 60 (restricted fed, $n = 11$), or 140% (overfed, $n = 10$) of NRC requirements for TDN beginning at d 30.2 ± 0.2 of gestation. Ewes were euthanized at d 90 ($n = 11$) and 135 ($n = 10$) of gestation or allowed to undergo parturition and lambs were euthanized within 24 h of birth ($n = 11$) and male offspring LM tissue was collected ($n = 3$ to 4 per treatment per time point). Offspring from control-fed, restricted-fed, and overfed ewes are referred to as CON, RES, and OVER, respectively. Ribonucleic acid was isolated from LM tissue and libraries were prepared and sequenced (Illumina NextSeq500). Data were aligned to the *Ovis aries* reference annotation using STAR aligner, and differentially expressed genes were identified using Ht-seq and DEseq2. The average number of raw reads was 26,065,509 with 85% mappability to the reference annotation. Main effect of diet was observed ($q \leq 0.05$; RES vs. CON; 2 genes upregulated and 5 genes downregulated; OVER vs. CON; 3 genes upregulated and 9 genes downregulated; OVER vs. RES; 2 genes upregulated and 2 genes downregulated). This included genes involved in cell signaling (*Endoplasmic reticulum to nucleus signaling 2* and *SH2 Domain Containing 6*), regulation of inflammation (*C-C motif chemokine 2 ligand* and *Pentraxin-related protein*), and epigenetic regulation (*Histone Deacetylase 10* and *Histone H1.3*). Similarly, a main effect of time ($q \leq 0.05$) was observed with significant differences for d 135 vs. 90 (137 genes upregulated and 172 genes downregulated), birth vs. d 90 (693 genes upregulated and 2,378 genes downregulated), and birth vs. d 135 (80 genes upregulated and 291 genes downregulated). No significant interactions of diet × day of gestation were observed ($q \geq 0.2$). Pathway analysis using PANTHER determined that genes involved in metabolic, cellular, and developmental processes were most affected over time. In conclusion, poor maternal nutrition may alter offspring muscle development through genes involved in cell signaling, inflammation, and epigenetic regulation.

Key Words: maternal nutrition, muscle transcriptome, sheep
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304 Fetal and placental growth during the first 90 days of gestation in beef heifers, and effects of maternal nutrition.

N. Negrin Pereira*[1,2], C. R. Dahlen[1,2], P. P. Borowicz[1,2], J. S. Caton[1,2], M. S. Crouse[1,2], K. J. McLean[3], X. Sun[1], A. K. Ward[1,2], and L. P. Reynolds[1,2], [1]*Department of Animal Sciences, North Dakota State University, Fargo,* [2]*Center for Nutrition and Pregnancy, NDSU, Fargo, ND,* [3]*Department of Animal and Food Sciences, University of Kentucky, Lexington.*

Early gestation is the critical period for successful establishment of pregnancy and placentation. Numerous factors are associated with altered conceptus growth and pregnancy loss, including maternal nutritional status. To document the patterns of fetal and placental growth, in Study 1, crossbred Angus heifers ($n = 16$) were estrous synchronized, bred via AI, and ovariohysterectomized at 5-d intervals from d 25 to 90 of gestation. To examine the effects of maternal nutrition, in Study 2, crossbred Angus heifers ($n = 27$) were synchronized and assigned to 2 dietary intakes at AI (100% of requirements [CON] and 60% of CON [RES]) and were ovariohysterectomized on d 16, 34, or 50 after AI. The gravid uteri were cleaned of adnexa, opened with scissors, blunt dissected, and photographed. A ruler was included in each photo to indicate sizes. Fetal straight crown–rump (C-R) lengths (all days in Study 1 and d 34 and 50 in Study 2) or embryonic disc long axis length (d 16 in Study 2) and surface area of the 2 to 3 largest placentomes (Study 1) were determined by image analysis of the photographs. For Study 1, fetal C-R length increased from 2.2 mm on d 25 to 174.3 mm on d 90, as described by a quadratic equation: $y = 0.0223x^2 + 0.1018x - 16.077$ ($R^2 = 0.996$, $P < 0.01$), in which y = fetal C-R length in mm and x = day of gestation. Placentome surface area increased from 91.4 mm^2 on d 25 to 2,277.9 mm^2 on d 90, as described by an exponential equation: $y = 14.999e^{0.0546x}$ ($R^2 = 0.903$, $P < 0.01$), in which y = placentome surface area in mm^2, e = the base of the natural log, and x = day of gestation. For Study 2, on d 16, embryonic disc long axis lengths for CON vs. RES embryos were 1.084 vs. 0.587 mm (SEM 0.396, $P = 0.198$), and on d 34 and 50, C-R lengths for

CON vs. RES were 1.20 and 4.15 vs. 1.17 and 3.79 cm (SEM 0.154 [$P = 0.46$] and 0.114 [$P = 0.12$] for d 34 and 50, respectively). These observations will serve as a useful “baseline” for future studies of factors that can affect pregnancy establishment and fetal and placental growth. Additionally, we successfully applied our ovariohysterectomy method to study fetal and placental growth from d 16 to 90 of gestation. Supported by the North Dakota State Board of Agricultural Research and Education, a USDA – National Institute of Food and Agriculture – Agriculture and Food Research Initiative grant (2016-67016-24942), and additional local funds.

Key Words: beef heifer, early gestation,
fetoplacental growth
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305 Beef cows nutrition and the effect in the fetal development – A meta-analysis.

D. Zago[1], M. E. A. Canozzi[1], E. D. Sartori[1], M. Bitello[1], and J. O. Barcellos[*1,2], *[1]NESPRO/UFRGS – Department of Animal Science, Federal University of Rio Grande do Sul, Porto Alegre, Brazil, [2]Federal Council of Veterinary Medicine (CFMV), Brasília, Brazil.*

To quantify the effects of the TDN and CP in the diet of pregnant beef cows on fetal weight and birth weight of calves, a systematic review and meta-analysis were performed. We searched on 2 electronic databases (Scopus and ISI Web of Knowledge) from 1945 to October 2016, and we checked references of relevant review papers. Data were extracted using predefined protocols. Inclusion criteria were complete studies using pregnant beef cows receiving different diets that analyzed fetal weight and/or birth weight of calves. Random effect meta-analyses were conducted for each indicator separately with the mean of the control and the treated group. The analysis was conducted with the TDN and CP levels in relation to cows’ requirements (NRC, 1996). The results were presented with the pooled mean difference (MD) and I^2 (the percentage of total variation between studies that is due to heterogeneity rather than chance). For fetal weight at 4 mo (FW4), we included 4 studies reporting 6 trials involving 170 animals; for fetal weight at 8 mo (FW8), we included 4 studies, 4 trials, and 156 animals; and for birth weight of calves (BiW), we included 48 studies, 125 trials, and 9,053 animals. The heterogeneity between studies was high for FW4 (I^2 = 94.4%), FW8 (I^2 = 91.08%), and BiW (I^2 = 96.9%). When control cows received 20 to 40% less TDN than the treated group, the FW4 was reduced by 2.27 kg ($P < 0.001$; I^2 = 65.06), because both groups received 19 to 25% more TDN than their requirements. The cows from control group tended to show ($P = 0.057$) a lower MD (1.57 kg; I^2 = 91.08%) when consuming 30% of CP above their requirements. The fetuses from control group were 2.23 kg lighter ($P < 0.001$; I^2 = 0%) when their cows consumed 20% TDN above their requirements. The BiW was lower (MD = −0.761; I^2 = 96.4%; $P < 0.001$) only for cows in the third period of pregnancy. The calves from both groups were born 0.560 and 0.761 kg lighter when cows consumed CP ($P = 0.0015$; I^2 = 97.1%) and TDN ($P < 0.001$; I^2 = 96.4%) more than their requirements, respectively. Our study demonstrates that FW4, FW8, and BiW were reduced when CP was 19 to 25% and TDN was 30% above of cows’ requirements as published by the NRC (1996).

Key Words: birth weight, bovine fetus,
fetal programming
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306 Maternal under- and overnutrition during gestation alters pancreatic DNA methylation in fetal offspring.

M. L. Hoffman[*], S. M. Pillai, A. K. Jones, M. C. Wynn, K. K. McFadden, S. A. Reed, S. A. Zinn, and K. E. Govoni, *Department of Animal Science, University of Connecticut, Storrs.*

Poor maternal nutrition during gestation can increase insulin production and reduce β-cell proliferation in the pancreas tissue of the offspring, with the effects persisting into postnatal life and across multiple generations. However, the mechanisms by which these changes occur are poorly understood. Changes to pancreas DNA methylation patterns during gestation may be mediating some of these effects. We hypothesized that maternal under- and overnutrition during gestation would increase fetal pancreatic DNA methylation in the offspring. Twenty pregnant Western White-faced ewes were fed 100, 60, or 140% of NRC requirements for TDN for a ewe pregnant with twins beginning at d 30.2 ± 0.2 of gestation. Fetuses are referred to as CON, RES, and OVER, respectively. Ewes (n = 6 to 7 per diet) were euthanized at d 135 of gestation and fetal pancreas tissue was collected. Deoxyribonucleic acid was isolated and reduced representation bisulfate sequencing library preparation was performed (3 to 4 fetuses per treatment per gender), and libraries were sequenced (Illumina MiSeq). Data were mapped to the *Ovis aries* reference annotation (Oar_V.3.1) using Bismark. Differentially methylated loci ($q \leq 0.01$; Table 306) and differentially methylated regions (DMR; $P \leq 0.001$; $\Delta = 0.1$; Table 306) were determined using the dispersion shrinkage for sequencing data analysis package in R. Offspring from ewes were fed 100 (CON), 60 (RES), or 140% (OVER) of NRC requirements for TDN from d 30.2 to 135 of gestation. In RES females, 62% of DMR were hypomethylated compared with CON females ($P \leq 0.001$). In contrast, 93% of DMR were hypermethylated in RES males

Table 306. Total number of differentially methylated loci (DML) and regions (DMR) identified in the pancreas tissue of fetal offspring

Treatment comparison	DML	DMR
CON vs. RES females	2,416	34
CON vs. RES males	1,514	64
CON vs. OVER females	1,874	48
CON vs. OVER males	608	25

compared with CON males ($P \le 0.001$). In OVER, 66 and 80% of DMR were hypermethylated in females and males compared with CON females and males, respectively ($P \le 0.001$). These data demonstrate that maternal nutrition affects the DNA methylation patterns in the pancreas tissue of offspring in a diet-specific manner and that the changes in pancreatic DNA methylation are gender dependent.

Key Words: DNA methylation, maternal nutrition, pancreas
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307 Effect of maternal melatonin supplementation during mid to late gestation on fatty acid composition in maternal and fetal plasma and perirenal adipose tissue collected from bovine fetuses at 240 days of gestation.

R. C. Thompson[*1], K. J. McCarty[1], A. T. Sukumaran[1], R. L. Lemire[1], E. H. King[2], R. M. Hopper[2], C. O. Lemley[1], T. T. N. Dinh[1], and D. D. Burnett[1], [1]*Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State,* [2]*Department of Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Mississippi State.*

Melatonin supplementation during mid to late gestation increases uterine blood flow, thereby altering the flux of nutrients delivered to the developing fetus by the dam. Changes in the amount and composition of fatty acids available to the fetus can alter the long-term growth and developmental potential of the offspring in postnatal life. The objective of this study was to determine the effect of supplementing melatonin to beef heifers during mid to late gestation on fatty acid composition of maternal, umbilical, and fetal plasma as well as fetal perirenal adipose tissue. A total of 32 pregnant heifers were treated with (MEL) or without (CON) two 24-mg melatonin implants every 30 d starting on d 180 and ending on d 240 of gestation. On d 240 of gestation (approximately 85% of gestation), 6 CON and 6 MEL heifers were randomly selected to undergo Cesarean sections to collect fetal blood and tissues. Maternal blood (MB) was collected from the tail vein of the dams immediately prior to the surgery. Before excising the fetus, the umbilical cord was clamped on the fetal and maternal ends to collect blood from the umbilical artery (UA) and umbilical vein (UV). Fetal peripheral blood (FB) was collected during exsanguination, and perirenal (PR) adipose tissue was dissected from the fetal kidney following evisceration. Plasma and PR adipose tissue samples were directly derivatized for fatty acid quantification on a gas chromatography system to determine fatty acid concentration and percentage by internal calibration. Data were analyzed using the GLIMMIX procedure of SAS 9.4 (SAS Inst. Inc., Cary, NC), and statistical significance was determined at $P \le 0.05$. There was no difference in total plasma fatty acid concentrations between the CON and MEL groups in MB, UA, UV, FB or PR ($P > 0.324$). Total SFA, MUFA, and PUFA in UA, UV, MB, FB, or PR also did not differ between treatments ($P \ge 0.11$). However, MEL tended to increase C22:6 fatty acid concentration in MB ($P = 0.065$), UV ($P = 0.079$), and FB ($P = 0.068$). Additionally, there was a tendency for increased ($P = 0.080$) C20:5*n*-3 fatty acid in PR adipose tissue in fetuses from MEL-treated dams. Both C22:6 and C20:5*n*-3 fatty acids improve fetal development and immune function. Therefore, additional research is warranted to determine the specific effect of MEL on these fatty acids and their long-term impacts on offspring growth and physiology.

Key Words: fatty acids, melatonin, perirenal adipose tissue
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308 Fetal brown fat deposition is increased by melatonin implants in sheep.

F. Sales[*1], V. H. Parraguez[2], S. McCoard[3], E. Cofré[2], O. A. Peralta[2], and I. Subiabre[4], [1]*Instituto de Investigaciones Agropecuarias, Punta Arenas, Chile,* [2]*Faculty of Veterinary Sciences, University of Chile, Santiago, Chile,* [3]*AgResearch Limited, Palmerston North, New Zealand,* [4]*Instituto de Investigaciones Agropecuarias, Osorno, Chile.*

The major cause of lamb mortality in grazing systems at birth is starvation and/or exposure to cold complex, with hypothermia being a primary contributing factor. In precocial species such as sheep, the ability to produce the heat required to prevent hypothermia during the first 12 h after birth relies heavily on the nonshivering thermogenesis, via brown adipose tissue (BAT). Therefore, insufficient BAT deposits, or inability to metabolize BAT, are the major factors contributing to lamb death resulting from starvation/exposure. Circulating concentration of melatonin is associated with proper amount and functionality of BAT. However, there is limited information on the effect of increased melatonin levels, via maternal supplementation, on fetal BAT deposition. The objective was to establish the effect of melatonin implants (M) in single- and twin-bearing ewes, on fetal BAT deposits. Corriedale ewes were synchronized, superovulated, mated to Suffolk rams, and managed under commercial grazing conditions. Single (S)- and twin (T)-bearing ewes received 0 (M0), 1 (M1), or 2 (M2) commercial 18-mg melatonin implants (Regulin) at 100 d of gestation ($n = 8$ per group). Ewes were euthanized at d 140 of gestation, and total fetal perirenal fat (BAT) was excised and weighed. The effect of litter size (S vs. T), number of implants (M0, M1, or M2), and their interaction on fetal biometrics were analyzed using ANOVA. A rank × treatment interaction ($P = 0.002$) was observed for total BAT, where SM2 fetuses tended to have 18% more BAT compared with SM0 ($P = 0.1$) and SM1 fetuses ($P = 0.09$; 22.8 ± 1.6 vs. 19.3 ± 1.5 or 19.2 ± 1.5 g), whereas TM1 fetuses had approximately 35% more BAT compared with TM0 ($P = 0.0002$) and TM2 fetuses ($P = 0.0003$; 22.9 ± 1.1 vs. 17.1 ± 1.0 or 16.9

± 1.1 g). Single and twin M2 fetuses tended to be 5 to 8% heavier compared with single and twin M0 and M1 fetuses (4.1 ± 0.1, 3.8 ± 0.1, and 3.9 ± 0.1 kg, respectively; $P = 0.09$). In addition, M2 fetuses, compared with M0 and M1 fetuses, showed greater fetal thorax diameter (34.6 ± 0.4, 33.8 ± 0.3, and 33.9 ± 0.3 cm, respectively; $P = 0.047$) and presented a trend for increased crown–rump length (44.1 ± 0.5, 43.0 ± 0.4, and 42.6 ± 0.5 cm, respectively; $P = 0.056$). These results indicate that maternal melatonin implants from d 100 of gestation increases BAT deposition, especially in twin fetuses, and may increase BW. Both effects may have important implications for newborn lamb survival under commercial grazing conditions. Funded by CONICYT project number 11150998.

Key Words: brown adipose tissue, lamb survival, melatonin
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309 Changes in fetal muscle microRNA expression from exposure to ergot alkaloids in utero.

M. F. Miller Jr.*, *Clemson University, Clemson, SC.*

MicroRNA (miRNA) are small noncoding RNA that help regulate gene expression and metabolic function. Some miRNA, called MyomiR, are expressed predominately in skeletal muscle and regulate myogenesis. The objective of this study was to identify miRNA in skeletal muscle of fetuses exposed to ergot alkaloids in utero. Thirty-six pregnant Suffolk ewes (78.24 kg ± 9.5) were randomly assigned to dietary treatments of endophyte-free tall fescue seed (E−; 0.0 µg ergovaline + ergovalinine/ewe per day) or endophyte-infected tall fescue seed (E+; 1,722 µg ergovaline + ergovalinine/ewe per day) at specific stages of gestation (d 35–85 or d 86–133) in a 2 × 2 factorial arrangement of treatments. Fetal and maternal necropsies were performed at d 133 of gestation. Semitendinosus (ST) muscle was removed from each fetus and immediately frozen in liquid nitrogen for storage at −80°C. Total cellular RNA was extracted using the *mir*Vana miRNA Isolation Kit (Ambion, Austin, TX). Quality analysis of RNA was performed using an Agilent 2100 Bioanalyzer, with a RNA integrity number threshold of 7.0. The translational control RNA from 3 fetuses per treatment from the ST was used for miRNA sequencing and data analysis (LC Sciences, Houston, TX). MicroRNA sequencing yielded 113,252,743 reads with 92,177,228 mappable to the ovine reference genome. Of the mappable reads, 27% were specific to the *Ovis aries* genome and 18% were specific to mammals. There were 4,242 unique miRNA identified by sequencing, which included 208 that were specific to the *Ovis aries* genome and 676 that were mammalian but novel to *Ovis aries*. Known MyomiR (miR-1, miR133a, miR133b, miR206, miR-208b, miR-486, and miR-499) in skeletal muscle were present in our samples but not ($P > 0.05$) differentially expressed due to treatment. miR-148b, miR-300-3p, miR-431-3p, miR-299-3p, and miR-541-5p were upregulated ($P < 0.05$) in E+/E+ compared with E−/E− fetal ST muscles. miR-652, miR-628, miR-2427, miR-22-3p, miR-8118-p5, miR-376d, and miR-677 were downregulated ($P < 0.05$) in E+/E+ versus E−/E−. Skeletal muscle miR-148b has been shown to reduce glucose uptake in response to insulin in humans. miR-541 promotes vascular smooth muscle cell proliferation. Exposure to ergot alkaloids in utero alters miRNA expression in fetal skeletal muscle.

Key Words: fescue, fetal muscle, MyomiR
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310 Genetics is the essential factor for the precocious puberty in Nellore heifers.

M. V. C. Ferraz Junior*[1,2], D. M. Polizel[2], A. A. Miszura[2], G. B. Oliveira[2], A. V. Bertoloni[2], R. Sartori[1], G. P. Nogueira[3], and A. V. Pires[1,2], [1]*ESALQ/University of São Paulo, Piracicaba, Brazil,* [2]*FMVZ/University of São Paulo, Pirassununga, Brazil,* [3]*FMVA/São Paulo State University, Aracatuba, SP, Brazil.*

There is a paradigm that Nellore heifers' reproductive life starts at ≥24 mo of age due to nutritional conditions of low-quality pasture. This study aimed to determine the genetics and nutrition effects on puberty attainment in Nellore (*Bos indicus*) heifers. Fifty-eight weaned heifers (174 ± 6 kg initial BW and 8 ± 1 mo of age) were assigned to 28 feedlot pens. Heifers were born from 4 sires: 2 were precocious (P; negative EPD to age at first calving; $n = 33$) and 2 were nonprecocious (NP; positive EPD to age at first calving; $n = 25$). Heifers of each EPD were randomly assigned to 2 nutritional strategies (high ADG [HG; 0.7 kg] or low ADG [LG; 0.3 kg], resulting in 4 treatments: heifers from P sires were submitted to either HG (PHG; $n = 17$) or LG (PLG; $n = 16$) and heifers from NP sires were submitted to either HG (NPHG; $n = 12$) or LG (NPLG; $n = 13$). The HG heifers were fed with 75% concentrate diet, whereas the LG heifers were given 93% forage in their diet. Blood samples were collected at 9, 14, 18, 24, and 28 mo of age for plasma IGF-I determination. Transrectal ultrasonography and progesterone concentration were assessed weekly to determine puberty onset. The proportion of heifers that attained puberty at 18, 26 and 30 mo of age and BW at puberty were assessed by GLIMMIX procedure using a binomial and normal option, respectively. The MIXED procedure, with repeated measure analysis, was used to assess the interaction between treatment and time in IGF-I concentration. There was a treatment effect ($P < 0.01$) in the percent of heifers that attained puberty by 18 (62, 0, 0, and 0% for PHG, PLG, NPHG, and NPLG, respectively), 24 (100, 6, 54, and 0% for PHG, PLG, NPHG, and NPLG, respectively) or 36 mo of age (100, 100, 100, and 38% for PHG, PLG, NPHG, and NPLG, respectively). The BW at puberty was 360, 340, 468, and 390 ± 15 kg for PHG, PLG, NPHG, and NPLG, respectively. Plasma IGF-I concentrations were higher in P heifers than NP cohorts in all ages and in the same ADG ($P < 0.01$, treatment × age interaction). In conclusion, EPD of age at first calving was the essential factor for puberty onset at 18 mo of age in Nellore heifers, but ADG was a limiting factor at puberty.

Key Words: *Bos indicus*, IGF-I, nutrition
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311 Effect of compensatory growth on puberty of Nellore heifers.

A. A. Miszura*[1], M. V. C. Ferraz Junior[1,2], D. M. Polizel[1], G. B. Oliveira[1], A. V. Bertoloni[1], J. P. R. Barroso[1], L. G. M. Gobato[1], G. P. Nogueira[3], and A. V. Pires[1,2], [1]*FMVZ/University of São Paulo, Pirassununga, Brazil,* [2]*ESALQ/University of São Paulo, Piracicaba, Brazil,* [3]*FMVA/São Paulo State University, Aracatuba, SP, Brazil.*

The objective in this study was to determine the effect of growth rates and compensatory growth on age and BW at puberty of heifers. One hundred twenty Nellore (*Bos indicus*) heifers, weaned at 8 ± 0.75 mo of age, born from 6 bulls (block effect), were assigned to 40 feedlot pens according to initial BW (180 ± 8.6 kg) to receive 1 of 4 treatments: 1) high gain (HG), in which heifers were submitted to high ADG and ad libitum DMI; 2) medium ADG (MG; 0.6 kg); 3) restricted gain (RG), which was feed restriction for 4 mo (0.2 kg) followed by ad libitum DMI with compensatory growth; and 4) alternate gain (AG), which was ad libitum DMI for 2 mo alternated with 2 mo of feed restriction (ADG = 0.2 kg) during 10 mo. The experimental period lasted 10 mo. All heifers received the same diet composed of ground corn (70%), sugarcane bagasse (12%), soybean meal (16%), mineral mixture (1%), and urea (1%). The lower gain was attained by restriction of DMI. Transrectal ultrasonography and progesterone concentration was assessed weekly to determine puberty onset. At 18 mo of age, heifers that did not reach puberty were submitted to a puberty induction with a progesterone inset by 9 d. The continuous variables were analyzed by the MIXED procedure and the binomial variables were evaluated by the GLIMMIX procedure (SAS 9.3). There was no effect of treatments in the percentage of pubertal heifers at 18 mo of age (66, 40, 69, and 51% for HG, MG, RG, and AG, respectively; $P = 0.17$), BW (351, 339, 339, and 337 ± 15 kg for HG, MG, RG, and AG, respectively; $P = 0.74$), and age at puberty (17.4, 18.2, 18.7, and 18.1 ± 0.35 mo for HG, MG, RG, and AG, respectively; $P = 0.15$). However, the ADG during the total experimental period (0.771, 0.607, 0.630, and 0.688 ± 0.05 kg; $P < 0.01$) and ADG until puberty (0.836, 0.725, 0.667, and 0.727 ± 0.04 kg; $P < 0.01$) was greater in heifers submitted to HG compared with heifers from the other treatments. Moreover, heifers submitted to HG had greater ($P < 0.01$) DMI than heifers submitted to RG (5.9, 4.7, 4.6, and 5.4 ± 0.12 kg/d for HG, MG, RG, and AG, respectively). About 80% of the heifers responded to induction, and there was no difference ($P = 0.90$) among treatments. Compensatory growth was an efficient nutritional strategy to reduce DMI and did not affect puberty in Nellore heifers until 18 mo of age.

Key Words: *Bos indicus*, nutritional strategy, puberty induction
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312 Consequences of birth weight differences on carcass traits as well as muscle and adipose tissue cellularity in crossbred bulls.

E. Albrecht[1], C. Kühn[1], and S. Maak*[2], [1]*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany,* [2]*Muscle Biology and Growth, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Birth weight differences have been shown to affect body composition in pigs and other species. However, data on effects of birth weight differences on morphological and cellular traits of carcass in bulls with a longer fattening period are scarce. Consequently, we have analyzed 2 groups of bulls from an experimental F_2 cross (Charolais × Holstein) with low birth weight (LBW; 35.6 ± 0.7 kg; $n = 20$) and high birth weight (HBW; 59.4 ± 0.9 kg; $n = 20$). All animals were kept in a tight stall barn from d 121; were fed a standardized, concentrate-based diet ad libitum; and were slaughtered at an age of 547 d. The feed intake was higher in the HBW group but feed conversion ratio was not different. Live weights were not different between the 4th and 15th month of age but then diverged, resulting in significantly higher weights at slaughter at 18 mo in the HBW group (717 ± 13 vs. 661 ± 10 kg; $P < 0.05$). Bulls of the HBW group accreted more protein (14.9 ± 0.15 vs. 14.4 ± 0.17%; $P = 0.017$) and LBW bulls accreted more fat (17.2 ± 0.81 vs. 14.3 ± 0.79%; $P = 0.016$) in the carcass. The absolute and relative weights of omental, perirenal, and visceral adipose depots were significantly higher in LBW bulls. Weight of longissimus (MLD) was higher in the HBW bulls (8.6 ± 0.15 vs. 7.7 ± 0.13 kg; $P < 0.001$) compared with LBW animals. However, there were no significant differences in muscle fiber traits in MLD. The intramuscular fat (IMF) content of MLD from LBW bulls was significantly increased compared with that of HBW animals (3.9 ± 0.5 vs. 2.5 ± 0.3%; $P = 0.012$). Analysis of cellular parameters of the IMF revealed increased diameters (94.4 ± 1.7 vs. 81.4 ± 2.4 μm; $P < 0.01$) of adipocytes and larger but not more marbling flecks as cause for higher IMF in LBW bulls. Our results demonstrate long-lasting effects of large differences in birth weight on carcass traits. Crossbred bulls could not compensate low birth weights even under ad libitum feeding regimen within a period of 18 mo in this experiment. Our data indicate that metabolic differences resulted in different partitioning of nutrients with a shift to lipid accumulation in bulls with lower birth weight in this crossbreed population.

Key Words: adipocyte morphology, birth weight, crossbred bulls
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313 Heat-shock protein beta 1 is related to muscle growth and development in beef cattle.

Y. S. Kim*[1,2], Y. Lee[3], J. S. Lee[1,2], W. S. Kim[1,2], D. Q. Peng[1,2], M. H. Bae[1,2], Y. H. Jo[1,2], and H. G. Lee[1,2], [1]*Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea (South),* [2]*Team of an Educational Program for Specialists in Global Animal Science, Brain Korea 21 Plus Project, Konkuk University, Seoul, Republic of Korea (South),* [3]*Department of Biotechnology, Hankyung National University, Anseong-si, Gyeonggi-do, Republic of Korea (South).*

Muscle growth and development is critical for the meat production of beef cattle. Previous studies have suggested that heat-shock protein beta 1 (HSPB1) is a candidate protein related to muscle development in cattle. In this study, we aimed to examine the association between HSPB1 and muscle development in Korean native cattle. In addition, we also sought to identify novel SNP of *HSPB1* gene, which may be related to muscle growth in Korean native cattle. In this research, we conducted both in vitro cell culture and *HSPB1* SNP genotyping experiments. In in vitro cell culture experiments, we used MyoD (myogenic lineage determinant) overexpressed immortalized bovine embryonic fibroblast cell line (BEFS-MyoD cells) to find out the role of *HSPB1* in bovine myogenesis. First, a small interfering RNA assay of *HSPB1* expression was conducted in BEFS-MyoD cells to evaluate the effect of reduced HSPB1 expression on myogenic differentiation stages. Second, to elucidate the role of higher HSPB1 expression in myogenesis, we also carried out glutamine (HSPB1 inducer)-mediated bovine myogenesis in BEFS-MyoD cells. For genotyping experiments, direct DNA sequencing of *HSPB1* gene was performed to find out novel SNP associated with muscle development in 20 unrelated Korean native cattle. The inhibition of HSPB1 expression was shown to repress the expression of myogenic marker genes (*MyoD*, *Myogenin*, and *Desmin*; $P < 0.01$) and formation of myotubes. In contrast, higher expression of HSPB1 enhanced the expression of myogenic marker genes ($P < 0.01$), myotube formation, and protein synthesis ($P < 0.01$). Direct DNA sequencing of *HSPB1* revealed 3 sequence variants located in the coding region, 5′ untranslated region, and intron region in 20 unrelated Korean native cattle. Among these SNP, g.2352 T>C and g.111 T>C SNP are located near a splicing site and a *cis*-regulatory site. According to the results, it is concluded that HSPB1 enhances muscle growth and development and that novel variants found in 3 distinct genomic regions might be used as candidate markers for muscle development in Korean native cattle.

Key Words: *HSPB1* gene, muscle growth, single nucleotide polymorphism
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314 A high-roughage diet alters performance, carcass characteristics, and adipogenic gene expression of bovine longissimus thoracis.

K. Y. Chung*, S. S. Chang, S. H. Yang, K. S. Ki, E. M. Lee, and E. G. Kwon, *National Institute of Animal Science, RDA, KOREA, Pyeongchang, Republic of Korea (South).*

Three groups of calf-fed steers were used to evaluate the effects of control (100% concentrate), Italian rye grass (IRG) silage (ad libitum with 66% concentrate), and IRG hay (ad libitum with 66% concentrate) on adipogenic gene expression in longissimus thoracis (LT) muscle. Eight randomly selected Hanwoo steer from each group were fed with a 3-step diet, which were calf diet (6 to 11 mo), early fattening diet (12 to 20 mo), and final fattening diet (21 to 30 mo). One gram of muscle biopsy samples was taken from cattle on 7, 12, 24, and 30 mo on both sides of the LT area. Real-time PCR determined the levels of adipogenic marker (C/EBPβ, PPARγ, SCD, and GPR43) and myogenic marker (Pax3, Myf5, myogenin, GLUT4, MHC I, MHC IIA, and MHC IIX) mRNA. Data were analyzed as a completely randomized design using the MIXED model, and each treatment was performed in triplicate. Means were considered different at $P < 0.05$. Average daily gain at calf and early fattening period of study were not different, but final fattening period of the study was lower in the IRG hay group ($P < 0.05$) than in control steers. Back fat thickness, rib eye area, and carcass weight of the control group were greater than those of the IRG diet group ($P < 0.05$). However, marbling score and shear force (kg/0.5 in^2) were not different among the control and IRG diets. Relative PPARγ and SCD mRNA levels in biopsy samples were increased ($P < 0.05$) on the days of fattening diet, but relative C/EBPβ mRNA level was decreased ($P < 0.05$). The level of Pax3, Myf5, and myogenin were decreased on the days of fattening diet ($P < 0.05$). Relative MHC IIX mRNA levels were greater ($P < 0.05$) in 12-mo-old Hanwoo steer than in control steers. Italian rye grass hay group cattle had greater MHC IIX mRNA levels than the other groups ($P < 0.05$). These data indicate that relative mRNA levels of adipogenic genes in LT muscle are decreased during the days of high-roughage diet (IRG silage and hay). The high-roughage diet also decreased back fat thickness and rib eye area but not affect marbling score.

Key Words: adipogenesis, muscle biopsy, roughage diet
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315 Vitamin C induces PRDM16 of bovine muscle-derived cells isolated from semimembranosus and longissimus dorsi tissues.

K. Y. Chung*, D. H. Kang, S. S. Jang, S. H. Yang, K. S. Ki, E. M. Lee, and E. G. Kwon, *National Institute of Animal Science, RDA, KOREA, Pyeongchang, Republic of Korea (South).*

Vitamin C (VC) supplements have been used for enhancing marbling fat in high-quality beef cattle. However, mode of action of VC was not clearly studied for a long time. The aim of this experiment was to determine the effect of VC dose titration in bovine muscle-derived cells (MDC) from semimembranosus (SM) and longissimus dorsi (LD) muscle tissues. We hypothesized that VC may affect adipogenesis of bovine MDC isolated from different muscle depots. Bovine MDC were pronase liberated from SM and LD muscle tissues of 3 newborn Hanwoo calves. Bovine SM and LD MDC were incubated with Dulbecco's modified Eagle's medium (DMEM) with 10% fetal bovine serum for proliferation and differentiation was induced with DMEM with 3% horse serum. Bovine MDC were treated with various levels of VC (control and 10 and 100 μ*M*) with insulin, oleic acid, and ciglitizone to induce transdifferentiation in bovine MDC cultures. Relative mRNA abundance of adipogenic markers (PRDM16, C/EBPβ, PPARγ, SCD, and GPR43) and myogenic markers (Pax3, Myf5, myogenin, GLUT4, MHC I, and MHC IIX) were analyzed with real-time quantitative PCR for 2, 3, and 7 d after differentiation treatment. Data were analyzed as a completely randomized design using the MIXED model, each and treatment was performed in triplicate. Means were considered different at $P < 0.05$. Relative PRDM16 mRNA abundance was increased in dose-dependent levels in both SM and LD MDC with VC treatments compared with the control ($P < 0.05$). The levels of C/EBPβ and PPARγ were increased during differentiation ($P < 0.05$) but the level of SCD was not changed during differentiation ($P > 0.05$). The levels of Pax3, Myf5 and myogenin were increased with treatment of 100 μ*M* VC but MHC IIX was greater only at 100 μ*M* VC in SM MDC than those in LD MDC ($P < 0.05$). There was not a tissue × time interaction ($P > 0.05$) but there were main effects ($P < 0.05$) among adipogenic and myogenic mRNA concentration. These results indicated that VC has a dose-dependent effect on not only PRDM16 but also on adipogenic markers in bovine MDC isolated from LD and SM muscle tissues.

Key Words: Hanwoo, muscle-derived cells, vitamin C
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316 Different dietary calcium and phosphorus inclusion levels alter satellite cell activity in neonatal pigs.

K. Kroscher*[1], R. L. Murray[2], W. Zhang[2], L. Zhao[1], C. H. Stahl[2], and R. P. Rhoads[1], *[1]Virginia Tech, Blacksburg, [2]University of Maryland, College Park.*

Postnatal skeletal muscle growth requires satellite cell activation and fusion with existing myofibers. Delay or absence of satellite cell proliferation and differentiation leads to a reduction in postnatal muscle hypertrophy and reduced growth potential. Calcium and phosphate are necessary for normal muscle development, and deficiencies cause altered satellite cell function and reduced muscle accumulation. Dietary PO_4 deficiencies were shown to cause decreased satellite cell proliferation in vitro whereas excess PO_4 caused increased proliferation. The objective of this study was to determine proliferation and differentiation of satellite cells in response to combined Ca–PO_4 deficient, adequate, and excess diets in neonatal pigs. Twenty-seven newborn piglets (24 ± 6 h age) were assigned to dietary treatments, based on NRC requirements, containing an adequate Ca–PO_4 available diet, a 25% deficient Ca–PO_4 available diet, or a 25% excess Ca–PO_4 available diet over a 17-d trial. Feed intake and BW were recorded daily, and blood samples were collected at 8 and 16 d. Oral bromodeoxyuridine (BRDU) was administered 18 h prior to sacrifice. Following sacrifice, longissimus dorsi muscle was collected for immunohistochemistry and satellite cell (SC) isolation. Isolated SC were cultured for in vitro proliferation and differentiation assays. Dietary treatments altered serum phosphate whereas adequate treatment increased serum phosphate by 8% compared with the deficient diet at 8 d but was 12% less in the excess diet compared with the deficient at 16 d ($P < 0.05$). There were no differences in ADG between treatments ($P = 0.16$). Dietary deficiency reduced proliferating satellite cells (BRDU/MyoD+) in vivo ($P = 0.02$) compared with adequate and excess diets. However, in vitro SC from excess diets tended to proliferate 13.7% ($P = 0.08$) less than SC from adequate diets, with deficient diets being intermediate and not different from the other 2 ($P \geq 0.49$). Similarly, myoblast fusion rates were greatest in adequate diets, with deficient diets having 9.2% lower fusion rates ($P = 0.05$) and excess diets exhibiting 20.7% lower fusion rates than those fed adequate diets ($P < 0.001$). These data indicate that diets deficient in Ca–PO_4 decrease satellite cell activity, which may lead to a reduction in postnatal muscle growth. Additionally, excess dietary Ca–PO_4 appears to reduce satellite cell proliferation and differentiation in vitro. Diets adequate in Ca–PO_4 have the greatest proliferation and differentiation rates, which may improve the growth potential of the animal.

Key Words: mineral, pig, satellite cell
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317 In vitro betaGRO supplementation stimulates myogenesis of porcine fetal myoblasts and porcine satellite cells in a divergent manner.

O. S. Khatri*, M. A. Vaughn, K. J. Phelps, and J. M. Gonzalez, *Kansas State University, Manhattan.*

Two separate experiments were conducted to evaluate the effect of betaGRO supplementation on proliferation rate, fusion rate, and myotube growth of porcine fetal myoblasts (PFM) and porcine satellite cells (PSC) in vitro. The PFM were isolated from the LM of d 60 of gestation fetuses and PSC from the LM of piglets within 24 h of birth. Proliferation assays were conducted as 4 × 3 factorial arrangements with time of culture (24, 48, 72, and 96 h) and media treatment as main effects. Media treatments consisted of a positive control, which contained high-glucose Dulbecco's modified Eagle medium supplemented with 10% (vol/vol) fetal bovine serum, 2% (vol/vol) porcine serum, 100 units/mL penicillin, 100 μg/mL streptomycin, and 20 μg/mL gentamicin (HS); a negative control, which consisted of HS without 10% FBS (LS); and LS supplemented with 10 mg/mL betaGRO (BG). Fusion rate and myotube growth assays were conducted as 2 × 2 factorial designs with serum concentration and betaGRO inclusion as the main effects. There was a treatment × time interaction ($P < 0.01$) for proliferation rate of PFM. At all time points, HS and BG PFM had greater proliferation rates compared with LS PFM ($P < 0.01$). The HS treatment had greater proliferation rates than the BG treatment ($P < 0.02$) except at 72 h of culture ($P = 0.44$). There were betaGRO × serum interactions for PFM fusion rate and myotube growth ($P < 0.01$). When betaGRO was added to LS media of PFM, fusion percentage and myotube diameter decreased ($P < 0.01$), whereas fusion percentage increased ($P < 0.01$) and myotube diameter was unaffected ($P = 0.63$) when betaGRO was added to HS media. There were treatment × time and betaGRO × serum interactions for proliferation rate and fusion rate of PSC ($P < 0.01$). At all time points, HS had greater proliferation rates than LS and BG ($P < 0.01$) and LS had greater proliferation rates than BG ($P < 0.02$). When betaGRO was added to LS and HS media of PSC, fusion percentage increased for both media types ($P < 0.01$). There was no betaGRO × serum interaction ($P = 0.63$) for PSC myotube growth; however, betaGRO-supplemented myotubes were larger ($P < 0.01$) than non-betaGRO-supplemented myotubes. These 2 experiments indicate betaGRO supplementation to culture media stimulates divergent responses based on the type of cell examined, with BG increasing proliferation in PFM and fusion rate and myotube growth in PSC. These findings suggest betaGRO supplementation may enhance both myogenesis in utero as well as postnatal muscle hypertrophy.

Key Words: betaGRO, porcine fetal myoblast, porcine satellite cell
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318 Comparison of a point-of-care glucometer and an automated biochemical analyzer to measure glucose concentrations in whole blood, serum, and plasma from porcine blood samples.

M. K. Gohlke*, W. Z. Nunnelley, and T. D. Brandebourg, *Auburn University, Auburn, AL.*

Accurate measurement of circulating glucose concentrations is critical when evaluating the metabolic status of swine. Point-of-care glucometers (POCG) represent an expedient method for measuring glucose concentrations in whole blood samples given the insignificant blood volume required and the rapid results, but often this technology yields less reliable estimates of blood glucose concentrations compared with biochemical analyzers used in clinical diagnostic laboratories, likely due to a confounding effect of packed cell volume on POCG readings. Our objective was to test this hypothesis by determining the correlation between glucose concentrations measured by a POCG in serum, plasma, and whole blood compared with values measured in plasma by a biochemical analyzer. To accomplish this, blood samples were collected via jugular venipuncture from 152 grow–finish Yorkshire swine during the postprandial state. Glucose concentrations were measured in whole blood, serum, and plasma (in the presence and absence of the glycolytic inhibitor fluorine) by a POCG and in fluorinated plasma using a biochemical analyzer. Resulting values were compared using correlation and Bland–Altman analyses to determine if sampling methods were interchangeable. Glucose concentrations in whole blood as measured by a POCG were highly variable and poorly correlated with plasma glucose concentration measured by a biochemical analyzer ($r^2 = 0.34$). However, glucose concentrations in serum and plasma measured by a POCG were more strongly correlated with the plasma glucose concentration measured by a biochemical analyzer (serum, $r^2 = 0.57$, and plasma, $r^2 = 0.64$). Plasma glucose concentration measured by a POCG in the presence of fluorine correlated the strongest with plasma glucose concentration measured by a biochemical analyzer ($r^2 = 0.89$). Bland–Altman analysis revealed the mean differences in glucose concentrations determined by biochemical analyzer and by POCG in whole blood, serum, plasma, and fluorinated plasma were 43.5, 33.5, 12.4, and 4.5 mg/dL, respectively. These results indicate that the use of a human POCG to measure glucose concentration in fluorinated porcine plasma yields results that are most similar to those produced by a biochemical analyzer. Next, whole blood was collected from 24 grow–finish Yorkshire hogs that were subjected to an oral glucose tolerance test following an overnight fast to determine if the POCG can successfully measure physiologically relevant differences in circulating glucose concentrations. As expected, values obtained 30 min following consumption of a glucose bolus were 171% higher than fasted values as determined by the POCG ($P < 0.01$). These results indicate POCG can reliably estimate circulating porcine glucose concentrations when measured in plasma.

Key Words: glucometer, glucose, swine
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319 Metabolomic analysis of the longissimus muscle revealed differences between underperforming and normal preweaning growth piglets.

T. G. Ramsay*, M. J. Stoll, A. E. Shannon, and L. A. Blomberg, *USDA, ARS, BARC, Beltsville, MD.*

The present study was designed to determine if normal birth weight pigs that grow poorly during the preweaning period have altered skeletal muscle 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/d until 21 d of age. At 21 d, slow-growing (SG) pigs weighed 5.47 ± 0.22 kg whereas control (CON) littermates weighed 6.98 ± 0.28 kg ($P < 0.001$). Samples of longissimus were collected for metabolomic analysis at d 21. Metabolomic analysis was performed by Metabolon (Durham, NC) using ultrahigh performance liquid chromatography–tandem mass spectroscopy. Analysis of the longissimus from these SG pigs identified 68 metabolites that were increased and 33 that were decreased relative to longissimus from CON littermates using matched pairs *t*-tests for analysis ($P < 0.05$). A reduction in central carbon metabolism was apparent in longissimus from SG pigs relative to CON pigs. Specifically, SG pigs exhibited decreases in several pentose sugars and alcohols, including sedoheptulose 7-phosphate ($P = 0.016$), 6-phosphogluconate ($P = 0.022$), ribose 5-phosphate ($P = 0.031$), and ribitol ($P = 0.048$), indicative of reduced pentose phosphate shunt activity. Decreases were also apparent in the glycolytic intermediates glycerol 3-phosphate ($P < 0.001$) and lactate ($P = 0.013$). The key glycolysis-derived intermediates glucose-6-phosphate ($P = 0.015$) and fructose-6-phosphate ($P = 0.012$) were also reduced in longissimus of SG pigs relative to CON pigs. Increased levels of carnitine ($P = 0.003$), acetylcarnitine ($P = 0.019$), and deoxycarnitine ($P = 0.026$), coupled with increased levels of several phospholipids ($P < 0.05$), diacylglycerols ($P < 0.05$), and sphingolipids ($P < 0.05$), suggest more fatty acid synthesis and utilization in longissimus of SG pigs than in that of CON pigs. Longissimus of SG pigs exhibited higher levels of 3-methylhistidine ($P = 0.003$), pro-hydroxy-pro ($P = 0.034$), and trans-4-hydroxyproline ($P = 0.002$), which are associated with increased muscle breakdown and extracellular matrix remodeling. In conclusion, muscle from SG pigs displayed limited accretion of pentose phosphate metabolites, with corresponding increases of many lipid classes that suggest a shift to β-oxidation over carbohydrate oxidation. This further corresponded with increased markers of muscle and collagen breakdown, consistent with a more catabolic state in the SG pig.

Key Words: metabolomics, neonatal swine, skeletal muscle
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320 The effects of biweekly administration of recombinant bovine somatotropin during the first trimester on fetal development in gestating beef heifers.

C. D. Sanford*[1], N. Oosthuizen[1], P. L. P. Fontes[1], L. B. Canal[1], K. A. Vonnahme[2], C. O. Lemley[3], N. DiLorenzo[1], and G. C. Lamb[4], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*Department of Animal Science, North Dakota State University, Fargo,* [3]*Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State,* [4]*Texas A&M University, Department of Animal Science, College Station.*

To evaluate the effects of recombinant bovine somatotropin (bST; sometribove zinc, Posilac; Elanco Animal Health, Indianapolis, IN) on fetal and placental development during the first trimester of gestation, 97 Angus heifers were exposed to a 7-d CO-Synch + controlled internal drug release ovulation control protocol and then either received 500 mg of bST (BST) biweekly or received no bST (CONT) immediately prior to fixed-timed AI (TAI; d 0). On d 0, 15, 29, 43, and 57, BST heifers received a single subcutaneous injection in the neck. Heifer BW was assessed on d −9, −3, 0, 15, 22, 29, 43, 50, 57, 64, and 77. Blood samples were collected on d 0, 22, 50, and 64 for analysis of concentrations of plasma IGF-1. Pregnancy was diagnosed via transrectal ultrasonography on d 29 and 64 after TAI. A subset of pregnant heifers ($n = 7$ for BST and $n = 5$ for CONT) were retained for assessment of fetal and placental characteristics. Heifers were harvested, and complete gravid reproductive tracts and liver tissue were collected for analysis. Mean change in BW (71.9 kg) and ADG (0.95 kg ± 0.27) of the heifers from TAI to d 77 did not differ between treatments ($P > 0.05$). Likewise, no differences were detected between treatments with regards to carcass quality grade, carcass yield, or carcass weight. Mean concentrations of IGF-1 were greater ($P < 0.001$) in BST-treated heifers (346.50 ± 27.7 ng/mL) than in CONT heifer (134.70 ± 32.8 ng/mL). Mean placental weight (66.46 g), fetal membrane weight (0.256 kg), and uterine weight (1.42 g) as well as ovarian and corpus luteum weights (15.1 and 4.8 g, respectively) did not differ ($P > 0.05$) between treatments. Similarly, fetal crown to rump length, fetal weight, heart girth, and liver weight did not differ between treatments ($P > 0.05$). However, extraembryonic samples collected from heifers receiving bST (521.6 ± 22.9 g) resulted in greater ($P = 0.027$) quantities of fetal fluid compared with CONT heifers (429.6 ± 27.14 g). There was also a tendency for BST heifer reproductive tracts to have fewer

placentomes ($P = 0.084$) and greater umbilical diameter ($P = 0.091$) than CONT heifers. In conclusion, administration of bST during the first trimester of gestation increased concentrations of IGF-1, which resulted in an increase in extraembryonic fluid, a decreased quantity of placentomes, and greater umbilical diameter but failed to alter fetal development.

Key Words: beef heifers, bovine somatotropin, fetal programming
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321 The effects of fescue toxicosis at different stages of gestation on fetal development.

M. F. Miller Jr.*, *Clemson University, Clemson, SC.*

The objective of this study was to determine the effects of ergot alkaloids fed to ewes during 2 gestational time periods on fetal growth and development. Suffolk ewes ($n = 36$) were synchronized and bred to a single ram. Ewes (78.02 ± 9.53 kg BW) identified by ultrasound at d 35 to be pregnant with twin fetuses were fed endophyte-infected tall fescue seed (E+; 1,772 µg/ewe per day ergovaline + ergovalinine) or endophyte-free tall fescue seed (E−; 0 µg/ewe per day ergovaline + ergovalinine) during the 2 gestational time periods (d 35–85 or d 86–133). This created 4 unique dietary treatments E+/E+, E+/E−, E−/E+, and E−/E−. Ewes were pair fed to maintain similar DMI. Maternal and fetal necropsies were performed at d 133 of gestation. Data was analyzed as a randomized block design with a 2 × 2 factorial with treatment (E+ or E−), time of gestation (d 35–85 or d 86–133), and 2-way interaction in the model. Feeding ergot alkaloids during early gestation did not alter ($P > 0.05$) fetal BW or muscle or organ weights. Feeding ergot alkaloids during late gestation reduced fetal BW at d 133 of gestation by 10% compared with the E− treatment. Thoracic circumference was smaller ($P < 0.05$) for E+ fetuses than for E− fetuses; crown–rump length and abdominal circumference also tended ($P < 0.10$) to be smaller for E+ fetuses. Total muscle weight was reduced ($P < 0.05$) by 13% in fetuses from ewes fed E+ seed during late gestation. Weights of the psoas major, semitendinosus, semimembranosus, and quadriceps femoris were lighter ($P < 0.05$) for fetuses from ewes fed E+ seed during late gestation. Weight of the heart and liver were lighter ($P < 0.05$) for fetuses from ewes fed E+ seed during late gestation. There were interactions ($P < 0.10$) between fescue treatment and time of gestation for kidney, pancreas, spleen, and brain weights. Brain weight expressed on a fetal BW basis was higher ($P = 0.01$) in fetuses from ewes fed E+ fescue seed, indicating asymmetrical fetal growth. Feeding endophyte-infected seed containing ergovaline + ergovalinine during late gestation (d 86–133) reduces fetal growth and muscle mass.

Key Words: ergot alkaloid, fescue toxicosis, fetal development
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322 Altered messenger RNA expression in placental tissues of ewes exposed to ergot alkaloids during gestation.

J. L. Britt*, A. Feltus, M. F. Miller Jr., B. M. Koch, M. C. Miller, and S. K. Duckett, *Clemson University, Clemson, SC.*

Consuming ergot alkaloids found in endophyte-infected tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh.] seed causes intrauterine growth restriction due to uteroplacental insufficiency. The objective of this study was to assess the impact on gene expression levels in placental tissue from feeding ergot alkaloids during gestation. Thirty-six Suffolk ewes (78.24 kg ± 9.5) estimated to be carrying twins at d 35 of gestation were randomly assigned to 1 of 2 treatments—endophyte-free tall fescue seed (E−; 0.0 µg ergovaline + ergovalinine/g) or endophyte-infected tall fescue seed (E+; 4.14 µg ergovaline + ergovalinine/g)—from d 35 through 85 and d 86 through 133 of gestation, creating 4 unique dietary treatments: E−E−, E−E+, E+E−, and E+E+. Endophyte-infected tall fescue seed was fed at a level to provide 1,772 µg of ergovaline + ergovalinine/ewe per day for E+ treatments, and an equal weight of endophyte-free seed (0.0 µg ergovaline + ergovalinine) was fed for E− treatments. Ewes were pair fed across treatments in order to maintain equal DMI. Fetal and maternal necropsies were performed at d 133 of gestation. Placental samples were weighed, frozen in liquid nitrogen, and stored at −80°C. Total RNA was extracted from cotyledon placental tissue using TRIzol and a PureLink RNA Mini Kit (ThermoFisher Scientific). Total RNA was quantified and quality was assessed using an Agilent 2100 Bioanalyzer. Ribonucleic acid integrity numbers of >7 were considered sufficient quality. A subsample ($n = 4$) was selected for both the E+E+ and E−E− treatment groups, and total cotyledon RNA was submitted for gene expression profiling via Illumina RNA-Seq (LC Sciences). Numerous genes were upregulated ($P \leq 0.01$; $n = 131$) in E+E+ compared with E−E− and included genes involved in angiogenesis and vasoconstriction (FGA, APOH, and HPX), hemostasis and coagulation (KNG1, FGA, PLG, and FGB), oxidative reduction (PYROXD2 and CYP2E1), cholesterol import and lipoprotein particles (APOC3, APOH, APOA2, GC, and PON1), cell activation (FGA), and immune response (KNG1 and AHSG). Several genes were downregulated ($P < 0.01$; $n = 56$) in E+E+ compared with E−E−, including genes involved in fatty acid metabolism, lipid oxidation, and beta-oxidation (ADIPOQ), G-protein coupled receptor (GPR151), signal transduction (HRH4), and cell proliferation (PODN). The consumption of ergot alkaloids during gestation directly effects the mRNA expression in cotyledon tissues.

Key Words: fescue, placenta, RNA sequencing
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323 Does genotype play a role in resistance to fescue toxicosis in the ovine?

S. K. Adams*[1], C. J. Kojima[2], J. L. Britt[1], M. F. Miller Jr.[1], B. M. Koch[1], J. G. Andrae[1], and S. K. Duckett[1], [1]*Clemson University, Clemson, SC,* [2]*Department of Animal Science, University of Tennessee, Knoxville.*

The objective of this study was to evaluate the effect of genotype in ewes consuming ergot alkaloids found in endophyte-infected tall fescue seed. Genotype at the DRD2 gene has been associated with serum prolactin concentrations in beef cattle grazing E+ tall fescue. Genomic DNA samples were obtained from 32 Suffolk ewes and used to initially screen the ovine DRD2 gene for SNP. One SNP in exon I, g270a, was discovered and further investigated due to favorable allele and genotypic frequencies. Allele frequencies at the g270a SNP were 0.64 for G and 0.36 for A; genotypic frequencies were 0.47, 0.34, and 0.19 for GG, AG, and AA genotypes, respectively. A genotyping assay was designed, tested, and found to be 100% concordant with sequencing results. Pregnant ewes ($n = 32$) were fed 1 of 2 dietary treatments—endophyte-free tall fescue seed (E−; 0.0 μg ergovaline + ergovalinine/g) or endophyte-infected tall fescue seed (E+; 4.14 μg ergovaline + ergovalinine/g)—during 2 time periods—d 35 through 85 (T2) and d 86 through 133 (T3) of gestation—in a 2 × 2 factorial arrangement. Endophyte-infected seed was fed at a level of 1,772 μg of ergovaline + ergovalinine/ewe per day for E+ treatments and an equal weight of endophyte-free seed for E− treatments. All ewes were pair fed across treatments to maintain equal DMI. Data were analyzed with dietary treatment (E+ or E−), time of gestation (T2 or T3), genotype (AA, AG, and GG), and all interactions in the model. Significance was set at $P < 0.05$. Prolactin concentrations during gestation were higher for AA and AG than GG genotype regardless of dietary treatment or gestation time. Lamb fetal weight was reduced due to E+ exposure during T3 but did not differ by ewe genotype or any interactions with treatment or gestation time. A subsample ($n = 16$) of ewes were used to assess changes in cortisol and thyroid hormones (Th3, triiodothyronine, and thyroxine). Cortisol, triiodothyronine, and thyroxine concentrations were elevated in AA genotype compared with GG. Dietary treatment, gestation time, or interactions with genotype had no effect on cortisol, triiodothyronine, or thyroxine. Genotype at the ovine DRD2 SNP appears to be associated with circulating hormone concentrations in the ewe, regardless of dietary fescue treatment or stage of gestation.

Key Words: fescue, genotype, ovine
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324 Altered expression of placental microRNA in ewes with uteroplacental insufficiency due to consumption of endophyte-infected tall fescue seed.

J. L. Britt*, A. Feltus, M. F. Miller Jr., B. M. Koch, M. C. Miller, and S. K. Duckett, *Clemson University, Clemson, SC.*

Differential microRNA (miRNA) expression levels have been reported for placental tissues in cases of uteroplacental insufficiency and fetal growth restriction. Ergot alkaloids found in endophyte-infected tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh] seed induces intrauterine growth restriction (IUGR) due to uteroplacental insufficiency. The objective of this study was to assess the impact on placental miRNA levels due to consumption of ergot alkaloids during mid to late gestation. Thirty-six Suffolk ewes (78.24 kg ± 9.5) estimated to be carrying twins at d 35 of gestation were randomly assigned to 1 of 2 treatments—endophyte-free tall fescue seed (E−; 0.0 μg ergovaline + ergovalinine/g) or endophyte-infected tall fescue seed (E+; 4.14 μg ergovaline + ergovalinine/g)—from d 35 through 85 and d 86 through 133 of gestation, creating 4 unique dietary treatments: E−E−, E−E+, E+E−, and E+E+. Endophyte-infected tall fescue seed was fed at a level to provide 1,772 μg of ergovaline + ergovalinine/ewe per day for E+ treatments, and an equal weight of endophyte-free seed (0.0 μg ergovaline + ergovalinine) was fed for E− treatments. Ewes were pair fed across treatments in order to maintain equal DMI. Fetal and maternal necropsies were performed at d 133 of gestation. Placental samples were weighed, frozen in liquid nitrogen, and stored at −80°C. Total RNA was extracted from cotyledon placental tissue using TRIzol and a PureLink RNA Mini Kit (ThermoFisher Scientific). Total RNA was quantified and quality was assessed using an Agilent 2100 Bioanalyzer. Ribonucleic acid integrity numbers of >7 were considered sufficient quality. A subsample ($n = 4$) was selected for both the E+E+ and E−E− treatment groups, and total cotyledon RNA was submitted for gene expression profiling via Illumina RNA-Seq (LC Sciences). Numerous miRNA transcripts were upregulated ($P < 0.01$; $n = 15$) in E+E+ compared with E−E− and included miR-21, miR-221, miR-99a, miR-152, miR-381, miR-30a, miR-143, and miR-122. miR-21 exhibited a 9.89-fold increase in expression level for E+E+ compared with E−E−. miR-21 has previously been implicated as a potential biomarker for fetal hypoxia due to upregulation in both placental and plasma/serum samples. Similar increases in miR-21 and miR-122 levels have been correlated to other pathological diseases of the placenta including placental insufficiency, IUGR, and preeclampsia.

Key Words: fescue, placenta, RNA sequencing
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325 Genes in skeletal muscle associated with gain and intake identified in a multiseason study of crossbred beef steers.

A. K. Lindholm-Perry*, B. N. Keel, C. M. Zarek, J. W. Keele, L. A. Kuehn, W. M. Snelling, W. T. Oliver, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

The purpose of this study was to identify genes differentially expressed in the muscle of beef cattle associated with gain and intake regardless of breed of origin and season or year of study. Crossbred animals of 19 different breeds with variation in BW gain and feed intake were selected from fall and spring seasons over 3 yr to reduce the influence of gene expression that was either breed specific or related to environment or cohort. Ribonucleic acid sequencing was performed on longissimus dorsi muscle from 80 selected steers (5 cohorts, each with 16 animals). Each cohort displayed a clear segregation of phenotypes; therefore, a meta-analysis for the main effects of gain, intake, and their interaction was chosen to identify differentially expressed genes across the 5 RNA sequencing data sets. A total of 148 genes were differentially expressed for the main effect of gain, 1,738 genes for intake, and 59 genes for the gain × intake interaction. There were 9 genes associated with gain and 12 genes associated with intake that shared the same gene expression directionality across all 5 groups of steers. The 9 genes with common directionality associated with gain were *LDHB*, *PITHD1*, *PDLIM1*, *MYHB7*, *GSTM2*, *MYL12A*, *NFKBIA*, and 2 LOC genes. These genes have been associated with functions including protein oxidation, oxidative metabolism, oxidative stress and cytokine inhibition. The 12 genes identified for feed intake were *ART5*, *ALDH5A1*, *ARHGEF25*, *BGN*, *C15H11orf31*, *CC2D1B*, *CLSTN2*, *CAMK1D*, *LOC101902407*, *PON1*, *SOCS3*, and *UBE2B* involved in ion binding, G-coupled receptor signaling, signal transducer activity, and striated muscle contraction. Pathway analysis of the complete list of 1,738 genes for feed intake identified genes overrepresented in oxidative phosphylation, mammalian target of rapamycin, and *EIF2* signaling pathways; however, many of these genes displayed different effects by season. The variation among the lists of genes identified as differentially expressed by cohort in this study underscores the importance of including animals from more than one cohort of livestock to obtain biologically relevant data for complex traits. The USDA is an equal opportunity provider and employer.

Key Words: beef cattle, feed efficiency, growth
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326 Shifts in hepatic transcriptome profiles of growing versus finished beef steers.

J. Huang*, P. Bridges, and J. C. Matthews, *University of Kentucky, Lexington.*

Transcriptome analysis was conducted to gain a greater understanding of hepatic metabolic shifts associated with the change in whole-body compositional gain of growing vs. finished beef steers. Weaned Angus steers (209 ± 29.4 kg BW) were randomly assigned ($n = 8$) to develop through lean (GROW; 301 kg final BW) or lipid (FINISH; 576 kg final BW) growth phases and individually fed enough of a cottonseed hull-based diet to achieve a constant ADG (1.5 kg/d). Marbling score (668 and 296) and yield grade (3.65 and 2.13) were greater ($P < 0.01$) but liver weight (1,005 and 1,341 g/100 kg BW) was less ($P < 0.01$) for FINISH vs. GROW steers, respectively. Total hepatic RNA was isolated and subjected to microarray (Bovine Affymetrix Gene 1.1 ST GeneChip) analysis, and differences in gene expression (false discovery rate < 10%; $P < 0.01$) between treatment groups were determined by 1-way ANOVA (Partek Genomics Suite). Expression of 405 mRNA was increased (5 to 567%) and the expression of 695 mRNA was decreased (6 to 638%) in FINISH vs. GROW steers. Bioinformatic (Ingenuity Pathway Analysis) analysis found that the top functional gene category was cell death and survival (47 genes; $P \leq 0.025$) and the top canonical cell signaling pathway was calcium-induced T lymphocyte apoptosis (13 genes; $P \leq 0.0005$). Functional analysis of canonical metabolic pathways found that FINISH steers had increased ($P \leq 0.009$; 17 to 414%) capacities for ammonia (*GLS2*, *GLUD1*, and *GPT2*), Arg (*OAT*, *GOT1*, *ASS1*, and *ASL*), and urea production (ARG2) and shunting of AA carbons into pyruvate (*ALT2*, *SDS*, and *LDHB*). For carbohydrate metabolism, capacity for glycolysis (*PGK1* and *PKM2*) was inhibited ($P \leq 0.003$; 19 and 42%) whereas glycogen synthesis (*GYG2* and *GYS2*) was greater ($P \leq 0.002$; 30 and 31%) in FINISH steers. For lipid metabolism, FINISH steers showed decreased ($P \leq 0.008$; 28 to 163%) capacity for fatty acid activation (*ACSL5* and *ACSF2*) and desaturation (*SCD*, *FADS1*, and *FADS2*) but increased ($P \leq 0.009$; 26 to 61%) capacity for fatty acid β-oxidation (*ACADL* and *ACAA1*) and lipid storage (*LIPA* and *PLIN3*). In addition, redox capacity (*GPX1*, *GSS*, and *GGT1*) and inflammatory responses (*NOS2*, *SOCS2*, *CCL2*, *IL6R*, and *TLR3*) were decreased ($P \leq 0.008$; 18 to 191%) in FINISH steers. Network analysis identified liver X receptor/retinoid X receptor activation as the most probable ($P = 0.015$) mechanism coordinating lipid metabolism and immune response events. These findings elaborate the shift in hepatic metabolic capacities as compositional gain shifted from lean to lipid phenotype in beef steers.

Key Words: finishing steers, liver, transcriptome analysis
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327 GTRAP3-18 protein negatively modulates canalicular glutamate transport and glutamine synthesis capacity in the liver of finishing versus growing beef steers.

J. Huang*[1], Y. Jia[1], Q. Li[1], W. R. Burris[2], P. Bridges[1], and J. C. Matthews[1], [1]*University of Kentucky, Lexington,* [2]*University of Kentucky, Princeton.*

In rodents, system X^{-}_{AG} Glu transporters, EAAC1 and GLT-1, are linked to glutamine synthetase (GS) activity and glutathione content, respectively. The goal of this study was to determine if the hepatic content and activities of these proteins, and GTRAP3-18, an inhibitor of EAAC1 and GLT-1, change as steers developed from predominately lean to lipid growth phases. Weaned Angus steers (209 ± 29.4 kg BW) were randomly assigned ($n = 8$) to develop through lean (GROW; 301 ± 7.06 kg final BW) vs. lipid (FINISH; 576 ± 36.9 kg final BW) growth phases and individually fed enough of a cotton seed hull–based diet to achieve a constant ADG (1.5 kg/d) throughout the trial. The effect of development on experimental parameters was assessed by 1-way ANOVA using the GLM procedure of SAS. As expected, final BW (576 and 301 kg), 12th-rib adipose (1.73 and 0.54 cm), marbling score (668 and 296), and yield grade (3.65 and 2.13) were greater ($P < 0.01$) for FINISH vs. GROW steers, respectively. Western blot analysis of hepatic homogenates ($n = 8$) found more GTRAP3-18 (63%; $P = 0.01$) in FINISH vs. GROW steers, whereas EAAC1 content was less (32%; $P = 0.05$) and GLT-1 did not differ ($P \geq 0.66$). System X^{-}_{AG} activity (pmol·10 min^{-1}·μg^{-1} protein) in canalicular membrane vesicles (cMV) was greater ($P = 0.07$) in GROW steers (2.78; $n = 6$) than in FINISH steers (0.0; $n = 4$) but did not differ ($P = 0.55$) between basolateral membrane vesicles (bMV) of GROW (1.85; $n = 6$) and FINISH (1.15; $n = 4$) steers. Western blot analysis of MV ($n = 4$) found that EAAC1 content in bMV was less (25%; $P = 0.05$) and tended to be less (47%; $P = 0.09$) in cMV for FINISH vs. GROW steers, whereas GLT-1 content in bMV and cMV was not affected ($P \geq 0.50$). Glutamine synthetase activity in liver homogenates ($n = 8$) of FINISH steers (0.67 nmol·min^{-1}·mg^{-1} wet tissue) was less (32%; $P = 0.01$) than GROW steers, whereas GS content did not differ ($P = 0.72$). Hepatic glutathione content (mg/g wet tissue) did not differ ($P = 0.96$) between GROW (1.08) and FINISH (1.07) steers. We conclude that as steer compositional gain changes from lean to lipid, the change in Gln synthesis capacity is related to canalicular membrane-associated EAAC1 function, which is inversely proportional to GTRAP3-18 content.

Key Words: finishing steers, glutamate transporters, liver
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328 Effect of maternal nutrition and sex on skeletal muscle gene expression in Angus cattle during immune challenge.

L. M. Pereira Sanglard*[1], M. Nascimento[2], P. Moriel[3], M. Merrill[1], M. Poore[1], M. S. Duarte[2], and N. V. Serão[1], [1]*North Carolina State University, Raleigh,* [2]*Universidade Federal de Viçosa, Viçosa, Brazil,* [3]*UF/IFAS Range Cattle Research and Education Center, Ona, FL.*

Maternal nutrition during gestation has long-term effects on skeletal muscle development of the offspring. The objective of this work was to identify differentially expressed genes and their biological functions as an effect of maternal energy restriction in Angus steers and heifers during immune challenge. Twenty-four purebred Angus pregnant cows were fed 1 of 2 diets: 70 (restricted) or 100% (control) of the NE requirements for maintenance of a pregnant beef cow. Three weeks after weaning, and 3 d after vaccination for bovine viral diarrhea virus, longissimus dorsi muscle biopsies were collected from 12 steers and 12 heifers and snap frozen in liquid nitrogen. Total RNA was extracted and sequenced for 150 bp paired-end reads. A total of 2,076,680,240 reads were generated. Reads were checked for quality with FASTQC software. Sequence reads were mapped to *Bos taurus* UMD3.1 reference genome using Bowtie2. For statistical analysis, raw counts were normalized by the trimmed mean of M values (TMM) procedure and then $\log_2$ transformed. A linear model including the fixed effects of maternal diet, sex, diet × sex interaction, sequencing lane (2 lanes), and RNA integrity number score (as a covariate) was used. Statistical analyses were performed in R using the gls function from the nlme package. Multiple testing correction was conducted using the Benjamini and Hochberg false discovery rate method. For the differentially expressed genes, an enrichment analysis was performed in DAVID Bioinformatics Resources 6.8. A total of 719, 658, and 1,041 differentially expressed genes ($P < 0.10$) were identified for the effects of diet, sex, and diet × sex interaction, respectively. The most significant differentially expressed gene ($P < 0.0001$) for each of these effects was RSPH3, DDX3Y, and LRRFIP1, respectively. For diet, differentially expressed genes were enriched for protein synthesis and degradation activity. For sex, most differentially expressed genes were involved in the apoptotic process, indicating a potential difference in homeostatic potential during challenge. For sex × diet interaction, a greater range of biological processes was identified for differentially expressed genes, such as glycolysis and gluconeogenesis processes, myofibril assembly, actin filament elongation, and fatty acid metabolism. Differences in protein metabolism between steers and heifers are expected due to effects of sex hormones. Maternal energy restriction also can alter protein metabolism due to lack of nutrients for embryo muscle development. Therefore, these results suggest that the expression profiles of genes controlling protein turnover differ in the skeletal muscle of animals born from dams

with or without energy restriction during pregnancy under immunological challenge.

Key Words: fetal programming, gene expression, muscle development
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329 Impact of fetal versus maternal contributions of *Bos indicus* and *Bos taurus* genetics on early embryonic development.

P. L. P. Fontes[*1], N. Oosthuizen[1], D. D. Henry[1], F. M. Ciriaco[1], C. D. Sanford[1], L. B. Canal[1], V. R. G. Mercadante[2], S. E. Johnson[3], A. D. Ealy[3], N. DiLorenzo[1], and G. C. Lamb[4], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]Virginia Tech – Animal and Poultry Sciences, Blacksburg, [3]Virginia Tech, Blacksburg, [4]Department of Animal Science, Texas A&M University, College Station.*

To evaluate maternal and fetal system influence on early embryonic and fetal development in *Bos indicus* and *Bos taurus* cattle, a reciprocal embryo transfer approach was used in a completely randomized design with a $2 \times 2 \times 2$ factorial arrangement of treatments in order to generate 55 pregnancies over 2 consecutive years ($n = 55$). Recipient cows were placed into the University of Florida Feed Efficiency Facility, containing a GrowSafe feed intake monitoring system, and were randomly assigned to 1) a diet to meet daily maintenance requirements (MAINT) or 2) a diet that restricts intake of nutrients to 70% of energy maintenance requirements (RESTR). Angus (AN) and Brangus (BN) embryo donors were superovulated and artificially inseminated with female sexed-sorted semen from the same breed. Embryos were then randomly transferred 7 d after insemination (d 7) to either AN or BN recipients fed the respective diets for 20 d. Recipients remained on the dietary scheme until d 91, at which time cows were commingled and fed a common diet that met their energy and protein requirements to the same feeding regime until calving. Transrectal ultrasonography was performed to assess fetal crown to rump length (CRL) weekly from d 42 to 91. Blood samples were collected weekly from d 28 to 91 to determine plasma concentrations of pregnancy-specific protein B (PSPB). All analyses were performed using the MIXED procedure of SAS. There was an effect of diet ($P < 0.001$) and day ($P < 0.001$) on recipient BW, with RESTR recipients having lower BW than MAINT. Similarly, diet altered recipient BCS from d 70 to 91 (diet × day, $P = 0.005$). Embryos from BN donors transferred to recipients fed the RESTR diet resulted in a greater (embryo breed × diet, $P < 0.001$) plasma concentrations of PSPB. Although no effects of embryo breed ($P > 0.05$) or diet ($P > 0.05$) were observed on fetal morphometries, fetuses from AN recipients had greater CRL on d 91 (breed × day, $P = 0.021$) when compared with BN recipients (167.7 ± 1.8 vs. 160.7 ± 1.6 mm, respectively). No effect of recipient breed, embryo breed, or diet was detected on gestation length ($P > 0.05$) or birth weight of the offspring ($P > 0.05$). In conclusion, *Bos indicus* genotype was a significant factor altering concentrations of PSPB during early gestation, whereas *Bos taurus* recipient genotype positively impacted early fetal growth.

Key Words: *Bos indicus*, *Bos taurus*, fetal development
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330 Effect of heat stress on serum and tissue fatty acid profile in pigs.

H. Qu[*1] and K. M. Ajuwon[2], *[1]Purdue University, West Lafayette, IN, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN.*

Studies have shown that heat stress (HS) increases adipose tissue accretion in pigs. However, effects of HS on fatty acid composition are still unknown. The objective of this study was to investigate HS effects on tissue fatty acid composition in pigs and differentiated pig adipocytes under HS. Pigs were divided into 3 treatments: control (CON), with ad libitum feed intake and maintained at 22°C ambient temperature; pair fed (PF), in which pigs were pair fed to the feed intake of HS pigs and maintained at 22°C; and HS, in which pigs had ad libitum feed intake but were kept at a constant ambient temperature of 29.4°C. Pigs were in these treatments for 7 d. Fatty acid composition of serum, adipose tissue, liver, and muscle were analyzed by gas chromatography. Heat stress pigs had higher serum ($P < 0.05$) linoleic acid than PF pigs (21.29 vs. 11.34%). Both linoleic (10.90 vs. 13.47%) and gadoleic (0.30 vs. 0.47%) acids were decreased ($P < 0.05$) in LD muscle in HS pigs compared with PF, respectively. In vitro, heat-stressed adipocytes differentiated under HS (41.5°C) had a higher ($P < 0.05$) percent total SFA (69.16 vs. 59.34%) and higher ($P < 0.05$) MUFA (28.85 vs. 20.53%) compared with cells at 37.0°C (CON). In conclusion, heat stress induces distinct tissue fatty acid profile in pigs and adipocytes and this could be associated with tissue and cellular heat stress adaptation.

Key Words: fatty acids, heat stress, pig
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HORSE SPECIES

331 Influence of short-term dietary starch inclusion on the equine cecal microbiome.

C. M. Warzecha*[1], J. C. McCann[2], J. Coverdale[1], J. Janečka[3], W. E. Pinchak[4], T. A. Wickersham[1], and J. L. Leatherwood[1], [1]*Department of Animal Science, Texas A&M University, College Station,* [2]*Department of Animal Sciences, University of Illinois, Urbana,* [3]*College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station,* [4]*Texas A&M AgriLife Research, Vernon.*

The objective of this study was to determine bacterial community profiles of the equine cecum in response to abrupt inclusion of varying levels of dietary starch. Seven cecally cannulated Quarter horse geldings (497 to 580 kg) were used in a crossover design with two 28-d periods and a 28-d washout between them. Horses were randomly assigned to dietary treatments consisting of a commercial concentrate offered as fed at either 0.6 (LS) or 1.2% BW (HS) daily that was divided into 2 meals at 12-h intervals. Prior to the start of each period, horses were allowed ad libitum access to coastal bermudagrass (*Cynodon dactylon*) hay. Concentrate was fed on d 1 with no adaptation. Cecal fluid was collected on d 1 at h 0 and 3, 6, 9, and 12 h relative to the morning concentrate meal on d 1. Additional samples were collected 6 h after feeding on d 2, 3, and 7 of each period. Cecal contents were used to determine pH and VFA concentrations and to extract genomic DNA. The V4 through V6 region of 16S rRNA gene was amplified by PCR and sequenced on the Roche 454 FLX platform. Sequence analysis was performed with QIIME, and data were analyzed using the MIXED procedure of SAS. Cecal pH tended to decrease ($P \leq 0.09$) in HS horses for the first 12 h after the first concentrate meal and remained lower ($P \leq 0.05$) the following 7 d in HS horses. Total VFA were greater ($P < 0.05$) in HS horses in the initial 12 h and 7 d after addition of concentrate. Although species richness determined by Chao1 was unchanged ($P > 0.2$) over the initial 12 h, it did decrease ($P = 0.01$) over 7 d for both treatments. Community diversity determined by the Shannon index tended to decrease ($P = 0.06$) over the 7 d, with the greater decrease ($P = 0.09$) in HS horses. Relative abundances of Paraprevotellaceae increased ($P < 0.01$) and Streptococcaceae tended to increase ($P \leq 0.10$) in HS horses in the first 12 h. Over 7 d, relative abundances of Paraprevotellaceae, Veillonellaceae, and Succinivibrionaceae increased ($P \leq 0.02$) in HS horses compared with LS horses. Abrupt and short-term exposure to dietary starch does alter cecal fermentation and microbial community structure in horses; however, the contributions of specific bacterial communities to horse health need further investigation.

Key Words: cecum, equine, microbiome
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332 Effect of dietary L-arginine on blood flow dynamics, gestation length, and placental efficiency of mares.

L. B. Hodge*[1], B. J. Rude[1], and C. O. Lemley[2], [1]*Mississippi State University, Mississippi State,* [2]*Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

Objectives were to determine effects of arginine supplementation during different times of gestation to mares on uterine blood flow, placental efficiency and uterine involution. Pregnant mares ($n = 20$) were randomly assigned to 1 of 4 diets beginning 21 d prior to expected foaling date until 84 d of next gestation: diet 1 (CON), the basal diet; diet 2, CON plus arginine during late gestation; diet 3 (E), CON plus arginine during early gestation; and diet 4, CON plus arginine during both early and late gestation. Arginine was supplemented at 1% of diet. Ultrasonography was conducted to measure uterine blood flow at 21 d prior to expected foaling date (late gestation); then every 2 wk until foaling; d 1, 4, and 7 after foaling to measure uterine involution; and then every 14 d after breeding until 84 d of gestation (early gestation). Placentas were weighed, and surface area and displacement volume were determined. Placental efficiency was calculated using foal weight and placental weight. Mixed procedures with repeated measures in SAS were used for blood flow parameters and uterine involution parameters, and placental efficiency and gestation length data were subjected to Mixed procedures. Treatment did not affect ipsilateral or contralateral uterine artery measurements during late gestation of resistance index (RI; $P > 0.05$), pulsatility index (PI; $P > 0.05$), and blood flow ($P > 0.05$) or during early gestation of PI ($P > 0.05$), blood flow ($P > 0.05$), and heart rate (HR; $P > 0.05$). Ipsilateral uterine artery measurements during late gestation of RI ($P = 0.03$) increased as trial progressed. Ipsilateral uterine artery measurements for early gestation of RI ($P = 0.03$) were different over time. There was a treatment × time interaction for RI in the contralateral uterine artery in early gestation ($P = 0.04$), in which mares on E had increased RI on d 84. Total blood flow for mares in late or early gestation ($P = 0.52$ and $P = 0.74$, respectively) was not effected by treatment. Average HR ($P = 0.04$) increased over time and was decreased ($P = 0.01$) for all mares consuming arginine. Total blood flow for mares during 7 d after foaling ($P = 0.29$) was not effected by treatment. Whole uterine diameter during 7 d after foaling had a treatment × day interaction ($P < 0.01$), with mares receiving arginine prior to foaling having a smaller uterine diameter during 7 d after foaling compared with mares on either CON or E. Uterine fluid during 7 d after foaling was not affected by treatment ($P = 0.01$). Further research is continuing on arginine supplementation to gestating mares.

Key Words: arginine supplementation, equine nutrition, gestation
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333 Beta 1-3,1-6 glucan supplementation modulates the immune response of horses undergoing a glucocorticoid challenge.

R. D. Jacobs*[1], M. E. Gordon[2], M. J. Felippe[3], and R. H. Raub[4], [1]*Purina Animal Nutrition, Gray Summit, MO,* [2]*Purina Animal Nutrition, LLC, Gray Summit, MO,* [3]*Cornell University College of Veterinary Medicine, Ithaca, NY,* [4]*Hubbard Feeds, Mankato, MN.*

An appropriate immune response is critical to the maintenance of systemic health across species. Specifically related to the horse, pathogenic exposure, exercise or travel-induced stress, age, and metabolic status may play a role in the development of disease. Yeast-derived β-glucans have been implicated for their role in modulating the immune response. The objective of the study was to evaluate the potential for a beta 1-3,1-6 glucan supplement to modify the immune response in horses challenged through a glucocorticoid induced model of immune suppression. It was hypothesized that supplemented horses would have an improved immune response to a glucocorticoid challenge as demonstrated by immune cell proliferation and activation. Sixteen horses were randomly assigned to 1 of 4 groups: a base diet (Purina Strategy, fed at 0.5% BW) with no supplementation (CON; $n = 4$), base diet + 1 mg/kg BW β-glucan (LOW; $n = 4$), base diet + 2 mg/kg BW β-glucan ($n = 4$), and base diet + 4 mg/kg BW β-glucan (HIGH; $n = 4$). Horses were acclimated to the experimental rations for 2 d and then received supplementation for 15 additional days. Baseline blood samples were obtained following acclimation at d 0. A glucocorticoid challenge (0.1 mg/kg BW) was intravenously administered on d 15, and blood samples were obtained at 0, 8, 24, and 48 h after challenge. Blood samples were analyzed for neutrophil and lymphocyte counts, serum ACTH and cortisol levels, lymphocyte subpopulation distribution ($CD4^+$ T cells, $CD8^+$ T cells, B cells, and CD4:CD8 ratio), and leukocyte LFA-1 and MHC class II expression via flow cytometry. The data were analyzed via ANOVA to determine differences due to time and treatment and time × treatment interactions using the GLIMMIX procedure in SAS 9.4 (SAS Inst. Inc., Cary, NC). Glucocorticoid administration resulted in an increase in neutrophil numbers and decrease in lymphocyte numbers at 8 h after administration. Horses receiving β-glucan regardless of concentration displayed an increase in $CD8^+$ T cells at 8 h after glucocorticoid administration ($P < 0.01$). Horses in the LOW group displayed an increase in Mo LFA 1 at 8 h after challenge compared with horses in the CON and HIGH groups ($P < 0.01$). Taken together, these data indicate that the immune challenge was successful in suppressing the immune response and that β-glucan supplementation modulated the immune system during challenge. More research is necessary to fully elucidate the potential role of β-glucan supplementation on horse health.

Key Words: β-glucan, immune, nutritional additive
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334 Muscle metabolic effects of whole-body vibration in yearling horses.

C. S. Hyatt*, D. H. Sigler, and M. M. Vogelsang, *Texas A&M University, College Station.*

This study was designed to determine the effects of whole-body vibration (WBV) on select muscle metabolites in yearling horses on stall rest. Twenty yearling horses (17 ± 2 mo) were randomly divided into a split plot consisting of treatment ($n = 10$) and control groups. Horses were assigned uniform stalls at the Texas A&M University Horse Center and given ad libitum access to water and trace mineral salt blocks. Horses were fed a diet for 100% DE and 110% protein, calcium, and phosphorus of the NRC recommendations using coastal grass hay and pelleted concentrate. The treatment group completed WBV on a theraplate at 50 Hz for 30 min 5 d/wk for 120 d. Serum was collected via jugular venipuncture in lithium heparin tubes on d 0, 30, 60, and 120 before a 30-min turnout and after turnout (control group) or vibration (treatment group). A single blood draw was collected on Day 0 as a baseline value to serve as a covariant. Samples were analyzed by Texas A&M University Veterinary Medical Teaching Hospital Clinical Pathology Laboratory for blood urea nitrogen (BUN), aspartate aminotransferase (AST), gamma-glutamyltransferase (GGT), creatine kinase (CK), and lactic acid (LA) within 24 h of collection. Statistical analysis was completed using PROC MIXED of SAS 9.4, and significance was set to $P \leq 0.05$. Aspartate aminotransferase showed significant ($P < 0.05$) reduction across all collections from an average of 301.27 ± 11.42 units/L before treatment to 287.73 ± 11.42 units/L after treatment in control horses. Gamma-glutamyltransferase values for both groups showed a significant ($P < 0.05$) decline between collections, with the control group having a greater reduction. Creatine kinase values had a significant ($P < 0.05$) treatment × day interaction, with the control group value decreasing and the treatment group value increasing. Elevated CK and AST values are indicative of muscle degradation; LA presence in blood is an indicator of anaerobic conditions during high-intensity physical exertion. Gamma-glutamyltransferase is a biomarker used to exclude liver disease as a reason for elevated CK. Whole-body vibration of young horses on stall rest does not provide significant sustained muscular benefits. Further studies using uniform muscle biopsies and hourly blood

Table 334. Effect of vibration treatment in select blood metabolites: means across all collections

Response variable	Control	Vibration	SE	*P*-value
BUN	13.96 mg/dL	14.11 mg/dL	0.35	0.76
AST	294.5 units/L	303.13 units/L	11.23	0.59
GGT	21.2 units/L	21.31 units/L	0.43	0.86
CK	187.94 units/L	211.08 units/L	9.59	0.1
LA	8.6 mg/dL	8.57 mg/dL	0.28	0.95

collections after vibration are recommended for further understanding of the potential therapeutic applications of WBV.

Key Words: equine, muscle, vibration
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335 Oral administration of L-citrulline increases plasma concentrations of L-citrulline and arginine in horses.

J. A. Daniel*[1], M. G. Stockwell-Goering[1], A. R. Crane[1], C. M. Hernandez[1], D. F. Qualley[1], and B. K. Whitlock[2], [1]*Berry College, Mt. Berry, GA,* [2]*University of Tennessee, Knoxville.*

L-Citrulline can influence circulating concentrations of arginine and thus enhance nitric oxide (NO) generation to increase blood flow to tissue. This experiment was conducted to determine the dose response of horses to oral L-citrulline administration. The day before blood collection, mature gelding American Quarter Horses (n = 5; 521 ± 27 kg BW) were sedated with xylazine (0.5 mg/kg IV) and fitted with an IV catheter in the jugular vein. The horses were then placed in individual stalls and allowed water and bermudagrass hay ad libitum. The following day, 1 h prior to treatment administration, hay was removed. Blood samples were collected via jugular catheter at −60, −30, 0, 30, 60, 90, 120, 240, 360, 720, and 1,440 min relative to treatment administration. At time 0, horses received treatments of 0 (water), 0.018 (low), 0.09 (medium), or 0.18 g/kg (high) of L-citrulline dissolved in 200 mL of distilled water orally via nasal gastric tube, and hay was returned. Plasma was harvested and frozen at −20°C for analysis of L-citrulline and arginine concentrations in circulation by HPLC as well as nitrate and nitrite levels by colorimetric assay (Cayman Chemical, Ann Arbor, MI). Horses were administered a 7-d washout period, and the study was repeated until all horses received all treatments. Data were tested for effects of replication, dose, time, and dose × time interaction using procedures for repeated measures with JMP software (version 10; SAS Inst. Inc., Cary, NC). Circulating concentrations of L-citrulline were greater with the high dose compared with those of the water or low dose ($P < 0.04$). Circulating concentrations of arginine were greater with the high and medium dose than with the water or low dose ($P < 0.01$). There was also a dose × time effect on circulating concentrations of arginine such that the medium dose had greater arginine concentrations than the water at 120 min as well as the water and low dose at 240, 360 and 720 m. The high dose had greater arginine concentrations than the water and low dose at 120, 360, and 720 min. There was no effect of dose or dose × time interaction on plasma concentration of nitrate and nitrites ($P > 0.56$). These results indicate oral L-citrulline administration can alter circulating concentrations of both L-citrulline and arginine in horses.

Key Words: arginine, citrulline, horse
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336 The effect of dietary microalgae on American Association of Equine Practitioners lameness scores and whole blood cytokine gene expression following a lipopolysaccharide challenge in mature horses.

K. M. Brennan*[1], C. Whorf[2], L. E. Harris[1], and E. Adam[2], [1]*Alltech Inc., Nicholasville, KY,* [2]*University of Kentucky, Lexington.*

Joint inflammation in horses can lead to reduced performance and mobility whereas chronic joint inflammation can lead to permanent damage. In horses, an intra-articular injection of lipopolysaccharide (LPS) can be used to produce a model of moderate but transient joint inflammation. The objective of this study was to determine if daily supplementation with microalgae could alter the clinical assessment of physiological measures, lameness score, and whole blood mRNA levels of cytokines following an intra-articular LPS challenge in mature, healthy horses. Mature, mixed-sex Thoroughbred horses were assigned to 1 of 2 treatments (n = 5 per treatment), basal diet (CON) or basal diet plus 190 g/horse per day of a docosahexaenoic acid (DHA)-rich microalgae (ALG). After 60 d on diets, a localized inflammation was induced by injecting 1.0 ng of LPS diluted into lactated Ringers solution into the medial carpal joint of a randomly selected leg. Sampling occurred at 0 (before injection), 12, 24, and 48 h after injection. Cytokine mRNA levels in blood were measured using real-time PCR with β-actin as a housekeeping gene. At 0 h, American Association of Equine Practitioners (AAEP) lameness scores did not differ between treatments. Respiration rate and body temperature were not different at any time point. Heart rate tended to be higher ($P = 0.07$) at 12 h in CON horses than in ALG horses. At 12 h, AAEP lameness scores were higher ($P < 0.05$) in CON horses compared with ALG horses. At 24 and 48 h, lameness scores did not differ. At 0 h, mRNA levels of IL-1β tended ($P = 0.06$) to be lower in ALG horses compared with CON horses (0.92-fold and 1.27-fold, respectively). At 12 h, mRNA levels of IL-1B were increased ($P < 0.05$) in CON horses compared with ALG horses (1.71-fold and 1.2-fold, respectively). IL-8 mRNA levels tended ($P = 0.06$) to be higher in CON horses compared with ALG horses (2.50-fold and 1.62-fold, respectively). There were no differences in mRNA levels between treatments at 24 and 48 h. These results suggest that high-DHA dietary microalgae can mitigate increases in lameness scores, heart rate, and cytokine gene expression in a model of an intra-articular LPS challenge in horses

Key Words: algae, horse, inflammation
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Table 337. Effect of treatment on VFA (mM)

Item	Control	SCFP	Inulin	SEM
Acetate, m*M*	17.68^{b}	22.83^{a}	14.20^{c}	0.54
Propionate, m*M*	3.54^{b}	6.58^{a}	6.79^{a}	0.30
Butyrate, m*M*	4.09^{b}	5.80^{a}	5.58^{a}	0.13
Total VFA,[1] m*M*	25.51^{b}	35.58^{a}	26.76^{b}	0.93

[a–c] Means within a row without a common superscript letter differ by $P < 0.05$.

[1] Total VFA is the sum of acetate, propionate, butyrate, isobutyrate, isovalerate, and valerate.

337 *Saccharomyces cerevisiae* fermentation product, but not inulin, increases total volatile fatty acid production in an equine in vitro intestinal model.

J. M. Butler*, *Diamond V, Cedar Rapids, IA.*

A study was conducted to evaluate the effect of a *Saccharomyces cerevisiae* fermentation product (SCFP; Diamond V Original XPC) on in vitro VFA production using an equine fecal-inoculated intestinal model. Gas-tight culture tubes (50 mL) containing 0.3 g predigested Timothy grass hay and 0.15 g treatment (ground grain [Control], SCFP, or inulin) were inoculated with an anaerobic buffered homogenate of fresh equine manure and incubated for 24 h at 39°C. Five replicate samples were tested per treatment, and data were analyzed using the GLM model of JMP. Significance was defined as $P \leq 0.05$. The SCFP treatment significantly increased acetate, propionate, butyrate, and total VFA concentrations compared with the Control (Table 337; $P < 0.05$). Compared with inulin, the SCFP significantly increased acetate ($P < 0.05$) and total VFA ($P < 0.05$) with there were no differences in propionate or butyrate concentrations between the 2 treatments. Interestingly, inulin reduced acetate compared with the SCFP and Control ($P < 0.05$). In conclusion, in an in vitro intestinal model, *Saccharomyces cerevisiae* fermentation product increased acetate, propionate, butyrate, and total VFA production when using Timothy grass hay as a fermentation substrate.

Key Words: equine, in vitro, XPC
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LACTATION BIOLOGY

338 The effect of stage of lactation and parturition on galectin expression in cow blood.

E. Asiamah*, S. Adjei-Fremah, K. Ekwemalor, B. Osei, H. Ismail, and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

The aim of this study was to evaluate the expression of galectins in cow blood and to evaluate their modulation in periparturient cows at different stages of lactation. Galectins are multipotent, evolutionarily conserved, carbohydrate- binding proteins that, by crosslinking cell surface glycoconjugates, trigger a cascade of transmembrane signaling events such as cell activation, cytokine secretion, migration, and apoptosis There are 15 galectin protein subtypes that all share the shared characteristic of AA sequences and affinity for β-galactoside sugars. Galectins are known to have an impact on immunomodulation and are involved in uterine immunoregulation during pregnancy. The cows were grouped into 3 lactation periods (first, second, and third lactations). Blood was taken 2 wk close to parturition (close up) and 7 d after parturition(c+7) at Michigan State University dairy farm and shipped in Paxgene tubes for analysis. Total RNA was isolated, reverse transcribed to cDNA, and then used in real-time PCR experiments. With the use of Primer-Blast from the National Center for Biotechnology Information, specific primers for galectins 1, 2, 3, 4, 7, 8, 9, and 12 and β-actin (forward and reverse) were sequenced and used for this project. β-actin was used as internal control. Fold change in transcript abundance was calculated using the Livak method. In first-lactation cows, Galectin 1 was turned off after parturition. Galectin 2 was absent in both close up and c+7 cows. Galectins 3 and 7 were present in both close up and c+7 cows but levels did not change after parturition (fold change < 2). Galectin 4 was present before parturition but absent a week after parturition, Galectin 9 expression increased after parturition (fold change = 2). Galectin 12 was turned off after parturition. In the second-lactation cows, Galectin 1 was turned off after parturition, and Galectins 2, 3, 7, and 9 increased in transcription after parturition (fold change > 2). Galectins 1, 4, 8, and 12 were present before and after parturition but their fold changes were not significant. In third-lactation cows, all 8 galectins except for Galectin 8 were detected in both close ups and c+7 cows. Expression levels for these galectin genes did not change (fold change < 2). All genes tested were expressed in cow blood at varying levels. It is clear from this study that galectin gene expression is affected by stage of lactation and parturition. Further studies are needed to determine the factors that contribute to the different galectin expressions in cow blood during the periparturient period.

Key Words: galectins, gene expression, periparturient
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339 1H-NMR–based metabolomics identifies new predictive urinary biomarkers and highlights the pathobiology of ketosis in periparturient dairy cows.

B. N. Ametaj*[1], E. Dervishi[1], R. Mandal[2], D. S. Wishart[2], and G. Zhang[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to investigate metabolic fingerprints in the urine of preketotic cows as well as during and after the occurrence of disease and to identify newly predictive and diagnostic urine biomarkers that can be used to distinguish cows with ketosis from healthy controls (CON). In this study, proton nuclear magnetic resonance–based metabolomics was performed to analyze urine samples from 6 cows with ketosis and 20 CON cows at −8 wk, −4 wk, disease diagnosis, +4 wk, and +8 wk relative to parturition. Univariate (*t*-test or Wilcoxon–Mann–Whitney test; significance, $P < 0.05$) and multivariate analyses (permutation test; $P < 0.05$) and biomarker analysis (empirical; $P < 0.05$) were used to select metabolite sets for the noninvasive prediction and diagnosis of ketosis. All data analyses were performed using MetaboAnalyst 3.0. A total of 14, 21, 14, 2, and 2 differential metabolites between the 2 groups were identified at −8 wk, −4 wk, disease diagnosis, +4 wk, and +8 wk, respectively. VIP plots ranked the most significant differential metabolites that contributed to the onset and progression of ketosis. Specifically, concentrations of pantothenic acid (i.e., 3.42 vs. 1.44 μM/mM creatinine at −8 wk [$P = 0.04$], 2.9 vs. 1.26 μM/mM creatinine at −4 wk [$P = 0.01$], and 3.04 vs. 1.54 μM/mM creatinine at the disease week [$P = 0.03$]) and *myo*-inositol (i.e., 31.89 vs. 10.73 at −8 wk [$P < 0.01$], 26.35 vs. 9.17 at −4 wk [$P < 0.01$], and 21.85 vs. 13.26 at the disease week [$P = 0.04$]) were persistently greater in the urine of both preketotic and ketotic cows when compared with CON cows. Urinary concentrations of urea were lower in preketotic and ketotic cows versus the CON group at −8 wk (41.79 vs. 146.55; $P < 0.01$), −4 wk (44.51 vs. 144.3; $P = 0.04$), and the disease week (43.77 vs. 194.57; $P < 0.01$). Moreover, 2 promising biomarker models were identified for prediction of ketosis with an excellent level of sensitivity and specificity. Overall, multiple urine metabolite alterations were identified in preketotic, ketotic, and postketotic cows, which could be used as potential screening biomarkers as well as to better understand the pathobiology of disease and to develop new preventive treatments in the future.

Key Words: dairy cows, ketosis, urine 1NMR
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340 Metabolomics-based profiling identifies serum signatures that predict the risk of metritis in transition dairy cows.

G. Zhang[1], Q. Deng[1], R. Mandal[2], D. S. Wishart[2], and B. N. Ametaj[*1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]University of Alberta, Edmonton, AB, Canada.*

The objectives of this study were to identify metabolite signatures in the blood of dairy cows before, during, and after diagnosis of metritis that could be used to predict the risk of metritis in transition dairy cows. Direct-injection liquid chromatography–tandem mass spectroscopy was used to analyze serum samples collected from both 20 healthy (CON) and 6 metritic cows during −8 and −4 wk, at disease diagnosis, and +4 and +8 wk relative to parturition. Univariate (Wilcoxon–Mann–Whitney test by R; statistical significance: $P < 0.05$) and multivariate data (i.e., principal component analysis and partial least squares discriminant analysis [PLS-DA]; permutation test for the PLS-DA model, $P < 0.05$) analyses were conducted to examine alterations of serum metabolites throughout the progress of the disease. Results from univariate analysis indicated that cows with metritis experienced altered concentrations of multiple serum AA, glycerophospholipids, sphingolipids, acylcarnitines, and hexose during the entire experimental period. Principal component analysis and PLS-DA analyses showed clearly separated clusters for the 2 groups on the basis of measured serum metabolites during 5 time points. It is interesting to note that throughout the 17 wk of the study, several serum metabolites (e.g., PC aa C30:0, PC ae C30:1, SM [OH] C24:1, and SM C24:0) appeared to play a consistent role in distinguishing between the CON and metritic cows. For example, concentrations of PC ae C30:1 were consistently 2-fold greater in premetritic (i.e., mean of 3.10 μM [SEM 0.46] vs. mean of 1.32 μM [SEM 0.18; $P = 0.002$] at −8 wk prepartum and mean of 1.91 μM [SEM 0.22] vs. mean of 0.83 μM [SEM 0.10; $P = 0.001$] at −4 wk prepartum) and metritic (1.89 ± 0.23 vs. 0.90 ± 0.11; $P = 0.001$ at the disease week) cows compared with CON cows. Furthermore, 5 metabolic pathways (i.e., Lys degradation, biotin metabolism, Trp metabolism, Val–Leu–Ile degradation, and protein biosynthesis) were altered in both premetritic and metritic cows. These new findings give insights into the pathomechanism of metritis in dairy cows. Moreover, the area under the curve for 5 ROC curves was 0.995 (95% CI 0.945 to 1) at −8 wk, 0.992 (95% CI 0.938 to 1) at −4 wk, 0.988 (95% CI 0.913 to 1) at disease week, 1 (95% CI 1 to 1) at +4 wk, and 0.99 (95% CI 1 to 1) at 8 wk, respectively, which suggests that serum biomarkers identified have pretty accurate predictive, diagnostic, and prognostic abilities for metritis in transition dairy cows.

Key Words: dairy cows, metritis, serum metabolomics
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341 Comparison of five commercial kits for total RNA isolation including microRNA from three bovine milk fractions.

P. L. Dudemaine, B. Fomenky[*], A. Dutoit, L. Béjanin, and E. M. Ibeagha-Awemu, *Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada.*

Many different commercial kits are available for the extraction of total RNA including microRNA (miRNA) from different tissues and cells other than milk. Total RNA isolation from different milk fractions (fat, cells, and whey) is possible, but the challenge is having high yield and quality. The aims of this study were to 1) compare the performance of 5 commercial kits used for the extraction of total RNA including miRNA on bovine milk fractions (fat, whey, and somatic cells) and 2) determine which kit is most suitable for RNA extraction from each milk fraction. Milk samples were collected from 12 Holstein cows in mid lactation and separated into fractions (fat, whey, and cells) by centrifugation. The whey fraction was further subjected to lyophilization treatment. Total RNA including miRNA was extracted from each fraction using 5 different commercial kits E (Exiqon miRCURY RNA Isolation Kit), L (Life Technologies mirVana miRNA Isolation Kit), P (Promega ReliaPrep miRNA Cell and Tissue Miniprep System), Q (Qiagen miRNeasy Mini Kit), and Z (ZymoResearch Direct-Zol RNA MicroPrep). Following RNA extraction, samples were treated with deoxyribonuclease (DNase) and the quantity (ng/mL) and quality (RNA integrity number [RIN]) were assessed. Polymerase chain reaction amplifications covering different lengths of 1 highly expressed gene (LALBA) and 1 lowly expressed gene (FABP3) were done to further verify the integrity of mRNA extracted with kit Q from the fat fraction. Differences between means were calculated with the Student's *t*-test. Kit Q showed higher ($P < 0.05$) concentrations of total RNA after DNase treatment from the fat and whey fractions (102.50 ± 24.39 and 82.39 ± 9.98, respectively) than the other kits (55.42 ± 16.20 and 19.22 ± 2.42, respectively, for L; 21.27 ± 3.84 and 17.55 ± 3.87, respectively, for Z; 30.18 ± 5.46 and 43.45 ± 10.71, respectively, for E; and 44.85 ± 7.05 and 27.51 ± 6.88, respectively, for P). Deoxyribonucleic acid contamination was higher ($P < 0.05$) in the fat (kits L and Z) and whey (kit L) fractions compared with other kits. Overall RIN in the cell fraction was better for kit L (8.5) compared with the other kits. Full length transcripts were detected in fat, although fat RIN values (2 to 2.9) were low. Kit Q gave the best overall yield (approximately 90 ng/mL); meanwhile, kit L gave the best quality (RIN = 8.5) for the cell fraction. Similarly, kit Q and L had expected (better) small RNA pattern following Bioanalyzer results with small RNA Chip in cells, compared with the other kits. From our findings, kits Q and L should be preferred for the isolation of total RNA, including miRNA, from milk cells, whereas kit Q is the most reliable regardless of the fraction.

Key Words: commercial RNA isolation kits, microRNA fraction, total RNA isolation
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342 Injections of oxytocin in the early postpartum period affect the status of mammary tight junctions in swine.

C. Farmer*[1], H. Quesnel[2], M. Lessard[1], and C. H. Knight[3], [1]*AAFC, Sherbrooke R & D Centre, Sherbrooke, QC, Canada,* [2]*UMR, Saint Gilles, France,* [3]*University of Copenhagen, Copenhagen, Denmark.*

The goal of this project was to determine if injections of oxytocin in the early postpartum period affect the quality of mammary tight junctions, milk composition and immune status of sows and piglets. Post-parturient sows received im injections of either saline (CTL, n = 10) or 75 IU of oxytocin (OXY, n = 10). A total of 4 injections were given, the first 12 h after the end of farrowing, then twice per day (08:00 and 16:30). Milk samples were obtained following an iv injection of 20 IU of oxytocin before the first treatment injection, before the second injection, and 24 and 48 h after the last injection. Standard milk composition was measured as well as the Na/K ratio, and IGF-1, IgG and IgA concentrations. Blood samples were obtained from sows prior to the first, second and last milkings to measure prolactin, IGF-1, lactose, IgG and IgA concentrations. On d 5 of lactation, a blood sample was obtained from 3 piglets per litter to measure immunocrit and concentrations of IGF-1, IgG, IgA, and interleukin-2 (IL-2). The MIXED procedure of SAS was used for statistical analyses and means were compared using the Tukey's test. Circulating concentrations of prolactin, IGF-1, lactose and IgA in sows did not differ between treatments at any time ($P > 0.10$) but OXY sows had less IgG than CTL sows ($P < 0.01$) before the second oxytocin injection. There were also differences in milk composition before the second injection, with OXY sows having more IGF-1 ($P < 0.01$), DM ($P < 0.05$), protein ($P < 0.001$), energy ($P < 0.05$), and IgA ($P < 0.01$) and a greater Na/K ratio ($P < 0.001$) than CTL sows. These differences were not seen in the next 2 milk samples, except for protein and IgA that still tended ($P < 0.10$) to be greater in OXY vs CTL sows 24 h (for protein) and 48 h (for IgA) after the last injection. Values for immunocrit, IGF-1, IgG and IgA in piglet blood did not differ between treatments ($P > 0.10$), whereas concentrations of IL-2 tended to be greater ($P < 0.10$) in OXY compared with CTL piglets. Data demonstrate that injecting oxytocin in the early postpartum period increases leakiness of the mammary tight junctions, improves composition of early milk, and potentially affects immune status in neonatal piglets.

Key Words: oxytocin, sows, mammary tight junctions
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343 Effect of once daily milking on mammary transcriptome and cell turnover in dairy goat.

M. Boutinaud*[1], V. Dris-Kerdreux[2], S. Wiart[1], J. M. Aubry[2], D. Laloe[3], F. Jaffrezic[3], E. Devinoy[3], and L. Galio[3], [1]*UMR 1348 PEGASE, Agrocampus Ouest, INRA, Saint-Gilles, France,* [2]*UMR 1348 PEGASE, Agrocampus Ouest, INRA, Saint Gilles, France,* [3]*INRA UMR 1313 GABI, Jouy en Josas, France.*

Once-daily milking is known to modify cell number and activity in the bovine mammary gland. However, in goats, the effect of once-daily milking on mammary cell death is controversial. To assess the effect of once-daily milking on mammary transcriptome and cell turnover and the effect of the duration of once-daily milking, 10 goats producing 2.5 kg of milk per day at 100 DIM were divided into 2 groups. All goats were twice daily milked during a pre-experimental period of 2 wk. Then, the goats were once daily milked for the 3 following weeks. Mammary biopsy samples were collected at d −1 and 7 after the start of once-daily milking for one group of 5 goats and at d −1 and 21 for a second group of 5 goats. Cell apoptosis and proliferation rates were analyzed in mammary tissue by immunohistological analyses after TUNEL and PCNA staining, respectively. Ribonucleic acid was extracted from mammary tissues. A transcriptomic analysis using the Agilent Bovine 4x44k microarrays has been performed to compare the effect of once-daily milking on mammary transcript profiles. Data were normalized and statistical significant raw *P*-values were adjusted for multiple comparisons using the Benjamini–Hochberg procedure. A similar reduction in milk yield (−19%) was observed in both groups of goats during once-daily milking compared with twice-daily milking. Cell apoptosis was higher during once-daily milking than during twice-daily milking for both groups of goats ($P < 0.05$) whereas cell proliferation did not vary ($P = 0.27$). The transcriptomic analysis showed a differential gene expression of 4,039 transcripts, 2,238 and 1,801 transcripts up- and downregulated, respectively, by once-daily milking compared with twice-daily milking. More than 1,000 transcripts were commonly regulated between the 2 groups of goats. IPA analysis showed that these transcripts were part of networks associated with DNA replication, cellular growth and proliferation, and cell-to-cell signaling and interaction in both groups of goats. RT-qPCR analysis of 11 genes confirmed the differential gene expression with a downregulation of genes involved in milk synthesis and an upregulation of genes involved in cellular cycle and apoptosis. These results showed that once-daily milking induce cell turnover in goat mammary tissue, with a small impact of time.

Key Words: cell turnover, dairy goat, transcriptome
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344 Supplementing different forms of l-methionine and acetate alters the expression patterns of messenger RNA, proteins, and metabolites related to milk protein synthesis and energy metabolism in bovine mammary cells.

J. R. V. Conejos*[1], S. W. Jeon[1], M. H. Bae[1,2], J. E. Lee[3], B. S. Lee[3], J. S. Park[3], J. O. Moon[3], and H. G. Lee[1,2], [1]*Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea (South),* [2]*Team of an Educational Program for Specialists in Global Animal Science, Brain Korea 21 Plus Project, Konkuk University, Seoul, Republic of Korea (South),* [3]*CJ CheilJedang Research Institute of Biotechnology, Suwon, Republic of Korea (South).*

N-Acetyl-l-methionine (NALM) can be used as a rumen-protected methionine, which is cleaved into l-Met and acetate in the small intestine or liver, with high bioavailability. This study was conducted to compare the efficacy of NALM and its digested forms on milk protein synthesis using an immortalized bovine mammary epithelial cell line (MAC-T cell); l-Met, conjugated l-Met, and acetate (NALM) and the nonconjugated form (l-Met + acetate; digested form of NALM). Then, the mechanism of milk protein synthesis was also elucidated through omics analysis. The l-Met + acetate group showed the highest milk protein concentration in the media ($P < 0.05$) as well as in the total protein ($P < 0.05$) and also showed the highest beta casein ($P < 0.05$) and S6K1 ($P < 0.05$) mRNA expression levels compared with l-Met and NALM. On the other hand, the l-Met–treated group showed the highest mTOR gene expression level compared with the NALM and l-Met + acetate groups ($P < 0.05$). A total of 39 upregulated and 77 downregulated proteins, 62 upregulated and 80 downregulated proteins, and 50 upregulated and 81 downregulated proteins were observed in l-Met–, NALM-, and l-Met + acetate–treated groups, respectively. Interestingly, based on metabolic pathway analysis, in the l-Met + acetate–treated group, the ATP synthesis, cell cycle, ubiquitin proteasome, and TGF-β signaling pathways were stimulated, but not in the NALM-treated group. On the other hand, in the NALM- and l-Met–treated groups, the PI3 kinase and pyruvate metabolism pathways were stimulated, but not in the l-Met + acetate–treated group, indicating that acetate group conjugated in NALM cannot be utilized as an energy source in MAC-T cell, and consequently resulting cells to produce energy via the pyruvate pathway. Metabolite analysis showed, in the NALM-treated group, the increase of 12 metabolites and the decrease of UMP ($P < 0.05$). On the other hand, the l-Met + acetate–treated group showed the increase of 13 metabolites and the decrease of IMP and pantothenate ($P < 0.05$). In summary, the l-Met + acetate–treated group showed better performance in the expression of the beta casein and S6K1 mRNA, the stimulation of pathways and metabolites involved in ATP synthesis, and the increase of other metabolites related to energy production. As a result, the l-Met + acetate–treated group showed higher protein concentration ($P < 0.05$) in the MAC-T cells compared with other groups, possibly suggesting that digested forms of NALM (l-Met and acetate) can be effectively utilized for the increase of milk protein synthesis in the mammary gland after absorption and digestion of NALM in small intestine or liver.

Key Words: acetate, l-methionine, milk protein
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345 Feed restriction increases mammary epithelial cell exfoliation rate in dairy cows.

L. Herve*, M. Veron, P. Lamberton, S. Wiart, P. Debournoux, S. Philau, C. Mustière, H. Quesnel, and M. Boutinaud, *UMR 1348 PEGASE, Agrocampus Ouest, INRA, Saint-Gilles, France.*

In dairy cows, feed restriction is known to decrease milk yield by reducing the number of mammary epithelial cells (MEC) in the udder, due to an increased rate of MEC apoptosis. The exfoliation of MEC from the mammary epithelium into milk is another process that could participate in regulating MEC number. We hypothesized that the decreased number of MEC in the udder of feed-restricted cows might also result from an increase in MEC exfoliation rate. Nineteen Holstein dairy cows producing 40 ± 0.7 kg at 80 ± 4 DIM were divided into 2 groups, control ($n = 9$) and feed restricted ($n = 10$). Ad libitum DMI was recorded during a pre-experimental period of 2 wk. For 29 d (period 1), cows were fed either 100 or 80% of their DMI measured during the pre-experimental period. Then, all cows were fed ad libitum for 35 d (period 2). Feed intake and milk production were recorded daily. Blood and milk samples were collected once during the pre-experimental period and 5, 9, and 27 d after the beginning of periods 1 and 2. Mammary epithelial cells were purified from milk samples using an immunomagnetic method. Lipid mobilization was assessed by plasma NEFA concentration. Mammary epithelium integrity was assessed by plasma lactose concentration, milk Na, and milk Na:K ratio. Mammary tissue samples were collected by biopsy at the end of each period in order to analyze the rate of cell proliferation and apoptosis. Data were analyzed using the mixed procedure of SAS. Compared with control feeding, feed restriction induced a decrease in DMI by 20% ($P < 0.001$), an increase in plasma concentration of NEFA ($P < 0.001$), and a 3-kg/d milk yield loss ($P < 0.001$) but had no effect on the rate of proliferation and apoptosis in the mammary tissue. Daily MEC exfoliation rate was 65% greater in feed-restricted cows compared with control cows ($P < 0.05$). Feed restriction had no effect on plasma lactose concentration and milk Na:K ratio but increased milk Na concentration, which does not allow conclusions about the integrity of the mammary epithelium. In period 2, when all cows returned to ad libitum feeding, no significant difference was observed on DMI, milk yield, MEC exfoliation rate, and mammary epithelium integrity between feed-restricted and control cows. These results show that the exfoliation process could play a role in regulating the number of MEC in the udder of dairy cows during a feed restriction without a carryover effect on their milk production.

Key Words: dairy cow, feed restriction, mammary epithelial cell exfoliation
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346 Impact of arterial nutrient concentration on the uptake of nutrients by the mammary glands in sows.

U. Krogh*[1] and P. K. Theil[2], [1]*Aarhus University, Foulum, Denmark,* [2]*Aarhus University, Tjele, Denmark.*

The high nursing frequency observed in sows results in a relatively constant demand for nutrients for milk synthesis, whereas the supply of nutrients in arterial blood is greatly affected by the time relative to feeding. Therefore, characterization of the mammary uptake of nutrients at different times relative to feeding could provide a better understanding of how macronutrients are utilized for milk synthesis. The objective was to characterize the use of nutrients by the mammary glands by measuring arterial concentrations and mammary arterial–venous differences (AV-diff) of nutrients in catheterized sows at different times relative to feeding. Indwelling catheters were surgical inserted in the femoral artery and the cranial mammary vein of 8 multiparous sows at d 76 ± 2 of gestation. Eight sets of blood samples were simultaneously sampled from the catheters in hourly intervals from 0.5 h before to 6.5 h after feeding at d 17 (range 15 to 19) of lactation. Plasma samples were analyzed for glucose, NEFA, triglycerides (TG), lactate, and essential AA. Arterial concentration of NEFA and TG decreased postprandially ($P < 0.05$), whereas all other studied metabolites showed a postprandial increase, although leucine ($P = 0.06$) and histidine ($P = 0.11$) did not reach significance. Mammary AV-diff of glucose (1.4 mmol/L; $P = 0.38$) and TG (49 µmol/L; $P = 0.39$) were not affected by time after feeding, suggesting that the liver and other organs were capable of buffering mammary uptake after feeding. In contrast, the AV-diff for lactate, lysine, methionine, and threonine ($P < 0.001$) increased by 20 to 40% postprandially compared with preprandial levels, whereas a postprandial decrease in AV-diff was observed for NEFA ($P < 0.001$). Arterial concentrations were positively correlated to the AV-diff for NEFA ($r = 0.88$, $P < 0.001$), lactate ($r = 0.78$, $P < 0.001$), methionine ($r = 0.61$, $P < 0.001$), threonine ($r = 0.60$, $P < 0.001$), leucine ($r = 0.56$, $P < 0.001$), and lysine ($r = 0.46$, $P < 0.001$), suggesting that the arterial concentration of these AA was, to some extent, important for the transfer into the mammary glands. Collectively, the mammary uptake of lactate, NEFA, lysine, methionine, and threonine changed with time after feeding and were associated with arterial concentrations, whereas glucose, TG, and the remaining essential AA seemed to be independent of the arterial supply.

Key Words: colostrum, mammary gland, nutrient metabolism
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347 Prolactin, prolactin receptor, and adiponutrin messenger RNA abundances in mammary extraparenchymal tissue of gilts are affected by body condition.

M. F. Palin*[1], C. R. Amaral Duarte[2], M. Comi[3], and C. Farmer[1], [1]*Agriculture and Agri-Food Canada, Sherbrooke R & D Centre, Sherbrooke, QC, Canada,* [2]*Faculdade de Ciências Agrárias, Biológicas e da Saúde, Universidade do Estado de Mato Grosso, Tangará da Serra, Brazil,* [3]*Dipartimento VESPA, Universitá Studi Milano, Milano, Italy.*

Study objectives were 1) to determine if different body conditions in late gestation, which were maintained from mating to d 110 of gestation, affect the mRNA abundance of adipokines and their receptors in mammary extraparenchymal tissue and 2) to look for associations between mammary gland composition variables and the gene expression of selected adipokines in extraparenchymal tissue. A total of 45 gilts were selected at mating according to their backfat thickness: low (LBF; 12–15 mm; $n = 14$), medium (MBF; 17–19 mm; $n = 15$), and high (HBF; 22–26 mm; $n = 16$) backfat. Throughout the gestation period, LBF, MBF, and HBF gilts received different amounts of a conventional diet to maintain similar backfat thicknesses from mating until the end of gestation. Gilts were slaughtered on d 110 of gestation. One side of the udder was dissected to evaluate mammary gland composition. Extraparenchymal tissue (mammary fat) was collected from the fourth teat of the other side to measure mRNA abundance of adipokines (*ADIPOQ*, *LEP*, *PNPLA3*, and *PRL*) and their receptors (*ADIPOR1*, *ADIPOR2*, *LEPR-LF*, and *PRLR-LF*) using real-time PCR amplifications. Statistical analyses were performed with the mixed procedure of SAS using a univariate model (3 levels), and means were compared with a Tukey test. PROC CORR of SAS was used for correlation analyses. In the extraparenchymal tissue, there was a greater *PRL* mRNA abundance in HBF gilts than in LBF and MBF gilts ($P < 0.05$). The *PNPLA3* mRNA abundance was lower for HBF gilts than for MBF gilts ($P < 0.05$), and lower *PRLR-LF* mRNA abundance was found in LBF gilts than in HBF gilts ($P < 0.05$). In the overall gilt population, there was a negative correlation between the *PNPLA3* mRNA abundance in extraparenchymal tissue and the percentage of parenchymal tissue fat ($r = -0.30$, $P < 0.05$) and a positive correlation with the percentage of protein ($r = 0.32$, $P < 0.05$). The *PRL* mRNA abundance in the extraparenchyma positively correlated with percent parenchymal DM ($r = 0.42$, $P < 0.01$) and percent fat ($r = 0.37$, $P < 0.05$). A negative correlation was observed between *PRL* mRNA abundance and the percent protein in parenchymal tissue ($r = -0.31$, $P < 0.05$). Maintaining different backfat thicknesses from mating to the end of gestation affected *PNPLA3*, *PRL*, and *PRLR-LF* gene expression in mammary extraparenchymal tissue. Correlation analyses show a relationship between *PNPAL3* and *PRL* gene expression in extraparenchymal tissue and mammary gland composition at the end of gestation.

Key Words: adipokines, gene expression, mammary composition
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348 Effect of feed restriction and nature of forage on the mammary exfoliation rate in dairy cows.

L. Herve*, M. Veron, E. Vanbergue, H. Quesnel, C. Hurtaud, and M. Boutinaud, *UMR 1348 PEGASE, Agrocampus Ouest, INRA, Saint-Gilles, France.*

Diet, in term of quantity and quality, is one of the main factors that affect milk yield and composition in dairy cows. The mammary epithelial cell (MEC) exfoliation process, together with the cell proliferation/apoptosis balance, participates in regulating the MEC number in the mammary gland and thus milk yield. Little is known about the effect of diet in the regulation of MEC number in the mammary tissue. This trial aimed to investigate the effect of feeding level and nature of forage on the MEC exfoliation rate. Sixteen multiparous dairy cows producing 37.0 ± 0.68 kg at 99 ± 4.6 DIM were divided into 4 groups of 4 cows each according to their diet. After a pre-experimental period of 3 wk, cows were fed either 100 or 75% of their ad libitum DMI with diets based on corn silage or conserved grass for 3 wk (Period 1). The feeding level was then reversed for the 3 following weeks (Period 2). Milk samples were collected at the end of the pre-experimental period and 15 d after the beginning of each period for milk MEC purification using an immunomagnetic method to assess the daily MEC exfoliation rate. The percentage of apoptotic MEC in milk was determined by flow cytometry after annexin V/propidium iodide labeling. Mammary epithelium integrity was assessed by milk Na:K ratio determination. Data were analyzed using the mixed procedure of SAS. After 15 d of treatment, feed restriction decreased milk yield by 10% ($P < 0.05$) without affecting the MEC exfoliation rate. The Na:K ratio was greater with feed restriction, suggesting a loss of mammary epithelium integrity ($P < 0.05$). The nature of forage affected neither milk yield nor mammary epithelium integrity, but the daily MEC exfoliation rate was greater in cows fed with the corn silage–based diet ($P < 0.01$). When cows were fed 100%, the percentage of apoptotic cells among exfoliated MEC was lower with the corn silage–based diet than with conserved grass–based diet ($P < 0.05$). These results show that the MEC exfoliation rate was not affected by a 15-d feed restriction whereas it was affected by the nature of forage. Mammary epithelial cell exfoliation rates did not vary along with variations of milk yield. The effect of the duration of feed restriction on the MEC exfoliation rate and the effect of the nature of forage on the cell proliferation/apoptosis balance need to be investigated further.

Key Words: dairy cow, diet, mammary epithelial cell exfoliation
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MEAT SCIENCE AND MUSCLE BIOLOGY

349 Duration of high-concentrate diet prior to forage finishing I: Effects on animal performance, glucose/insulin levels, carcass traits, and tissue fatty acid composition of beef steers.

B. M. Koch*, J. L. Britt, L. E. Koch, W. C. Bridges, N. M. Long, and S. K. Duckett, *Clemson University, Clemson, SC.*

Thirty-two Angus-influenced steers (255 ± 15.1 kg) were used to evaluate the effect of duration of exposure to a high-concentrate–based diet after weaning prior to forage finishing on performance, plasma insulin and glucose levels, carcass characteristics, and tissue fatty acid composition. Steers were randomly assigned to 1 of 4 feeding treatments: 0 d on high concentrate (CNT), 40 d on high concentrate, 80 d on high

concentrate (80D), and 120 d on high concentrate (120D) followed by finishing on pasture to 485 kg. The high-concentrate diet consisted of cracked corn, corn gluten feed, chopped hay, and mineral supplement; high-quality pasture included winter annuals (ryegrass and oats), alfalfa, and nontoxic tall fescue. Weight and blood samples were collected at 21-d intervals. At 24 h postmortem, carcass characteristics and a rib section (11th–12th rib) from the left side was collected for proximal analysis and a section of subcutaneous adipose tissue collected for histology cell sizing. Due to harvesting steers at equal final BW, there was no difference for total gain or total ADG ($P > 0.19$); however, HCW and dressing percentage linearly increased ($P < 0.031$) with time on concentrate. There was no difference across treatments for rib eye area or yield grade ($P > 0.11$), but 12th-rib fat thickness and KPH fat quadratically and linearly increased ($P < 0.015$), respectively. Marbling score and total lipid of the longissimus dorsi (LM) linearly increased with time on concentrates ($P < 0.001$). This increase in lipid within the LM resulted in a linear decrease with increased time on concentrate for moisture ($P < 0.001$). Crude protein content of the LM quadratically differed ($P = 0.001$) and was the greatest in steers from 80D whereas 120D had the least. Within the LM, there was no difference across treatments for SFA or MUFA ($P > 0.27$) whereas *n*-6 PUFA quadratically differed ($P = 0.002$), being the greatest at 80D, and *n*-3 PUFA linearly decreased as time on concentrates increased ($P < 0.001$). These changes in *n*-6 PUFA and *n*-3 PUFA resulted in a linear increase of the *n*-6:*n*-3 PUFA ratio as time on concentrate increased ($P < 0.001$). There was no difference across treatments for plasma glucose concentration ($P > 0.64$), whereas there was an interaction between treatment and time for plasma insulin concentration ($P = 0.012$), with a quadratic difference across treatments, with the greatest levels occurring in the CNT and 120D treatments. The consumption of a high-concentrate–based diet immediately after weaning increases dressing percentage, carcass weight, and marbling deposition in cattle subsequently finished on forages.

Key Words: glucose tolerance, grass finished, high-concentrate diet
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350 Duration of high-concentrate diet prior to forage finishing II: Effects on glucose and insulin levels under challenge, and gene expression of beef steers.

B. M. Koch*, J. L. Britt, L. E. Koch, W. C. Bridges, N. M. Long, and S. K. Duckett, *Clemson University, Clemson, SC.*

Twelve Angus-influenced steers (227 ± 10.1 kg) were used to evaluate the effect of duration of exposure to a high-concentrate–based diet after weaning prior to forage finishing on plasma insulin and glucose levels under challenge and lipogenic gene expression. Steers were randomly assigned to 1 of 4 feeding treatments—0 d on high concentrate (CNT), 40 d on high concentrate, 80 d on high concentrate, and 120 d on high concentrate (120D)—followed by finishing to 485 kg on pasture. The high-concentrate diet consisted of cracked corn, corn gluten feed, chopped hay, and mineral supplement, whereas high-quality pasture included winter annuals (ryegrass and oats), alfalfa, and nontoxic fescue. Weights and blood samples were collected at 21-d intervals. Muscle biopsies taken from the right longissimus dorsi (LM) when steers started the feeding period and at their respective days on treatment. Intravenous glucose tolerance tests (IVGTT) were performed at 40-d intervals until 160 d. At 24 h postmortem, carcass characteristics and a rib section (11th–12th rib) from the left side was collected for proximate analysis. There was an interaction between treatment and time for plasma glucose concentration ($P = 0.03$), whereas there was no interaction and no difference across treatments for plasma insulin concentration ($P > 0.20$). There was no difference across treatments for initial glucose concentration during IVGTT ($P = 0.86$) whereas adjusted area under the curve for glucose concentration linearly decreased as treatment increased ($P = 0.022$), with CNT and 120D being significantly different at 120 d ($P = 0.008$). There was no difference across treatments for initial insulin concentration during IVGTT ($P = 0.46$), however, 120D had a greater initial insulin concentration than CNT at 120 d ($P = 0.024$). Adjusted area under the curve for insulin was not different across treatments ($P < 0.40$). Gene expression of acetyl CoA carboxylase, stearoyl CoA desaturase, and glucose transporter 4 were not different ($P > 0.21$) between CNT and 120D at 120 d. Fatty acid synthase mRNA expression increased 3.2-fold ($P < 0.05$) for 120D compared with CNT and the ΔCT values for FASN correlated (−0.80; $P < 0.017$) to the quantity of de novo lipogenesis products within the LM at the time of harvest. The consumption of a high-concentrate–based diet immediately after weaning may alter insulin and glucose dynamics and lipogenic gene expression of cattle finished in a pasture-based system.

Key Words: gene expression, glucose tolerance, grass finished
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351 Fatty acid composition and expression of lipid metabolism-related genes in longissimus dorsi muscle of grazing beef heifers offered supplements containing either safflower oil or ruminally protected fish oil.

A. P. Moloney*[1], F. M. Cicognini[2], and S. M. Waters[3], [1]*Teagasc, Grange, Dunsany, Meath, Ireland,* [2]*Institute of Food Science and Nutrition, Faculty of Agriculture, Università Cattolica del Sacro Cuore, Piacenza, Italy,* [3]*Animal and Bioscience Research Department, Teagasc Grange, Dunsany, Meath, Ireland.*

There is increasing interest in enhancing the nutritional value of ruminant-derived foods for human consumption. Beef from grass-fed cattle contains more fatty acids considered to benefit

human health, including the *n*-3 fatty acids eicosapentaenoic acid (EPA; 20:5*n*-3), docosahexaenoic acid (DHA; 22:6*n*-3), and *cis*-9, *trans*-11 CLA, than beef from concentrate-fed cattle. The objective of this study was to determine the effect of long-term supplementation of grazing beef heifers with rumen protected fish oil (PFO) or safflower oil (SAFF) on longissimus dorsi muscle concentrations of EPA + DHA and CLA, respectively, and associated effects on the expression of selected genes coding for proteins involved in muscle lipid metabolism. Spring-born Aberdeen Angus × Friesian (AA; $n = 24$) and Belgian Blue × αFriesian (BB; $n = 24$) heifers were assigned ($n = 8$/breed), at 4 mo old, to either a standard grass-based production system (CON) or, within that system, to supplementation with the experimental oils. Heifers were slaughtered from pasture at 21 mo of age and muscle tissue was collected. The fatty acid profile was measured by gas chromatography whereas mRNA was extracted and gene expression analyzed by RT-qPCR. The proportion of EPA + DHA in muscle was 4.6, 2.5, 19.0, 8.0, 4.2, and 24.1 g/kg (SED 1.77) fatty acids for AACON, AASAFF, AAPFO, BBCON, BBSAFF, and BBPFO, respectively. The corresponding proportion of CLA was 8.6, 27.0, 6.1, 8.0, 23.4, and 5.5 g/kg (SED 1.28) fatty acids. Expression of acetyl-CoA carboxylase and stearoyl-CoA desaturase (SCD) genes was higher in BB ($P = 0.013$ and $P = 0.055$, respectively), whereas fatty acid synthase (FAS) gene expression was higher in AA ($P = 0.007$). FAS and SCD expression were increased by PFO supplementation ($P = 0.006$ and $P = 0.074$, respectively) compared with CON. There was an interaction between breed and diet for peroxisome proliferator-activated receptor α (PPARα; $P = 0.006$) and adiponectin (ADIPOQ; $P = 0.055$) gene expression; PPARα expression was reduced by PFO in AA and increased in BB, and ADIPOQ expression was increased by SAFF in AA and deceased in BB. The expression of delta-6-desaturase, delta-5-desaturase, fatty acid elongase 5, activated protein kinase α, G protein-coupled receptor, adipose differentiation-related protein, sterol regulatory element-binding protein, peroxisome proliferator-activated receptor γ, statin 5 and glucose transporter 4 genes did not differ. In conclusion, provision of PFO to heifers for 17 wk enhanced muscle EPA + DHA content, whereas provision of SAFF effectively increased muscle CLA. In general, the effects of oil supplementation on gene expression were small, with some evidence of breed specificity.

Key Words: beef heifers, fatty acids, gene expression
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352 Two-year study comparing high-energy forage and feedlot finishing impact on beef consumer acceptability and sensory characteristics in the Upper Midwest.

R. M. Martin*[1], J. E. Rowntree[1], J. P. Schweihofer[2], J. B. Harte[1], and S. Cho[1], [1]*Michigan State University, East Lansing,* [2]*Michigan State University Extension, Bad Axe.*

The 2-yr study determined consumer acceptability and sensory attributes of beef longissimus thoracis steaks from steers grazing high-energy forages vs. a conventional feedlot diet. Steaks were from 62 steers fed 1 of 4 treatment diets: mixed pasture (MIX), simple cereal grain/brassica mixture (SIMP), complex cereal grain/brassica mixture (COMP), and conventional feedlot ration (FLOT). Steers grazed perennial mixed pasture prior to treatment assignment. Steers were fed the FLOT ($n = 8$/yr) diet for 92 (yr 1) and 128 d (yr 2). Steers in the MIX ($n = 8$/yr), SIMP ($n = 8$ in yr 1 and $n = 6$ in yr 2), and COMP treatments ($n = 8$/yr) grazed respective pastures for 76 (yr 1) and 70 d (yr 2). All steers were slaughtered on the same day each year. Marbling scores were evaluated 48 h postmortem. Carcasses were aged 7 d prior to fabricating 2.54-cm steaks. Vacuum-packaged steaks were aged an additional 8 d and frozen (−20°C) until evaluation for Warner–Bratzler shear force (WBSF). Consumer panelists ($n = 106$ in yr 1 and $n = 107$ in yr 2) evaluated cooked steaks aged 15 d for flavor, texture and firmness, juiciness, and overall acceptability using a 9-point hedonic scale (1 = dislike extremely and 9 = like extremely). Sensory characteristics and consumer acceptability data were analyzed using PROC MIXED (SAS 9.4). Marbling scores of steaks from FLOT (541) were greater ($P < 0.01$) compared with those from MIX (436), SIMP (428), and COMP (431). There was a treatment effect ($P < 0.05$) for WBSF, where steaks from FLOT steers (3.12 ± 0.34 kg) were more tender compared with those from MIX (4.01 ± 0.34 kg), SIMP (3.94 ± 0.34 kg), and COMP steers (3.99 ± 0.34 kg). Panelists preferred ($P < 0.01$) the texture and firmness of steaks from steers fed the FLOT (7.09) diet compared with steaks from steers fed the SIMP (6.73), MIX (6.30), and COMP diets (6.43). There was a preference ($P < 0.01$) for the juiciness and overall acceptability of steaks from steers fed the FLOT (6.48 and 6.76) and SIMP diets (6.34 and 6.66) compared with steaks from steers fed the MIX (6.09 and 6.24) and COMP diets (5.94 and 6.23). There was a year effect ($P < 0.05$), where yr 2 was preferable to yr 1 for overall acceptability (6.59 vs. 6.35) and flavor (6.67 vs. 6.39) and there was no treatment difference ($P > 0.05$) for flavor. Because there was no year effect for marbling score and WBSF, the basis for year differences is inconclusive. Results indicate that steaks from steers finished on FLOT or SIMP had greater overall acceptability when compared with other treatments.

Key Words: consumer panel, forage finished, sensory
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353 A plant extract with manganese, Vali MP, promotes myotube hypertrophy in mouse C2C12 skeletal muscle cells.

M. Y. Park*[1], S. W. Choi[1,2], S. W. Jung[2], and K. Y. Whang[1], [1]*Department of Biotechnology, Graduate School, Korea University, Seoul, Republic of Korea (South),* [2]*CTCBIO INC., Seoul, Republic of Korea (South).*

As animals grow, rate of fat deposition accelerates once protein growth reaches its genetic potential and results in decreased feed efficiency. Use of β-adrenergic agonists was considered as one of the strategies to improve lean growth via nutrient repartitioning. However, its use has been disputed due to residues in the meat that might cause detrimental effects. As an alternative, many phytogenics have been developed including Vali MP. Vali MP is a mixture of plant extract with manganese. In previous studies, dietary supplementation of Vali MP to finishing pigs has been shown to reduce body fat and increase lean growth. It was also demonstrated that adipogenesis was decreased in 3T3-L1 preadipocytes by Vali MP. However, its effect on skeletal muscle has not yet been investigated. Therefore, the present study was conducted to examine the effects of Vali MP on skeletal muscle hypertrophy in vitro by using mouse C2C12 myotubes. C2C12 myoblasts were differentiated into myotubes for 8 d, and then Vali MP solution (10% dissolved in PBS) was supplemented for the next 4 d at final concentration of 0 (CON), 1, 10, or 100 ppm. Myotubes were stained by the Giemsa method for quantification of myotube width as a hypertrophic marker. Complementary DNA was constructed for mRNA levels of the genes, and protein was extracted for western blot analysis. Myotube width was increased by 20% in the 10-ppm Vali MP treatment but it was reduced by 40% in the 100-ppm Vali MP treatment compared with that of the CON ($P < 0.01$). At the mRNA level, *MuRF1*, one of the upregulated markers during loss of skeletal muscle mass, was suppressed by Vali MP treatment at all doses ($P < 0.05$). Also, mRNA level of the atrophy genes *FoxO1* and *FoxO3* was 0.73-fold and 0.52-fold lesser less at the 1-ppm Vali MP and 0.75-fold and 0.70-fold less at 10-ppm Vali MP treatments compared with CON ($P < 0.01$). Protein expression level of phosphorylated p70 ribosomal S6 kinase to total p70 ribosomal S6 kinase (p-S6K/total S6K), which is involved in protein synthesis pathway, was not changed by Vali MP treatment. However, ratios of phosphorylated FoxO3a to total FoxO3a (p-FoxO3a:FoxO3a ratio), a marker for protein degradation, were decreased in the cells treated with Vali MP at 10 and 100 ppm by 0.75-fold and 0.72-fold, respectively ($P < 0.05$). In summary, Vali MP has exhibited hypertrophic effects on mouse C2C12 myotubes via inhibiting protein degradation rather than stimulating protein synthesis pathway.

Key Words: lean growth, protein degradation, Vali MP
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354 Betaine enhances skeletal muscle cell lipid accumulation by promoting adipogenic genes expression.

W. Wu*, *College of Animal Science, Zhejiang University, Hangzhou, P.R. China.*

Meat quality and the value of meat are dependent, to a great extent, on intramuscular fat. Therefore, enhancing intramuscular fat accumulation is particularly important. Betaine is a widely used feed additive and appears to increase intramuscular fat in growing pigs. However, the underlying regulatory mechanism of betaine on intramuscular fat deposition remains elusive. Here, we demonstrated that betaine enhanced C2C12 cellular lipid accumulation through regulating the expression of lipid metabolism related genes. We found 10 m*M* betaine treatment significantly upregulated lipid content in C2C12 after adipogenic differentiation. Next, we found that after 24 h of treatment, betaine could markedly enhance C2C12 cellular lipid accumulation, other than 12 or 48 h. Subsequently, we analyzed the expression of lipid metabolism–related genes by using RT-PCR. Our results showed that betaine treatment promoted the expression of adipogenic genes *PPARγ*, *aP2*, and *LPL*. Meanwhile, betaine did not affect the expression of lipidolytic genes *ATGL* and *HSL* as well as fatty acid transportation related genes *FAbp3* and *CD36*. We also observed betaine enhanced mitochondrial function by upregulating *PGC1α* and *PGC1β* expression. Together, these results suggest that betaine enhances skeletal muscle cell lipid accumulation mainly through modulating the expression of adipogenic genes *PPARγ*, *aP2*, and *LPL*, which sheds light on the effect of betaine on intramuscular fat accumulation.

Key Words: betaine, lipid metabolism, skeletal muscle cell
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355 Cholecalciferol supplementation in heifer diets increases beef vitamin D concentration and improves beef tenderness.

A. K. Kelly*[1], J. V. O'Doherty[2], and S. K. Duffy[1], [1]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland,* [2]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland.*

This study investigated the effects of cholecalciferol (vitamin D_3) supplementation on beef vitamin D concentration, beef tenderness, and sensory evaluation. Thirty Continental heifers were blocked on the basis of live weight and age and randomly allocated to 1 of 3 dietary treatments: basal + 0 IU of vitamin D_3 (T1), basal + 2,000 IU of vitamin D_3 (T2), and basal + 4,000 IU of vitamin D_3 (T3). Dietary treatments were offered for the final 28 d of an 80-d intensive finishing period. The basal diet consisted of a standard ad libitum finishing regime of concentrates and forage (straw) offered at a 90:10 ratio. Animal growth was recorded weekly, and individual DMI were

recorded using Calan Broadbent Controlled feeding system. Blood samples were taken prior to slaughter for blood serum 25-OH-D_3concentration. Longissimus dorsi (LD) muscles were excised 10 d after slaughter for D_3 analysis carried out by analytical HPLC. Data were analyzed using mixed model ANOVA in SAS. Increasing dietary D_3 resulted in a linear response ($P < 0.05$) in systemic 25-OH-D_3 blood concentrations (88.63 vs. 132.52 vs. 165.45 n/mol per liter in T1, T2, and T3, respectively [SEM 10.692]). Similarly, D_3 ($P < 0.05$) content of LD beef also showed a linear response to dietary D_3 inclusion. Heifers fed 4,000 IU of vitamin D_3 had higher LT cholecalciferol and 25-hydroxyvitamin D_3 activity compared with those fed 0 IU of vitamin D_3 and 2,000 IU of vitamin D_3. Indeed, D_3 content in the highest inclusion treatment (T3) and showed 33% enhanced D_3 content compared with T2 and 72% compared with T1 (0.019 vs. 0.045 vs. 0.067 µg/100 g in T1, T2, and T3, respectively [SEM 0.0240]). Heifers offered 4,000 IU of vitamin D_3 diet had a decreased spinalis dorsi Warner–Bratzler shear force (WBSF) value ($P < 0.05$) in 14-d-old steaks compared with other dietary treatments. Heifers offered the 2,000 and 4,000 IU of vitamin D_3 also had a decreased ($P < 0.05$) WBSF values compared with the 0 IU of vitamin D_3 treatment. Mean sensory score parameters including appearance, odor, texture, flavor, overall acceptance, and off-flavor were not affected ($P > 0.05$) by dietary treatments. In conclusion, results indicate that D_3 content of beef can be successfully enhanced through short-term dietary supplementation and that biofortification of beef may be a potential food-based strategy for increasing human vitamin D dietary intake.

Key Words: beef, biofortification, vitamin D
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356 Comparative analysis of the N6-methyladenosine of skeletal muscle in Jinhua and Landrace pigs.

Q. Jiang*, X. Wang, and Y. Wang, *College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China.*

Methylation of the N6 position of adenosine (m^6A) is the most prevalent internal mRNA modification in eukaryotes; it is a reversible modification, and it plays important roles in cell differentiation and tissue development. Jinhua, a Chinese pig breed, contains considerably higher levels of intramuscular fat (IMF) than does Landrace, a Danish pig breed. However, how m^6A methylation dictates the difference in IMF of skeletal muscle between lean and obese pigs remains unclear. In this study, the longissimus dorsi muscles of Jinhua and Landrace pigs ($n = 4$) at 180 d were used 1) to investigate the difference in m^6A:A ratio between Jinhua and Landrace pigs, 2) to analyze the differences in the expression of m^6A modification–related proteins between Jinhua and Landrace pigs, and finally 3) to perform a comparative analysis of whole N6-transcriptome methylation between Jinhua and Landrace pigs. The results showed that 1) the ratio of m^6A to A was significantly lower in Jinhua pigs than in Landrace pigs ($P < 0.05$); 2) the expression of m^6A "readers" (YTHDF1 and YTHDF2) was significantly lower in Jinhua pigs than in Landrace pigs ($P < 0.01$), whereas that of the "eraser" FTO was significantly higher in Jinhua pigs than in Landrace pigs ($P < 0.05$); and 3) the differentially methylated genes (DMG) were significantly associated with lipid metabolism, oxidative stress, and muscle development; among the identified DMG, 53 genes were associated with obesity. The expression of the genes UCP2, FAM134B, and MTCH2 was probably associated with the m^6A methylation levels of their mRNA; these genes were associated with oxidation–reduction and fatty acid metabolism. Ribonucleic acid methylation potentially influences the propensity for obesity by affecting gene expression in skeletal muscle. The findings of this study provide valuable information on the epitranscriptome that will be useful for pig breeding and nutrition research.

Key Words: intramuscular fat, messenger RNA m^6A, skeletal muscle
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357 All-*trans* retinoic acid impacts myogenic gene expression in bovine satellite cells.

J. Kim*, K. B. Pritchett, Z. K. F. Smith, and B. J. Johnson, *Texas Tech University, Lubbock.*

All-*trans* retinoic acid (ATRA) has been associated with the enhancement of myogenesis, the alteration of muscle fiber type, and can subsequently alter lipid metabolism through various transcriptional reactions in skeletal muscle. A completely randomized design cell culture study used orthogonal contrasts for unequally spaced treatments to examine dose effects of ATRA on expression of genes related to skeletal muscle fiber type and hypertrophy. Bovine satellite cells were isolated from the semimembranosus of two 14-wk-old crossbreed steers. The isolated muscle satellite cells were incubated in Dulbecco's modified Eagle's medium (DMEM) solution with 10% fetal bovine serum, 1x antibiotic–antimycotic at 37°C under a humidified atmosphere of 95% O_2 and 5% CO_2. Upon reaching 80 to 90% confluence, the growth medium was replaced with differentiation medium composed of DMEM and 2% horse serum to induce myogenic differentiation. Along with differentiation media, various doses (0, 0.01, 0.1, 1, and 10^{-6} M) of ATRA were randomly administered to wells (6 wells/dose). After 96 h of incubation, cells were harvested for mRNA analysis. Real-time quantitative PCR was used to measure the quantity of protein kinase B (Akt), AMP-activated protein kinase α (AMPKα), glucose transporter 4 (GLUT4), myogenin, myosin heavy chain (MHC) I, MHC IIA, MHC IIX, IGF-I, PPARγ, and transforming growth factor-beta effector protein (SMAD3) mRNA relative to ribosomal protein subunit 9 (RPS9). No differences for control vs. ATRA were detected for mRNA expression of Akt ($P = 0.17$), AMPKα ($P = 0.46$), or GLUT4 ($P = 0.30$). A tendency ($P = 0.09$) for a linear increase of MHC I mRNA expression

was detected with increasing doses of ATRA. Expression of PPARγ, known to induce oxidative muscle fiber type formation, linearly increased ($P < 0.01$) with ATRA. The mRNA expression of IGF-I was linearly increased ($P < 0.01$) by ATRA. The mRNA abundance of SMAD3 ($P < 0.01$) and myogenin ($P < 0.01$) both linearly increased with ATRA. A novel finding in this study is that PPARγ expression was increased by ATRA in bovine muscle cells. It is well known that ATRA inhibits expression of PPARγ and other adipogenic genes in adipocytes. In muscle cells, ATRA appears to push muscle fibers toward the MHC isoform that prefers oxidative metabolism, primarily via increased expression of genes associated with MHC I isoform and myogenic differentiation.

Key Words: bovine satellite cells, myogenesis, retinoic acid
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358 Effects of rumen protected–histidine supplementation dose on finishing beef cattle.

B. N. Sandberg*, C. W. Hunt, M. E. Doumit, R. Richard, and G. K. Murdoch, *University of Idaho, Moscow.*

This study examined the effect of dietary rumen-protected histidine (HIS) supplementation in cattle on growth and carcass traits/product quality. Three levels of daily HIS (Balchem Corp.) were tested (control, low dose [D_L], and high dose [D_H]) over a 55-d finishing period in 48 crossbred steers implanted with Revalor-XS. Cattle were randomly allocated into 8 pens of 6 steers each and fed twice daily using Calan gates. Morning feed was top-dressed with the HIS as follows: control (no HIS), 50 g/steer per day (D_L), or 100 g/steer per day (D_H). Individual intakes were recorded, and feed and orts were analyzed every 5 d during the feeding period. Steers were harvested, carcass data was recorded, and carcasses were fabricated at a USDA-inspected facility. One longissimus lumborum (LL) and 1 gluteus medius (GM) was acquired from each animal, aged under vacuum (21 and 14 d respectively), and cut into 2.54-cm steaks. One steak was used for retail display for which subjective (to evaluate visual color components) and objective (L*, a*, and b*) color scores were recorded. Lipid oxidation on d 0 and 9 of retail display were assessed using thiobarbituric acid reactive substances. Another steak was used to evaluate cooking loss and tenderness using Warner–Bratzler shear force. Sensory taste panels were conducted (1 panel for each muscle) to determine consumer perception of the product. Muscles were analyzed using HPLC for HIS metabolite (anserine and carnosine) and HIS content. Histidine supplementation increased ADG during d 1 to 21 (D_H, $P = 0.07$), d 42 to 60 (D_L and D_H, $P = 0.07$), and the final 50 d (D_H, $P = 0.07$) of feeding. Supplementation with HIS also increased the lightness (D_L GM, $P = 0.05$), degree of yellow hue (D_L and D_H LL, $P = 0.01$), oxygenated lean color (D_L GM, $P = 0.004$), uniformity (D_H GM, $P = 0.03$, and D_H LL, $P = 0.06$), and overall color stability of the product from d 3 through 9 of retail display. The percent surface discoloration (D_L and D_H GM, $P = 0.04$, and D_L and D_H LL, $P < 0.0001$), degree of browning (D_L and D_H GM, $P = 0.002$, and D_L and D_H LL, $P < 0.0001$), and discoloration (D_L and D_H GM, $P = 0.01$, and D_H LL, $P = 0.05$) of the product was decreased. The D_L GM steaks were juicier ($P = 0.07$), more acceptable ($P = 0.05$), and more satisfying ($P = 0.01$) than the control steaks. Seventy-seven percent of panelists would purchase the D_L GM product (control, 61%, and D_H, 60%). In conclusion, 55 d of rumen-protected HIS treatment positively impacts consumer perception and may optimize product quality and marketability in beef cattle.

Key Words: beef quality, histidine, muscle
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359 Effects of dietary glycerin on carcass characteristics, fatty acid profile, and volatile compounds in longissimus dorsi muscle of Korean steers.

S. W. Na*, M. Y. Piao, H. I. Yong, H. J. Lee, C. Jo, and M. Baik, *Department of Agriculture Biotechnology, College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea (South).*

Dietary glycerol may improve beef quality by affecting glycogen content and marbling. This study was performed to evaluate the effect of a glycerin-increased diet on growth performance, carcass characteristics, chemical composition, sensory traits, fatty acid profile, and volatile compounds in longissimus dorsi muscle (LM) of beef cattle. Twenty Korean steers (647 ± 10.49 kg BW and 27 mo of age) were divided into a control diet group ($n = 10$) and a glycerin-increased diet group ($n = 10$). Diets were formulated to meet or exceed NRC (2000) requirements. The control diet, which was conventionally designed for finishing period of Korean cattle, was used in this study. For the glycerin-increased diet, the portion of molasses and distiller's dried grains with solubles in the control diet were replaced with a 3% crude glycerin with isoenergy nutrient levels (TDN = 87%, DM basis) compared with the control diet. All steers were allowed daily to receive a concentrate with the amount of 1.5% of BW and 1.0 kg of rice straw. The feeding trial was performed for 5 wk. Water was allowed ad libitum. All data were analyzed by ANOVA using GLM of SAS. Concentrate intake was 14% higher ($P < 0.01$) in the glycerin group compared with control group, whereas rice straw intake was not different between the 2 groups. Average daily gain and feed efficiency (G:F) were not different between the 2 groups ($P > 0.05$). Animals were slaughtered after the feeding trial, and LM samples were collected from hot carcasses within 2 h after slaughter and frozen for chemical analyses. The carcasses were kept at 4°C for 24 h and graded with Korean standard grading methods. Longissimus dorsi muscle samples were also collected from cold carcasses at 24 h for analysis of sensory traits. Carcass weight, LM muscle area, back fat thickness, marbling score, yield grade, and quality grade were not different between the 2 groups ($P > 0.05$). Contents of protein, fat, collagen, reducing sugar, and glycogen in the LM were not different between the 2 groups ($P > 0.05$). Sensory traits (appearance, flavor, taste, tenderness, juiciness, and overall acceptance) and percentages of fatty acids and volatile compounds in the LM were not different between the 2 groups ($P > 0.05$). In conclusion, the glycerin-increased diet improved feed intake, although it did not affect daily gain and feed efficiency. The glycerin-increased diet did not affect beef quality, including marbling, glycogen contents, sensory traits, and percentages of fatty acids and volatile compounds in the LM.

Key Words: beef quality, glycerin, Korean cattle
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360 Characterization of rigor mortis process in longissimus dorsi of crossbred calves.

A. A. G. Lobo*[1], A. C. F. Rocha[2], M. L. Chizzotti[2], A. C. B. Menezes[2], A. S. Trece[2], M. M. D. Castro[2], J. Dias[2], V. R. Vardiero[2], and M. I. Marcondes[2],
[1]*University of São Paulo (USP), Pirassununga, Brazil,*
[2]*University of Viçosa (UFV), Viçosa, Brazil.*

This study, conducted at the University of Viçosa, Brazil, aimed to characterize the process of conversion of muscle into meat of crossbred Holstein × Gir veals. Thirty-five calves with an initial mean BW of 35 ± 5 kg were used. We used 35 carcasses of crossbred Holstein-Gir calves subjected to 2 treatments: 1) fed only milk (LL) and 2) milk plus concentrated (LC).The animals were slaughtered at 44 d old. The temperature, pH, and sarcomere length were measured at different intervals of time after slaughter (0200, 0400, 0600, 0800, 1000, 1200 and 2400 h). The temperature of the cold chamber was adjusted by −2°C every 2 h, starting at 16°C. For all parameters, we used a 5% significance. The carcasses were kept for 24 h in the cold chamber at 4°C, and after that, the longissimus dorsi muscle was removed from each half carcass. The muscle was vacuum-packaged and frozen. The pH variation was significant for hour and diet ($P < 0.05$). Over time, the pH decreased, presenting a mean of 6.71 at time 0 and 5.51 at 2400 h. The carcasses of the animals submitted to the LC treatment had a lower mean (5.98) than the carcasses of the LL treatment (6.06). The monitoring of the pH drop is an important tool to analyze the quality of the meat. Depending on your speed of decrease and the level of glycogen available, the quality may vary, leading to a softer or harder meat. The temperature variation was not significant between treatments ($P > 0.05$). Statistical analysis did not show a significant difference ($P > 0.05$) regarding the length of sarcomere values in time, diet, and time and diet intervals. Therefore, carcasses of animals submitted to the diet with or without concentrate did not present differences in length of sarcomere and temperature during the process of rigor mortis. The decrease in pH was observed to act faster in calves fed with concentrate during their development phase.

Key Words: pH, sarcomere length, temperature
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361 Focal adhesion kinase–mammalian target of rapamycin pathway–mediated different proliferation, migration, and differentiation abilities of satellite cells in Lantang and Landrace piglets.

C. Gao*, C. Jin, H. Yan, and X. Wang,
College of Animal Science, South China Agricultural University, Guangzhou, P.R. China.

Compared with the Landrace pig, Lantang is an indigenous Chinese pig breed that possesses excellent meat quality but low rates of lean meat deposition. The different muscle characteristics may be related to the different features of skeletal muscle satellite cells (SC). Therefore, 3 experiments were conducted to explore SC proliferation, migration, and differentiation abilities in Lantang and Landrace piglets as well as focal adhesion kinase (FAK) and mammalian target of rapamycin (mTOR) pathways to preliminarily explore the molecular mechanisms. In Exp. 1, the different proliferation capacity of these SC was determined. Cell count assay showed that there was a greater ($P < 0.05$) number of Lantang SC compared with Landrace at 72 h. Higher percentages of Lantang SC in the S and G2/M phases were found ($P < 0.05$) whereas the those in the G0/G1 phase was lower ($P < 0.05$) in comparison with the Landrace. The mRNA abundances of myogenic differentiation antigen, myogenic factor 5, myogenin, and paired box 7 in SC from Lantang were higher ($P < 0.05$), whereas those of myostatin, Sekelsky mothers against dpp family member 3, protein kinase B (Akt), tuberous sclerosis complex 1, mTOR, ribosomal protein S6 kinase 1 (S6K1), and ribosomal protein S6 (S6) were lower than those in Landrace SC ($P < 0.05$). In Exp. 2, for the migration study, we found that Lantang SC had greater ability of migration and adhesion ($P < 0.05$) than Landrace SC. Meanwhile, the levels of p-FAK and p-paxillin were higher ($P < 0.05$) in Lantang SC than Landrace SC at 24 h after migration. Similarly, treatment with the FAK inhibitor PF-573228 restrained Lantang SC migration ($P < 0.05$) and decreased p-paxillin and p-Akt levels ($P < 0.05$). In Exp. 3, for the differentiation study, the creatine kinase activity and fusion index in Lantang SC were higher than that in Landrace SC at 72 h during differentiation ($P < 0.05$). Meanwhile, the levels of differentiation markers such as myogenin and myosin heavy chain I in Lantang SC were higher compared with Landrace SC at 72 h during differentiation ($P < 0.05$). However, the levels of p-Akt, p-mTOR, p-S6K1, and p-S6 in Lantang SC were lower than those in Landrace SC ($P < 0.05$). In conclusion, these findings show that SC in Lantang piglets had higher proliferation, migration, and differentiation abilities than those in Landrace piglets. It is interesting for us to find that the mTOR pathway was positive to cell proliferation, whereas it was negative to differentiation; nevertheless, the FAK pathway plays a key role in the regulation of SC migration.

Key Words: focal adhesion kinase–mammalian target of rapamycin pathway, proliferation, differentiation, and migration, satellite cells
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362 Identification of a beneficial role of proteasome-mediated protein degradation in the differentiation of bovine myoblasts into myotubes.

X. Leng* and H. Jiang, *Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg.*

The objective of this study was to determine the role of proteasome-mediated protein degradation in the differentiation of bovine myoblasts into myotubes. This objective stemmed from an earlier, unexpected observation that the ubiquitin–proteasome pathway in bovine myoblasts was upregulated during their differentiation into myotubes. Satellite cells, the myogenic progenitor cells in adult skeletal muscle, were isolated from 5 Angus or Angus crossbred steers (experimental unit) and were expanded as myoblasts in growth medium. Myoblasts were then induced to differentiate into myotubes in differentiation medium in the presence or absence of 5 μM lactacystin, a specific inhibitor of the 20S proteasome, for 6, 12, 24, 48, and 72 h. The differentiation status of myoblasts was assessed by reverse-transcription quantitative PCR of myosin heavy chain 3 (MYH3), muscle creatine kinase (CKM), and Myomaker (TMEM8) mRNA, markers of myotubes. Compared with control myoblasts, lactacystin-treated myoblasts expressed less MYH3, CKM, and TMEM8 mRNA at 24, 48, and 72 h of differentiation ($P < 0.01$). These differences indicated that lactacystin inhibited the differentiation of bovine myoblasts into myotubes. Differentiation of myoblast into myotubes is primarily controlled by myogenin at the transcriptional level. The DNA binding and transcriptional activity of myogenin can be inhibited by the inhibitor of DNA-binding 1 (ID1) protein. Based on western blot analyses, ID1 protein expression was decreased ($P < 0.05$) during bovine myoblast differentiation into myotubes, and this decrease was reversed ($P < 0.05$) by including lactacystin in the differentiation medium. Collectively, these results suggest a beneficial role of proteasome-mediated protein degradation in bovine myoblast differentiation into myotubes, and this role may involve the degradation of the ID1 protein.

Key Words: myogenin, proteasome, skeletal muscle
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363 Color and lipid oxidation of meat from young bulls finished in feedlot supplemented with clove or cinnamon essential oils.

J. A. Torrecilhas*[1], C. Mottin[2], M. G. Ornaghi[2], P. A. C. Rodrigo[2], M. V. Valero[2], K. A. Souza[2], F. Zawadzki[2], A. M. Bridi[3], and I. N. Prado[2], *[1]São Paulo State University (UNESP) School of Agricultural and Veterinarian Sciences, Jaboticabal, Brazil, [2]Maringá State University, Maringá, Brazil, [3]Londrina State University, Londrina, Brazil.*

This study examined color and lipid oxidation of meat, from young bulls finished in feedlot supplemented with clove (84.5% of eugenol) or cinnamon (78.8% of cinnamaldehyde) essential oils. Forty bulls (1/2 Brown Swiss - 1/2 Nellore) 10 ± 2.2 month-old and with initial average BW of 219.0 ± 11.7 kg were used in a complete randomized design, assigned to individual pens. The diet consisted of 90% concentrate and 10% of sugar cane pellets. The young bulls were randomly assigned to the groups: CON control, no clove or cinnamon oil, CLO35 inclusion of 3500 mg/animal/d of clove oil, CLO70 inclusion of 7000 mg/animal/d of clove oil, CIN35 inclusion of 3500 mg/animal/d of cinnamon oil, and CIN70 inclusion 7000 mg/animal/d of cinnamon oil. After 187 d the bulls reached an average of 443.5 ± 26.2 kg BW, and were transported to a slaughterhouse. The carcasses were stored in a chilling chamber at 4°C. After 24 h, Longissimus muscle samples were collected for analysis. Three steaks (two-half centimeters thick) were cut, packed in polystyrene trays over wrapped with a retractile film (oxygen permeable) and stored in expositor (4°C) during 1, 7, and 14 d. The color was evaluated using a Minolta colorimeter (CM 700). The lipid oxidation was evaluated by thiobarbituric acid-reactive substances protocol, and the results were expressed in mg of malondialdehyde (MDA) per kg/meat. The data were assessed via analysis of variance using GLM procedures with SPSS v21.0 and the averages were compared at the 5% level of significance. The inclusion of oil in diets did not affect the color on 1, 7, and 14 d, the average values were 40.0, 40.27, and 32.05 for lightness (L*), 11.73, 16.08, and 7.6 for redness (a*), and 11.82, 14.91, and 7.98, for yellowness (b*). The concentration of MDA in meat on 1 and 14 d of storage was not influenced ($P = 0.832$ and $P = 0.183$, respectively) by the treatments. However, on the 7 d, the MDA concentration of meat were lower ($P = 0.001$) for animals from groups fed with diets supplemented with both oils, compared to animals from control group (0.681, 0.594, 0.540, 0.592, 0.573 mg/kg for CON, CLO35, CLO70, CIN35, CIN70, respectively). The essential oils added to the cattle diet did not alter the color parameters of meat and were efficient in the protection of the lipid oxidation.

Key Words: antioxidant, natural additive, shelf life
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364 Effect of breed and finishing system on meat quality from beef cattle.

J. A. Torrecilhas*[1], O. R. Machado Neto[2], M. G. Ornaghi[3], E. San Vito[1], L. O. Lima[1], T. Adriano Simioni[1], E. E. Dallantonia[1], and T. T. Berchielli[1], *[1]São Paulo State University (UNESP) School of Agricultural and Veterinarian Sciences, Jaboticabal, Brazil, [2]São Paulo State University, Botucatu, Brazil, [3]Maringá State University, Maringá, Brazil.*

This study evaluated the meat quality of 3 cattle breeds finished in 2 feeding systems. Bulls of 3 genetic groups (n = 113)—Nellore (NL), one-half Angus × one-half Nellore (AN), and one-half Senepol × one-half Nellore (SN)—were randomly assigned to 2 feeding systems groups: pasture (PA; $n = 57$) and feedlot (FE; $n = 56$). Bulls from both systems were supplemented (2% BW) daily with a high-concentrate diet (16% CP and 78% TDN). After 110 d, the bulls were slaughtered at a commercial beef plant. The carcasses were stored in a chilling chamber at 4°C. Three steaks from LM (2.5-cm thick) were cut between the 11th to 13th ribs, individually vacuum-packaged, and assigned to 1-, 7-, and 14-d ageing periods. Muscle pH, thawing loss (TL), cooking loss (CL), water holding capacity (WHC), color, and Warner–Bratzler shear force (WBSF) were analyzed. The results were analyzed by ANOVA using GLM procedures in SAS 9.0, with a 3 × 2 factorial arrangement, and the averages were compared at 5% level of significance. The muscle pH (1-, 7-, and 14-d ageing time) was not influenced by feeding system or breed. The feeding system affected some quality parameters: TL was lower for the PA group compared with the FE group at 1 d ageing time (7.86 and 10.18%, respectively; $P = 0.006$), CL was greater on d 7 for the FE group (26.16 and 24.31%; $P = 0.047$), and WHC was greater on d 1 for the PA group (68.13 and 64.34%; $P < 0.001$) and on d 14 as well (69.37 and 67.75%; $P = 0.004$). The meat color of the FE group was greater compared with the PA group, lightness (L*) was greater on all days examined (d 1, 7, and 14; $P < 0.001$), redness (a*) was greater on d 1 ($P = 0.020$) in the FE group but was lower on d 7 and 14 ($P = 0.026$ and $P = 0.002$, respectively) compared with the PA group, and yellowness (b*) was greater on d 1 and 14 in the FE group ($P < 0.001$ and $P = 0.047$). The WBSF was better in the FE group during all ageing times. The breed influenced L*: on 7 d ageing time, the SN group was greater compared with NE group; however, the SN and AN groups did not differ from each other. On 14 d ageing time, the AN and SN groups were similar, but both were greater than the NL group. In this study, the meat quality parameters were more affected by feeding systems than by breed.

Key Words: feedlot, longissimus muscle, pasture
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365 Effect of growth rate on beef fatty acid profile from Hereford steers finished either on pasture or in feedlot.

A. M. Ferrinho*[1], E. Peripolli[2], G. Banchero[3], A. S. C. Pereira[4], G. Brito[3], A. F. La Manna[3], E. Fernandez[3], F. Montossi[3], and F. Baldi[5], *[1]School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil, [2]Sao Paulo State University (UNESP), School of Agricultural and Veterinarian Sciences (FCAV), Department of Animal Science, Jaboticabal, Brazil, [3]INIA, Colonia, Uruguay, [4]Universidade de São Paulo, Pirassununga, Brazil, [5]School of Agricultural and Veterinarian Sciences, Sao Paulo State University – FCAV/UNESP, Jaboticabal, Brazil.*

Different nutritional management during the rearing and finishing periods can determine changes on beef fatty acid profile. Beef lipid composition was quantified in 224 male Hereford calves weaned at 8 wk of age with an average initial live weight (LW) of 170 ± 17 kg. After weaning, 4 nutritional treatments were imposed to obtain different daily LW gains (LWG; kg/d) during the first winter. Nutritional management groups were high LWG in feedlot (HF), low LWG in feedlot (LF), high LWG in pasture (HP), and low LWG in pasture (LP). The finishing phase began when each group reached a mean LW of 350 ± 28 kg. During the finishing phase, one-half of the HF, LF, HP and LP animals were finished on pasture and the other half in a feedlot. The animals were slaughtered when calves in each treatment attained a mean LW of 500 kg. Analysis of beef fatty acids was performed by extraction and methylation from LM, and the fatty acids were quantified using a gas chromatography. The statistical model included the groups at growing phase (HF, LF, HP, and LP) and the groups at finishing phase (feedlot or pasture) and the interaction between growing and finishing phase as fixed effects and LW at the beginning of the finishing phase as a covariable. Tukey's test was applied to compare the means ($P < 0.05$). There was interaction between the growing and finishing phases for myristic acid and CLA *cis* 9, *trans* 11. Animals from HF finished on pasture presented the highest concentration of myristic acid (2.54%) when compared with the other treatments. The LP and HP groups finished on pasture had more CLA *cis* 9, *trans* 11 in their beef composition (0.60 and 0.58%, respectively), whereas animals finished in the feedlot presented the lowest concentrations (average of 0.28%). Finishing phase affected the fatty acid profile ($P < 0.05$). Higher concentrations of palmitic, oleic, and linoleic acids were observed in beef from animals finished in the feedlot than in beef from those finished on pasture. However, the beef from animals finished on pasture presented high concentrations of stearic, docosapentaenoic, and docosaexaenoic acids. Animals finished on pasture had higher concentrations of linolenic, arachidonic, and eicosapentaenoic acids compared with those finished in feedlot. Interestingly, the LP group presented higher concentrations of

linolenic and eicosapentaenoic acids, regardless of the finishing phase. The same results were observed in the LF group for arachidonic acid. In general, the LP and HP groups finished on pasture resulted in healthy beefs, with the greatest CLA and omega-3 concentrations.

Key Words: finishing system, growth out, lipid composition
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366 Gender status effects on beef fatty acid profile of Angus × Nellore cattle.

L. F. Mueller[1], J. C. D. C. Balieiro[2], A. M. Ferrinho*[3], J. D. J. M. Furlan[4], M. L. N. Furlan[2], M. Zanata[2], T. R. Amorin[2], I. H. S. Fuzikawa[2], T. S. Martins[2], F. Baldi[5], and A. S. C. Pereira[2], [1]*University of Sao Paulo (USP), School of Animal Science and Food Engineering (FZEA), Department of Animal Science (ZAZ), Pirassununga, Brazil,* [2]*Universidade de São Paulo, Pirassununga, Brazil,* [3]*School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil,* [4]*University of Sao Paulo (USP), School of Veterinary Medicine and Animal Science (FMVZ), Department of Animal Science (VNP), Pirassununga, Brazil,* [5]*School of Agricultural and Veterinarian Sciences, Sao Paulo State University– FCAV/UNESP, Jaboticabal, Brazil.*

Beef fatty acid profile can be modified by the sex of the animals. Therefore, the goal of this study was to evaluate the influence of gender status on beef fatty acid profile of feedlot Angus × Nellore cattle. A total of 176 cattle, 20 wk of age, from the Brazilian Certified Angus Beef Program were assigned to 4 sex classes: 32 bulls, 48 steers, 48 immunocastrates, and 48 heifers, presenting initial mean weights of 251.4 ± 3.62 kg for bulls, 266.6 ± 2.95 kg for immunocastrates, 226.4 ± 2.95 kg for steers, and 255.4 ± 2.95 kg for heifers. Cattle were fed during 190 d an ad libitum high-grain diet containing 80% concentrate. At the end of the experimental period, cattle were slaughtered. Steaks were collected from the LM and stored at −80°C pending analysis for fatty acid profile. Beef fatty acid was extracted and then the methyl esters were formed. Fatty acids were quantified using a gas chromatography. Statistical analyzes were performed using PROC MIXED of SAS, including the fixed effect of gender status and the random effect of cattle within gender groups. The gender status had no effect on the total SFA, but significant differences were observed for MUFA, PUFA, CLA, *n*-6, the *n*-6:*n*-3 ratio, and the PUFA:SFA ratio ($P < 0.05$). Beef from heifers had greater levels of MUFA (45.77%; $P < 0.01$) and CLA (0.42%; $P = 0.0006$) when compared with bulls (41.56 and 0.30%, respectively), steers (44.21 and 0.30%, respectively), and immunocastrates (43.95 and 0.36%, respectively). The highest levels of MUFA in the heifers' beef was mainly related to the higher levels of the major single fatty acids in this group, namely C18:1 *n*-9 (35.65%; $P < 0.01$) and C16:1 *n*-9 (2.94%; $P < 0.01$). On the other hand, the levels of PUFA and *n*-6 and the PUFA:SFA and *n*-6:*n*-3 ratios were greater ($P < 0.01$) in beef from bulls (9.76, 8.36, 0.22, and 4.83%, respectively) compared with the other gender statuses. In conclusion, beef from heifers can be considered healthier to humans because it presented lower levels of *n*-6 and myristic acid and higher levels of CLA, MUFA, and oleic acid.

Key Words: beef cattle, fatty acid composition, sexual condition
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367 Chemical treatment of poultry litter does not affect the chicken meat quality.

J. D. J. M. Furlan[1], L. F. Mueller[2], A. M. Ferrinho*[3], M. L. N. Furlan[4], M. Zanata[4], M. C. Izeppi[4], T. R. Amorin[4], I. H. S. Fuzikawa[4], T. S. Martins[4], F. Baldi[5], and A. S. C. Pereira[4], [1]*University of Sao Paulo (USP), School of Veterinary Medicine and Animal Science (FMVZ), Department of Animal Science (VNP), Pirassununga, Brazil,* [2]*University of Sao Paulo (USP), School of Animal Science and Food Engineering (FZEA), Department of Animal Science (ZAZ), Pirassununga, Brazil,* [3]*School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil,* [4]*Universidade de São Paulo, Pirassununga, Brazil,* [5]*School of Agricultural and Veterinarian Sciences, Sao Paulo State University – FCAV/UNESP, Jaboticabal, Brazil.*

Many studies have demonstrated the damaging effect of gases such as ammonia in the production of broilers chickens, especially on the performance and blood parameters. However, few studies have evaluated the effect of using additives to treat poultry litter on the chicken meat quality. Therefore, the goal of this study was to evaluate the effects of aluminum sulfate doses ($Al_2(SO_4)_3 \cdot 18H_2O$; 0, 200, 400, and 600 g/m^2) to treat poultry litter and stocking density (12 and 14 birds/m^2) on chicken meat quality traits. A total of 532 broiler male Cobb 500 chicks presenting an initial mean weight of 46 g ± 2.3 were used and housed in a completely randomized experimental design, with 4 × 2 factorial arrangement, totaling 8 treatments with 7 replicates each. Standard industry diets were used throughout the study, including starter (0 to 21 d), grower (21 to 35 d), and finisher (35 to 42 d) diets. At the end of the experimental period (42 d), 2 birds per replicate were randomly chosen and harvested. The traits analyzed in chicken meat were pH (24 h postmortem), color (L*, a*, and b*), cooking loss, and shear force. Statistical analyses were performed using PROC MIXED of SAS, including the fixed effect of factors (aluminum sulfate and stocking density) and interactions. No interaction was detected between treatments for any meat quality trait evaluated ($P > 0.05$). The treatments with a highest sulfate levels and density presented the lowest

cooking loss (28.80%). There was a curvilinear response (cubic) of aluminum sulfate doses for meat color on the a* value ($P = 0.0214$), with the addition of aluminum sulfate (0 to 200 g/m^2) decreasing the a* value. However, the a* values increased when the doses of aluminum sulfate were 400 and 600 g/m^2. In conclusion, the addition of aluminum sulfate ($Al_2(SO_4)_3 \cdot 18H_2O$) and stocking densities evaluated did not affect chicken meat quality.

Key Words: aluminum sulfate, broiler, litter
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368 Effects of functional oils and vitamin E addition on meat sensory traits from feedlot lambs.

M. L. N. Furlan[1], L. F. Mueller[2], A. M. Ferrinho*[1], J. D. J. M. Furlan[3], M. Zanata[1], I. H. S. Fuzikawa[1], T. R. Amorin[1], T. S. Martins[1], S. B. Gallo[4], and A. S. C. Pereira[1], *[1]Universidade de São Paulo, Pirassununga, Brazil, [2]University of Sao Paulo (USP), School of Animal Science and Food Engineering (FZEA), Department of Animal Science (ZAZ), Pirassununga, Brazil, [3]University of Sao Paulo (USP), School of Veterinary Medicine and Animal Science (FMVZ), Department of Animal Science (VNP), Pirassununga, Brazil, [4]School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil.*

The use of functional oils replacing additives, such as antibiotics, ionophores, and growth promoters, has shown good results. Furthermore, there is an increasing demand from consumers for healthier meat. Therefore, the aim of this study was to evaluate the effects of the inclusion of functional oils (*Ricinus communis* and *Anacardium occidentale*) and vitamin E in high-grain diets on meat sensory traits of lambs. A total of 30 crossbred lambs (12 males and 18 females), 5 mo of age, were used. Lambs presenting initial mean weights of 26 ± 3.6 kg for females and 28 ± 3.6 kg for males were grouped into a randomized block design, confined, and assigned to the following treatments, with 10 replicates each: no additives inclusion (CON), inclusion of functional oils (500 mg/kg DM; OIL), and inclusion of functional oils (500 mg/kg DM) + vitamin E (500 IU vitamin E/kg DM; OILVIT). Animals were fed ad libitum with a high-grain diet containing 85% concentrate. At the end of the experimental period (77 d), the animals were harvested with final mean weights of 38.59 ± 4.15 kg (females) and 47.11 ± 4.24 kg (males). Vacuum-packaged steaks (2.54-cm thick) from the LM were collected and stored at −18°C pending analysis for sensory traits. An acceptance test was used, in which 100 untrained laboratory consumer panelists evaluated 1 sample from each treatment class. Each panelist evaluated the samples using an evaluation form including a 9-point hedonic scale, where 1 = dislike extremely and 9 = like extremely, for sensory attributes such as aroma, flavor, tenderness, and juiciness and a scale from 1 to 5, where 1 = very strong and 5 = absent, for off-flavor and off-aroma. Statistical analyses were performed using PROC MIXED of SAS (version 9.2). No difference was found between treatments for aroma, off-flavor, and off-aroma ($P > 0.05$). The best scores were observed in OILVIT for the tenderness and juiciness attributes when compared with the other treatments ($P < 0.05$). For the flavor attribute, the best scores were observed in OILVIT and CON when compared with the OIL treatment ($P < 0.05$). The inclusion of functional oils and vitamin E in the sheep diets appears to be a good option to improve lamb sensorial traits.

Key Words: additive, sensory analysis, sheep
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369 Performance and carcass quality of Nelore cattle evaluated during termination phase in integrated agricultural production systems.

P. A. C. Luz*[1], C. Andrighetto[2], G. C. Lupatini[3], H. S. Aranha[3], A. S. Aranha[4], E. A. R. D. Santana[4], J. A. M. D. Almeida[3], R. F. Vaz[3], and A. M. Jorge[1], *[1]Universidade Estadual Paulista – FMVZ, Botucatu, Brazil, [2]Universidade Estadual Paulista – UNESP, Dracena, Brazil, [3]São Paulo State University (UNESP), Dracena, Brazil, [4]São Paulo State University (UNESP), Botucatu, Brazil.*

Integrated agricultural production systems have been gaining prominence in recent years, especially those that advocate the use of trees, which, in addition to being an alternative income per unit area, protect animals against extreme weather conditions that can influence animal performance and, consequently, carcass characteristics. Therefore, the present study was developed with the aim of evaluating the animal performance and carcass characteristics of Nelore cattle during the termination phase in integrated agricultural production systems without shade availability (ICL) and with 2 densities of trees (ICLF-1L and ICLF-3L). The experimental design was performed in nonrandomized complete blocks with 3 treatments—integrated crop–livestock (ICL); integrated crop–livestock–forest, with eucalyptus trees planted in simple lines (196 trees/ha; ICLF-1L); and integrated crop–livestock–forest, with eucalyptus trees planted in triple lines (448 trees/ha; ICLF-3L)—and 4 replicates per treatment, totaling 12 experimental plots. A total of 60 castrated Nelore cattle were used, weighing 382.51 ± 27.17 kg, with an age of 28.0 ± 2.81 wk, and 453.68 ± 29.69 kg, with and age of 34.0 ± 2.81 wk, at the start and end of the termination phase, respectively. The variables evaluated were ADG; final live weight; warm carcass weight; carcass yield; weight and yield of the forequarter, special hindquarter, and flank; rib eye area; back fat thickness; and marbling. All data was initially tested for normality with the Shapiro–Wilk test from the UNIVARIATE procedure. Also, it was normally distributed ($W \geq 0.90$). The analysis was developed by using the Student's *t* test, at the significance level of 5%, as well as

PROC MIXED of SAS. According to the data, no difference was observed between treatments for the ADG ($P > 0.05$). However, higher final live weight was observed in the ICL system compared with ICLF-1L and ICLF-3L ($P = 0.009$). Consequently, the same behavior was verified in the forequarter weight ($P = 0.043$) and the weight and yield of the flank ($P = 0.001$ and $P = 0.041$, respectively). On the other hand, no differences were observed between treatments for carcass yield, forequarter yield, and special hindquarter weight and yield, which is indicative of noble meat quantity, back fat thickness, and marbling ($P > 0.05$). Therefore, the study concludes that although the animals kept in wooded pastures presented lower final live weight, the trees planted in the pasture do not compromise their performance or the carcass yield and characteristics of higher amount of noble meat.

Key Words: carcass yield, crop–livestock–forest, rib eye area
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370 Relationships between fatty acid composition, trained panel descriptors, and volatile aroma compounds of ground beef patties of brisket, flank and plate with 10, 20, and 30% total fat.

A. R. Cabral*[1], T. L. Blackmon[2], R. K. Miller[1], C. R. Kerth[1], and S. B. Smith[1], [1]*Texas A&M University, College Station,* [2]*Kansas State University, Manhattan.*

The aim of this study was to determine the relationships, through principal component analysis (PCA), among fatty acid composition, trained panel descriptors, and volatile aroma compounds of ground beef patties produced from lean and fat trims of brisket, flank, and plate primals with 10, 20, or 30% total fat. We hypothesized that these primals would produce ground beef products with distinct flavor descriptors and aromatics. Four USDA Select carcasses from *Bos taurus* steers were randomly selected in a commercial packing plant. Brisket, flank, and plate were collected from both sides of the carcass and frozen at −20°C. Primals and subcutaneous fat were coarse ground (1.27 cm) and then fine ground (0.32 cm), formed into hamburger patties (136-g patties), vacuum-packaged, and stored at −20°C until testing (<14 d). Fatty acid composition, trained sensory analysis, and volatile aroma compounds from gas chromatography–mass spectrometry were determined. The data were analyzed using PCA. The PCA generated with flavor descriptors and fatty acids for 20 and 30% flank beef patties indicated clusters with the flavor descriptors medicinal, refrigerator stale, heated oil, and myristic and vaccenic acids, whereas 10, 20, and 30% brisket patties were clustered with sour, sour aromatics, green hay–like, bloody, metallic, and eicosapentanoic and docosahexaenoic acids. Patties from plate that contained 20% fat were associated with elaidic acid. A loading plot of PCA with aromatic volatiles and sensory attributes indicated that plate 10, 20, and 30% were located at the positive principal component (PC) 1 and PC2 axes and clustered with 2-octanone, dodecane, and cyclotrisfloxane whereas brisket 10, 20, and 30% aromatics were located at negative PC1 and positive PC2, clustered with 2-nonenal, green hay–like, metallic, fat and methane, and thiobis. Flank 10 and 30% were located at negative PC1 and PC2 and associated with medicinal, refrigerator stale, and 2-butanone. Upon loading plot with fatty acid and aromatic volatile compounds, brisket 10, 20, and 30% were located close to the negative portion of the PC1 axes and clustered with 2-nonenal, benzeneethanol, and docosahexaenoic, lignoceric, and pentadecanoic acids. Plate 20% and flank 20% were close to the positive side of PC1 and clustered with pentanal, nonenal, and elaidic, eicosenoic, and palmitic acids. In conclusion, flank patties were highly associated with undesirable flavors, and brisket patties were associated with flavor attributes of iron influence, acidic compounds, and some PUFA. These results confirm our hypothesis that patties from brisket, flank, and plate primals have distinct flavor descriptors and aromatics.

Key Words: gas chromatography, principal component analysis, sensory
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371 The effect of feeding a high-fiber and -fat diet on pig meat quality.

S. Conte*[1], C. Pomar[1], D. Paiano[2], Y. Duan[3], P. Zhang[4], J. Lévesque[5], F. Guay[6], M. Ellis[7], N. Devillers[1], and L. Faucitano[1], [1]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada,* [2]*Department of Animal Science, Universidade do Estado de Santa Catarina, Chapecó, Brazil,* [3]*College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, P.R. China,* [4]*College of Animal Science, Inner Mongolia Agricultural University, Hohhot, P.R. China,* [5]*Centre de Recherche en Sciences Animales de Deschambault, Deschambault, QC, Canada,* [6]*Universite Laval, Quebec City, QC, Canada,* [7]*University of Illinois, Urbana-Champaign.*

The application of strategic finishing diets to reduce the muscle glycogen content at slaughter is considered a method to improve pork meat quality. The objective of this study was to assess the effects of feeding pigs with high-fat and low-digestible-carbohydrate diets in the late finishing period (last 29 d) on meat quality. Four dietary treatments were applied: 1) a control diet (CON; 67.2% corn, 15.5% soybean meal, and 15.0% hard wheat), 2) a high-fat and -fiber diet (HFF; 38.0% corn, 17.9% soybean meal, 15.0% hard wheat, 20.0% oat hulls, and 6.9% fat), 3) a blend of 50:50% CON and HFF diets, and 4) the CON diet for 11 d and then the HFF diet for 11 d after a 7-d diet transition. A total of 160 pigs (119.2 ± 6.2 kg), balanced by gender (barrows and gilts), were raised in 20 pens of 8 pigs each (5 pens per treatment). At the end of the finishing period, pigs were weighed and fasted between 16 and 19 h before slaughter. The whole-blood lactate level was assessed at exsanguination using a hand-held Lactate Scout Analyzer (EKF Diagnostic GmbH, Magdeburg, Germany). On the slaughter day, HCW was recorded and pH was measured at 1 h postmortem in the LM and semimembranous (SM) muscles. Meat quality was also assessed at 24 h postmortem by measuring pHu in the LM, SM, and adductor muscles; color (Minolta L*, a*, and b*) in the LM and SM muscle; and EZ-drip loss in the LM. Analyses were performed using the MIXED procedure of SAS, with the pen as the experimental unit, using treatment, sex, and their interactions in the model. Results indicated neither differences between treatments nor an interactive effect ($P > 0.05$) between sex and treatment for final live weight and any of the postmortem measured variables. These results may indicate either the inefficiency of the applied dietary treatments for meat quality improvement or, based on the low exsanguination blood lactate values (mean and confidence interval of 5.2 mmol/L and 5.8–6.7 mmol/L, respectively), that the stress imposed on pigs before slaughter in this study might not have been sufficiently high to result in meat quality variation.

Key Words: meat quality, pig, strategic feeding
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372 Effect of yeast polysaccharide on meat quality of finishing pigs.

X. Ma*, Z. Tian, Y. Xiong, Y. Qiu, D. Deng, and L. Wang, *Institute of Animal Science, Guangdong Academy of Agricultural Sciences, The Key Laboratory of Animal Nutrition and Feed Science (South China) of Ministry of Agriculture, State Key Laboratory of Livestock and Poultry Breeding, Guangzhou, P.R. China.*

This study was conducted to investigate the roles of yeast polysaccharide (a kind of yeast polysaccharide from Institute of Animal Science, Guangdong Academy of Agricultural Sciences) on meat quality of finishing pigs. A total of 72 Du × (Chang × Da) (about 60 kg BW) were randomly allotted to 1 of 2 dietary treatments on the basis of BW in a completely randomized design. Each treatment consisted of 6 replicates with 6 pigs per replicate. All pigs received the same wheat–soybean meal diet. The pigs in Group 1 (the control) were fed a corn and soybean meal–based diet, whereas pigs in Groups 2 were fed the basal diet supplemented with 0.5 g/kg yeast polysaccharide. This experiment ended when the pigs reached 110 kg BW. On the last day of the experiment, pigs were deprived of food for 16 h before blood samples were obtained for analysis of biochemical indexes. Immediately thereafter, pigs were slaughtered for determination of carcass composition, muscle biochemical parameters, and meat quality. The results showed that yeast polysaccharide did not affect the growth performance of pig. However, yeast polysaccharide significantly decreased the backfat thickness and suet weight. Yeast polysaccharide decreased drip loss of muscle at 24 and 48 h postmortem, and although it increased intramuscular fat content ($P < 0.05$), it also improved the meat color (a* had a trend to increase and b* value had a trend to decrease). Yeast polysaccharide decreased the cortisol level in serum and enhanced antioxidant capacity and glutathione peroxidase activity in serum ($P < 0.05$); yeast polysaccharide also increased the IL-10 and TGF-β and decreased IL-1β and IL-6. Additionally, yeast polysaccharide increased glutathione peroxidase activity and decreased the concentration of malondialdehyde in skeletal muscle ($P < 0.05$) and decreased the concentration of aflatoxin in the liver ($P < 0.05$). We conclude that yeast polysaccharide improved the meat quality by improving the antioxidant and immune function of finishing pigs. The funds are from Key project of Natural Science Foundation of Guangdong Province (2014A030311010) and the earmarked fund for Modern Agro-industry Technology Research System (CARS-36, 2016LM1080).

Key Words: finishing pigs, meat quality,
yeast polysaccharide
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373 Chemical composition, color, and tenderness of beef from Nellore and Nellore × Angus steers fed whole shelled corn diets.

A. C. Rodrigues, M. M. Ladeira*, T. C. Coelho, M. P. Gionbelli, J. M. Oliveira Júnior, and G. M. Moreira, *Universidade Federal de Lavras, Lavras, Brazil.*

The objective was to evaluate quality of beef from Nellore and Nellore × Angus steers fed whole shelled corn (WSC) diets. Thirty-two steers with average BW of 353 kg were used in a completely randomized design using a 2 × 2 factorial arrangement (2 breeds and 2 diets). One diet containing 80% WSC and 20% of a commercial pellet based on soybean meal and minerals (15.1% CP and 2.84 Mcal/kg). The other diet had 74% WSC, 20% of the same proteic-mineral pellet, and 6% of sugarcane bagasse (14.7% CP and 2.75 Mcal/kg). Feeding period was 116 d, steers were fed individually and final BW was 431 and 463 kg for Nellore and crossbred steers ($P < 0.05$), respectively. Twenty-four hours after slaughter, samples were taken from the LM muscle of the left half carcass between 12th and 13th ribs for chemical composition analysis, color (L*, a*, and b*), cooking loss (CL), and shear force (SF). The statistical model included the effects of breed, diet, time, and their interactions. There was no effect ($P > 0.05$) of breed and diet on chemical composition, with mean values for moisture, CP, ether extract, and ash equal to 72.2, 22.88, 3.05, and 1.84%, respectively. There was no effect of diets on CL, SF and color indices (Table 373). However, there was a tendency ($P < 0.10$) of the beef from Nellore steers be less tender than Nellore × Angus steers, only 24 h after slaughter. Aging time increased tenderness and CL and reduced a* values. Beef from Nellore steers had lower CL. In conclusion, beef from Nellore are tougher than beef from Nellore × Angus steers after slaughter but similar after 14 d of aging. In addition, color,

Table 373. Beef quality traits from Nellore and Nellore × Angus steers fed whole shelled corn diets

	Nellore		Angus × Nellore			*P*-value			
Item	Time 0	Time 14	Time 0	Time 14	SEM	Breed	Diet	Time	Breed × time
Tenderness	7.10	3.76	6.42	3.83	0.25	0.19	0.24	<0.01	0.10
Cooking loss	21.4	24.7	25.7	26.8	0.61	<0.01	0.48	0.01	0.13
L*	40.72	40.15	41.85	39.97	0.60	0.57	0.54	0.06	0.30
a*	18.77	14.1	19.29	13.82	0.41	0.83	0.44	<0.01	0.38
b*	12.07	12.73	13.02	12.62	0.28	0.30	0.56	0.71	0.14

CL, and chemical composition of beef from Nellore and Nellore × Angus steers are similar.

Key Words: *Bos indicus*, crossbreed, shear force
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374 Mechanism of continuous high ambient temperature affecting meat quality of finishing pigs.

X. Ma*, Z. Jiang, X. Yang, L. Wang, Y. Xiong, and Z. Tian, *Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, P.R. China.*

This study investigated the effect of high ambient temperature on meat quality and its mechanism in finishing pigs. All pigs received the same wheat–soybean meal diet. Twenty-four Landrace × Large White pigs (60 kg BW) were assigned to 3 groups—those fed ad libitum at 22°C, those fed ad libitum at 35°C, and those fed at 22°C, but fed the amount consumed by those kept at 35°C—and the experiment lasted for 30 d. Feed intake, weight gain, and intramuscular fat content of pigs were reduced, both directly by high temperature and indirectly through reduced feed intake. Transcriptome analysis showed that downregulated genes caused by feed restriction were mainly involved in muscle contraction, muscle development, and muscle system process or differentiation and that upregulated genes were mainly involved in response to nutrient levels or extracellular stimulus. Downregulated genes caused by high temperature were mainly involved in muscle structure and development, energy, or catabolic metabolism, whereas upregulated genes were mainly involved in DNA or protein damage or recombination, cell cycle process or biogenesis, stress response, or immune response. The mechanisms by which high temperature and reduced feed intake affected meat quality were not completely consistent. Apart from its effects of reducing feed intake, a direct effect of high temperature on meat quality also was involved in negatively regulating cell cycle, stimulating protein, DNA damage and cell apoptosis, and heat stress response. Based on this work, microRNA profiles were analyzed and the integrated analysis of microRNA–mRNA expression levels highlighted an inverse correlation between microRNA and their putative target genes, which further verified the negative effects of high ambient temperatures on feed intake and BW gain in finishing pigs. The results in this study indicate that high temperature decreased energy metabolism and muscle tissue development and increased DNA damage or stress response through regulating microRNA and their targets genes.

Key Words: finishing pigs, high temperature, meat quality
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375 Effect of oregano essential oil supplementation to a reduced-protein diet on meat quality, fatty acid composition, and oxidative stability of longissimus thoracis muscle in growing–finishing pigs.

C. Cheng, H. Wei, and J. Peng*, *Department of Animal Nutrition and Feed Science, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, P.R. China.*

This study investigated the effects of reduced-protein diet supplementation with oregano essential oil (OEO) in pigs, from growing period to slaughter (98 d), on meat quality, fatty acid composition, and oxidative stability of longissimus thoracis (LT) muscle. A total of 36 barrows (Large White × Landrace) with an initial BW of 29.0 ± 1.00 kg were obtained from a commercial farm in the Hubei province of China. Pigs were randomly allotted into 1 of 3 treatments based on BW in a randomized complete block design with 12 replicates of 1 pig per replicate. Pigs were individually penned. The three following experimental treatments were applied: 1) normal-protein diet (NPD), 2) reduced-protein diet (RPD), and 3) identical reduced-protein diet supplemented (250 mg/kg feed) with OEO. The 3 diets were based on corn–soybean meal–distiller's dried grains with solubles. The pigs in the NPD group were offered diets that contained 17 and 15.6% protein during the growing (d 0–49) and finishing (d 51–98) periods, respectively, whereas the pigs in the RPD group were offered diets that contained 15 and 13.6% protein during their growing and finishing periods, respectively. Experimental diets were balanced with 4 AA (L-lysine, L-methionine, L-threonine, and L-tryptophan) to meet the requirements of growing–finishing pigs (NRC, 2012). Dietary RPD and OEO increased the Minolta $b^*_{45\text{min}}$, tenderness, overall acceptance, and intramuscular fat (IMF) content of pork compared with dietary NPD ($P < 0.05$). The percentage of n-3 PUFA and the percentage of MUFA in OEO muscle were higher ($P < 0.05$) and lower ($P < 0.05$), respectively, than those in RPD muscle. Dietary OEO improved oxidative stability, total antioxidative capacity, and catalase ($P < 0.01$) but decreased drip loss in LT muscle compared with dietary NPD

and RPD ($P < 0.01$). In our study, reduced-protein diet supplementation with oregano essential oil enhanced the sensory attributes and antioxidative status of pork meat by improving IMF and *n*-3 PUFA percentage and antioxidative capacity.

Key words: reduced-protein diet, oregano essential oil, pigs
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376 Effect of fatty acids on myogenesis and mitochondrial biosynthesis during murine skeletal muscle cell differentiation.

T. Y. Hsueh*, X. Wang, and Y. Huang, *University of Arkansas, Fayetteville, AR.*

Polyunsaturated fatty acids are important nutrients for human health, especially omega-3 fatty acids such as docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA), which have been found to play positive roles in the prevention of various diseases. However, previous studies have reported that DHA and EPA can inhibit myoblast proliferation. In this study, we investigated the effect of fatty acids on mitochondrial function and gene expression in C2C12 myoblast cells in presence during skeletal muscle differentiation. C2C12 myoblasts were cultured to confluency and then treated with differentiation medium that contained fatty acids (50 μM EPA and DHA). After 72 h of myogenic differentiation, cell mRNA was collected and gene expression was analyzed by real-time PCR. Microscopy was used to examine cell morphology following treatment with fatty acids. In addition, the effect of DHA/EPA on cellular oxygen consumption was measured using a Seahorse XF24 Analyzer. Cells treated with fatty acids had fewer myotubes formed compared with control cells. The expression of MRF4 (myogenic regulatory factor 4), MyoD (myogenic differentiation), MyoG (myogenin), and Pax7 (paired box 7), genes related to myogenesis, was significantly lower in cells treated with fatty acids. Genes associated with adipogenesis, aP2 (adipocyte protein 2), c/EBPa (CCAAT/enhancer-binding protein alpha), c/EBPb, PPARg (peroxisome proliferator-activated receptor gamma), CPT1 (carnitine palmitoyltransferase I), and FAT/CD36 (fatty acid translocase), had higher expression after treatment with fatty acids. In addition, the mitochondrial biogenesis decreased with lower Mfn2 (mitofusin 2), ERRa (estrogen related receptor alpha), TFAM (mitochondrial transcription factor A), and PGC1a (peroxisome proliferator-activated receptor gamma coactivator 1-alpha) expression and lower mitochondrial DNA:nuclear DNA ratio in cells treated with fatty acids compared with control cells. However, the expression of PMP70 (70-kDa peroxisomal membrane protein), Pex2 (peroxisomal biogenesis factor 2), and Pex19, genes related to peroxisome biosynthesis, was higher in cells treated with fatty acids. Moreover, fatty acid treatment reduced oxygen consumption rate under oligomycin-inhibited (reflecting proton leak) and uncoupled conditions. Our preliminary data implies that fatty acids might reduce myogenesis and increase adipogenesis in myotube formation. Fatty acids may also decrease cell metabolism by reducing mitochondrial biogenesis as well as respiration rate. This data suggests that a high-fat diet or supplement may affect myotube formation during myogenesis in fetal stage and regeneration of skeletal muscle in adults via impaired mitochondrial metabolism.

Key Words: fatty acids, mitochondria, myogenesis
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NONRUMINANT NUTRITION

A2 Early Career Award Speaker: Optimizing nutrition to support immune and brain development in livestock and humans.

R. Dilger*, *University of Illinois at Urbana-Champaign.*

Strong evidence links establishment of a stable microbiota with development of tissues and organ systems, immunity, and cognitive abilities, and this communication network is often referred to as the gut-brain axis. Nutrition serves as a powerful tool capable of exerting influence over each of these domains, and optimal early-life nutrition is particularly important to avoid permanent alterations in structure and function within the body. Activation of the immune system elicits a coordinated set of metabolic, physiological, and behavioral events, all of which result in reduced animal growth. Thus, immune stimulation serves to alter whole-body protein metabolism to repartition amino acids away from lean tissue accretion and toward production of specialized immune cells and mediators. Additionally, normal gastrointestinal function may be compromised during sickness, as evidenced by decreases in nutrient digestion and absorption. From a nutritional perspective, these circumstances are quite challenging to manage because disease-challenged animals not only consume less feed, but also experience metabolic shifts that compromise profitability. Complex interrelationships between the periphery and brain permit nutritional status, immune activation, and microbial-derived products to alter neurodevelopment and cognitive function. Based on similarities in patterns of gut and brain development, the pig has emerged as a translational animal model for studying effects of early-life nutrition on cognitive function. Use of sensitive analytical techniques, including neuroimaging, behavioral assessments, and molecular quantification, permits an in-depth understanding of how nutrition affects neurodevelopmental patterns. Recent advances to quantify longitudinal volumetric changes during the pre-pubertal period, along with the integration of a high-quality brain atlas and magnetic resonance imaging sequences optimized for the domestic pig, have permitted researchers to establish quantifiable neurodevelopmental links between pigs and humans.

As such, nutritional strategies designed to support immune and brain development, potentially through alteration of the microbiota, are currently being tested to benefit health and well-being of animals and humans alike.

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377 DL-Methionyl-DL-methionine as a methionine source for weaned and growing pigs.

L. S. D. Santos[*1], J. K. Htoo[2], C. Fracaroli[1], W. C. D. Silva[1], J. D. P. Gobi[1], A. M. Veira[1], N. A. Barbosa[3], and L. Hauschild[1], *[1]Sao Paulo State University, Jaboticabal, Brazil, [2]Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany, [3]Evonik Industries do Brazil, São Paulo, Brazil.*

Methionine is often limiting in typical swine diets and balancing with supplemental Met sources to ensure optimal performance of pigs. Two studies were conducted to evaluate the relative bioavailability (RBV) of DL-methionyl-DL-methionine (DL-Met-Met) compared with DL-Met as Met sources in pigs. In Exp. 1, 42 barrows (PIC; 21.0 ± 1.37 kg initial BW) were allotted to 7 experimental diets with 6 replicate pigs per treatment in a nitrogen balance study to evaluate the RBV of DL-Met-Met compared with DL-Met. A basal diet was formulated based on corn and soybean meal using analyzed ingredient AA contents to be deficient in Met (0.23% standardized ileal digestible [SID] Met, 0.47% SID Met + Cys, and 1.15% SID Lys; diet 1) but adequate in all AA. Three graded levels of DL-Met (0.03, 0.06, and 0.09%) or DL-Met-Met (0.0306, 0.0612, and 0.0919%) were supplemented to the basal diet on top to create diets 2 to 7. In Exp. 2, 216 weaned pigs (PIC; 10.2 ± 0.98 kg initial BW) were used. The dietary treatments consisted of a Met-deficient basal diet (0.24% SID Met, 0.53% SID Met + Cys, and 1.30% SID Lys; diet 1), and the same supplemental levels of DL-Met and DL-Met-Met for Exp. 1 were used to produce diets 2 to 7. In Exp. 1, fecal and absorbed N were not different among the 2 Met sources. A linear increase ($P < 0.05$) in N retained (g/d), N retention (% of intake), and N retention (% of absorbed) were observed for supplementations with DL-Met or DL-Met-Met. The linear slope-ratio regression estimated the RBV of 109% (95% confidence interval [CI] 57–160%) for N retention (% of intake), 111% (95% CI 63–158%) for N retained (g/d), and 98% (95% CI 43–154%) for N retention (% of absorbed), respectively, on an equimolar basis. In Exp. 2, the ADG and G:F linearly increased ($P < 0.001$) with additions of DL-Met or DL-Met-Met. Using a slope-ratio procedure, the RBV of DL-Met-Met to DL-Met were estimated to be 104 (95% CI 66–141%) and 117% (95% CI 61–174%) on an equimolar basis for ADG and G:F, respectively. In conclusion, the 95% CI for the RBV of DL-Met-Met covers 100%, indicating DL-Met-Met is at least equally bioavailable as DL-Met as a Met source for pigs.

Key Words: bioavailability, DL-methionyl-DL-methionine, methionine
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378 Effects of replacing pharmacological levels of dietary zinc oxide with lower dietary levels of zinc oxide nanoparticles for weaned piglets.

M. Wang[*1], B. Wang[1], L. Liu[1], J. Zhu[1], J. Zou[2], and D. Leng[2], *[1]College of Animal Science, Zhejiang University, Hangzhou, P.R. China, [2]Jiangxi Innovating Science and Technology Co., Ltd., Nanchang, P.R. China.*

Pharmacological dosage (3,000 mg/kg) of zinc oxide (ZnO) in pig nursery diets was commonly used to improve growth performance and gut health. However, high zinc excretion in animal wastes poses environmental contamination. Zinc oxide nanoparticles (nano-ZnO), with small size and bigger specific surface area, have potential to be used as a substitute for pharmacological ZnO. This study aimed at comparing the effects of nano-ZnO with conventional ZnO. One hundred fifty crossbred (Landrace × Large White × Duroc) weaned piglets (9.37 ± 0.48 kg BW) were randomly allotted to 5 dietary treatments with 3 replicates for 21 d, including a basal diet (BD); the BD + 150, 300, or 450 mg/kg Zn from nano-ZnO; and the BD + 3,000 mg/kg Zn from conventional ZnO. After the feeding trial, 6 pigs from the BD, 450 mg/kg nano-ZnO, and 3,000 mg/kg ZnO treatments were selected and slaughtered to collect samples. All studied parameters were analyzed with 1-way ANOVA, taking into account the experimental treatment as the main factor with α level of 0.05. Supplementation of either 300 or 450 mg/kg nano-ZnO or ZnO increased ($P < 0.05$) ADG, ADFI, and G:F compared with pigs fed the BD. Pigs diarrhea incidence in treatments of 300 and 450 mg/kg nano-ZnO and 3,000 mg/kg ZnO was significantly decreased (57.24, 79.14, and 58.09%, respectively; $P < 0.05$) compared with that in the BD treatment. Supplemental nano-ZnO and ZnO improved ($P < 0.05$) the concentration of Zn in the serum, heart, liver, spleen, and kidney. Compared with the BD, villus height (VH), crypt depth (CD), and the VH:CD ratio in pigs supplemented with 450 mg/kg nano-ZnO exhibited greater ($P < 0.05$) improvement, and CD and the VH:CD ratio were also improved ($P < 0.05$) with 3,000 mg/kg ZnO. The abundance of *Escherichia coli* community of 450 mg/kg nano -ZnO was reduced in the cecum, colon, and rectum (13.85, 13.03, and 11.13%, respectively; $P < 0.05$). The abundance of *Lactobacilli*, *Bifidobacterium*, and *Salmonella* community in different large intestine segments did not differ between the treatments. The results indicated that the nano-ZnO product in low dosage (450 mg/kg) has potential to exhibit beneficial effects, in weaned pigs, which are similar to or better than that of pharmacological dosage (3,000 mg/kg) of conventional

ZnO. Zinc oxide nanoparticles may reduce Zn excretion, which consequently may lower the environmental challenges.

Key Words: weaned piglets, zinc oxide, zinc oxide nanoparticles
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379 Dietary supplementation of microalgal astaxanthin produced dose-dependent enrichments of the phytochemical and elevations of radical absorbance capacity in tissues and eggs of layer hens.

A. D. Magnuson*[1], T. Sun[1], R. Yin[1], G. Liu[1], S. Tolba[1], S. Shinde[2], and X. G. Lei[3], [1]*Cornell University, Ithaca, NY,* [2]*Heliae Development, Gilbert, AZ,* [3]*Department of Animal Science, Cornell University, Ithaca, NY.*

Astaxanthin is a well-known antioxidant phytochemical that has limited bioavailability to humans. The present study was conducted to determine if astaxanthin present in full and defatted microalgae was bioavailable to layer hens and if dietary astaxanthin affected antioxidant status of the hens' tissues and eggs. A total of 50 White Leghorn Shavers (21 wk old) were divided into 5 groups (n = 10/group), individually caged in an environmentally controlled room, and fed a corn–soybean meal basal diet supplemented with microalgal (*Haematococcus pluvialis*) astaxanthin (Heliae, Gilbert, AZ) at 0, 20, 40, 60, and 80 mg/kg for 6 wk. Body weight, feed intake, and egg production and quality were recorded weekly. At the end of study, blood and eggs were collected from all hens and liver samples were collected from 6 hens/group for biochemical analysis. Data were analyzed by 1-way ANOVA. Supplemental astaxanthin showed no effect on feed intake, BW gain, egg production, and egg quality (component weights or shell thickness). Supplemental microalgal astaxanthin resulted in dose-dependent enrichments ($P < 0.05$) of astaxanthin and total carotenoids in the plasma, liver, and egg yolk of hens. The maximal concentrations of astaxanthin reached 4.1 µg/mL, 5.8 mg/kg, and 36 mg/kg whereas those of total carotenoids reached 7.0 µg/mL, 75 mg/kg, and 114 mg/kg (on fresh tissue basis) in the plasma, liver, and egg yolk, respectively, of hens. The oxygen radical absorbance capacity was also enhanced ($P < 0.05$) in a dose-dependent fashion in the liver and egg yolk of hens. Meanwhile, total glutathione concentration and activities of glutathione peroxidase and glutathione reductase in the liver of hens were decreased ($P < 0.05$) by the high dose of astaxanthin (80 mg/kg) supplementation compared with the control. Although the color of egg yolk was changed ($P < 0.05$; more orange) by the astaxanthin supplementation, there were no major changes in the fatty acid profiles of egg yolk caused by the diet treatments. In conclusion, supplemental dietary microalgal astaxanthin seemed to be highly bioavailable to be digested and deposited in the plasma, liver, and eggs of hens and to improve their antioxidant status, except at the highest dose of 80 mg/kg.

Key Words: astaxanthin, bioavailability, redox
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380 Transgenerational effect of feeding genetically modified *maroACC* corn to laying hens and offspring roosters on offspring roosters growth and reproduction.

R. Zhong*[1,2], L. Chen[1], L. Zhang[2], and H. Zhang[2], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P.R. China,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

The aim of this study was to evaluate the chronic effect of feeding a transgenic corn line containing the *maroACC* gene from the *Agrobacterium tumefaciens* strain (CC) to laying hens and their offspring roosters on growth and reproduction of offspring roosters. Healthy White Leghorn laying hens (n = 72 placed in cages; 3 hens/cage) were randomly allotted to 3 corn–soybean meal dietary treatments (8 cages/treatment) formulated with nontransgenic near-isoline control corn (CT), CC corn, or commercially available nontransgenic reference corn (RF). After 12 wk, fertile eggs were collected and hatched for 21 d. A total 108 offspring cockerels were assigned to 3 dietary treatments for 32 wk: 1) CT corn–fed parental hens/CT corn–fed offspring cockerels (CT/CT), 2) CC corn–fed parental hens/CC corn–fed offspring cockerels (CC/CC), and 3) RF corn–fed parental hens/RF corn–fed offspring cockerels (RF/RF). Each dietary treatment had 36 offspring cockerels and was assigned to 6 replicates with 6 offspring cockerels per replicate. Body weight and feed intake were determined weekly. The semen quality was measured at the end of 28 and 30 wk. At the end of 32 wk, offspring roosters were harvested and the carcass yield were recorded (n = 6/treatment). Secondary sex characteristics (the size and weight of rooster cockscomb and whisker) of offspring roosters were measured at the same time. Testes were weighed and sampled for histological analysis. Serum was collected for sex hormone analysis. There was no difference in BW, feed intake, and carcass yield between the CT/CT diet and the CC/CC diet. The testis weight, histology, and health were not affected by the dietary treatment. No difference was observed in semen quality indices between roosters consuming the CT/CT diet and roosters consuming the CC/CC diet. The serum concentration of prolactin and estradiol for roosters fed the CC/CC diet were lower ($P < 0.05$) than for those fed the CT/CT diet. The concentration of FSH, LH, and testosterone were not affected by dietary treatment. The weight and height of rooster cockscomb and the weight and size of rooster whisker for roosters fed the CC/CC diet were similar to those fed the CT/CT diet, but the length and thickness of cockscomb for roosters fed the CC/CC diet were less ($P < 0.01$) than those

fed the CT/CT diet. In conclusion, transgenerational feeding of *maroACC* corn has no negative effect on growth and reproductive performance of offspring roosters.

Key Words: rooster, transgenerational safety, transgenic corn
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381 2-Hydroxy-4-methylselenobutanoic acid exerted a unique regulation of selenogenome, selenoproteins, and selenocystenine-related genes in tissues of broiler chicks.

L. Sun[1], L. Zhao[1], M. Briens[2], S. W. Xu[3], and X. G. Lei[*4], [1]*Department of Animal Nutrition and Feed Science, Huazhong Agricultural University, Wuhan, Hubei, P.R. China,* [2]*Adisseo France S.A.S., Antony, France,* [3]*Department of Veterinary Medicine, Northeast Agricultural University, Harbin, P.R. China,* [4]*Department of Animal Science, Cornell University, Ithaca, NY.*

A new organic Se compound, 2-hydroxy-4-methylselenobutanoic acid (SeO), was shown to be more bioavailable than Na_2SeO_3 or seleno-yeast (SeY) to chicks, hens, and pigs. This study was to determine regulations of 26 selenoprotein genes, 5 selenoproteins (GPX1, GPX4, SELENOP, SELENOW, and SELENOU), and 5 selenocystenine biosynthesis and degradation-related genes (*Pstk*, *SeciSbp2*, *Sephs1*, *SepSecS*, and *Scly*) by the 3 sources of Se in the liver, breast, thigh, and/or plasma of chicks. Day-old male broilers (6 cages/diet and 6 chicks/cage) were fed a Se-deficient, corn/soy–based diet (BD; 0.05 mg Se/kg) or the BD supplemented with Na_2SeO_3, SeY, or SeO at 0.2 mg Se/kg for 6 wk. Growth performance was recorded weekly, and blood and tissue samples were collected from 6 chicks/group for analyses at the end of study. Data were analyzed using 1-way ANOVA. The 3 sources of Se produced no significant differences in the growth performance compared with the BD control. Although all sources of Se enhanced ($P < 0.05$) mRNA levels of *Gpx1*, *Gpx3*, *Selenop*, *Pstk*, and *SepSecS* in the 3 tissues over the BD group, only SeO upregulated ($P < 0.05$) the expression of *Selenos* and *Mrsb1* in the liver and thigh. Compared with Na_2SeO_3, SeO caused greater increases ($P < 0.05$) in expression of *Gpx3* mRNA and GPX4, SELENOU, and SELENOP proteins in the 3 tissues and/or plasma. A greater ($P < 0.05$) expression of GPX4 and SELENOP protein in the 3 tissues and/or plasma and *Selenop* and *SepSecS* mRNA in the 2 muscles was produced by SeO than by SeY. In conclusion, SeO exhibited a unique ability to induce the expression of *Selenos* and *Mrsb1* mRNA and to enhance the production of GPX4 and SEPP1 proteins in the chick tissues. (Supported in part by NSFC 31501987 and 31320103920, NSTSPC-2013BAD20B04, and Adisseo.)

Key Words: chick, muscle, selenium, selenoprotein
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382 Interaction between feeding techniques and ambient temperature on growing pigs' performance and body composition.

L. S. D. Santos[1,2], P. H. R. F. Campos[3], L. Hauschild[*2], W. C. D. Silva[2], A. M. Veira[2], A. Z. Fraga[2], and C. Pomar[4], [1]*FAPESP Scholarship, Sao Paulo, Brazil,* [2]*Sao Paulo State University, Jaboticabal, Brazil,* [3]*UFVJM, Diamantina, Brazil,* [4]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

Pigs maintained in hot environments voluntarily reduce feed intake, and thus growth performance, to lower the heat dissipation burden. Feeding pigs with low-protein diets has been proposed to attenuate the negative effects of heat stress in pigs reared in hot climate areas. The aim of this study was to evaluate the performance and body composition of pigs fed in conventional group-phase feeding systems (CONV) or individually fed with daily tailored diets (precision feeding [PREC]) under 2 thermal conditions (thermoneutral, 23°C, and high temperature, 30°C). Forty-eight 41-kg (±0.98) BW barrow pigs were assigned to treatments (12 animals per treatment) in a 2 × 2 factorial arrangement. The experiment lasted 55 d (phase 1 from d 0 to 27 and phase 2 from d 28 to 55). Conventional group-phase feeding systems–fed pigs received, within each phase, a constant blend of diets A (high nutrient density) and B (low nutrient density) supplying the estimated nutrient requirements of the group, whereas PREC pigs received daily a personalized blend providing the estimated amount of nutrients. Body mineral and lean and fat masses were assessed by dual-energy X-ray absorptiometry at the beginning and at the end of each phase. Data were analyzed using the MIXED procedure of SAS, including the fixed effects of feeding system (FS), ambient temperature (AT), and their interactions. Initial BW was included as a covariate. Average daily feed intake, ADG, NE intake, and lysine intake were lower at 30°C than at 23°C ($P < 0.01$) but were similar within FS. Lysine intake was lower in PREC pigs than in CONV pigs at both 23 and 30°C (−16.9 and −14.1%, respectively) but had similar growth performance. The means of protein and lipid gain and body protein and lipid content were different ($P < 0.01$) for AT independently of FS. In the PREC pigs, bone mineral content was lower ($P = 0.01$) than in the CONV pigs (1.16 and 1.26 kg) at 23°C. The results of this study indicate that precision feeding may be an efficient strategy for high as well as thermoneutral temperatures, reducing the excessive nutrient intake of pigs without impairing the performance and body composition.

Key Words: dual X-ray absorptiometry, lysine requirement, precision feeding
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383 Highly processed soy protein is an alternative protein source to fishmeal for weaned piglets.

M. A. Ton Nu*[1], H. Hall[2], H. MaseyONeill[2], and H. Schulze[2], [1]*Agro Korn a/s, Videbæk, Denmark,* [2]*AB Agri Ltd., Peterborough, UK.*

The objective of the study was to evaluate the effect of replacing fishmeal with highly processed soy proteins with low content of anti-nutritional factors (ANF), AlphaSoy 530 (SP1), AlphaSoy (SP2), and HP 300 (SP3), on growth performance of weaned piglets. A total of 180 weaned piglets (JSR Genpacker and 90 PIC Camborough; 8.55 kg initial BW) were randomly allocated to 4 dietary treatments. There were 5 pigs/pen and 9 replicate pens/treatment (5 pens with barrows and 4 pens with gilts). Three diets based on wheat, barley, and SBM were fed from d 0 to 9 (Phase 1), d 9 to 22 (Phase 2), and d 22 to 36 (Phase 3). In phases 1 and 2, fishmeal (6 and 3%, respectively) was replaced by 7.5% of SP1, SP2, or SP3. A commercial grower diet without dietary treatments was fed to all groups in Phase 3. All diets in each phase were isocaloric and isonitrogenous. Growth performance was measured at d 9, 22, and 36. Diet, sex, and diet × sex served as fixed effects in the statistical model. No interaction of diet and sex was detected; therefore, only main effects are discussed. The in vitro enzyme digestible OM at the ileal level was comparable among treatments in Phase 1 (84.2–85.9%) and Phase 2 (83–86.5%). The stachyose and raffinose content of diets was in the range of 0.92 to 1.43% (Phase 1) and 1.06 to 1.26% (Phase 2). The trypsin inhibitor activity was low in all treatments (<0.5–0.5 mg/g in Phase 1 and 0.5–0.6 mg/g in Phase 2). In Phase 1, pigs fed highly processed soy proteins had a lower ADG and BW (except pigs fed SP2) compared with pigs fed fishmeal ($P < 0.05$). However, the FCR of pigs was the same between treatments ($P > 0.1$). In Phase 2, feeding SP1 diets improved the FCR of pigs compared with feeding fishmeal (7% increase) or SP3 (10% increase; $P = 0.017$). The growth performance of pigs was similar between treatments in Phase 3 and over the whole period of d 0 to 36 ($P > 0.1$). Barrows tended to have a lower FCR than gilts in Phase 2 and 3 and overall (d 0 to 36; $P < 0.1$); however, sex had no effect on other parameters ($P > 0.1$). In conclusion, highly processed soy protein with low ANF, especially SP1 and SP2, is a good alternative protein source to fishmeal in the diet of weaned piglets.

Key Words: alternative protein, piglet, soybean
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384 Effects of dietary supplementation of natural feed additives on growth performance of nursery pigs.

S. M. Mendoza*[1], G. R. Murugesan[1], E. G. Hendel[1], E. Kadas-Toth[2], and A. Kovacs[2], [1]*BIOMIN America Inc., San Antonio, TX,* [2]*BIOMIN Holding GmbH, Getzersdorf, Austria.*

The present experiment investigates the effects of 2 natural feed additives (Biotronic Top3 [OA], a blend of formic, propionic, and acetic acids combined with cinnamaldehyde and permeabilizing complex, and Digestarom P.E.P. [EO], a phytogenic blend of oregano, anise, and citrus oil and fructooligosaccharide) on growth performance of nursery pigs. Weaning pigs (PIC 280 × 1050; $n = 360$; 6.22 ± 1.4 kg BW; 22 d) were allotted 10 pigs per pen, for a total of 36 pens, and pens were assigned within weight blocks to 1 of the 3 dietary treatments (12 pens/diet). The dietary treatments were 1) basal diet (NC), 2) NC + 0.1% OA, and 3) NC + 0.1% OA + 0.0125% of EO (OA+EO). Experimental diets were provided in 2 phases (phase 1, 0–8 d, and phase 2, 8–22 d after weaning). Diets were corn–soybean meal–dry whey based and formulated to contain 4.35 and 4.10 g standardized ileal digestible lysine/Mcal ME for phase 1 and 2, respectively. Diets did not contain in-feed antibiotics. Body weight and feed disappearance were measured weekly. Least squares means were analyzed using a *t*-test. For the 22-d period, supplementation of OA+EO, compared with the NC, increased final BW (10.53 vs. 10.85 kg; $P = 0.012$) and G:F (0.722 vs. 0.775 g/g; $P = 0.015$), tended to increase ADG (193 vs. 210 g/d; $P = 0.062$), and did not affect ADFI (272 vs. 267 g/d; $P = 0.341$). For the 22-d period, supplementation of OA did not affect BW (10.76 kg; $P \leq 0.135$), ADG (0.202 g/d; $P \leq 0.135$), ADFI (0.273 g/d; $P \leq 0.393$), and G:F (0.273 g/g; $P \leq 0.097$) compared with OA+EO and NC. Overall, the supplementation of OA in combination of EO improved nursery pig performance. Biotronic Top3 and Digestarom P.E.P. provided a viable natural alternative to promote growth and feed efficiency in nursery pigs.

Key Words: essential oil, gain to feed, organic acid
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385 Effects of supplementing sow diets with *Saccharomyces cerevisiae* refermented sorghum dried distiller's grains with solubles from late gestation to weaning on the performance of sows and progeny.

D. Song*[1], F. Wang[1], Z. Lu[2], and Y. Wang[1], [1]*College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China,* [2]*Institute of Feed Science, College of Animal Science, Zhejiang University, Hangzhou, P.R. China.*

Limited nutrient intake in combination with the increased demand for milk production required to support a large litter often leaves sows in a severe catabolic condition and reduces sow longevity for reproduction. Dietary supplementation with

yeast culture (YC) in the gestation and lactation diets of sows has been shown to increase the performance of progeny. In the present study, a novel type of YC, *Saccharomyces cerevisiae* refermented SDDGS (SSDDGS), was developed, and the effects of supplementing sow diets with SSDDGS from late gestation to weaning on the performance of the sows and their progeny were studied. In Exp. 1, 24 sows at 85 d of gestation were allocated to the following 3 dietary treatments: 1) sows fed a basal diet from late gestation to weaning ($n = 8$), 2) sows fed a diet with 2% SSDDGS ($n = 8$), and 3) sows fed a diet with 4% SSDDGS ($n = 8$). The 4% SSDDGS treatment significantly improved the sows' ADFI, the litter weaning alive rate, and the individual piglet weaning weights and significantly reduced the litter stillbirth rate and the levels of urea N and somatic cell counts (SCC) in the milk. However, the 2% SSDDGS treatment did not alter the performance of the sows or progeny. Therefore, we considered the volume of 4% SSDDGS to be more efficient than 2% SSDDGS. To verify the results of Exp. 1, we performed Exp. 2, in which 60 sows at 85 d of gestation were allocated into the following 2 dietary treatments: 1) sows fed a basal gestation diet from 85 d of gestation to weaning ($n = 30$) and 2) sows fed a basal diet with 4% SSDDGS from 85 d of gestation to weaning ($n = 30$). The 4% SSDDGS supplementation tended to increase the sows' ADFI, litter weaning size, litter weight gain during lactation, and individual piglet weaning weight and weight gain during lactation, and it also increased the milk yield and the fat and DM contents of the milk. This treatment also decreased the levels of urea N and SCC in the milk. Therefore, the present study indicates that supplementing sow diets with 4% SSDDGS from late gestation to weaning has the potential to 1) increase sow ADFI, 2) promote progeny growth performance, 3) increase sow milk production and quality, and 4) improve the maternal health status as indicated by improved protein utilization and reduced potential inflammatory response.

Key Words: *Saccharomyces cerevisiae* fermented sorghum distiller's grains, sow, yeast culture
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386 Dietary calcium and phosphate levels affect bone development and marrow adipose tissue deposition in neonatal pigs.

W. Zhang*[1], R. L. Murray[1], C. Guiltinan[1], L. Zhao[2], K. Kroscher[2], R. P. Rhoads[2], and C. H. Stahl[1], [1]*University of Maryland, College Park,* [2]*Virginia Tech, Blacksburg.*

A deficit in bone development during early life has been associated with increased likelihood of developing osteoporosis later in life. Dietary Ca and phosphate play a pivotal role in bone development, which is largely orchestrated by the cellular activities osteogenesis, ostoclastogenesis, and adipogenesis. This study aims to determine the impact of different concentrations of dietary Ca and phosphate supplementation on bone development and mesenchymal stem cell (MSC) programming. Twenty-seven newborn neonatal pigs ($n = 27$; 24 ± 6 h) were randomly assigned into 3 groups and received a milk replacer diet for 16 d. Diets were isonitrogenous and isocaloric but had varying concentrations of Ca and phosphate. The diets were designed to be 25% deficient, adequate, or 25% in excess (NRC standard) of Ca and phosphate requirements. Bone mineral content, serum mineral and hormone concentrations, and activity of MSC were determined. Serum phosphate concentrations were significantly higher in pigs receiving the adequate diet compared with those fed the deficient diet on d 8 but lower among pigs fed the excess diet compared with those fed the deficient diet on d 16 ($P < 0.05$). Serum FGF23 concentrations were greater among the pigs fed the deficient diet than those fed the excess diet on d 16 (77.21 ± 1.90 vs. 70.38 ± 1.90 pg/mL; $P < 0.05$). Pigs receiving the diet containing excess Ca and phosphate had significantly higher bone ash and bone volume compared with the deficient group. We determined in vivo proliferation of the MSC with BrdU, and there was greater cell proliferation in pigs fed the adequate diet than in those fed the deficient diet (8.9% ± 0.7 vs. 6.3% ± 0.7; $P < 0.05$). Calcium and phosphate deficiency shifted MSC towards adipogenic differentiation, as indicated by both Oil Red O staining and increased gene expression of key adipogenic factors such as PPARγ2, FABP4, and LPL. Meanwhile, osteogenesis in the deficient group was reduced compared with adequate group, which was illustrated by lower expression of master osteogenic regulator osteocalcin. This study demonstrates the importance of even minor deficiencies in neonatal Ca and phosphate intake and their impact on bone mineral acquisition and in shaping MSC activity and lineage allocation.

Key Words: calcium and phosphate, mesenchymal stem cell, neonatal pigs
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387 A comparison of total collection and index method estimates of energy values of full fat soybean using regressing method for growing pigs.

F. Zhang*, *Purdue University, West Lafayette, IN.*

This experiment was conducted to compare total collection (TC) and index method (IM), including Cr_2O_3, TiO_2, and AIA, for determining the energy values of full fat soybean (FFS) using the regression method. Twenty-four barrows with an average initial BW of 20 kg were assigned to 3 diets in a randomized complete block design. The 3 diets consisted of a corn–soybean meal reference diet (RD) and the RD + 75 or 150 g/kg FFS, and all diets contained 3 index markers (5 g/kg Cr_2O_3, 5 g/kg TiO_2, and 20 g/kg AIA). Each diet was fed to 8 barrows in individual metabolism crates for a 5-d acclimation followed by a 5-d total collection of feces and urine separately. All data were analyzed as split-plot experiments, where the FFS level was the main-plot factor and measurement method including TC or IM with different markers was the split-plot factor. Results showed that the fecal marker recovery was

90.0, 90.9, and 93.3% for TiO_2, Cr_2O_3, and AIA, respectively, when compared with total collection. The substitution of FFS linearly reduced ($P < 0.05$) both dietary DE and ME. With the increase of FFS level, the dietary DE was linearly decreased based on TC, AIA, and TiO_2 measurements, but not for Cr_2O_3, resulting in an FFS level by measurement method for dietary DE ($P = 0.056$). The results also showed that the determined dietary DE was lower using TiO_2 compared with TC, Cr_2O_3, and AIA ($P < 0.05$). And the dietary ME determined by TiO_2 was lower than TC and AIA ($P < 0.05$) but similar to Cr_2O_3. The energy value of FFS was determined by the regression method. The TC-derived DE and ME of FFS were 4,131 and 3,873 kcal/kg, respectively. The DE and ME of FFS were 4,072 and 3,814 kcal/kg DM, respectively, using Cr_2O_3; 3,935 and 3,867 kcal/kg DM, respectively, using TiO_2; or 3,991 and 3,734 kcal/kg DM, respectively, using AIA. The DE of FFS using TC method was not different from those obtained from Cr_2O_3 and AIA but higher than the DE value obtained from TiO_2 ($P < 0.05$). In conclusion, the IM is as robust as TC to derive DE of FFS using the regression method, but the accuracy may be dependent on the marker.

Key Words: index method, regression method, total collection
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388 Fitting prediction equations of the metabolizable energy of corn obtained from different harvests for piglets.

L. A. C. Esteves[1], L. D. Castilha[2], M. R. Fachinello[1], N. T. E. D. Oliveira[3], R. V. Nunes[4], and P. C. Pozza*[5], [1]*Universidade Estadual de Maringá/CAPES, Maringá, PR, Brazil,* [2]*Universidade Estadual de Maringá, Maringá, Brazil,* [3]*Universidade Estadual do Oeste do Paraná, Marechal Cândido Rondon, Brazil,* [4]*Universidade Estadual do Oeste do Paraná/CNPq, Marechal Cândido Rondon, Brazil,* [5]*Universidade Estadual de Maringá/CNPq, Maringá, Brazil.*

This study aimed to fit prediction equations of the ME from the chemical composition of corn obtained from different harvests for piglets. Two experiments were carried out in a controlled-temperature room to determine the ME values of 18 corn cultivars. In Exp. 1 and 2, the corn from the second (planting from January–March) and the first (planting from August–December) harvests, respectively, were evaluated. In each experiment, 40 crossbred barrows (9.48 ± 0.06 kg in Exp. 1 and 8.75 ± 0.22 kg in Exp. 2) were individually housed in metabolic cages and allotted in a randomized block design with 9 treatments (corn cultivars replaced 25% of the reference feed), 4 replicates, and 1 animal per experimental unit. The amount of daily feed was calculated based on metabolic weight ($BW^{0.75}$). Feed was provided 4 times a day (0700, 1030, 1330, and 1600 h) and the water was provided on the same feeder at 5 mL/g of feed. The experiment lasted 12 d, with a 7-d adjustment period followed by a period of 5 d of total collection of feces and urine. The fit prediction equations of ME of corn were carried out by means of the simple and multiple linear regression procedure through indirect disposal techniques (backward). The regressors used to fit the model were GE, CP, ether extract (EE), ash, starch (ST), NDF, ADF, Ca, and P, on a DM basis. In general, the ME values of corn for the first and second crops ranged from 3,281 to 3,509 kcal/kg and from 3,143 to 3,652 kcal/kg, as-fed basis, respectively. The greater variation of the ME in the second crop justified the fit of equations for the different crops or that corn from both crops was used to fit these equations. The equations fitted to predict ME presented determination coefficients (R^2) that demand the validation of these equations. The best fit to predict the ME of corn for piglets was represented by $ME = -6{,}306.15 + 400.652ADF + 117.286ST + 24{,}924.7Ca + 2{,}489.66P - 148.406CP$ ($R^2 = 0.44$) for the first corn crop; $ME = -7{,}560.08 + 2.66895GE - 120.688ADF$ ($R^2 = 0.48$) for the second corn crop; and $ME = 2{,}848.95 + 68.5714NDF + 161.938EE - 5{,}563.51Ca - 1{,}454.15P$ for the combined period of both crops.

Key Words: chemical composition, metabolizability, range
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389 Energy values of wheat bran are additive in corn–soybean meal–based swine diets.

S. H. Lee, H. Jo*, and B. G. Kim, *Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea (South).*

The objective of this experiment was to verify the additivity of energy value of wheat bran (WB) in corn–soybean meal (SBM)–based diets fed to pigs. Four experimental diets based on the corn and SBM were formulated to contain 0, 10, 20, or 30% of WB with the constant ratio of corn and SBM at 3.4:1. Eight crossbred barrows with a mean initial BW of 63.1 kg ± 3.4 were individually housed in metabolism crates equipped with a feeder. The animals were allocated to a replicated 4 × 4 Latin square design with 4 diets, 4 periods, and 8 pigs.

Table 389. Energy values of experimental diets fed to pigs, as-fed basis

	Wheat bran, %					*P*-values	
Item	0	10	20	30	SEM	Linear	Quadratic
Diet DE, kcal/kg	3,667	3,592	3,551	3,493	32	<0.001	0.794
DE:GE ratio	0.919	0.895	0.879	0.861	0.008	<0.001	0.698
Diet ME, kcal/kg	3,613	3,542	3,494	3,431	34	<0.001	0.909
ME:DE ratio	0.985	0.986	0.984	0.982	0.001	0.077	0.364

Each period consisted of a 4-d period of adaptation to the experimental diet and a 4-d collection period. Feces were collected using the marker-to-marker procedure and urine was collected from 1400 h on d 5 to 1400 h on d 9 of each period. The daily fecal output and daily fecal energy output linearly increased ($P < 0.001$) with WB inclusion rate. The DE:GE ratio linearly decreased ($P < 0.001$) as WB inclusion rate increased. As dietary WB increased, the DE and ME values of the experimental diets linearly decreased ($P < 0.001$) without quadratic effect. Based on the linear changes of DE and ME values with WB inclusion rate, we conclude that the DE and ME values of WB are additive up to 30% inclusion rate in corn–SBM–based diets fed to pigs.

Key Words: additivity, metabolizable energy, pigs
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390 The effects of length of feeding, dietary electrolyte balance, and energy source on ileal endogenous amino acid losses in pigs fed nitrogen-free diets.

S. Adedokun*, K. Dong, and D. L. Harmon, *University of Kentucky, Lexington.*

An experiment was conducted to investigate the effect of dietary factors on ileal endogenous AA (EAA) losses in pigs fed a N-free diet (NFD). Sixteen cannulated pigs were used to evaluate the effect of length of feeding, dietary electrolyte balance (DEB; low vs. high), and energy source (corn starch vs. dextrose) on ileal EAA losses. Pigs were fed 4 diets for 2 periods in a crossover design with 4 blocks of 4 pigs per block within each of the 2 periods. The average initial BW in periods 1 and 2 were 28.3 ± 0.95 and 30.6 ± 1.09, respectively. Each period lasted 7 d with a 12-h ileal digesta collection on d 3 and 4 and d 6 and 7. Pigs received a daily feed allowance of approximately 4% of their BW. There were no 3- or 2-way interactions except for DEB × energy source, where low DEB and dextrose resulted in higher ($P < 0.05$) endogenous loss of N, Arg, Lys, Ala, Gly, Pro, and total AA compared with losses from pigs fed a NFD with high DEB and dextrose. The length of feeding of the NFD was not significant for most of the AA except for Arg, Gly, Pro, total AA, and N, where feeding for 6 to 7 d resulted in higher ($P < 0.05$) losses. Low dietary DEB resulted in higher ($P < 0.05$) Thr, Cys, Gly, and Ser losses. Dextrose as a source of energy resulted in higher endogenous losses for most of the AA except for Arg, Lys, Ala, Gly, Pro, and total AA. The effect of length of feeding was most pronounced for Pro, where endogenous loss increased by 82% (2,620 vs. 4,780 mg/kg DMI) with increasing length of feeding. Finally, dextrose resulted in higher EAA loss and the length of feeding of the NFD could be reduced to 3 to 4 d without any significant effects on losses compared with when the diet is fed for 6 to 7 d.

Key Words: cannulated pig, endogenous amino acid, length of feeding
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391 Ileal amino acid and phosphorus digestibility of fermented corn–soybean meal mixed feed with *Bacillus subtilis* and *Enterococcus faecium* fed to pigs.

C. Shi*[1], Z. Yu[1], Y. Yin[2], Z. Lu[1], and Y. Wang[3], [1]*Institute of Feed Science, College of Animal Science, Zhejiang University, Hangzhou, P.R. China,* [2]*Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, P.R. China,* [3]*College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China.*

In the present study, a 2-stage solid-state fermentation (TS-SSF) process using *Bacillus subtilis* followed by *Enterococcus faecium* was carried out with the purpose of improving the nutritional quality of corn and soybean meal mixed feed (MF). The matrix of native MF and fermented mixed feed (FMF) was analyzed using scanning electron microscopy to determine external structures during solid-state fermentation. Results of the present study indicated that the FMF contained a greater concentration of CP and total P compared with the unfermented feed, whereas the contents of β-conglycinin, glycinin, phytate P, and NDF in FMF declined by 77.6, 86.7, 41.2, and 38.9%, respectively. It is worth noting that the content of trichloroacetic acid–soluble protein, particularly those of small peptides and free AA, increased more than 3 times after TS-SSF. Scanning electron microscopy revealed that irregular shapes and rough surfaces were mainly observed in FMF whereas the microstructure of untreated MF was regular and the surface was smooth. Two animal experiments were conducted to evaluate the digestibility of CP and P in FMF when fed to pigs. In Exp. 1, 6 barrows (15.20 ± 1.27 kg initial BW) fitted with a T-cannula in the distal ileum were allotted to a 3 × 3 Latin square with 3 diets and 3 periods per square. Two diets containing unfermented MF or FMF as the only source of protein and a N-free diet were formulated. Results indicated that the apparent ileal digestibility of 6 indispensable AA (Arg, Ile, Leu, Lys, Met, and Thr) and 2 dispensable AA (Ala and Gly) in FMF were greater ($P < 0.05$) than in untreated MF. The standardized ileal digestibility of 4 AA (Ile, Leu, Lys, and Ala) in FMF was also greater ($P < 0.05$) than in MF. In Exp. 2, 16 barrows (17.57 ± 1.08 kg initial BW) were allotted to 2 diets formulated to contain MF or FMF as the sole source of P to determine the digestibility of P. The apparent total tract digestibility and standard total tract digestibility of P in FMF were 58.14 and 64.72%, respectively. These values were greater ($P < 0.01$) than in untreated MF (37.11 and 44.89%, respectively). Our results suggest that the TS-SSF process using *B. subtilis* followed by *E. faecium* offers an effective approach to improving the quality of corn and soybean meal MF.

Key Words: corn–soybean meal mixed feed, digestibility, two-stage solid-state fermentation
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392 Effect of dietary fiber type with different viscosity and fermentability on the standardized ileal digestibility of amino acids and intestinal digestion of carbohydrate component in a corn–soybean meal diet fed to growing pigs.

L. Chen*[1], L. Gao[2], R. Zhong[1], L. Zhang[2], J. Liu[1], X. Tang[1], and H. Zhang[2], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P.R. China*, [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

Two experiments were conducted to determine the effect of 2 dietary fiber with different viscosity and fermentability on the ileal AA digestibility and intestinal digestion and hindgut fermentation of carbohydrate (CHO) component in growing pigs. In Exp. 1, 6 ileal-cannulated gilts (21.4 ± 1.5 kg initial BW) were allotted to a replicated 3 × 3 Latin square design with 3 diets and 3 periods. The pigs were provided a corn–soybean meal control diet or a diet with 5% inulin (INU) or carboxymethylcellulose sodium (CMC). The apparent ileal digestibility (AID) of AA was measured. The AID and apparent total tract digestibility (ATTD) of carbohydrate components were also determined in the ileal and fecal samples. In Exp. 2, 6 ileal-cannulated pigs were fed a N-free diet and standardized ileal digestibility (SID) of AA was calculated for 3 diets. The AID and SID of Arg, His, Ile, Leu, Lys, Phe, Thr, and Val were greater ($P < 0.05$) in the CMC diet than in the control and INU diets. Pigs fed the CMC diet had greater ($P < 0.05$) AID and SID of Ala, Asp, Cys, Gly, and Ser compared with pigs fed the control and INU diets. There was also a tendency ($P = 0.09$) for the AID of Met to be greater in the CMC diet than in the INU diet. The SID of all AA was not affected by incorporation of 5% INU into the corn–soybean meal diet. Inclusion of 5% CMC in the diet increased ($P < 0.01$) the AID of starch and β-glucan compared with the INU diet. Inclusion of 5% INU (6.3%) in the diet reduced ($P < 0.01$) the AID of soluble nonstarch polysaccharides (NSP) compared with the control (20.9%) and CMC (29.7%) groups. Addition of 5% CMC in the diet reduced ($P < 0.01$) the ATTD of total CHO, soluble NSP, insoluble NSP, total NSP, and cellulose compared with the control and INU diets. Inclusion of 5% CMC in the diet reduced ($P < 0.01$) the hindgut fermentation of soluble NSP, insoluble NSP, total NSP, β-glucan, and cellulose compared with the control and INU diets. In conclusion, addition of 5% INU into a corn–soybean meal diet had a low digestibility of the carbohydrate component in the upper gut and high hindgut fermentation for total NSP. In contrast, the CMC increased the ileal AA digestion and reduced total tract digestion and hindgut fermentation of the carbohydrate component.

Key Words: amino acid, carbohydrate component, digestibility
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393 Amino acid digestibility of full-fat canola seed and solvent-extracted and expeller-derived canola meals in broiler chickens and pigs.

C. S. Park*[1], A. Helmbrecht[2], J. K. Htoo[2], and O. Adeola[1], [1]*Department of Animal Sciences, Purdue University, West Lafayette, IN*, [2]*Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany.*

The objective of this study was to compare the apparent ileal digestibility (AID) and standardized ileal digestibility (SID) of CP and AA in full-fat canola seed (FFCS), solvent-extracted canola meal (SECM), and expeller-derived canola meal (EXCM) for broiler chickens with those for pigs. Three semipurified diets were prepared to contain FFCS, SECM, or EXCM as the sole source of nitrogen. A nitrogen-free diet was also formulated to estimate the basal ileal endogenous losses of CP and AA. A total of 272 male broiler chickens (932 ± 80.6 g initial BW; 21 d after hatching) were allotted to 4 experimental diets in a randomized complete block design with BW as a blocking factor. Birds had free access to experimental diets for 5 d, and ileal digesta samples were collected after birds were euthanized by sodium pentobarbital. Sixteen barrows (18.8 ± 0.75 kg initial BW) surgically fitted with T-cannula at the distal ileum were divided into 4 blocks based on BW and assigned to experimental diets for 2 consecutive periods. In each experimental period, ileal digesta samples were collected during 2 d of collection periods. A 2 × 3 factorial treatment arrangement was applied to determine the effect of species (broiler chickens or pigs) and 3 feed ingredients (FFCS, SECM, or EXCM). Pairwise comparison among digestibility of CP and AA in feed ingredients were conducted within species. There were interactions ($P < 0.05$) between species and feed ingredients in digestibility of indispensable AA except for Lys. In broiler chickens, the AID of most of indispensable AA in FFCS were greater ($P < 0.05$) than those in SECM but were not different from those in EXCM. In pigs, however, the AID of most of indispensable AA in EXCM were greater ($P < 0.05$) than those in FFCS but were not different from those in SECM. The SID of Arg, His, Leu, and Thr in broiler chickens fed FFCS were greater ($P < 0.05$) than in those fed SECM but were not different from those fed EXCM. In pigs, the SID of Arg, His, Ile, Leu, Phe, Thr, and Val in EXCM were greater ($P < 0.05$) than those in FFCS but were not different from those in SECM. The SID of Arg, Ile, Leu, Lys, Met, Phe, Trp, and Val in broiler chickens were greater ($P < 0.05$) than those in pigs. In conclusion, species differences in digestibility of AA exist among canola seed products.

Key Words: poultry, protein, swine
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394 Effect of supplemental protease on growth performance, nutrient digestibility, and gut health in nursery pigs fed diets with corn or sorghum.

H. Chen[*], I. Park, S. Zhang, and S. W. Kim, *North Carolina State University, Raleigh.*

A total of 144 pigs (18.4 ± 2.3 kg initial BW at 6 wk of age) were used in a 40-d trial to evaluate effects of protease (300,000 units/kg feed; BioResource International, Inc., Durham, NC) on growth performance, apparent ileal digestibility (AID) of nutrients, and gut health of nursery pigs fed diets with sorghum. Pigs were randomly allotted to 4 treatments (12 pens per treatment and 3 pigs per pen) in a 2 × 2 factorial arrangement (corn or sorghum basal diet and 0 or 0.05% protease as 2 factors) with sex and initial BW as blocks. The experimental period had phase 1 (d 1 to 21) and phase 2 (d 22 to 40). About 65 (phase 1) and 72% (phase 2) of cereal grains were used in corn- or sorghum-based diets. Both cereals were ground to 400 µm. Body weight and feed intake were recorded weekly. On d 35, serum was collected to quantify tumor necrosis factor-alpha (TNF-α) and malondialdehyde (MDA). On d 40, 32 pigs (8 pigs per treatment) were euthanized to collect digesta from the jejunum and ileum (for viscosity and AID), tissues (for morphology), and mucosa samples (for TNF-α and MDA) from the duodenum, jejunum, and ileum. Replacing corn with sorghum in the diet increased ($P < 0.05$) overall ADG (from 756 to 787 g/d) and ADFI (from 1,374 to 1,473 g/d), reduced ($P < 0.05$) overall G:F (from 0.553 to 0.537), and did not affect nutrient digestibility. Pigs fed diets with sorghum had a lower ($P < 0.05$) MDA content in serum (from 14.61 to 6.48 µ*M*) and the jejunum (1.42 to 0.91 µmol/g protein) and a reduced ($P < 0.05$) villus height (from 492 to 396 µm) and crypt depth (from 310 to 257 µm) in the jejunum. Dietary protease improved ($P < 0.05$) AID of CP (from 81.8 to 86.0%), decreased the MDA level (from 1.20 to 0.98 µmol/g protein) in the duodenum, and increased ($P < 0.05$) the ratio of villus height to crypt depth (from 1.08 to 1.21) in the duodenum. Overall, use of sorghum fully replacing corn in nursery diets could be beneficial to nursery pigs with enhanced feed intake and growth of nursery pigs potentially by reducing oxidative stress. Supplementation of protease improved protein digestion and gut health, irrespective of sorghum- or corn-based diets.

Key Words: growth performance, protease, sorghum
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395 Effects of dietary lysophospholipid complex on apparent ileal digestibility of fatty acids, intestinal morphology and barrier function, and growth performance in nursery pigs.

L. Zheng[*], I. Park, and S. W. Kim, *North Carolina State University, Raleigh.*

It was hypothesized that dietary lysophospholipid complex could actively be incorporated into the plasma membrane of enterocytes, enhancing cell viability, which could improve intestinal morphology and barrier function. The objective of this experiment was to evaluate the effect of lysophospholipid complex (LPL; Lipidol; Easy Bio, Inc., Korea) on growth, fat utilization, intestinal morphology, barrier function, and immune response of nursery pigs. The LPL was produced by an enzymatic modification of phospholipids with elimination of 1 molecule fatty acid at the sn-2 position. Twenty-four newly weaned pigs (12 barrows and 12 gilts; 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 diet supplemented with either 0 or 0.1% LPL based on 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, ileal digesta were collected to measure apparent ileal digestibility (AID) of crude fat, fatty acids, DM, CP, and GE. Blood samples were collected for analysis of immune response. Duodenum and jejunum segments were collected for morphology evaluation, and mucosa samples were collected for analysis of barrier function and immune response. Data were analyzed using the MIXED procedure of SAS. Dietary LPL increased ($P < 0.05$) ADG (681 to 774 g/d) and ADFI (1,000 to 1,089 g/d) of nursery pigs from d 14 to 19 and tended to increase AID of crude fat (72.7 to 84.2%; $P = 0.086$) and C18:2 (86.7 to 96.4%; $P = 0.059$). Dietary supplementation with LPL increased ($P < 0.05$) villus height in the duodenum (509.3 to 589.2 µm) and in the jejunum (463.1 to 524.2 µm) and tended to increase villus height–to–crypt depth ratio in the duodenum (1.9 to 2.2; $P = 0.086$) and in the jejunum (184.7 to 200.9 µm; $P = 0.062$). Dietary LPL tended to increase claudin-1 (0.21- to 0.25-fold increase; $P = 0.062$) and zonula occludens-1 (0.26- to 0.30-fold increase; $P = 0.056$) in the jejunal epithelial cells and tended to decrease IgG (1.13 to 1.16 mg/mL; $P = 0.083$) in serum. In conclusion, dietary supplementation of LPL improved fat digestibility, intestinal morphology and barrier function, and growth of nursery pigs.

Key Words: apparent ileal digestibility, lysophospholipid, growth performance
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396 Excess dietary leucine level increases the optimal dietary isoleucine-to-lysine ratio in 8- to 21-kilogram pigs.

J. K. Htoo[*1], K. Männer[2], and J. Zentek[2], [1]*Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany,* [2]*Freie Universität Berlin, Berlin, Germany.*

Feeding diets containing excess Leu can lead to branch-chained AA antagonisms, which may increase Ile requirement for pigs. A 28-d study was conducted to evaluate the effect of dietary Leu levels on the dietary standardized ileal digestible (SID) Ile:Lys ratio to optimize performance of 8- to 20-kg pigs. A total of 210 mixed-sex pigs (Danbred × Pietrain; 7.8 ± 0.20 kg initial BW) were assigned to 6 diet regimes using a 2 × 3 factorial arrangement with 2 levels of SID Leu:Lys ratio (110 and 165%) and 3 levels of SID Ile:Lys ratio (50, 54, and 58%) with 7 pen replicates (5 pigs per pen) per treatment. Diets were formulated based on corn, soybean meal, corn gluten meal, and spray-dried blood cells using analyzed ingredient AA contents to meet requirements for AA except for Lys. Lysine was second limiting (1.21% SID Lys) in all diets. Pigs had ad libitum access to mash feed and water. Data were analyzed by ANOVA using the GLM procedure of SAS with initial BW and diets included in the model. Orthogonal–polynomial contrasts were used to determine the effect of SID Leu:Lys ratio (110 vs. 160%) and SID Ile:Lys ratio (50 vs. 54% and 54 vs. 58%) on performance responses. There was no Leu × Ile:Lys ratio interaction ($P > 0.05$) for any measured parameter. During d 0 through 28, increasing SID Leu:Lys ratio from 110 to 160% increased ($P < 0.05$) the final BW, ADG, and G:F. When the diets contained the 110% SID Leu:Lys ratio, the final BW, ADG, ADFI, and G:F increased ($P < 0.05$) by increasing the SID Ile:Lys ratio from 50 to 54%; however, no further improvements were observed by increasing the dietary SID Ile:Lys ratio from 54 to 60% ($P < 0.05$). Under excess dietary Leu (160% SID Leu:Lys ratio), increasing the SID Ile:Lys ratio from 50 to 54% increased ($P < 0.05$) the final BW, ADG and ADFI. The final BW, ADG, and ADFI further increased ($P < 0.01$) by increasing the SID Ile:Lys ratio from 54 to 58% in diets with excess Leu. However, the G:F was not affected by dietary Ile:Lys ratio under excess dietary Leu condition. These results suggest that a dietary SID Ile:Lys ratio of 54% is optimal for 8- to 21-kg pigs when Leu is not in excess. However, pigs need a higher Ile (58% SID Ile:Lys ratio) when the diets contain excess Leu (160% SID Leu:Lys ratio) to maximize the ADFI and ADG.

Key Words: isoleucine, leucine, pigs
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397 Metabolome profile of intestinal content of pigs fed diets with wheat and corn fiber supplemented with multicarbohydrase enzymes.

Z. K. Zeng*[1], G. C. Shurson[1], C. Chen[1], and P. E. Urriola[2], [1]*Department of Animal Science, University of Minnesota, St. Paul,* [2]*University of Minnesota, St. Paul.*

This study evaluated the effects of multienzyme supplementation on growth performance, digestibility of GE and nutrients, and characteristics of intestinal content in growing pigs fed diets containing corn distiller's dried grains with solubles (DDGS) or wheat middlings (WM). Fifty-four individually housed pigs (25.33 ± 0.41 kg) were blocked by BW and sex and randomly assigned to 1 of 6 dietary treatments ($n = 9$) in a 2 × 3 factorial design with 2 levels of carbohydrases (0 vs. 100 mg/kg; 1,500 units/g xylanase, 1,100 units/g beta-glucanase, 110 units/g mannanase, and 35 units/g galactosidase) and 3 basal diets (corn–soybean control [CSB], CSB + 40% DDGS, or CSB + 30% WM). Titanium dioxide (0.5%) and phytase (1,000 phytase units/kg) were added to all diets. On d 29, pigs were euthanized and digesta (jejunum, ileum, and cecum) was collected. The whole digesta was directly submitted to liquid chromatography–mass spectrometry for metabolome analysis. The mono-sugar concentrations at the liquid portion of digesta (centrifuged at 18,000 × g for 10 min) were determined. The partial least squares discriminant analysis model clearly separated cecal metabolomes of the CSB, DDGS, and WM diets (positive and negative detection mode) but not with or without carbohydrases. Dietary treatments differences were not separated based on ileal metabolome. The addition of carbohydrases increased ($P < 0.05$) xylose concentration of jejunal and ileal digesta supernatant only in the WM diet, but not in the CSB and DDGS diets, as indicated by the interaction ($P < 0.05$) between basal diets and carbohydrases addition. The interaction ($P < 0.05$) was also observed for the galactose concentration of ileal fluid, which was increased ($P < 0.05$) by carbohydrase addition into the CSB diet but not into the WM and DDGS diets. The glucose concentration of ileal fluid was improved ($P < 0.05$) by carbohydrase addition regardless of basal diets. Pigs fed CSB diets had greater ($P < 0.05$) glucose and mannose concentration at the ileum and galactose concentration at the cecum compared with pigs fed WM and DDGS diets. The inclusion of DDGS resulted in decreases in the glucose concentration of jejunal fluid and galactose concentration of ileal fluid compared with CSB diets. Pigs fed WM diets had greater mannose concentration at the jejunum and galactose concentration at the ileum compared with pigs fed DDGS diets. The addition of WM also resulted in increases in the xylose concentration of ileal and cecal fluids compared with the CSB and DDGS diets. In conclusion, carbohydrase supplementation increased xylose release at the upper but not the lower digestive tract

Key Words: carbohydrases, metabolomes of digesta, pig
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398 Supplementation of xylanase and mannanase influences in vitro fermentation characteristics of distiller's dried grain with solubles in the large intestine of swine.

U. P. Tiwari* and R. Jha, *University of Hawaii at Manoa, Honolulu.*

Fermentation substrate modulates the composition of the microbial community and the end products of microbial metabolism; hence, substrate may influence nutritional, physiological, and immunological function in pigs. After arabinoxylan, mannan is the second most abundant hemicellulosic polysaccharide present in corn distiller's dried grains with solubles (DDGS) that is not degraded by endogenous enzymes in swine and subsequently reduces the digestibility of other nutrients. Use of byproducts such as DDGS in swine feeding can be enhanced by supplementing with enzymes. Distiller's dried grains with solubles with 3 enzymatic treatments (xylanase, mannanase, and xylanase + mannanase) and without enzymes along with inulin and a blank as a positive and negative control, respectively, were used in this in vitro study to evaluate the effect of supplemental enzymes on fermentation characteristics of DDGS in the large intestine of swine. After a 2-step enzymatic digestion, residues were fermented using fresh pig feces as a microbial inoculum and gas production was periodically recorded for 72 h by means of a pressure transducer. Gas production was then mathematically modeled. The VFA in the fermented liquid phase was measured by gas chromatography. Supplementation with xylanase significantly increased ($P < 0.05$) total gas production (223 to 256 mL gas/g sample incubated). Supplementation with xylanase also significantly increased ($P < 0.05$) production of acetate, total VFA, and propionate; that is, excess propionate produced would provide energy to the animal via gluconeogenesis. Conversely, mannanase supplementation significantly increased production of butyrate ($P < 0.05$), signifying its role in providing energy to colonocytes and supporting gut health.

Key Words: distiller's dried grain with solubles, in vitro fermentation, swine
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399 Prophylactic enrichment of sow milk and intestinal mucosa of piglets by supplementation of arachidonic and eicosapentaenoic acid to sows during lactation.

P. L. Chang*, J. Odle, and E. van Heugten, *North Carolina State University, Raleigh.*

Long-chain PUFA have been shown to improve intestinal barrier function and recovery following intestinal injury in young pigs. The objectives of this study were to determine dose and duration of arachidonic acid (ARA) and eicosapentaenoic acid (EPA) supplementation required to efficiently enrich sow milk and intestinal tissue of suckling piglets and to determine their effects on pre- and postweaning performance. Sows ($n = 60$) were assigned to a randomized complete block design with 5 dietary treatments, consisting of a control (palm kernel oil), 72.5 and 145 g/d of ARA, and 72.5 and 145 g/d of EPA. Sows were supplemented for 14 d prior to weaning with 343 g of lipid mixtures containing the targeted concentrations of ARA and EPA once daily. Concentrations of ARA in milk linearly increased ($P < 0.001$) with ARA supplementation on d 6 (0.53, 3.50, and 6.14% for 0, 72.5, and 145 g/d ARA, respectively) and 13 (0.50, 3.50, and 8.12%) and were greater ($P < 0.001$) on d 13 compared with d 6 for the 145 g/d ARA treatment. Concentrations of ARA in intestinal mucosa of piglets, measured after 7 and 14 d of supplementation in lactation and 7 d after weaning, linearly increased ($P < 0.01$; 9.59, 12.59, and 13.02%) with increasing dietary ARA. Mucosal ARA concentrations increased during lactation but decreased after pigs were weaned (quadratic, $P = 0.006$; 11.42, 13.81, and 9.97% for d 7 and 14 and 7 d after weaning, respectively). Milk EPA concentrations linearly increased ($P < 0.01$) with EPA supplementation on d 6 (0.05, 4.45, and 5.27%) and 13 (0.02, 3.07, and 7.24%) and tended ($P = 0.07$) to be higher on d 13 compared with d 6 when 145 g/d of EPA was fed. Similarly, EPA content of mucosa linearly increased ($P < 0.001$) with dietary supplementation on d 7 (0.15, 2.38, and 6.59%) and 14 (0.16, 3.14, and 5.55%) and 7 d after weaning (0.06, 1.50, and 2.33%). Concentrations of EPA were lower ($P < 0.05$) 7 d after weaning compared with d 14 for 72.5 g/d EPA and d 7 and 14 for 145 g/d EPA. Piglets ($n = 441$) from sows fed the control and 72.5 g/d EPA were 10% heavier at weaning and had 18% greater ADG ($P < 0.05$) than pigs from sows fed 145 g/d ARA, but postweaning performance was unaffected. Supplementation of sows with ARA and EPA progressively increased milk concentrations, which directly increased ARA and EPA profiles in piglet intestinal mucosa. However, intestinal enrichment did not affect postweaning and overall pig performance.

Key Words: intestinal enrichment, long-chain polyunsaturated fatty acids, sows
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400 Proteomic analysis of intestinal mucosa from weaning piglets with feeding *Clostridium butyricum*.

B. Xia*[1], Q. Meng[1], M. Pang[1], Q. Lu[1], and H. Zhang[2], [1]*The State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China.*

Modern breeding technology uses segregated early weaning to raise breeding efficiency at a minimum expense. However, early weaning is a stressful matter that results in intestinal dysfunction. Adding probiotics to the diet is gradually being accepted as an alternative to antibiotics for enteric disease. It has been found that dietary supplementation with probiotics could improve intestinal barrier function and also the ecosystem of the intestinal tract. Because the mechanism of action for improvement of intestinal health by probiotics in weaned piglets is currently unknown, this objective of this study is to determine the mechanism of dietary supplementation with *Clostridium butyricum* in relieving weaning-induced diarrhea. Six weaned pigs (21 d) were assigned to 2 groups according to their littermates and initial BW. The control group was fed a basal diet and the treated group received the basal diet supplemented with 500 mg/kg *Clostridium butyricum*. A label-based tandem mass tags technology was applied to investigate protein changes of the intestinal mucosa of weaned pigs fed with a probiotic. Quantitative proteins with a false discovery rate of less than 1% were identified ($n = 5,367$); of these, a total of 36 differentially expressed proteins were found. Functional analysis indicated that differentially expressed proteins were closely related to responses to stimulus and immune response. With respect to immune response, downregulated proteins,

such as transmembrane glycoprotein NMB and beta-galactoside alpha-2,6-sialyltransferase 1, participated in intestinal disease and innate immune response, whereas upregulated proteins took part in antigen presentation and complement activation pathways such as ficolin-2 and inverted formin-2. For cell growth and proliferation, downregulated proteins were involved in cell proliferation (such as methyl-CpG-binding domain protein 2), cell morphology (such as hexokinase-2), and tissue morphology (such as nuclear distribution protein nudE homolog 1). Additionally, glycoprotein, which is widely involved in immune response and adhesion of pathogens, was observed (such as fucose mutarotase). Based on these results, it could be concluded that adding a probiotic in diets could significantly improve intestinal immune response and adhesion of pathogens in the intestine, which provides new insights into the intestinal regulation mechanisms of probiotics.

Key Words: Piglet, Weaning stress, Intestinal health
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401 Effect of inclusion of a monocomponent amylase in a corn-soybean meal diet on performance and intestinal histology in 1- to 21-day-old broilers.

X. Zhang[*1,2], L. Chen[1], L. Zhang[1], R. Zhong[1,3], L. Zhang[2], and H. Zhang[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*Hebei University of Engineering, Handan, China,* [3]*Department of Animal Sciences, Purdue University, West Lafayette, IN.*

A study was conducted the to test the effects of inclusion of an exogenous monocomponent amylase in a corn-soybean meal diet fed to Arbor Acre broilers from 1 to 21 d of age. Broilers were randomly placed into 48 pens (5 birds/pen) and allocated to 4 treatments with 12 replicates. Amylase was added to a corn-soybean meal control diet (22.7% CP, DM basis) with 0 mg/kg, A0; 75 mg/kg, A75; 375 mg/kg, A375; and 750 mg/kg, A750. Growth performance was monitored weekly. Following slaughter at the end of 21 d of feeding (n = 12/treatment), carcass yield, organ weight, and serum biochemical parameters were determined; small intestine was also sampled for histological analysis. No differences in BW, ADF, ADFI, and G:F of birds were observed by inclusion of amylase in the corn-soybean meal diet. There were no differences in dressing weight, half eviscerated weight, eviscerated weight, abdominal fat weight, and thigh meat weight of birds fed the diets with amylase. Relative weight of heart, liver, spleen, lung, and kidneys were not affected by inclusion of amylase in the control diet. Urea nitrogen content was less ($P < 0.01$) in the A375 and A750 diets than in the A0 and A75 diets. Creatinine content of birds fed the A750 diet was less ($P < 0.01$) than those fed the A0 diet. Duodenal villus height increased (linear, $P < 0.01$) as the level of amylase in the diet increased. Villus height in the ileum decreased to reach a minimum at A75 (quadratic, $P = 0.08$). Crypt depth in the duodenum and jejunum were greater ($P < 0.01$) in the A750 diet than in the A0 diet, but no difference in crypt depth of the duodenum and jejunum of birds fed the A75, A375, and A0 diets. Villus height/crypt depth in the duodenum increased to reach a maximum in the control diet with 75 mg/kg of amylase (quadratic, $P = 0.08$), however, the villus height/crypt depth in the jejunum and ileum decreased to reach a minimum in the control diet with 75 mg/kg of amylase (quadratic, $P < 0.05$). Goblet cells in the duodenum and ileum decreased to reach a minimum in the control diet with 75 mg/kg of amylase (quadratic, $P < 0.05$). Data provided significant insight on histological profile in the small intestine associated with dietary exogenous monocomponent amylase. Inclusion of exogenous amylase in corn-soybean meal diet can improve the duodenum development of broilers.

Key Words: broilers, amylase, intestinal histology
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402 Effects of dietary protease on growth performance and intestinal morphology of weaned pigs.

I. H. Park[*1], J. Kang[2], J. Kim[2], S. Kim[2], J. J. Lee[2], K. Jang[2], B. Kim[2], S. Park[2], D. Mun[2], J. Baek[2], J. Choe[2], J. Y. Cho[1], S. H. Cho[1], and M. Song[2], [1]*DSM Nutrition Korea Ltd., Seoul, Korea, Republic of (South),* [2]*Chungnam National University, Daejeon, Korea, Republic of (South).*

A study was conducted to determine effects of dietary protease on growth performance and intestinal morphology of weaned pigs. A total of 75 weaned pigs (7.06 ± 0.18 kg BW; 28 d old) were randomly assigned to 3 dietary treatments (5 pigs/pen; 5 pens/treatment) in a randomized complete block design (block = BW). The dietary treatments were 1) a diet based on corn and soybean meal to meet or exceed the requirement of crude protein as a positive control (PC; CP = 24.17%), 2) a low protein diet as a negative control (NC; CP = 23.51%), and 3) NC + 0.02% protease (PRO). The protease used in this study was a commercial product (Ronozyme® ProAct, DSM nutrition products, Kaiseraugst, Switzerland) containing 75,000 protease units/g derived from *Bacillus licheniformis*. The dietary treatments did not include spray dried plasma, fishmeal, zinc oxide, and antibiotics to avoid their antibacterial or physiological effects. Pigs were fed respective dietary treatments for 6 weeks. Blood was collected from randomly selected 1 pig per replicate on d 1, 3, 7, and 14 after weaning. Ileum samples were collected from randomly selected 1 pig per replicate at the end of experimental period. Measurements were growth performance, frequency of diarrhea, packed cell volume (PCV) by an automated hematology analyzer calibrated for porcine blood, ileal morphology by the hematoxylin and eosin staining. Data were analyzed using the PROC GLM procedure of SAS. The statistical model for every measurement included dietary effect and BW as a covariate. Pigs fed PRO and PC had higher ($P < 0.05$) ADG (323 and 322 vs. 220 g/d)

and G:F (0.456 and 0.431 vs. 0.304 g/g) during overall experimental period and number of goblet cells (25 and 21 vs. 14) than those fed NC. Pigs fed PRO had higher ($P < 0.05$) villus height (318 vs. 282 μm) and villus height to crypt depth ratio (3.67 vs. 2.87 μm/μm) than those fed NC, but there was no difference on ileal morphology between PC and PRO. In addition, PRO decreased ($P < 0.05$) frequency of diarrhea for the first 2 weeks after weaning (16 vs. 36 and 41%) and PCV on d 14 after weaning (32.08 vs. 35.56 and 34.26%) compared with PC and NC. In conclusion, addition of protease in nursery diets with low protein level improved growth performance and decreased frequency of diarrhea of weaned pigs.

Key Words: Growth performance, Protease, Weaned pigs
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403 Effects of *Lactobacillus reuteri* LR1 on the growth performance, intestinal morphology and intestinal barrier function in weaned piglets.

H. Yi[*], L. Wang, and Z. Jiang, *Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, China.*

The objective of this study was to investigate the effects of *Lactobacillus reuteri* LR1 (LR1), a new strain isolated from the feces of weaning piglets, on the growth performance, intestinal morphology, immune response and intestinal barrier function in weaned piglets. A total of 144 weaned piglets (*Duroc*×*Landrace*×*Yorkshire*, 21 d of age) with an initial BW of 6.49 ± 0.02 kg were randomly assigned to 3 dietary treatments to give 8 pens per treatment and 6 piglets per pen. Piglets were fed with a basal diet (control group), a basal diet supplemented with 75 mg/kg aureomycin +100 mg/kg olaquindox (antibiotic group) or a basal diet supplemented with 5×10^{10} CFU/kg LR1 (LR1 group) for a 14-d period. At the end of study, the ADG, ADFI and G:F were calculated, and 8 randomly selected piglets from each treatment were euthanized for collecting samples. We found that LR1 treatment increased ADG (22.73%, $P < 0.05$) compared with the control group. However, no significant differences were observed in ADFI, ADG and G:F between the LR1 group and the antibiotic group. LR1 treatment decreased ($P < 0.05$) serum IL-6 concentration but increased ($P < 0.05$) IL-22 and TGF-β content in the mucosa of the ileum compared with the control and antibiotic treatment. We found LR1 treatment increased ($P < 0.05$) villus height of the ileum and reduced ($P < 0.05$) crypt depth of the jejunum, and increased ($P < 0.05$) the ratio of villus height/crypt depth in the jejunum and the ileum compared with the control and antibiotic treatment. Compared with control, LR1 increased ($P < 0.05$) the mRNA expression of the antimicrobial peptide *pBD2* and *PG1-5* in the mucosa of the ileum, whereas antibiotic treatment decreased ($P < 0.05$) expression. Additionally, we demonstrated that LR1 treatment increased ($P < 0.05$) toll-like receptor (*TLR*)*-2* expression but decreased ($P < 0.05$) the *TLR-4* expression in the mucosa of the ileum compared with the control group. Furthermore, compared with the control and antibiotic treatment, LR1 treatment increased ($P < 0.05$) the mRNA expression of tight junction protein *ZO-1* and *claudin-1* in the mucosa of jejunum, and also increased ($P < 0.05$) the mRNA expression of *ZO-1* and occludin in the mucosa of ileum. In conclusion, these data suggest that dietary LR1 supplementation at 5×10^{10} CFU/kg could improve the growth performance, intestinal morphology and intestinal barrier function in weaned piglets.

Key Words: Lactobacillus reuteri LR1, weaned piglet, intestinal barrier function
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404 Effect of supplementation of xylanase and live yeast on long-term growth performance of pigs.

H. Lu[*1], C. L. Bradley[2], P. Wilcock[2], O. Adeola[1,3], and K. M. Ajuwon[3], [1]*Purdue University, West Lafayette, IN,* [2]*AB Vista, Marlborough, United Kingdom,* [3]*Department of Animal Sciences, Purdue University, West Lafayette, IN.*

The objective of this study was to determine the effect of xylanase (Econase XT; XY) and live yeast (Vistacell; LY) supplementation, alone or in combination, on performance during the nursery and growing-finishing stages in pigs. A total of 128 weanling pigs (21 ± 2 d, BW: 6.24 ± 0.20 kg) were assigned to 4 treatments in a randomized complete block design (8 replicate pens, 4 pigs per pen) from weaning to market. The 4 treatments were as follows for two feeding periods; wean to 21 d and 21 to 154 d: T1) control-control, T2) XY; XY, T3) XY+LY; XY; T4) XY+LY; XY+LY. XY Pigs were fed a 6-phase feed program from weaning with a complex diet being fed from wean to 3 weeks after which pigs were fed a corn, soy, corn distillers based diet formulated to meet the pigs requirements (NRC 2012). Econase XT (XY) was added at 16,000 BXU/kg and LY was added at 1 g/kg from W-21 d after which if included in the diet it was reduced to 0.5g/kg from 21 to 156 d. Body weight and feed intake were recorded at the end of each nursery phase and then every two weeks. At d 21 there was no difference in body weight (BW), average daily gain (ADG), average daily feed intake (ADFI) and feed efficiency (G:F). During the grower phase (d 42 to 98) pigs fed T3 and T4 had higher ($P < 0.05$) ADG by 6.7% and 6.1%, respectively, compared with the control, with T2 being intermediate. In the finisher period (d98 to 156), pigs fed with T4 had higher ADG than T1. At the end of the trial, pigs fed T3 were heavier than T1 (114.1 v 108.1 kg; $P < 0.05$) with T2 (111 kg) and T4 (111.9 kg) intermediate and no difference ($P > 0.05$) from T1 (108.1 kg). There was a numerical increase in G:F with all XY supplemented diets (T1; 0.368, T2; 0.379, T3; 0.376 T4; 0.381; $P > 0.05$). In summary, early supplementation of a combination of XY and LY had a positive effect on future growth performance of weanling pigs.

Key Words: Xylanase, Weanling pigs, Live yeast
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405 Functional difference of free L-Lysine and L-Lysine HCl on growth performances, intestinal health, and intestinal integrity in newly weaned pigs.

W. Parnsen*, I. Park, and S. W. Kim, *North Carolina State University, Raleigh.*

This study was conducted to evaluate functional difference of liquid based free L-Lys and crystalline L-Lys HCl on the growth performances, intestinal health, and intestinal integrity in newly weaned pigs. Twenty four newly weaned pigs at 21 d of age (5.9 ± 0.1 kg BW), were randomly allotted to 2 treatments with 12 pens (1 pig per pen, 6 barrow and 6 gilt pens) per treatment, and fed experimental diets for 3 wk based on 2 phases (phase 1 for 10 d; and phase 2 for 11 d). Two treatments were, (1) a diet supplemented with crystalline L-Lys HCl (0.45%, Daesang Corp., Seoul, Korea) or (2) a diet supplemented with liquid based free L-Lys (0.71%, Daesang Corp., Seoul, Korea). These 2 diets were formulated to have equal SID Lys content and nutrients meeting the NRC requirements (2012). Body weight and feed disappearance were measured on d 7, 10, and 21 to calculate ADG, ADFI, and G:F ratio. Blood samples were taken on d 20 to obtain plasma. At the end of wk 3, all pigs were euthanized to obtain gut tissues and mucosal tissues from duodenum and jejunum. Plasma and mucosal tissues were used to measure tumor necrosis factor alpha (TNF-α), protein carbonyl, malondialdehyde, 8-OHdG, and total antioxidant capacity (TAC). Gut tissues were fixed for histological evaluation of gut morphology, for immunohistochemistry of Ki-67 protein to measure enterocyte proliferation, and for Western blot to quantify tight junction proteins (ZO-1, claudin-1, and occludin). Data were analyzed using PROC MIXED procedure in SAS with pen as the experimental unit and P values < 0.05 considered significant and < 0.10 considered tendency. Overall, source of Lys (free L-Lys vs. crystalline L-Lys HCl) did not affect ADG (0.319 and 0.319 kg/d), ADFI (0.384 and 0.397 kg/d), and G:F (0.828 and 0.804) of pigs. Liquid based free L-Lys decreased ($P < 0.05$) jejunal TNF-α (1.05 to 0.81 pg/mg protein), and plasma TNF-α (130 to 110 pg/mg protein) without affecting concentrations of protein carbonyl, malondialdehyde, and TAC. Liquid based free L-Lys increased ($P < 0.05$) villus height (346 to 386 μm) and villus height:crypt depth ratio (1.21 to 1.37 μm) in the jejunum. Collectively, this study indicates that free L-Lys supplementation improves intestinal health potentially by decreasing of systemic inflammatory status and improving jejunal morphology compared with the use of L-Lys HCl in newly weaned pigs.

Key Words: growth performance, intestinal health, lysine
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406 Effects of modified yeast cell wall extract on gut health and growth of newly weaned pigs under chronic dietary challenges of aflatoxin, deoxynivalenol, and fumonisin.

I. Park*[1], W. Parnsen[1], M. E. Duarte[1], A. Yiannikouris[2], and S. W. Kim[1], [1]*North Carolina State University, Raleigh,* [2]*Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY.*

The objective of this study was to evaluate the effects of modified yeast cell wall extract at 2 g/kg (YCWE; Integral A+, Alltech, Lexington, KY) on growth and health of pigs fed diets with aflatoxin (180 μg/kg), deoxynivalenol (1 mg/kg), and fumonisin (9 mg/kg). Forty-eight pigs (24 barrows and 24 gilts at 21 d of age with 6.0 ± 0.6 kg BW) were randomly allotted to 4 treatments (2 × 2 factorial arrangement) with 12 pens per treatment, and fed the experimental diets for 48-d. Factors were mycotoxin and YCWE. Experimental diets were formulated to meet the requirement suggested by the NRC (2012) in 2 phases (phase 1 for 20-d and phase 2 for 28-d). Body weight and feed consumption were measured every 5-d in phase 1 and weekly in phase 2. On d 14 and 45, all pigs were bled to collect serum for biochemical analysis and other measurements. On d 48, all pigs were euthanized to collect jejunal tissue and mucosa. Tissue was used to measure histology. Mucosa and serum were used to determine tumor necrosis factor-α, malondialdehyde, protein carbonyl (PC), and immunoglobulins (IgA and IgG). Data were analyzed using the Mixed procedure in SAS with 2 factors and sex as fixed effects and initial BW as a random effect. Overall, mycotoxin reduced ($P < 0.05$) BW (37.8 to 31.1 kg), ADG (481 to 416 g/d), and ADFI (726 to 601 g/d). The YCWE tended to improve G:F ($P = 0.079$, 0.670 to 0.691) and reduce WBC ($P = 0.071$, 18.7 to 16.3×10^3 cells/μL). Mycotoxins reduced ($P < 0.05$) villus height (526 to 515 μm), increased ($P < 0.05$) IgA (5.7 to 6.5 mg/g protein), and increased ($P < 0.05$) PC (2.32 to 2.67 nmol/mg protein) in the jejunum. The YCWE tended ($P = 0.088$) to increase villus height (515 to 523 μm), and reduced ($P < 0.05$) IgA (6.3 to 5.9 mg/g protein) and PC (2.6 to 2.4 nmol/mg protein) in the jejunum. Collectively, feeding diets with mycotoxin at moderate levels reduced growth and impaired gut health in newly weaned pigs. Supplemental YCWE could improve growth and gut health in newly weaned pigs at 3 to 10 wk of age.

Key Words: growth performance, mycotoxin, modified yeast cell wall extract
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407 Effects of *Bacillus*-based direct-fed microbials on growth and gut health of nursery pigs.

K. L. Brooks* and S. W. Kim, *North Carolina State University, Raleigh.*

The objective of this study was to determine the effects of *Bacillus*-based direct-fed microbials (DFM) on growth performance, gut health, immune status, and oxidative stress status in nursery pigs. Pigs (180 barrows and 180 gilts) at 21 d of age and 6.26 ± 1.02 kg BW were randomly assigned to 3 treatments based on a randomized complete block design with sex and initial BW as blocks: 1) Basal diet (CON); 2) Basal diet + DFM based on 1 *Bacillus* species (3.34×10^9 CFU/kg feed) (DFM-1); 3) Basal diet + DFM based on 2 *Bacillus* species (1.28×10^9 CFU/kg feed) (DFM-2). Pigs were distributed into 30 pens per treatment with 4 pigs per pen. Pen was the experimental unit and proc MIXED of SAS was used for statistical analysis using treatment and sex as fixed effects and BW block as a random effect. Pigs were given ad libitum access to feed and water for 42 d with d 1 to 14 representing phase 1 and d 15 to 42 representing phase 2. Feed intake and BW were measured at the beginning and end of each phase to calculate ADG, ADFI, and G:F. At d 42, 8 pigs (1 per pen) per treatment (4 barrows and 4 gilts) were euthanized for sample collection. Serum and jejunal mucosal tissues were obtained to measure tumor necrosis factor α (TNF-α), immunoglobulins G and A (IgG and IgA), protein carbonyl (PC) and malondialdehyde (MDA). Jejunal tissues were obtained to measure tight junction proteins (claudin, occludin, and ZO-1). The ADG was greater ($P < 0.05$) in the DFM-1 (550 and 427 g/d) and DFM-2 (546 and 424 g/d) compared to the CON (503 and 392 g/d) for both phase 2 and the overall experimental period, respectively. Overall ADFI was increased ($P < 0.05$) in the DFM-1 (552 g/d) and DFM-2 (555 g/d) compared to the CON (516 g/d), although there were no effects on G:F. The DFM-1 had higher ($P < 0.05$) ZO-1 than the CON. The DFM-1 had higher ($P < 0.05$) claudin and ZO-1 than the DFM-2. There were no differences in TNF-α, IgG, IgA, PC, or MDA concentrations in serum and jejunal mucosa among treatments. In conclusion, both *Bacillus*-based DFMs improved growth of nursery pigs primarily by increasing feed intake whereas the DFM with 1 *Bacillus* strain additionally improved gut integrity without affecting immune or oxidative stress status in the small intestine.

Key Words: Bacillus, direct-fed microbial, gut health
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408 Aromatic amino acids alleviate intestinal inflammation in piglets through calcium-sensing receptor activation.

B. Tan[1,3], B. Huang[1,2], J. Wang[1,2], G. P. Guang[1], C. B. Yang[2,3] and Yulong Yin[1*], *[1]National Engineering Laboratory for Pollution Control and Waste Utilization in Livestock and Poultry Production, Key Laboratory of Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha 410125, Hunan, China, [2]University of Chinese Academy of Sciences, Beijing 100008, China, [3] Department of Animal Science, Faculty of Agricultural and Food Sciences, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.*

Ca^{2+}-sensing receptor (CaSR) plays a key role in the maintenance of intestinal barrier function and represents a potential therapeutic target for inflammatory bowel diseases. CaSR strongly prefers aromatic amino acid ligands, such as tryptophan, phenylalanine and tyrosine. Therefore, this study was conducted to investigate the regulatory effects of dietary supplement with aromatic amino acid——tryptophan, phenylalanine and tyrosine (TPT) on CaSR signaling pathway and intestinal inflammatory response in piglets. A total of 40 weaned piglets (landrace ×large white) with similar weight were used in a 2 × 2 factorial design according to diet (basal diet or supplement with 0.24% Phe + 0.16% Trp + 0.24% Tyr) and inflammatory challenge (intraperitoneally injected with saline or LPS). On the morning of days 21 after the initiation of treatment, the piglets of each dietary treatment were intraperitoneally injected with LPS at 100 μg/kg body weight or the same amount of sterilized saline, respectively. Blood and intestine samples were collected 4 h after inflammation challenged. The results showed that piglets challenged with LPS have a significant increase in rectal temperature, histopathological injury as well as colon myeloperoxidase (MPO) activity, whereas dietary supplementation with TPT significantly alleviated piglets histopathological injury induced by LPS and significantly decreased MPO activity induced by LPS. Dietary supplement with TPT significantly decrease piglets serum pro-inflammatory cytokines concentrations of interleukin (IL)1β, IL6, IL8, IL12, GM-CSF and tumor necrosis factor alpha (TNF-β) as well as intestinal abundances of pro-inflammatory cytokines mRNA but significantly enhance anti-inflammatory cytokine IL4 and TGFβ level ($P < 0.05$). Dietary supplement with TPT significantly increased CaSR and PLCβ2 protein expressions level, but decreased p-NF-κB, IKKα/β, and IκB protein expressions level in LPS-challenged piglets ($P < 0.05$). Based on these results, supplement with TPT can alleviate intestinal inflammation in piglets induced by LPS, this may be concomitant with the activation of CaSR and the inhibition of NF-κB signaling pathways.

Key Words: aromatic amino acid, Ca2+-sensing receptor, inflammatory response
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409 Effects of combinational use of xylanase and protease on growth performance and gut health of newly weaned pigs.

M. E. Duarte*[1,2], I. Park[1], W. Parnsen[1], F. X. Zhou[3], and S. W. Kim[1], [1]*North Carolina State University, Raleigh,* [2]*Federal Rural University of Pernambuco, Recife, Brazil,* [3]*BioResource International, Inc., Durham, NC.*

This study was to investigate the effect of supplemental xylanase (Xylamax, BRI, Durham, NC) and protease (Versazyme, BRI) on growth performance, digesta viscosity, apparent ileal digestibility of nutrients, and gut health in nursery pigs. Forty-eight pigs (24 barrows and 24 gilts at 21 d of age with 7.2 ± 0.4 kg BW) were randomly allotted to 4 treatments (2 × 2 factorial arrangement). Factors were xylanase (0 or 45,000 XU/kg) and protease (0 or 300,000 U/kg). Experimental diets formulated to meet nutrient requirements suggested by NRC (2012) in 2 phases (phase 1 for 10 d and phase 2 for 24 d). Feed intake and BW gain were measured d 10 and 24. Titanium oxide (0.25%) was added to all diets as an indigestible external marker from d 20 to 24. On d 24, all pigs were euthanized to obtain jejunal and ileal digesta to measure viscosity and apparent ileal digestibility, respectively. Jejunal mucosa was collected to measure immune and oxidative stress status. Jejunal tissues were used to measure morphology, proliferation of crypt cells by immunohistochemistry of Ki-67, and tight junction proteins by Western blot. Data were analyzed using the MIXED procedure in SAS with 2 factors and sex as fixed effects and initial BW block as a random effect. In phase 2, xylanase increased ($P < 0.05$) ADG (0.518 to 0.560 kg/d) which was further increased ($P < 0.05$, interaction) with protease. Overall, combinational use of xylanase and protease increased ($P < 0.05$) ADG (0.503 vs. 0.442 and 0.437 kg/d) compared with the use of xylanase or protease alone, wheras protease improved ($P < 0.05$) feed efficiency (0.765 to 0.793). In jejunum, xylanase reduced ($P < 0.05$) viscosity of digesta (2.69 to 2.36 mPa.s), mucosal MDA (1.14 to 0.95 μM), crypt depth (220 to 198 μm) and crypt cell proliferation (20.3 to 17.6%), and protease increased ($P < 0.05$) villus height (439 to 493 μm), crypt depth (229 to 189 μm) and crypt cell proliferation (21.5 to 15.9%). Combinational use of xylanase and protease increased ($P < 0.05$) claudin (0.047 to 0.076 band intensity) and occludin (0.126 to 0.161 band intensity) in jejunum. Apparent ileal digestibility of nutrients was not different among treatments. Collectively, xylanase could improve growth, digesta viscosity, and oxidative stress, and protease could improve feed efficiency and gut integrity. Combinational use of xylanase and protease enhanced growth performance and tight junction proteins in newly weaned pigs.

Key Words: xylanase, growth performance, protease
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410 SID methionine+cystine levels and vitamin B6 supplementation on performance, blood parameters and metabolic enzymes gene expression of finishing barrows.

C. P. Sangali[1], L. D. Castilha[2], M. R. Fachinello[1], E. Gasparino[3], R. V. Nunes[4], and P. C. Pozza*[3], [1]*Universidade Estadual de Maringá/CAPES, Maringá, Brazil,* [2]*Universidade Estadual de Maringá, Maringá, Brazil,* [3]*Universidade Estadual de Maringá/CNPq, Maringá, Brazil,* [4]*Universidade Estadual do Oeste do Paraná/CNPq, Marechal Cândido Rondon, Brazil.*

This study aimed to evaluate the effects of dietary SID methionine+cystine (Met+Cys) levels and vitamin B_6 (B6) supplementation on performance, blood parameters and enzymes expression of finishing barrows. Fifty-six crossbred barrows (Talent x Topigs 20) averaging 75.11 ± 1.84 kg of body weight (BW) were distributed in a completely randomised block design arranged in a 2×4 factorial scheme consisting of two B_6 supplementation levels (1.58 and 3.58 mg/kg) and four SID Met+Cys levels (0.35, 0.45, 0.55 and 0.65%), with seven replicates and one animal per experimental unit. Average daily gain, average daily feed intake, feed/gain (F/G), plasma concentrations of glucose, urea, total proteins, creatinine and triacylglycerol, serum homocysteine levels and gene expression of methionine synthase (MS) and cystathionine γ-lyase (CGL) were evaluated. The F-test was used on the B_6 supplementation data. The degrees of freedom related to SID Met+Cys levels were used in orthogonal polynomials to obtain the regression equations. No interactions ($P > 0.05$) between B_6 supplementation and SID Met+Cys levels were observed. The highest B_6 supplementation (3.58 mg/kg) decreased ($P = 0.05$) the F/G and high ($P = 0.05$) plasma glucose concentration. Triglycerides showed a quadratic response ($P = 0.01$), wherein the lowest concentration (29.42 mg/dL) was estimated at 0.496% SID Met + Cys. Although treatments did not affect the expression of MS or CGL, there was a linear increase ($P = 0.01$) in serum homocysteine levels due to increasing SID Met+Cys in the diet. SID Met+Cys requirement for barrows (75–100 kg BW) was 10.46 g/day and high levels of these amino acids increased the homocysteine blood concentration. Dietary supplemention of 3.58 mg B_6/kg improved the F/G ratio but was not efficient to improve homocysteine metabolization by the trans-sulphuration pathway.

Key Words: cystathionine γ-lyase, homocysteine, methionine synthase
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411 Effects of dietary deoxynivalenol and zearalenone on the organ pro-inflammatory gene expressions and serum immunoglobulins of pigs.

K. E. Reddy[1], W. Lee[1], S. D. Lee[1], J. Y. Jeong[1], D. W. Kim[1], M. Kim[1], H. J. Lee[1], Y. K. Oh[1], and H. Jo[*2], [1]*Animal Nutrition & Physiology Team, National Institute of Animal Science, Rural Development Administration, Wanju, Korea, Republic of (South),* [2]*Department of Animal Science and Technology, Konkuk University, Seoul, Korea, Republic of (South).*

The aim of this study was to investigate effects of dietary deoxynivalenol (DON) and zearalenone (ZON) on pro-inflammatory genes in various pig organs and serum immunoglobulins of pigs. Fourteen 6-week-old pigs were randomly allocated to 3 dietary treatments in a completely randomized design with 4 or 5 replicates. Three experimental diets consisted of a corn-soybean meal-based control diet (4 animals), a diet containing DON at 8 mg/kg (5 animals), and a diet containing ZON at 0.8 mg/kg (5 animals). During a 4-week feeding period, the experimental animals had free access to feed and water. At the end of the feeding period, all pigs were slaughtered to collect the muscle, liver and kidney samples that were analyzed for mRNA expression of pro-inflammatory genes including IL-6, IL-10, IL-12β, tumor necrosis factor (TNF), interferon-gamma and prostaglandin-endoperoxide synthase 2 using quantitative reverse transcriptase PCR. Serum IgA, IgG and IgM concentrations were also measured using ELISA method. Dietary DON did not affect the gene expression of pro-inflammatory cytokines in the organs. However, dietary ZON resulted in mRNA down-regulations ($P < 0.05$) of IL-10, IL-12β, and TNF in the liver compared with the control group. Serum IgG and IgM of pigs fed the DON- or ZON-containing diet were less ($P < 0.05$) than those fed the control diet. However, serum IgA concentrations were unaffected by dietary mycotoxins. These results suggest that ZON could worsen organ inflammation particularly in the liver, and also provide a better understanding of the possible effects of either DON or ZON on the immunological defense mechanisms in the pig.

Key Words: immunoglobulin, mycotoxin, swine
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412 Supplementation of tea polyphenol mixed with sweetener to diet included with or without flax oil increased blood serum antioxidantive capacity without affecting growth performance of large white gilts.

F. F. Li[1], Y. Zhang[1,2], Y. D. Cao[1], and M. L. He[*2,3], [1]*Shenyang Agricultural University, Shenyang, China,* [2]*Lucta (Guangzhou) Flavours Co., Ltd., Guangzhou, China,* [3]*Zhejiang Agricultural and Forestry University, Hangzhou, China.*

Tea polyphenol (TP) that was extracted from green tea can be used as natural antioxidant to improve animal health and body antioxidative capacity. Flax oil (FO) contains high amount of omega-3 linolenic acid and can be added to diets as energy source and for increasing amount of functional fatty acids in animal body. This study designed as 2 by 2 factorial trial was to investigate effect of inclusions of TP and FO in diet on growth performance, body health and major antioxidative capacity of gilts. To avoid the possible negative influence of TP bitter taste on feed intake a sweetener was premixed with TP for inclusion in the diets. Total 40 growing Large White gilts with an average body weight of 59 kg were assigned to 4 groups (n = 10) fed ad libitum with following diets for 7 weeks: 1) a control (CON) diet; 2) CON diet+ 400mg/kg TP and 200mg/kg sweetener; 3) a diet containing 2% FO; 4) the FO diet + TP 400mg/kg and 200mg/kg sweetener. During the study daily growth and intake data were automatically collected through using Feed Intake Recording Equipment (FIRE). On the last day of feeding study fasting blood samples were taken from each group (n = 5). From the study it was found that inclusion of FO increased ($P < 0.05$) average daily gain (ADG) and feed intake (FI), however it resulted in larger ($P < 0.05$) ratio of FI:ADG. Within the normal ranges for health pigs, blood serum albumin and IgM were also increased ($P < 0.05$) by inclusion of FO, whereas AST, ALT, TP, glucose and IgG were not affected ($P > 0.1$) by all treatments. Supplementation of TP mixed with sweetener increased ($P < 0.01$) major antioxidative capacity related parameters e.g. GSH-Px, CAT, T-SOD and T-AOC in blood serum without affecting ($P > 0.05$) growth performance. However, blood MDA level was also increased ($P < 0.01$) by the treatment. In conclusion, inclusion of 2% FO to the diets of CON and FO increased feed intake, ADG and blood serum IgM but reduced feed efficiency of the gilts. Inclusion of 400 mg/kg TP mixed with Lucta sweetener to the diets of CON and FO increased major blood serum antioxidative capacity without affecting the animal growth performance. The results suggest that TP mixed with the sweetener can be included in swine diets for providing animal body with more antioxidative capacity.

Key Words: Antioxidant tea polyphenol, Flax oil, Large White gilts
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413 Supplementation of tea polyphenol mixed with sweetener in diet included with or without flax oil increased antioxidative capacity of blood serum and longissimus dorsi muscle of fattening pigs.

Y. Zhang[1,2], F. F. Li[1], Y. D. Cao[1], and M. L. He[*2,3], [1]*Shenyang Agricultural University, Shenyang, China,* [2]*Lucta (Guangzhou) Flavours Co., Ltd., Guangzhou, China,* [3]*Zhejiang Agricultural and Forestry University, Hangzhou, China.*

A natural antioxidant - tea polyphenol (TP) extracted from green tea can be used as feed additives to improve body antioxidative capacity. It can be applied together with a sweetener

to avoid possible negative influence by its bitter taste. As a major source of omega-3 fatty acids flax oil (FO) can be included in diet for increasing omega-3 fatty acids in meat. The current study was designed to investigate effect of supplementation of TP mixed with sweetener to diet included with or without FO on growth performance and body antioxidative capacity of fattening pigs. The study was a 2 by 2 factorial trial with two main factors of TP mixed with sweetener and FO inclusions. Total 40 Large White castrated growing pigs with an average body weight of 62 kg were assigned to 4 groups fed ad libitum with following diets for 5 weeks: 1) a control diet (CON); 2) CON diet + 400mg/kg TP and 200mg/kg Lucta sweetener; 3) a 2% FO diet; 4) FO diet + 400mg/kg TP and 200mg/kg Lucta sweetener. During the experimental period weekly body weight changes and daily feed intake data were collected. Fasting blood samples were taken for analyzing general health related parameters and antioxidative capacity. At the end of feeding trial 4-6 pigs from each group were slaughtered for carcass and meat quality measurements. From the study it was found that the animal growth performance and their general health related blood serum parameters were not affected ($P > 0.1$) by the treatments. Inclusion of TP with sweetener increased ($P < 0.01$) blood major antioxidative capacity parameters e.g. GSH-Px, CAT, T-SOD and T-AOC, whereas that of FO increased ($P < 0.05$) GSH-Px. On major carcass and meat quality characters, inclusion of FO resulted in more favorable ($P < 0.05$) meat colour whereas that of TP with sweetener resulted in a larger ($P < 0.05$) drop loss%. Inclusion of FO in the control diet also increased ($P < 0.05$) meat ribeye area. Inclusion of TP with sweetener increased ($P < 0.01$) longissimus dorsi muscle T-SOD and tended to increase ($P = 0.06$) GSH-Px whereas that of FO decreased ($P < 0.05$) it. In conclusion, inclusion of TP mixed with Lucta sweetener in either CON or FO diet increased antioxidative capacity of blood serum and the muscle without affecting growth performance of fattening pigs. The results suggest that inclusion of TP in FO diet is beneficial to prevent the possible oxidations in the muscle.

Key Words: Antioxidant tea polyphenol, Flax oil, Fattening pigs
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414 Inclusion of flax oil in diet supplemented with or without tea polyphenol increased omega-3 fatty acids in blood serum, subcutaneous fat, and longissimus dorsi muscle of fattening pigs.

M. L. He*[1,2], H. F. Wang[1,3], Y. J. Cui[1], Y. Zhang[2,4], F. F. Li[4], and Y. D. Cao[4], [1]*Zhejiang Agricultural and Forestry University, Hangzhou, China,* [2]*Lucta (Guangzhou) Flavours Co., Ltd., Guangzhou, China,* [3]*Zhejiang University, Hangzhou, China,* [4]*Shenyang Agricultural University, Shenyang, China.*

Flax oil (FO) is a major omega-3 source and can be used for increasing the amount of functional fatty acids in body tissues. Tea polyphenol (TP) from green tea can be applied as a natural antioxidant additive. A concurrent study found that inclusion of TP mixed with a sweetener to the diet increased the antioxidative capacity in blood serum and longissimus dorsi muscle of fattening pigs. The current study investigated the effect of including TP and a sweetener, FO, or both in the diet on body fatty acid profiles of fattening pigs. Forty castrated Large White pigs with an average BW of 62 kg were assigned to 4 groups ($n = 10$ per group) and fed, ad libitum, the following diets for 5 wk: 1) a control (CON), 2) the CON diet + 400 mg/kg TP and 200 mg/kg sweetener; 3) a 2% FO diet, and 4) the 2% FO diet + 400 mg/kg TP and 200 mg/kg sweetener. On the last day of the feeding study, 5 fasting blood samples were taken from each group. At slaughter, subcutaneous fat and longissimus dorsi muscle samples were taken from 4 to 6 pigs of each group for lipids extraction, methylation, and fatty acids analysis. Fatty acids methyl esters were analyzed using gas chromatography. Tt was found that inclusion of FO greatly increased ($P < 0.01$) weight percent of total n-3 fatty acids and individual 18:3n-3, 20:5n-3, and 22:5n-3 fatty acids, resulting in a reduced ($P < 0.01$) n-6:n-3 fatty acids ratio in blood serum, subcutaneous fat, and longissimus muscle. Supplementation of TP and sweetener did not ($P > 0.05$) affect either total and individual n-3 fatty acids or the n-6:n-3 fatty acids ratio, with exceptions: it reduced ($P < 0.05$) total n-3 fatty acids and increased ($P < 0.05$) the n-6:n-3 fatty acids ratio in blood serum when was added to the FO diet. In conclusion, inclusion of 2% FO in diets of fattening pigs significantly increased omega-3 fatty acids and reduced the n-6:n-3 fatty acids ratio, whereas inclusion of TP and sweetener did not affect these fatty acids in either subcutaneous fat or longissimus dorsi muscle. Together with results from our concurrent studies on meat quality and antioxidative capacity, these studies indicated that inclusion of FO plus TP mixed with a sweetener to the diet of fattening pigs could improve both meat omega-3 fatty acid levels and antioxidative capacity.

Key Words: Antioxidant tea polyphenol, Flax oil, Omega-3 fatty acids
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415 Effect of Cu provided As Bioplex® Cu or TBCC for weaned pigs: Growth performance, tissue mineral retention, and fecal mineral excretion.

Y. Guo[1], B. Liu[1], P. Xiong[1], J. He[1], L. Gang[2], Y. Xue[2], A. F. Koontz*[3], and D. Yu[1], [1]*College of Animal Sciences, Zhejiang University, Hangzhou, China,* [2]*Alltech Biological Products (Beijing) Co., Ltd., Beijing, China,* [3]*Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech Inc., Nicholasville, KY.*

Pharmaceutical Cu from CuSO4 is routinely added in diets of weaned pigs as a growth promoter. Excess Cu is excreted in feces then accumulates in soil and water, and has been shown

to reduce crop yield and pose a threat to environmental and human health. Bioplex® Cu (Alltech Inc.), a mineral proteinate chelated to soy protein hydrolysates, has been shown to be absorbed and utilized better than inorganic salts. However, the optimal supplementation for weaned pigs fed practical corn-soy diet has not been clearly determined. Eight hundred and forty crossbred piglets (Duroc x Landrace x Yorkshire, BW 7.4±0.6 kg), weaned at 28±3 d were used in this experiment. Bioplex® Cu or tribasic copper chloride (TBCC) were added to a basal corn-soybean diet. Copper was added at 0, 5, 10, 20, 40, 80 and 160 mg/kg from either Bioplex® or TBCC, and 200 mg/kg from TBCC (maximum allowed level in China). Growth performance, tissue retention, and fecal mineral excretion were measured for 38 days. Copper supplementation, regardless of source, quadratically increased ADG and quadratically decreased F:G ($P < 0.05$). Bioplex® Cu was more effective than TBCC in improving the ADG when supplemented at 40 or 80 mg/kg. No differences were observed in hepatic Cu retention for 80 mg/kg Bioplex® Cu compared to 160 mg/kg Cu as TBCC. Hepatic Zn content was affected by increasing dietary Cu supplementation especially as TBCC, indicating that Cu in organic forms may decrease the interactions between Cu and Zn. Copper supplementation, regardless of the source, quadratically increased fecal Cu excretion ($P < 0.05$). Bioplex® Cu decreased fecal Cu excretion compared to TBCC when supplemented equally. Bioplex® Cu was more effective than TBCC in improving piglet growth performance. To maximize performance, the optimal level of Bioplex® Cu is 78 mg/kg while TBCC is 140 mg/kg for weaned pigs fed practical corn-soy diet. Fecal Cu excretion can be reduced about 50% by using 80 mg/kg Bioplex® Cu to substitute inorganic Cu supplementation (160 mg/kg) in commercial production without compromising health and growth performance.

Key Words: Copper, Fecal Minerals, Nursery Piglets
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416 Effect of sodium butyrate protected with medium chain fatty acids or *Bacillus licheniformis* on behavior of weaned piglets oral challenged with ETEC K88.

M. Puyalto*, *NOREL S.A., Madrid, Spain.*

This study evaluated the effect of sodium butyrate protected with sodium salts of distilled coconut fatty acids (DICOSAN PLUS®; Norel S.A) or *Bacillus licheniformis* CECT4536 on behavior patterns of piglets at weaning when challenged with enterotoxigenic *Escherichia coli* (ETEC) K88. A total of 66 piglets of 3 weeks of age were divided in 22 pens (3 animals/pen) and 3 experimental groups: CTR, control group with plain diet (n = 8); DIP, plain diet supplemented with 3 kg/t of DICOSAN PLUS (0.3% in-feed of 50% sodium butyrate protected with sodium salts of distilled coconut fatty acids) (n = 8); and PRO, plain diet supplemented with 1 kg/t of *B. licheniformis* (10^6 cfu/g) (n = 6). After one week of adaptation, animals were orally inoculated with ETEC K88 ($1x10^9$ cfu). Scan sampling was used to evaluate animal behavior during the day before the challenge and two days post-inoculation (2 and 3 PI). Behavior measures were recorded during the morning and afternoon (0800 – 1000 h and 1600 – 1800 h). Use of the space (feeder, heat-light and drinker), active behaviors (exploration, feeding, drinking, walking and others) and inactive behaviors (lying ventrally or laterally, with or without pen mates contact) were registered. Before inoculation, animals treated with DIP and PRO spent more time in the feeder area ($P = 0.04$) compared to CTR and showed higher frequencies of active behaviors such feeding ($P < 0.001$) and exploring ($P < 0.01$), especially during the morning. On day 2 PI, sickness behaviors associated to the digestive disorder appeared such huddling under the heat-light ($P < 0.001$) and inactive behaviors ($P < 0.01$). On day 3 PI during the morning, DIP and PRO animals took up the behaviors associated to feed consuming ($P = 0.15$) and exploring ($P = 0.38$), with higher presence in feeder area ($P = 0.01$). The supplementation with sodium butyrate with sodium salts of distilled coconut fatty acids or *Bacillus licheniformis* in feed improved the welfare of the piglets during the first week after weaning. However, after the challenge with ETEC K88, these treatments could not totally compensate for the impact of the pathogen.

Key Words: *Escherichia coli* K88, sodium butyrate, *Bacillus licherniformis*
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417 Effects of dietary lysine supply on plasma concentrations of growth-related hormones in late-stage finishing pigs.

T. Wang[1], M. S. Hasan*[1], G. Wu[2], M. A. Crenshaw[1], and S. F. Liao[1], [1]*Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State,* [2]*Texas A&M University, College Station.*

The regulation of key metabolic pathways responsible for muscle protein turnover by dietary amino acids (AAs) in pigs is closely associated with the concomitant responses of some growth-related hormones. This study was undertaken to investigate the effects of dietary lysine supply at different levels on blood plasma concentrations of 3 key growth-related hormones in late-stage finishing pigs: insulin, growth hormone (GH), and insulin-like growth factor 1 (IGF-1). Nine crossbred (Large White × Landrace) finishing pigs (initial BW 94.4 ± 6.7 kg) were assigned to 3 dietary treatments according to a randomized experimental design (3 pigs/treatment). Three corn and soybean meal based diets were formulated to meet the NRC (2012) requirements for various nutrients except for lysine, whose concentrations were 0.43, 0.71, and 0.98% (as-fed basis) for Diets 1 (lysine-deficient), 2 (lysine-adequate), and 3 (lysine-excess), respectively. The feeding trial lasted 4 weeks, during which time the pigs were allowed ad libitum access to the experimental diets and fresh water. After 4 weeks, blood was collected from the jugular vein, and plasma samples were separated by centrifugation. The plasma concentrations of 3 hormones were measured by using 3 respective commercial assay kits. Data were statistically analyzed with the GLM Procedure of SAS (v9.4) with $P \leq 0.05$ and ≤ 0.10 as significant difference and a tendency, respectively. Results showed that there were no differences in the plasma insulin and GH concentrations ($P > 0.10$) among the three dietary treatments, which suggests that the plasma insulin and GH levels of the late-stage finishing pigs were not affected by the dietary lysine concentration, at least at the range from 0.43 to 0.98%. The plasma IGF-1 concentration of the pigs fed either Diet 1 or 3, however, was lower ($P < 0.05$) than that of the pigs fed Diet 2, which suggests that either dietary lysine deficiency or excess can lead to a lower level of plasma IGF-1 concentration in late-stage finishing pigs. Therefore, it can be concluded that IGF-1, instead of insulin or GH, in the blood circulation may be a controlling growth factor in response to dietary provision of lysine for regulating muscle growth in late-stage finishing pigs. This study was supported by a USDA-NIFA's Hatch/Multistate Project (under No. 1007691).

Key Words: Hormone, Finishing pig, Lysine
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418 Determination of adequate adaptation period in total tract digestibility studies using index method in lactating and gestating sows.

H. Jo*, and B. G. Kim, *Department of Animal Science and Technology, Konkuk University, Seoul, Korea, Republic of (South).*

Index methods are often employed in determining nutrient digestibility of sows due to the difficulties of quantitative fecal collection. A sufficient amount of time for reaching a constant index concentration in feces is critical in digestibility experiments. However, information on the adequate adaptation period for reaching the plateau of fecal index concentrations is lacking, particularly in sows. Therefore, the objective was to determine the minimum adaptation period in total tract digestibility experiment using index method of sows. Five lactating and 5 gestating sows with over 3-parities were housed in a commercial farm and used to determine the day for index-recovery. Indigestible indexes of 0.5% chromic oxide and 0.5% titanium dioxide were included to a diet based on corn and soybean meal. The daily feed allowance of lactating sow was at 6 kg and 3 equal meals were provided. Gestating sows were fed with 2 kg of feed per day with 2 equal meals. Following a 5-d period of feeding an index-free diet, feces were collected with 24-h intervals for 7 and 9 d for lactating and gestating sows, respectively. As collection days passed, the fecal index concentration increased quadratically ($P < 0.01$) in both lactating and gestating sows. Minimum adaptation periods were estimated by one-slope broken-line model, quadratic model, and quadratic broken-line model. Based on the R^2, the best-fitting model to determine the minimum adaptation period in lactating and gestating sows was the quadratic broken-line model and the one-slope broken-line model, respectively. The breakpoints of Cr and Ti concentration in feces were d 5.08 (SE = 0.48) and 4.67 (SE = 0.83) in lactating sows, respectively, and d 7.28 (SE = 0.31) and 6.16 (SE = 0.42) in the gestating sows, respectively. Based on the results of the present study, the recommended minimum adaptation period for reaching plateau of Cr and Ti concentration in feces was d 6 and 5 in lactating sows, respectively. For gestating sows, the minimum adaptation period for reaching plateau of Cr and Ti concentration in feces was d 8 and 7, respectively. Taken together, the minimum adaptation period in total tract digestibility study using index method in gestating sows was longer than in lactating sows.

Key Words: indigestible index, methodology, swine
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419 Influence of green tea on performance, nutrient utilisation and cecal microbiota of broiler chickens.

D. V. Thomas, A. L. Molan, and V. Ravindran*, *Massey University, Palmerston North, New Zealand.*

The present study was conducted to assess the influence of green tea supplementation on performance, nutrient utilisation and cecal microbiota of broiler chickens. Treatments consisted of a wheat-based basal diet and the basal diet supplemented with one of two types of green tea, namely normal (N-GTE) or selenium-rich (Se-GTE) at an inclusion rate of 1%. Bird performance, nitrogen-corrected apparent metabolizable energy (AMEn), and total tract digestibility of fat and starch were measured on d 7, 21 and 35. In addition, effects on cecal microbiota counts were determined in a cohort study. Green tea supplementation lowered ($P < 0.05$) weight gain and feed intake, but improved feed per gain ($P < 0.05$). Supplementation with N-GTE increased the AMEn on d 7 and 21, and with Se-GTE on d 7 ($P < 0.05$). AMEn increased with age for all treatments. Fat digestibility increased with N-GTE supplementation on d 21 and with Se-GTE supplementation on d 7 and 21 ($P <0.05$). Starch digestibility increased on d 21 with N-GTE supplementation and on d 7 with Se-GTE supplementation ($P < 0.05$). The abdominal fat pad, as a proportion of carcass weight, decreased in the Se-GTE diet ($P < 0.05$) and numerically in the N-GTE diet. Drip losses were lowered ($P < 0.05$) by both GTE treatments. There was no difference in cooking losses and breastmeat yield between treatments. Dietary inclusion of green tea had a positive effect on the cecal microbiota, with an increased ($P < 0.05$) number of beneficial bacteria (*Lactobacillus* spp. and *Bifidobacterium* spp.) and a reduced ($P < 0.05$) number of pathogenic bacteria (*Clostridium* spp and *Bacteroides* spp.). Differences were observed between the two green

tea types, with Se-GTE being more beneficial than N-GTE in the positive modulation of gut microbiota.

Key Words: Green tea, Cecal microbiota, Broilers
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420 Prediction equations for digestible and metabolizable energy concentrations based on feed ingredients and diets for pigs.

J. Y. Sung*, K. R. Park, and B. G. Kim, *Department of Animal Science and Technology, Konkuk University, Seoul, Korea, Republic of (South).*

The objectives of this study were to develop prediction models for DE and ME concentrations in feedstuffs and diets for pigs and to evaluate the accuracy of the DE prediction equations. A total of 398 data from experiments using marker to marker procedure in the literature were employed to develop equations for predicting DE and ME. The CORR procedure of SAS was used to determine correlation coefficients among variables and the REG procedure was used to generate prediction equations using CP, ether extract (EE), NDF, ash, GE, and DE as independent variables. The equations developed for estimating DE or ME concentrations in feed ingredients or diets for pigs are: DE = 3,968 + 14 × CP + 48 × EE – 21 × NDF – 73 × ash (Eq. 1; $R^2 = 0.723$, and $P < 0.001$); DE = 686 + 0.79 × GE – 25 × NDF – 24 × ash (Eq. 2; $R^2 = 0.729$, and $P < 0.001$); ME = 3,850 + 10 × CP + 49 × EE – 21 × NDF – 61 × ash (Eq. 3; $R^2 = 0.694$, and $P < 0.001$); ME = 1,232 + 0.63 × GE – 23 × NDF – 22 × ash (Eq. 4; $R^2 = 0.678$, and $P < 0.001$); ME = – 70 + 1.00 × DE – 5 × CP (Eq. 5; $R^2 = 0.967$, and $P < 0.001$), where GE, DE, and ME are in kcal/kg DM and all nutrients are in % DM. Data from 56 ingredients reported in NRC (2012) were employed to validate DE equations. To test the accuracy of DE prediction models, a regression analysis of the measured minus predicted DE concentration against the predicted minus average predicted DE concentration was conducted. A validation using Eq. 1 showed that the intercept (–87 ± 47; $P = 0.068$) representing the mean bias and slope (–0.021 ± 0.088; $P = 0.809$) representing the linear bias were not different from 0. A validation test of Eq. 2 showed that the intercept (–146 ± 53; $P = 0.008$) was different from 0 but slope (–0.068 ± 0.100; $P = 0.501$) was not different from 0. In conclusion, the DE or ME concentrations in feed ingredients or diets for pigs may be predicted using the prediction equations suggested herein.

Key Words: energy, prediction models, swine
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421 Effects of β-mannanase (CTCzyme®) supplementation on growth performance and nutrient digestibilities in comparison to multi-enzyme complexes in broilers.

D. J. Ha*[1,2], M. Y. Park[1], J. Kim[1], S. W. Jung[2], and K. Y. Whang[1], *[1]Department of Biotechnology, Graduate School, Korea University, Seoul, Korea, Republic of (South), [2]CTCBIO INC., Seoul, Korea, Republic of (South).*

As prices for feed ingredients rise, corn distillers dried grains with solubles (DDGS) have been used as a feed ingredient since DDGS production in the bioethanol industry has increased. However, DDGS contains a high percentage of non -starch polysaccharides (NSP) such as β-mannan, which is indigestible in non-ruminants. Therefore, supplementation of NSP-degrading enzymes in diets containing DDGS is widely accepted to increase nutrient utilization. A number of commercial products have been developed in the form of enzyme complexes due to concerns for various NSP in DDGS. The present study was conducted to evaluate the effects of β-mannanase (CTCzyme®) supplementation on growth performance and nutrient digestibilities in broilers, and to compare its efficacy with other multi-enzyme complex products. A total of 36 twenty-day-old broiler chicks were housed in individual cages and fed one of the 4 experimental diets for 10 days. Basal diet was formulated to contain 10% DDGS and used for the control group (CON). Each of CTCzyme® (800 U/g β-mannanase) and two enzyme complexes (product A: 7 U/g α-galactosidase, 22 U/g galactomannanase, 300 U/g xylanase, and 220 U/g β-glucanase; product B: 550 U/g xylanase and 50 U/g β-glucanase) were supplemented to the basal diet at 30% of recommended dosages (CTCzyme®, 0.015%; A, 0.030%; B, 0.030%). Body weight and feed intake were measured on days 0, 6, and 10. For total tract digestibility, excreta from each bird were collected during days 6 through 10. Average daily gain (ADG) of CTCzyme® treatment during day 6-10 was significantly higher ($P < 0.05$) than CON. Body weights of A and B treatments at day 6 were lower ($P < 0.05$) than CON, and BW of B treatment at day 10 was also lower ($P < 0.05$) than CON. Although average daily feed intake (ADFI) was not different among treatments, a concomitant decrease in ADG and feed efficiency was noted in the group supplemented with B compared to other groups ($P < 0.05$). There were no differences in nutrient digestibilities among treatments. Crude protein digestibility, however, tended to be higher in the group supplemented with CTCzyme® than other groups. These results may implicate the comparable aspects of CTCzyme® as a single NSP-degrading enzyme to multi-enzyme complexes A and B at 30% of recommended level in diets containing 10% DDGS.

Key Words: CTCzyme®, broilers, DDGS
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422 Effects of protease on growth performance and nutrient digestibility of growing pigs.

J. Baek*[1], S. Park[1], J. J. Lee[1], J. Kim[1], S. Kim[1], K. Jang[1], B. Kim[1], J. Kang[1], D. Mun[1], J. Choe[1], I. H. Park[2], J. Y. Cho[2], S. H. Cho[2], and M. Song[1], [1]*Chungnam National University, Daejeon, Korea, Republic of (South),* [2]*DSM Nutrition Korea Ltd., Seoul, Korea, Republic of (South).*

This study was conducted to investigate effects of dietary protease on growth performance and nutrient digestibility of growing pigs. A total of 96 growing pigs (initial BW 31.57 ± 2.97 kg; equal number of barrows and gilts) were randomly assigned to 2 dietary treatments (8 pigs/replicate; 6 replicates/treatment) in a randomized complete block design (BW as a block). Dietary treatments were 1) a diet based on corn, soybean meal, and wheat (CON) and 2) CON + 0.02% protease (PRO). The protease used in this study was a commercial protease product (Ronozyme® ProAct, DSM Nutritional Products, Kaiseraugst, Switzerland) containing 75,000 protease units/g derived from *Bacillus licheniformis*. Pigs were fed respective dietary treatments for 6 weeks. For the last week of the experimental period, pigs were fed respective dietary treatments containing 0.2% chromic oxide as an indigestible marker. Fecal samples from two randomly selected pigs in each pen were collected daily by rectal palpation for the last 3 days after the 4-day adjustment period. Measurements were growth performances and digestibility of dry matter, nitrogen, and energy by an index method. Data were analyzed using the PROC GLM procedure of SAS. The statistical model for every measurement included dietary effect and BW as a covariate. Pigs fed PRO had greater ADG (0.944 vs. 0.877 kg/d; $P < 0.05$) and G:F (0.450 vs. 0.401 kg/kg; $P < 0.05$) than those fed CON. However, no difference was found in ADFI between CON and PRO (2.16 vs. 2.10 kg/d). In addition, there were no differences in apparent total tract digestibility of dry matter (74.90 vs. 79.63%), nitrogen (69.62 vs. 76.23%), and energy (74.04 vs. 79.14%) between CON and PRO. In conclusion, addition of protease in grower diets improved growth performance and did not affect nutrient digestibility in growing pigs.

Key Words: protease, growing pigs, growth performance
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423 Effects of dietary protease on nutrient digestibility of weaned pigs.

D. Mun*[1], I. H. Park[2], J. Kim[1], S. Kim[1], J. J. Lee[1], K. Jang[1], B. Kim[1], S. Park[1], J. Kang[1], J. Baek[1], J. Choe[1], J. Y. Cho[2], S. H. Cho[2], and M. Song[1], [1]*Chungnam National University, Daejeon, Korea, Republic of (South),* [2]*DSM Nutrition Korea Ltd., Seoul, Korea, Republic of (South).*

This study was conducted to investigate effects of dietary protease on nutrient digestibility of weaned pigs. A total of 75 weaned pigs (initial BW = 7.06 ± 0.18 kg; 28 d old) were randomly assigned to 3 dietary treatments (5 pigs/pen; 5 replicates/treatment) in a randomized complete block design (block = BW). The dietary treatments were 1) a diet based on corn and soybean meal to meet or exceed the requirement of crude protein as a positive control (PC; CP = 24.17%), 2) a low protein diet as a negative control (NC; CP = 23.51%), and 3) NC + 0.02% protease (PRO). The protease used in this experiment was a commercial product (Ronozyme® ProAct, DSM nutrition products, Kaiseraugst, Switzerland) containing 75,000 protease units/g derived from *Bacillus licheniformis*. The dietary treatments did not include spray dried plasma, fishmeal, zinc oxide, and antibiotics to avoid their antibacterial or physiological effects. Pigs were fed each treatment for 6 weeks. For the last week of the experimental period, pigs were fed respective dietary treatments containing 0.2% chromic oxide as an indigestible marker. Fecal samples from 1 randomly selected pig per replicate were collected daily by rectal palpation for the last 3 days after the 4-day adjustment period. One randomly selected pig per replicate was euthanized to collect ileal digesta at the end of the experiment. Measurements were apparent ileal digestibility (AID) and apparent total tract digestibility (ATTD) of dry matter, crude protein, and energy by an index method. Data were analyzed using the PROC GLM procedure of SAS. The statistical model for every measurement included dietary effect and BW as a covariate. Pigs fed PRO and PC had higher ($P < 0.05$) AID of dry matter (74.36 and 74.88 vs. 68.59%), crude protein (74.71 and 73.71 vs. 68.86%), and energy (77.04 and 76.64 vs. 70.72%) than those fed NC. In addition, pigs fed PRO and PC had higher ($P < 0.05$) ATTD of dry matter (85.12 and 85.64 vs. 83.77%) and crude protein (79.63 and 79.90 vs. 75.34%) than pigs fed NC, but there was also no difference on ATTD of energy among dietary treatments. In conclusion, the addition of protease in nursery diets with low protein level improved nutrient digestibility of weaned pigs.

Key Words: Nutrient digestibility, Protease, Weaned pigs
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424 Effect of dietary net energy and digestible lysine levels on growth performance and carcass composition of finishing pigs.

J. K. Htoo*[1], and J. Morales[2], [1]*Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany,* [2]*PigCHAMP Pro Europa, Segovia, Spain.*

Studies evaluating the optimal dietary NE levels or standardized ileal digestible (SID) Lys:NE ratios in diets for finishing pigs are scarce. An experiment was conducted to evaluate the effects of dietary SID Lys and NE levels on performance and carcass composition of 60- to 100-kg pigs. A total of 288 mixed-sex pigs (PIC GP1050; initial BW of 59.2 ± 0.44 kg) were assigned to 6 dietary treatments with 8 pen replicates (3 barrows and 3 gilts/pen) per treatment using a 2 × 3 factorial

arrangement with 2 levels of SID Lys (0.70 or 0.80%) and 3 NE levels (9.40, 9.75 or 10.10 MJ/kg) for 45 d. Diets were formulated based on corn, soybean meal and wheat bran using the analyzed ingredient AA contents and published SID coefficients to meet ideal AA ratios. Pigs had ad libitum access to feed (mash) and water. Individual pigs and pen feed disappearance were weighed on bi-weekly basis to calculate ADG, ADFI and G:F. All pigs were slaughtered for carcass assessment after reaching approximately 107 kg BW. Data were analyzed using the GLM procedure of SAS. There were no SID Lys × NE interaction effects ($P > 0.05$) for any performance or carcass parameter. The ADFI was not affected ($P > 0.10$) by the dietary SID Lys (2,128 and 2,007 g/d) or NE levels (2,103, 2,035 and 2,065 g/d). Both ADG and G:F seemed to maximize at 0.80% SID Lys and 9.75 MJ NE. However, ADG and G:F were not affected by the NE levels. Increasing the SID Lys from 0.70 to 0.80% increased ($P < 0.05$) both the ADG (854 and 892 g/d) and G:F (0.418 and 0.460). Increasing SID Lys from 0.70 to 0.80% tended to reduce ($P = 0.06$) the amount of NE needed per kg BW gain from 24.3 to 22.1 MJ/kg BW gain. The SID Lys efficiency (g/kg of BW gain) was not affected ($P > 0.05$) by both Lys and NE levels. Supplying 0.80% SID Lys in the diets reduced the number of days on trial to reach the slaughter BW by about 3 d compared with 0.70% SID Lys. Carcass yield maximized at a dietary NE content of 9.75 MJ/kg. Carcass leanness and backfat thickness were not affected by dietary treatments. Overall, both performance and carcass composition optimized when the diet contains 0.80% SID Lys and 9.75 MJ/kg NE, which corresponds to 0.82 g SID Lys/MJ NE.

Key Words: Finishing pigs, Lysine, Net energy
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425 Time course of indigestible indexes in the ileal out flow of pigs fed a soybean meal-based or nitrogen-free diet.

B. G. Kim[1], K. R. Park[*1], and H. H. Stein[2], [1]*Department of Animal Science and Technology, Konkuk University, Seoul, Korea, Republic of (South),* [2]*University of Illinois at Urbana-Champaign, Urbana.*

The use of indigestible index is inevitable in ileal nutrient digestibility experiments due to the difficulties in quantitative collection of ileal digesta. A sufficient adaptation period before the initiation of ileal digesta collection is critical for accurate determination of ileal nutrient digestibility. The objective of this experiment was to identify the minimum adaptation period in ileal digestibility experiments using Cr, Ti, and acid insoluble ash (AIA) as indigestible indexes. Eight barrows with an initial BW of 58.1 kg (SD = 4.3) fitted with a T-cannula in the distal ileum were randomly allotted to a 2-period crossover design with 2 diets and 8 pigs in each period. The animals were housed in individual pens equipped with a feeder and a nipple drinker. A soybean meal (SBM)-based diet and an N-free diet were prepared. Both experimental diets contained 0.4% chromium oxide, 0.4% titanium dioxide, and 0.4% Celite (a source of AIA) as indigestible indexes. A washout diet with no indigestible index was provided ad libitum to the pigs for 7 d before each 9-d experimental period. The SBM and N-free diets were provided at daily levels of 3 times the estimated maintenance requirement for energy. Equal meals were provided at 0800 and 2000 h. Ileal digesta samples were collected from 0800 to 1600 h on each day during both experimental periods. In pigs fed the SBM diet, the break point for Cr, Ti, and AIA was 2.7 (SE = 0.6, $P < 0.001$), 2.4 (SE = 0.4, $P < 0.001$), and 3.8 d (SE = 1.8, $P = 0.091$), respectively, based on one-slope broken-line analysis. In pigs fed the N-free diet, the break point for Cr, Ti, and AIA was 2.5 (SE = 0.6, $P = 0.001$), 2.4 (SE = 0.5, $P = 0.002$), and 2.3 d (SE = 0.6, $P = 0.021$), respectively. Sum of squares of error term in quadratic broken-line models were not less than in one-slope broken-line models. Based on the present results, we suggest that at least 3 d of adaptation period is required before initiating digesta collection in ileal digestibility experiments using chromium oxide or titanium dioxide as an indigestible index and that at least 4 d of adaptation is required with Celite as an index. Further research is warranted to determine minimum adaptation periods for consistent ileal nutrient digestibility values.

Key Words: acid insoluble ash, chromium, titanium
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426 Ileal amino acid digestibility values vary depending on the exogenous indigestible indexes in pigs fed a soybean meal-based diet.

B. G. Kim[1], K. R. Park[*1], and H. H. Stein[2], [1]*Department of Animal Science and Technology, Konkuk University, Seoul, Korea, Republic of (South),* [2]*University of Illinois at Urbana-Champaign, Urbana.*

The objective was to test a hypothesis that ileal AA digestibility values may vary depending on the indigestible index sources including chromium oxide, titanium dioxide, and Celite. Eight barrows with an initial BW of 58.1 kg (SD = 4.3) fitted with a T-cannula in the distal ileum were randomly allotted to a 2-period crossover design with 2 diets and 8 pigs in each period. A soybean meal (SBM)-based diet and an N-free diet were prepared. Both experimental diets contained 0.4% chromium oxide, 0.4% titanium dioxide, and 0.4% Celite as indigestible indexes. A washout diet with no index was provided ad libitum to the pigs for 7 d before each 9-d experimental period. The diets were provided at daily levels of 3 times the estimated maintenance requirement for energy. Equal meals were provided at 0800 and 2000. Ileal digesta were collected from 0800 to 1600 on each day. In the same experiment, we found that the minimum adaptation period before ileal digesta collection to have constant index concentrations was 3 to 4 d. Therefore, the digestibility and endogenous loss of AA data were pooled from d 5 to 9 to investigate the influence of indigestible index on AA digestibility and endogenous losses. The ileal digesta are often collected during d 6 and 7 in many experiments, and thus, the data from d 6 and 7 were also pooled for testing index effects on AA digestibility and endogenous losses. Based on the pooled data from d 5 to 9, the apparent ileal digestibility (AID) and the standardized ileal digestibility (SID) of all AA except Tyr calculated using Cr or Ti as an index were greater ($P < 0.05$) than the digestibility values calculated using AIA. During d 5 to 9, the basal endogenous losses (BEL) of Arg, His, Ile, Leu, Lys, Thr, Trp, Val, Ala, Asp, Glu, Gly, Pro, and Ser calculated using Cr as an index were less ($P < 0.05$) than the BEL values calculated using Ti but greater ($P < 0.05$) than the BEL values calculated using AIA. When the data from d 6 and 7 were pooled, the AID, SID, and BEL of AA changes by indigestible indexes had the same pattern as the data from d 5 and 9. Overall, AA digestibility calculated using Cr or Ti was greater than that calculated using AIA.

Key Words: acid insoluble ash, chromium, titanium
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427 Using near-infrared spectroscopy to predict the metabolizable energy of corn for pigs.

S. L. Ferreira[1], M. R. Fachinello[1], L. M. Diaz Huepa[1], R. M. Rossi[2], R. V. Nunes[3], and P. C. Pozza*[4],
[1]Universidade Estadual de Maringá/CAPES, Maringá, Brazil, [2]Universidade Estadual de Maringá, Maringá, Brazil, [3]Universidade Estadual do Oeste do Paraná/CNPq, Marechal Cândido Rondon, Brazil, [4]Universidade Estadual de Maringá/CNPq, Maringá, Brazil.

The aim of this study was to determine the chemical composition and metabolizable energy (ME) of different varieties of corn, and to validate mathematical models for predicting the ME of corn for pigs using near-infrared spectroscopy (NIRS). The dry matter (DM), mineral matter (MM), neutral detergent fiber (NDF), acid detergent fiber (ADF), ether extract (EE), crude protein (CP) and gross energy (GE) content of 99 different cultivars of corn were determined by conventional laboratory analyses (LAB) and by NIRS technology. Eighty cultivars were used to establish and calibrate the NIRS model, nine samples were used for external validation and ten cultivars were used in the metabolism assay. Samples were read in the spectrum range from 1100–2500 nm, and the model parameters were estimated by the modified partial least squares (MPLS) method. The results for the chemical composition of corn obtained by LAB and by NIRS technology were compared in a paired manner (observed and predicted values). The estimated metabolizable energy (EME) values were obtained from 11 predictive models in the literature, and inserted into the NIRS model. The observed metabolizable energy values (OME) were obtained in the metabolism assay. The metabolism assay was carried out using 44 barrows with an average initial weight of 25.05 kg, which were distributed into 11 treatment groups based on a randomized block design, with four replicates per treatment and one animal per experimental unit. Validation of the prediction equations was performed by adjusting the linear regression models of the first degree of EME values due to the OME, following a Bayesian approach. The linear relationship between the estimated and observed values was evaluated by detecting the significance of the estimated posterior parameters β_0 and β_1, recorded where the null (zero) did not belong to the 95% credible intervals for each parameter. Near-infrared spectroscopy was effective for determining the NDF, EE, CP and GE contents of corn when compared to the conventional LAB method. The prediction equations $ME_1 = 4{,}334 - 8.1MM + 4.1E - 3.7NDF$, $ME_2 = 4{,}194 - 9.2MM + 1.0CP + 4.1EE - 3.5NDF$, $ME_7 = 344.272 + 0.90886GE + 57.9377EE - 86.9320CP$ and $ME_8 = 16.13 - 9.5NDF + 16EE + (23CP \times NDF) - (138MM \times NDF)$ were the most suitable ($P < 0.05$) for predicting the ME values of corn for pigs using NIRS compared to the LAB tests; however, neither method was accurate.

Key Words: Chemical composition, Prediction models, Validation
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428 Pig adipose depot-specific response to a reduced protein diet in combination with n-3/n-6 polyunsaturated fatty acid intervention.

D. Dannenberger*, C. Kalbe, and G. Nuernberg,
Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.

The clarification of mechanisms regulating de novo fatty acid synthesis in adipose depots in pigs is an important step in designing the strategies for producing pigs with "desirable" fatty acid composition. The objective of the study was to investigate adipose depot-specific responses to dietary protein/PUFA intervention with respect to lipid metabolism-related gene expression on mRNA and protein levels and fatty acid concentrations. In total, 40 male Landrace pigs were allocated into 4 experimental groups fed diets different in protein level (19.5 vs. 15.5%) and oil supplementation (sunflower seed vs. linseed oil), and 1 control group (17.4% protein level). The pigs were fed ad libitum from 60 kg to 100 kg live weight and restricted (2.8 kg/d) until 120 kg. After slaughtering, pig adipose depots (abdominal, omental, perirenal, intestinal, and back fat) were taken for real-time quantitative PCR, western blot, and fatty acid analysis. The effects of the dietary protein/PUFA intervention were estimated by 1-way ANOVA with a fixed factor of group (group 1 to 5) using the GLM procedure of the SAS software system. *n*-3 PUFA vs. *n*-6 PUFA intervention resulted in significant changes ($P < 0.05$) in *n*-3 and *n*-6 PUFA concentrations in 5 different adipose depots, independent of the dietary protein level. However, the changes in *n*-3 and *n*-6 PUFA concentrations are not reflected by corresponding diet-induced alterations of *ELOVL5*, *FADS1*, *FADS2*, and *SREBP1* mRNA and protein expression in investigated adipose depots. The mRNA expression of *ELOVL5* and *SREBP1* was highest in abdominal fat and *FADS1* and *FADS2* mRNA expression was highest in intestinal fat compared with the other pig adipose depots. Different diets did not affect the concentrations of single and sum SFA. This is in line with the *ACACA* and *FASN* gene expression, key enzymes involved in the de novo synthesis of SFA, and transcription factor SREBP-1, which was not affected by different dietary protein/PUFA intervention in all pig adipose depots, except higher protein expressions in abdominal fat of pigs fed a high-protein diet with sunflower seed oil. The gene expression of SCD, the key enzyme in the MUFA biosynthesis, was not diet affected in pig adipose depots and corresponds with the unchanged MUFA tissue concentrations. Because of the discrepancy between the highly different *n*-3 and *n*-6 PUFA concentrations and minor changes in lipogenic gene expression in pig adipose depots, alternative pathways of de novo fatty acids synthesis appear to be likely.

Key Words: pig, adipose tissue, PUFA
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429 Effect of increasing lead concentrations in diets on the lead residue of the liver and feather in broiler chickens.

D. Y. Koo*[1], J. H. Kim[1], G. H. Park[1], H. S. Choi[1], H. Jung[2], and D. Y. Kil[1], [1]*Chung-Ang University, Anseong, Korea, Republic of (South),* [2]*National Institute of Animal Science, Rural Development Administration, Wanju-Gun, Korea, Republic of (South).*

An experiment was conducted to investigate the effect of increasing lead concentrations in diets on the lead residue of the liver and feather in broiler chickens. A total of 800 2-d-old Ross 308 broiler chicks were used and allotted to 1 of 5 dietary treatments with 16 replicates consisting of 10 birds in a completely randomized design. Dietary lead concentrations were set to 0, 50, 100, 200, or 400 mg/kg by adding lead acetate ($\geq$ 54.6%) at the expense of the celite. The experimental diets were fed to birds for 5 weeks. At the conclusion of the experiment, 1 bird from each replicate was euthanized. Liver and feather samples were collected for the lead residue analysis. Results indicated that increasing lead concentrations in diets increased the lead residue of the liver (linear and quadratic, $P < 0.05$) and feather (linear, $P < 0.01$) in broiler chickens. Broiler chickens fed diets containing 400 mg/kg lead had greater ($P < 0.05$) lead residue in the liver than those fed the control diets. However, broiler chickens fed diets containing 200 mg/kg lead had greater ($P < 0.05$) lead residue in the feather than those fed the control diets. In conclusion, increasing lead concentrations in diets up to the level of 400 mg/kg increased the lead residue in the liver and feather tissues; however, only feather shows a dose-dependent linear response. A greater than 400 mg/kg lead in diets significantly increases the lead residue of the liver and feather in broiler chickens.

Key Words: Tissue lead residue, Broiler chicken, Dietary lead
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430 Effect of dietary mercury concentrations on growth performance and relative organ weight in male broiler chickens.

G. H. Park*[1], D. Y. Koo[1], J. H. Kim[1], H. S. Choi[1], F. M. Pitargue[1], H. Jung[2], and D. Y. Kil[1], [1]*Chung-Ang University, Anseong, Korea, Republic of (South),* [2]*National Institute of Animal Science, Rural Development Administration, Wanju-Gun, Korea, Republic of (South).*

An experiment was conducted to investigate the effect of dietary mercury concentrations on growth performance and relative organ weight in male broiler chickens. A total of 400 2-d-old Ross 308 male broiler chicks were housed in 40 battery cages for a 5-wk feeding trial. Birds were randomly allotted to 1 of 5 dietary treatments with 8 replicated cages. Each replicate had 10 birds per cage. Dietary mercury concentrations were set to 0, 50, 100, 250, or 500 mg/kg by adding mercury chloride ($\geq$ 73.9%) at the expense of the celite. The experimental diets were mash form. At the end of the experiment, 1 bird from each replicate was euthanized. The breast, liver, heart, kidney, spleen, lung, bursa of Fabricius, and small intestine were collected and weighed individually. The relative organ weights were calculated as a percentage of live body weight. Results indicated that increasing mercury concentrations in diets decreased (linear and quadratic, $P < 0.05$) body weight gain and feed intake of male broiler chickens. Birds fed diets containing greater than 250 mg/kg mercury showed significantly less body weight gain and feed intake ($P < 0.05$) than those fed the control diets. However, there were no differences in feed efficiency and mortality among dietary treatments. The relative weights of the small intestine were decreased (quadratic, $P < 0.05$) with increasing mercury concentrations in diets, whereas those of other organs were not affected by dietary treatments. In conclusion, a greater than 250 mg/kg mercury in diets is toxic to male broiler chickens. The small intestine is likely the most sensitive organ to the toxic concentrations of mercury in diets for male broiler chickens.

Key Words: Growth performance, Male broiler chicken, Mercury
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431 Effect of dietary mercury concentrations on growth performance and relative organ weight in female broiler chickens.

H. S. Choi*[1], G. H. Park[1], J. H. Kim[1], D. Y. Koo[1], F. M. Pitargue[1], H. Jung[2], and D. Y. Kil[1], [1]*Chung-Ang University, Anseong, Korea, Republic of (South),* [2]*National Institute of Animal Science, Rural Development Administration, Wanju-Gun, Korea, Republic of (South).*

An experiment was conducted to investigate the effect of dietary mercury concentrations on growth performance and relative organ weight in female broiler chickens. A total of 400 2-d-old Ross 308 female broiler chicks were housed in 40 battery cages for a 5-wk feeding trial. Birds were randomly allotted to 1 of 5 dietary treatments with 8 replicated cages. Each replicate had 10 birds per replicate. Dietary mercury concentrations were set to 0, 50, 100, 250, or 500 mg/kg by adding mercury chloride (≥ 73.9%) at the expense of the celite. At the conclusion of the experiment, 1 bird per replicate with a body weight (BW) close to the replicate mean BW (i.e., 8 birds per treatment) were euthanized by CO_2 asphyxiation, then immediately dissected. The breast, liver, heart, kidney, spleen, lung, bursa of Fabricius, and small intestine were collected and weighed individually. Relative organ weight was expressed as a percentage of live BW. Results indicated that increasing mercury concentrations in diets decreased BW gain (linear and quadratic, $P < 0.05$) and feed intake (linear, $P < 0.01$) of female broiler chickens. Birds fed diets containing 500 mg/kg mercury showed less ($P < 0.05$) body weight gain and feed intake than those fed the control diets. However, there were no differences in feed efficiency and mortality among dietary treatments. The relative weight of the liver was increased (linear, $P < 0.05$) with increasing mercury concentrations in diets. There was a quadratic relationship ($P < 0.01$) between the relative weight of the small intestine and increasing mercury concentrations in diets. In conclusion, the concentrations of 500 mg/kg mercury in diets are toxic to female broiler chickens. The liver is likely the most sensitive organ to the toxic concentrations of mercury in diets for female broiler chickens.

Key Words: Female broiler chicken, Mercury, Growth performance
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432 Alterations in bile acid profiling in large white pigs during heat stress.

W. Fang*[1,2], J. Xie[1], Q. Meng[3], and H. Zhang[4], [1]*The State Key Laboratory of Animal Science, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*University of Liège, Gembloux Agro-Bio Tech, Precision Livestock and Nutrition Unit, Gembloux, Belgium,* [3]*The State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [4]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China.*

Heat stress can reduce productivity through changes in feed intake, fat deposition and total tract digestibility of dietary fat. Bile acids are critical for dietary fat digestion and new roles in metabolism and endocrinology have been demonstrated recently. The objective was to investigate the alterations in plasma and gut bile acids profiles induced by heat exposure. Nine litters (3 pigs/litter) of male Large White pigs weighing 40.8 ± 2.7 kg were assigned to each of control kept at 23°C (CON), heat stress kept at 33°C (HS), or pair-feeding group (PF) kept at 23°C but given the same amount of feed as the HS group. On d 21, the average daily feed intake and average daily gain of the HS pigs was reduced to 55.6% and 41.2% of the controls ($P < 0.05$), respectively, and the rectal temperature was 0.8°C higher ($P < 0.05$). By using the LC-MS/MS, 15 bile acids were quantified. When compared with the CON, plasma taurocholates, including tauroursodeoxycholate (TUDCA) and taurohyodeoxycholate (THDCA), were reduced in the HS and PF groups ($P < 0.05$), but other bile acids did not differ from the CON group. The ratio of taurocholate to glycocholate (T:G) was reduced from 0.1 in the CON to 0.05 in the HS group ($P < 0.05$) and 0.04 in PF group ($P < 0.05$). In the ileum, where bile acids were reabsorbed and recycled, reduced TUDCA and glycoursodeoxycholate (GUDCA) was found in the PF group ($P < 0.05$) compared with the HS group. The T:G ratio was reduced from 0.46 in the CON group to 0.38 in the HS group and 0.27 in the PF group ($P < 0.05$). In the cecum, ursodeoxycholic acid (UDCA) was higher in the PF and HS groups than the CON group. The T:G ratio was reduced from 0.16 in the CON group to 0.08 in the HS group and 0.02 in the PF group. The HS group tended to have greater taurocholates compared with the PF group ($P = 0.08$). Our data clearly showed that reduced feed intake during heat exposure has profound impacts on the conjugation process of bile acids. Due to its protective role in endoplasmic reticulum (ER), the observed changes in UDCA conjugation could influence heat-induced oxidative stress.

Key Words: large white pigs, bile acids, heat stress
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433 Effects of protease on growth performance and carcass characteristics of finishing pigs.

J. Kang*[1], J. Choe[1], S. Park[1], J. Kim[1], B. Kim[1], S. Kim[1], J. J. Lee[1], K. Jang[1], D. Mun[1], J. Baek[1], I. H. Park[2], J. Y. Cho[2], S. H. Cho[2], and M. Song[1], [1]*Chungnam National University, Daejeon, Korea, Republic of (South),* [2]*DSM Nutrition Korea Ltd., Seoul, Korea, Republic of (South).*

The purpose of this study was to evaluate effects of protease on growth performance and carcass characteristics of finishing pigs. A total of 96 pigs (initial BW of 69.82 ± 2.30 kg; equal number of barrows and gilts) were randomly assigned to 2 dietary treatments (8 pigs/replicate; 6 replicates/treatment) in a randomized complete block design (BW as a block). Dietary treatments were 1) a diet based on corn, soybean meal, and wheat (CON) and 2) CON + 0.02% protease (PRO). The protease was a commercial product (Ronozyme® ProAct, DSM Nutritional Products, Kaiseraugst, Switzerland) containing 75,000 protease units/g derived from *Bacillus licheniformis*. Pigs were fed their respective diets for 6 weeks. All pigs were housed in environmentally controlled pens with free access to diets and water throughout the entire experiment period. After 6 weeks, pigs were fasted with only free access to water for 4 h and final BW of pigs was recorded prior to transportation. Pigs were transferred to a local commercial slaughter facility with a conventional scalding-singeing process. Measurements were growth performance and carcass characteristics of finishing pigs. All data were analyzed using the PROC GLM procedure of SAS. The statistical model for every measurement included dietary effect and BW as a covariate. There was no difference in ADG between CON and PRO (0.891 vs. 0.929 kg/d). However, pigs fed PRO had lower ADFI (2.92 vs. 3.29 kg/d, $P < 0.05$) and higher G:F ratio (0.319 vs. 0. 271 kg/kg, $P < 0.05$) than those fed CON. No differences were found in hot carcass weight (83.55 vs. 82.81 kg), dressing percentage (76.94 vs. 77.07%), final backfat depth (17.20 vs. 16.73 mm), and fat free lean (58.13 vs. 57.99%) between CON and PRO. In conclusion, addition of protease in finisher pig diets increased feed efficiency but did not affect carcass characteristics.

Key Words: Growth performance, Protease, Finishing pigs
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434 Energy values of passion fruit seed oil for broiler chickens.

L. H. Zanetti*[1], J. R. Sartori[2], A. C. Pezzato[2], J. C. Denadai[2], G. A. M. Pasquali[2], E. M. Muro[2], T. S. D. Santos[2], D. S. D. Souza[2], L. C. Dornelas[2], R. G. Ferreira Netto[2], A. C. Contin Neto[2], and P. G. Serpa[2], [1]*São Paulo State University (UNESP), Botucatu, Brazil,* [2]*FMVZ, UNESP, Botucatu, Brazil.*

Passion fruit (*Passiflora edulis*) is a tropical fruit with production concentrated primarily in South America, and Brazil is the main producer and consumer of this fruit. The byproducts obtained from the pulp and seeds can be used as an alternative food ingredient, and the oil is provided through the seeds. This study was conducted to determine the energy value of passion fruit seed oil for broiler chickens. A metabolism assay with seventy 21- to 31-d-old male Cobb broiler chickens was carried out using the method of total excreta collection. The birds were stored in 14 cages that were previously adapted with plastic-covered trays to collect excreta. The experimental design was completely randomized with 2 treatments and 7 replications of 5 birds per experimental unit. The treatments were a basal diet based on corn and soybean meal and a test diet (reference diet with 10% replacement of passion fruit seed oil). The experimental period lasted 10 d (5 d for adjustment + 5 d for excreta collection), and during that period, birds received ad libitum feed and water. The traditional method of excreta collection was used, with ferric oxide (1%) serving as a marker at the start and end of excreta collection, according to the methodology described by Sakomura and Rostagno. Feed was weighed at the start and the end of the full collection period in order to determine mean feed intake. The energy values were obtained using a colorimetric pump (IKA C-200). After laboratory analysis results were obtained for the reference feed, test feed, and excreta, the value of apparent ME (AME) was calculated using the equation in Matterson et al. The energy values of passion fruit seed oil obtained were 9,837 kcal/kg for GE and 9,378 kcal/kg for AME.

Key Words: by-product, digestibility, energy
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435 Spray-dried plasma on weaning piglets' feed with in diets with high or low mycotoxins levels.

D. Paiano*, *Universidade do Estado de Santa Catarina, chapecó, Brazil.*

Mycotoxins are a problem in swine production, especially after weaning, and ingredients such as spray-dried blood (PSD) may be an alternative to minimize the problem. The objective of this work was to assess the effects of PSD use for postweaning piglets feds diets with low or high mycotoxin levels. Fifty-six weaned, castrated male piglets (24 ± 2 d old and 7.15 ± 0.61 kg) were used in a 2 × 2 factorial design arrangement of diets without PSD and with 6% PSD and diets with low (0.95 μg/kg aflatoxins + 0.45 mg/kg fumonisins) or high mycotoxin levels (300 μg/kg aflatoxins + 8.0 mg/kg fumonisins), which resulted in 4 treatments, and there were 7 replicates and 2 piglets per experimental unit. The experimental period consisted of 15 d subdivided into three 5-d periods, in which feed intake, weight gain, feed efficiency, days with diarrhea, and economic viability were evaluated. There was no interaction ($P > 0.05$) between mycotoxins and PSD for the studied variables. Weight gain and feed efficiency were better in the diets with PSD in the first 2 periods and in the total experimental period. Feed intake was higher in diets with PSD in all periods. Diarrhea incidence was higher ($P < 0.05$) in the first 2 periods and the total experimental period for treatments without PSD. The high mycotoxin level reduced the gain in the third period ($P < 0.05$). Despite the technical feasibility of the PSD, there was economic viability just in the 2 first periods. Spray-dried plasma improved gain and feed intake and reduced the diarrhea incidence and should be used in low or high mycotoxin levels.

Key Words: Functional foods, economic feasibility, piglet nutrition
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436 Comparison of performance of finishing pigs fed diets containing different levels of distiller's dried grains with solubles.

J. M. Uriarte*[1,2], H. R. Guemez Gaxiola[2], J. M. Romo[3], and J. A. Romo[4], [1]*Facultad de Medicina Veterinaria y Zootecnia, CULIACAN, Mexico,* [2]*UNIVERSIDAD AUTÓNOMA DE SINALOA, CULIACÁN, Mexico,* [3]*FMVZ-Universidad Autonoma de Sinaloa, Culiacan, Mexico,* [4]*FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico.*

The present test was performed with the objective of determining the productive performance of pigs in finishing, using different percentages of distiller's dried grains with solubles

(DDGS) in the diet (10, 15, and 20%). Seventy-two pigs (78.01 ± 1.0 8 kg BW; Large White × Landrace × Large White × Pietrain) in groups of 6 were placed in 12 concrete floor pens (1.5 by 6 m). In a complete randomized experimental design, pigs received 1 of 4 diets similar in energy, CP, and lysine: 1) a diet with 12.97% CP and 3.30 Mcal of ME per kilogram, containing 85.0% corn, 12.2% soybean meal, 0.5% vegetable oil, and 2.3% premix (CONT); 2) a diet with 13.24% CP and 3.24 Mcal of ME per kilogram , with 79.2% corn, 10% DDGS, 8% soybean meal, 0.5% vegetable oil, 0.1% Lys, 0.1 calcium carbonate, and 2.1% premix (DDG10); 3) a diet with 13.3% CP and 3.21 Mcal of ME per kilogram, with 76.35% corn, 15% DDGS, 5.8% soybean meal, 0.5% vegetable oil, 0.15% Lys, 0.15 calcium carbonate, and 2.05% premix (DDG15); and 4) a diet with 13.46% CP and 3.19 Mcal of ME per kilogram, with 73.35% corn, 20% DDGS, 3.7% soybean meal, 0.5% vegetable oil, 0.20% Lys, 0.20 calcium carbonate, and 2.05% premix (DDG20). Pigs were weighed at d 0 and 35 of the experiment, and feed intake was recorded daily. Average daily gain and feed intake:gain ratio were calculated from these data. Body weight at d 35 was reduced ($P = 0.01$) in pigs fed the DDG20 diet, being 88.49 kg, and was 101.96, 102.53, and 100.49 kg for pigs fed the CONT, DDG10, and DDG20 diets, respectively. Average daily gain (0.685 kg for CONT, 0.739 kg for DDG10, 0.647 kg for DDG15, and 0.307 kg for DDG20) was also reduced ($P = 0.01$) by treatments containing DDG20. Feed intake (2.42, 2.56, 2.41, and 1.91 kg) was reduced in pigs fed DDG20 ($P = 0.01$). Feed:gain ratios (3.54 for CONT, 3.47 for DDG10, 3.74 for DDG15, and 6.24 for DDG20) were affected ($P = 0.01$) by these treatments. Given the results obtained, it is concluded that the 20% inclusion of DDGS in the diet of finishing pigs affects the productive performance of these animals.

Key Words: Pigs, DDGS, performance
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437 Effects of lipopolysaccharide challenge and weaning on serum biochemical parameters and hepatic hepcidin gene expression in piglets.

M. Li*[1], W. Li[1], Y. Liu[1], X. Yin[2], and M. Z. Fan[2], *[1]Henan University of Animal Husbandry and Economy, Zhengzhou, China, [2]University of Guelph, Guelph, ON, Canada.*

Hepcidin is a liver-derived peptide hormone that acts as a key regulator of intestinal iron absorption with antimicrobial properties in mammals, and its expression can be regulated by multiple stimuli. Two experiments were conducted to investigate the effects of lipopolysaccharide (LPS) challenge and weaning on serum parameters and hepatic hepcidin gene expression in piglets. In Exp. 1, 10 suckling piglets were randomly divided into a control group and a LPS group, with 5 piglets per group. The LPS group pigs were injected with 100 μg/kg BW LPS on suckling d 3, 5, and 7, and the control group piglets were injected with normal saline at the same dose. All piglets were sacrificed on d 7, and blood, liver, and spleen samples were collected. Total iron contents in the liver and serum were decreased ($P < 0.05$) in the LPS group. Serum total protein, albumin, total bilirubin, glucose, and triglyceride levels were reduced ($P < 0.05$) in the LPS group. Activities of serum Cu/Zn superoxide dismutase, catalase, and phospholipid hydroperoxide glutathione peroxidase were also decreased ($P < 0.05$) in the LPS group. However, erythrocyte malondialdehyde content was increased ($P < 0.05$) by the LPS challenge. Hepatic hepcidin mRNA abundance was increased ($P < 0.05$) in the LPS group compared with the control group. In Exp. 2, 55 piglets were randomly taken from 5 different sows at 21 d of age, and 5 piglets were sacrificed right before weaning at the age of 21 d. The remaining 50 piglets were weaned and divided into 5 pens with 10 pigs per pen. The weaning pigs were fed a corn and soybean meal–based weaning diet, and 1 pig per pen was sacrificed on d 2, 4, and d 8 after weaning. The alkaline phosphatase (AP) activity in serum was highest right before weaning and decreased ($P < 0.05$) after weaning. Serum Na, Cl, and K ion levels were not different ($P > 0.05$) before and after weaning. Serum globulin content was reduced ($P < 0.05$) on d 2 and was increased ($P < 0.05$) on d 4 and 8 after weaning. The hepatic hepcidin mRNA abundance was the lowest ($P < 0.05$) before weaning, peaked on d 2, and was then reduced ($P < 0.05$) on d 4 and 8 after weaning. In conclusion, LPS challenge and weaning enhanced hepatic hepcidin mRNA abundances whereas weaning decreased serum AP activity in the piglets.

Key Words: hepcidin, serum alkaline phosphatase activity, weaning piglets
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438 Estimating voluntary feed intake of slow-growing pigs fed progressive levels of diluted potato hash silage.

C. Ncobela*, *ARC- Animal Production Institute, Pretoria, South Africa; University of KwaZulu-Natal, Pietermaritzburg, South Africa.*

The objective of the study was to determine the effect of varying levels of potato hash silage on feed intake of growing Windsnyer pigs that are domestic in Southern Africa. A sequence and series of diets were formulated from a dilution of control diet (summit mixture) with 400 g/kg of ensiled potato hash diet (dilution mixture) at different proportions. The progressive diets were prepared by blending summit and dilution diets, respectively at different proportions to achieve 80 g/kg (320 g/kg: 80 g/kg), 160 g/kg (240 g/kg: 160 g/kg), 240 g/kg (160 g/kg: 240 g/kg), and 320 g/kg (80 g/kg: 320 g/kg) of ensiled potato hash silage. This produced six diets including summit (control) and dilution (400 g/kg) mixtures. There was a quadratic potato hash silage level effect (P <0.05) on average daily feed intake. As the inclusion levels of potato hash silage increased, the average daily feed intake increased at the increasing rate. Using piecewise regression, the maximum inclusion of potato hash silage was estimated to be 24 g/kg ± 4.72 and the maximum feed intake was predicted at 1.55 kg. The minimum feed intake was estimated at 1.34 kg ± 0.081. The rate of change of average feed intake was estimated to be 0.02 ± 0.009. The estimate of rate of increase of average daily feed intake was -0.002 ± 0.001. As the feed inclusion levels of potato hash increased, the average daily feed intake increased until the gut capacity was reached. Thereafter, the feed intake is reduced. There is a need to determine growth performance response of pigs fed increasing levels of potato hash silage. It is necessary to understand which chemical or physicochemical properties influence feed intake of slow growing pigs as an approach to accurately measure feed intake.

Key Words: feed intake, Windsnyer pigs, potato hash silage
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PHYSIOLOGY AND ENDOCRINOLOGY

048 Administration of lipopolysaccharide three times during gestation alters the postnatal acute phase and metabolic responses to a lipopolysaccharide challenge in weaned beef heifers.

A. B. Word*[1,2], N. C. Burdick Sanchez[3], J. A. Carroll[3], P. R. Broadway[3], G. M. Silva[4], J. Ranches[5], U. Pardelli[5], J. Warren[6], P. Moriel[5], and J. D. Arthington[5], [1]*USDA-ARS-Livestock Issues Research Unit, Lubbock, TX,* [2]*Texas Tech University, Lubbock,* [3]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX,* [4]*University of Florida, Range Cattle Research Center, Ona,* [5]*UF/IFAS Range Cattle Research and Education Center, Ona, FL,* [6]*University of Florida, Range Cattle Research and Education Center, Ona.*

This study evaluated whether 3 administrations of lipopolysaccharide (LPS) during gestation would alter the acute phase (APR) and metabolic responses to a postnatal LPS challenge in weaned heifers. Pregnant crossbred cows ($n = 50$) were randomized into prenatal immune stimulation (PIS; $n = 24$; administered 0.1 μg/kg BW LPS subcutaneously at 71 ± 2, 170 ± 2, and 234 ± 2 d of gestation) and saline groups (CON; $n = 26$). From these treatment groups, heifer calves ($n = 12$ PIS and $n = 11$ CON) were identified at weaning (244 ± 3 d of age) to subsequently receive an LPS challenge. On d 0, heifers were fitted with indwelling vaginal temperature (VT) devices and jugular catheters and moved into individual stalls. On d 1, heifers were intravenously challenged with LPS (0.5 μg/kg BW) at 0 h. Blood samples were collected and sickness behavior scores (SBS) were recorded at 0.5-h intervals from −2 to 8 h and at 24 h relative to LPS challenge. Serum was isolated and stored until analyzed for cortisol, cytokines, glucose, NEFA, and urea nitrogen (SUN) concentrations. Vaginal temperature was lesser in heifers in the PIS treatment group from 11 to 5 h before challenge (treatment × time, $P < 0.01$) compared with the CON group; however, the post-LPS VT response was similar between treatments ($P = 0.74$). There was a treatment × time interaction ($P < 0.01$) for SBS, with PIS heifers having lesser SBS from 0.5 to 2 h after challenge. There was a treatment × time interaction ($P = 0.04$) for cortisol with PIS heifers having greater cortisol at 0.5, 3, 3.5, and 6.5 h after challenge than CON heifers. There were treatment × time interactions for the postchallenge cytokine responses ($P \leq 0.05$). Specifically, PIS heifers had greater TNF-α at 2 and 2.5 h yet less TNF-α at 3 h than CON heifers ($P < 0.01$), and PIS heifers had greater IFN-γ from 3.5 to 5.5 h after challenge than CON heifers ($P < 0.01$). In contrast, IL-6 was less in PIS heifers than CON heifers from 2 to 8 h after challenge ($P \leq 0.02$). Glucose was greater in PIS heifers at −1.5 h but less at 2, 3, and 5.5 h compared with CON heifers (treatment × time, $P < 0.01$). Serum NEFA tended ($P = 0.06$) to be greater in PIS heifers than CON heifers. There was a treatment × time interaction ($P < 0.01$) for SUN with PIS heifers having greater SUN at −2, −1.5, 2, 3, 6.5, and 24 h than CON heifers. Therefore, in utero exposure to LPS 3 times during gestation reduced sickness behaviors and altered proinflammatory cytokine responses. These data suggest that prenatal exposure to LPS has the capability to alter the APR of offspring when presented with a similar challenge at weaning.

Key Words: immune, lipopolysaccharide, prenatal stress
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439 Supplementation of Omnigen-AF alters the metabolic response to a glucose tolerance test in beef heifers.

N. C. Burdick Sanchez*[1], J. A. Carroll[1], P. R. Broadway[1], T. H. Schell[2], S. B. Puntenney[3], and D. J. McLean[2, 1]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX,* [2]*Phibro Animal Health Corporation, Teaneck, NJ,* [3]*Prince Agri Products, Inc, Quincy, IL.*

This study was designed to determine whether feeding OmniGen-AF to feedlot heifers would alter metabolic profiles in response to a glucose tolerance test. Heifer calves (n = 184; 216±1 kg) were allocated into 2 treatment diets: 1) Control, fed a standard receiving ration, and 2) OmniGen-AF (OG), fed the Control diet supplemented with OmniGen-AF at 4.54 g/hd/d and were fed in a commercial feedlot for 42d. On d42, heifers (n = 16/trt) were selected based on BW, phenotype, temperament, and treatment history and transported to Lubbock, TX (130 km). Upon arrival, heifers were housed in outdoor pens according to treatment and fed respective diets until fitted with indwelling jugular catheters and vaginal temperature recording devices and moved into individual stanchions in an enclosed barn. After cannulation, heifers were fed their treatment diets at 1400h. All orts were removed at 2000h to allow for a 12-h fast prior to first blood collection. The following day, heifers were administered 0.5 mL/kg BW of a 50% dextrose solution at 0900h (0h). Blood samples were collected and serum isolated at -60, -45, -30, -15, 0, 10, 20, 30, 45, 60, 90, 120, and 150 min relative to bolus dextrose infusion immediately following the 0 min sample collection. Serum was stored at -80C until analyzed for cortisol, glucose, insulin, NEFA and serum urea nitrogen (SUN) concentrations. Data were analyzed using proc MIXED in SAS specific for repeated measures, with fixed effects of treatment, time and treatment x time. If main effects were significant, means were separated using the PDIFF option in SAS. Vaginal temperature was not affected by treatment ($P = 0.80$) but decreased post-infusion ($P < 0.01$). There was a treatment x time interaction for cortisol ($P < 0.01$) such that cortisol was greater in OG heifers than Control heifers from 10 to 45 min post-infusion. Glucose concentrations increased post-infusion ($P < 0.01$) and were lesser in OG (146±3 mg/dL) compared to Control heifers (161±3 mg/dL; $P < 0.01$). There was no treatment effect for serum insulin ($P = 0.61$). Serum NEFA concentrations were reduced ($P < 0.01$; 0.28 vs. 0.45±0.01 mmol/L) and SUN concentrations tended ($P = 0.06$; 89 vs. 98±3 mg/dL) to be reduced in OG heifers compared to Control heifers. Insulin sensitivity, measured via RQUICKI, was greater ($P < 0.01$) in OG heifers than Control heifers (0.36 vs. 0.35±0.002). These data suggest that OG heifers were more responsive to changes in glucose, perhaps affecting the storage and/or redistribution of energy deposits, and provide further evidence for altered metabolism in OmniGen-AF supplemented cattle.

Key Words: cattle, glucose, OmniGen-AF
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440 Influence of vaccination with a combined chemically altered/inactivated Bhv-1/BVD vaccine or a modified live vaccine on reproductive performance in beef cows and heifers.

G. A. Perry*[1], T. W. Geary[2], J. A. Walker[3], J. J. J. Rich[3], E. J. Northrop[3], S. D. Perkins[3], C. L. Mogck[3], M. Van Emon[4], A. L. Zezeski[2], and R. F. Daly[5], [1]*South Dakota State University, Brookings,* [2]*USDA-ARS Fort Keogh LARRL, Miles City, MT,* [3]*Department of Animal Science, South Dakota State University, Brookings,* [4]*Montana State University, Bozeman,* [5]*Department of Veterinary and Biomedical Sciences, South Dakota State University, Brookings.*

Previous research has indicated that vaccination with a modified live BHV-1/BVD vaccine (MLV) has negative effects on AI conception rates when performed 30 d prior to AI. To further investigate vaccine effects on reproductive performance, a field trial was conducted on 10 herds of well-vaccinated cows and heifers (n = 1565; all of which had been on a MLV vaccination program) to evaluate whether a MLV vaccine administered prebreeding would have negative impacts on conception rates compared to a combined chemically altered/inactivated BHV-1/BVD vaccine (CA/IV). Within herd, cows were blocked by parity and calving date and randomly assigned to receive one of the two treatments (MLV or CA/IV vaccine). Animals received a single (cows) or two injections (heifers) of either the MLV or CA/IV vaccine with the final injection occurring between 27 and 89 d prebreeding. All females were synchronized with the 7-d CO-Synch + CIDR protocol and inseminated (AI) at the appropriate time after CIDR removal (cows 60 to 66 hrs; heifers 52 to 56 hrs) and remained separated from bulls for at least 10 d after AI. Pregnancy success and fetal age were determined between d 34 and 86 after AI, and > 30 d after the breeding season. Data were analyzed using the GLIMMIX procedure in SAS with herd as a random variable. Conception rates to AI were greater in the CA/IV vaccine group compared to the MLV vaccine group ($P = 0.05$; 60% vs 52%). Furthermore, interval from vaccination with either vaccine until AI also influenced conception rates ($P = 0.02$). Animals vaccinated 27 to 30 d prebreeding and animals vaccinated 30 to 37 d prebreeding had similar ($P = 0.98$; 52% and 52%) conception rates; however, both were decreased compared to animals vaccinated 38 to 89 d prebreeding ($P < 0.03$; 64%). There was no treatment by interval interaction ($P = 0.79$). Furthermore, there was no effect of treatment ($P = 0.18$) or treatment by interval interaction ($P = 0.17$) on breeding season pregnancy rates. Days postpartum tended ($P = 0.07$) to influence conception rates with short postpartum cows (≤ 60 d) having decreased conception rates compared to cows that were further postpartum. In summary, vaccination of well-vaccinated beef cows and heifers with a MLV vaccine pre-breeding (28 to 89 d) decreased AI conception rates compared to a CA/IV vaccine.

Key Words: Modified-live vaccine, Inactivate vaccine, Reproductive success
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441 Effects of post-insemination dam nutrition on calf performance and DNA methylation.

E. E. Beck*[1], C. L. Mogck[1], J. A. Walker[1], and G. A. Perry[2], [1]*Department of Animal Science, South Dakota State University, Brookings,* [2]*South Dakota State University, Brookings.*

Nutritional changes immediately after insemination can result in increased embryonic mortality, but the impact of a nutritional change on the embryos that survive is not known. Therefore, the objective of this study was to evaluate the impact of a nutritional change immediately following AI on calf performance and global DNA methylation. Calving records were obtained for 142 heifers over two yr that were allotted into two developmental treatments: drylot or range. All heifers were fixed-time inseminated following the 7-day

CO-Synch plus CIDR protocol to a single sire each year and were turned out to pasture together and managed as a single group. Pregnancy success to AI was determined via ultrasonography, and calving data (calving date, birth weight, sex, and weaning weight) were collected. DNA was obtained from calves at weaning, and analyzed for global methylation (total methylation and 5-hmC methylation). Data were analyzed as a 2x2 factorial design using the mixed procedure in SAS with sex and replicate included in the model. Bull calves were heavier at birth compared to heifer calves (P = 0.04; 34.9±0.45 vs 34.3±0.60 kg) and both bull-bred calves (35.7±0.4 kg) and range (35.3±0.5 kg) calves were heavier (P < 0.01) at birth compared to AI-sired (32.9±0.5) and drylot (33.3±0.5 kg) calves. However, there was no replicate (P = 0.99) or development by sire interaction (P = 0.70). For weaning weights both development (P = 0.04) and sire (P < 0.01) impacted weaning weights with AI sired calves (221.8±5.1 vs 189.1±2.7 kg) and range developed (210.6±3.6 vs 200.2±3.4 kg) calves being heavier. Sex tended (P = 0.09) to influence weaning weight, but there was no development by sire interaction (P = 0.99). Total DNA methylation was not effected by development (P = 0.34), sex (P = 0.21), sire (P = 0.24), or any interactions (P > 0.70). For 5-hmC methylation there was a tendency for both development method and sex of the calf to impact global methylation, with range and bull calves tending (P = 0.10) to have decreased methylation compared to drylot and heifers. In addition there was a sire by development (P < 0.01) and sire by sex (P = 0.05) interaction with bull-bred drylot developed calves having greater methylation than all other groups and with AI-sired bull calves having decreased methylation compared to AI-sired heifer and bull-bred bull calves. In summary, method of heifer development and sire can impact future performance of the calf that is in utero as determined by BW and WW, and this change in performance may be regulated through DNA methylation.

Key Words: Birth weight, Weaning weight, DNA methylation
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442 Effects of parity on neonatal beef calf serum metabolites during the first 72 hours of age.

N. B. Duncan*, A. O. Redman, A. R. Rathert, K. S. Stoecklein, and A. M. Meyer, *Division of Animal Sciences, University of Missouri, Columbia.*

We have previously reported that neonatal calf metabolic status is impacted by calf age and gestational nutrition. Our current objective was to determine the effect of dam parity on neonatal calf nutrient supply, assessed through circulating metabolites. Neonatal calf blood samples were collected from multiparous (n = 15; parity = 4.2 ± 0.7; prepartum BW = 661 ± 17 kg; BCS = 5.3 ± 0.5; gestation length = 274.8 ± 0.6 d; 9 bull and 6 heifer calves) and primiparous (n = 13; BW = 560 ± 19 kg; BCS = 5.1 ± 0.2; gestation length = 276.6 ± 0.7; 8 bull and 5 heifer calves) dams. Pregnant dams were managed similarly in late gestation, then moved to dry lots (d 266 of gestation) and fed ad libitum tall fescue hay (6.7% CP and 63.9% NDF, DM basis) and 1.0 kg DM/d DDGS. Calf jugular blood samples were obtained at 0 (pre-suckling but after standing), 6, 12, 24, 48, and 72 h postnatally for blood chemistry analysis. Data were analyzed using a mixed model containing effects of parity, sampling hour, and their interaction, and hour was a repeated effect. Parity did not affect (P = 0.33) calf birth weight. A parity x sampling hour interaction ($P \leq 0.02$) was detected for serum glucose, blood urea nitrogen (BUN), creatinine, albumin, total protein, and globulin. Calves from primiparous dams had greater (P = 0.03) glucose at 0 h, but calves from multiparous dams had greater ($P \leq 0.04$) glucose at 6, 12, 24, and 72 h. Serum BUN tended to be greater (P = 0.09) in calves from primiparous dams at 12 h, but was greater (P = 0.03) in calves from multiparous dams at 72 h. Creatinine tended to be greater (P = 0.06) at 0 h and was greater ($P \leq 0.005$) at 12 and 24 h in calves from primiparous dams. Calves from primiparous dams had greater ($P \leq 0.03$) albumin at 6 and 12 h. Total protein was greater ($P \leq 0.04$) in calves from multiparous dams at 0, 6, and 12 h and tended to be greater (P = 0.07) at 72 h. Globulin was greater ($P \leq 0.003$) in calves from multiparous dams at 0, 6, and 12 h and tended to be greater (P = 0.06) at 48 and 72 h. Results indicate parity impacts metabolic status of calves, but likely in a time-dependent manner.

Key Words: metabolites, parity, neonates
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443 Residual feed intake in beef cattle and its association with ruminal epithelium gene expression.

A. A. Elolimy*[1,2], J. C. McCann[2], D. W. Shike[2], and J. J. Loor[1,2,3], [1]*Mammalian NutriPhysioGenomics, Department of Animal Sciences, University of Illinois, Urbana,* [2]*Department of Animal Sciences, University of Illinois, Urbana,* [3]*Division of Nutritional Sciences, Illinois Informatics Institute, University of Illinois, Urbana.*

Residual feed intake (RFI) describes an animal's feed efficiency independent of phenotypic performance. The objective of this study was to determine differences in gene expression of ruminal epithelium between the most-efficient and the least-efficient animals, and any interaction with sex. One-hundred and forty-nine Red Angus cattle were allocated to three groups according to sex and herd origin. Animals were fed a finishing diet in confinement for 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. Ruminal epithelium was collected immediately after slaughter for gene expression analysis using real-time RT-PCR. Data were analyzed using the MIXED procedure of SAS 9.3. Fixed effects in the model included RFI category, sex and RFI × sex. Individual animal was the experimental unit and incorporated into the statistical model as a random effect nested within group. Of the 48 genes evaluated, compared with steers, heifers had a higher expression of *FFAR2* ($P < 0.01$). The most-efficient cattle had a decrease in *ACADS* ($P < 0.01$) and *HMGCS2* ($P = 0.05$), both of which are involved in ketogenesis. Efficient animals also had lower expression of *SLC16A* ($P = 0.06$), a monocarboxylate VFA transporter. Results from RFI × sex interactions indicated that responses in gene expression between steers and heifers were based on differences in RFI. For example, compared with heifers, steers at the high-efficiency level had greater expression of *HIF1A*, *SLC25A20* and *COX8A* ($P < 0.05$), involved in VFA absorption and energy generation through oxidative phosphorylation, while heifers had greater expression for the VFA transporter *SLC9A1* ($P = 0.04$) compared with steers at the lower feed efficiency level. An RFI × sex effect also was observed where most-efficient steers had greater expression of *HIF1A*, *SLC9A1* and *COX8A* ($P < 0.05$) compared with least-efficient steers. In heifers, however, *SLC9A1* and *COX8A* had greater expression in least-efficient heifers ($P < 0.05$) compared with the most-efficient heifers. These findings indicate that differences in the ruminal epithelium gene expression that may play a role in feed efficiency in beef cattle could follow sex-dependent gene expression patterns.

Key Words: RFI, rumen epithelium, gene expression
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444 Influence of temperament on skeletal muscle mitochondrial capacity of Brahman cows.

S. H. White*[1], C. R. Long[2], R. D. Randel[2], and T. H. Welsh, Jr.[1], *[1]Texas A&M AgriLife Research and Department of Animal Science, College Station, [2]Texas A&M AgriLife Research, Overton.*

To investigate a potential relationship between animal temperament and mitochondrial function, 5-yr-old Brahman cows were stratified into one of three temperament groups based on herdsman scores: T1 (n = 4; calm), T2 (n = 4; normal), or T3 (n = 4; temperamental). The cows were processed at the departmental meats lab and samples from the longissimus dorsi (LD) and semitendinous muscles were collected. All samples were assessed for mitochondrial density (via citrate synthase activity) and function (via cytochrome *c* oxidase activity); samples from the LD were also evaluated for mitochondrial capacity utilizing high-resolution respirometry. Data were analyzed using the MIXED procedure of SAS (9.4). Relative to mg of tissue (integrative mitochondrial capacity), temperamental cattle (T3) had greater state 3 oxidative phosphorylation capacity with complex I substrates (P_{CI}), P_{CI} plus complex II substrates (P_{CI+II}), maximum electron transport capacity (E_{CI+II}), and E_{CII} than T1 ($P = 0.009$, $P = 0.03$, $P = 0.02$, and $P = 0.04$ for P_{CI}, P_{CI+II}, E_{CI+II}, and E_{CII}, respectively) or T2 ($P = 0.03$, $P = 0.02$, $P = 0.03$, and $P = 0.03$ for P_{CI}, P_{CI+II}, E_{CI+II}, and E_{CII}, respectively). Temperamental cattle (T3) also had a higher fractional control ratio of P_{CI+II} (0.890 ± 0.023) than T2 (0.780 ± 0.025; $P = 0.02$), with T1 being intermediate (0.814 ± 0.023). This indicates a greater contribution of complex II to oxidative phosphorylation and energy production in temperamental animals, the effects of which are unknown at this time. Temperamental animals (T3) also had the greatest citrate synthase activity across muscle groups (9.49 ± 0.70 nmol/min*mg tissue) compared to T1 (6.44 ± 0.68; $P = 0.009$) or T2 (5.29 ± 0.59; $P = 0.0008$), indicating greater skeletal muscle mitochondrial density in T3. Intrinsic mitochondrial capacity (relative to CS activity) and cytochrome *c* oxidase activity (mitochondrial function) were not different between muscles, nor between temperament groups. Research is needed to clarify the significance of different patterns of energy production in temperamental cattle. Further, skeletal muscle mitochondrial capacity may be a useful early indicator of animal performance and carcass quality at harvest.

Table 444. High-resolution respirometry data from longissimus dorsi muscles between calm (T1), normal (T2), and temperamental (T3) Brahman cows

O_2Flux (pmol/s*mg tissue)[1]	T1	T2	T3	SEM	*P*-value
P_{CI}	14.92	14.50	21.97	0.41	0.037
P_{CI+II}	19.35	18.73	31.01	2.65	0.039
E_{CI+II}	23.70	24.09	34.69	2.44	0.042
E_{CII}	13.54	12.81	22.19	2.23	0.056

[1]P = state 3 oxidative phosphorylation; $_{CI}$ = pyruvate + malate + glutamate; $_{CI+II}$ = pyruvate + malate + glutamate + succinate; E = electron transport system capacity.

Key Words: Brahman cows, Mitochondrial capacity, Temperament
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445 Toxy-Nil and Unike Plus modulate differences in gene expression of milk somatic cells isolated from mammary gland of lactating dairy cows fed aflatoxin B_1.

R. O. Rodrigues*[1], R. O. Rodrigues[1], D. R. Ledoux[1], G. E. Rottinghaus[1], R. Borutova[2], O. Averkieva[2], and T. B. McFadden[1], *[1]University of Missouri, Columbia, [2]Nutriad International NV, Dendermonde, Belgium.*

The objective was to investigate effects of Toxy-Nil (TN) or Unike Plus (UP) on gene expression profiles of blood leukocytes and milk somatic cells (MSC) in dairy cows challenged with dietary aflatoxin B_1 (AFB_1). Sixteen mid-lactation Holstein cows were assigned to receive one of the following treatments: 1) 2.8 mg of AFB_1/cow/day (positive control, PC); 2) 2.8 mg of AFB_1 + 100 g of TN/cow/day; 3) 2.8 mg of AFB_1 + 100 g of UP/cow/day; or 4) no AFB_1 and no adsorbents (negative control, NC). Treatments were administered for 7 days by top-dressing onto a standard TMR diet. Feed and water were available ad libitum throughout the trial. Blood and milk samples were obtained on day 7. Subsequently, mRNA from blood leukocytes and MSC were isolated and sequenced. Genes were considered differentially expressed (DE) when $P < 0.001$ and FDR ≤ 0.10. There were few differences in gene expression of blood leukocytes. No DE genes were observed when comparing cows not fed AFB_1 to those that were fed AFB_1 (NC vs average of PC/TN/UP). Comparing cows fed AFB_1 alone to cows also receiving adsorbents (PC vs average of TN/UP) revealed one downregulated gene, which was related to mitotic processes and five upregulated genes, which related to nitric oxide generation, signaling, and platelet activation. Comparing TN to UP revealed downregulation of two genes related to platelet activation and iron ion and oxygen binding. In MSC, numerous changes in gene expression were observed. Three annotated genes were DE between NC and TN/UP. No genes were DE between adsorbent treatments (TN vs UP). However, comparing cows not fed AFB_1 to those fed AFB_1 alone (NC vs PC) revealed 120 DE genes, and 70 genes were DE between cows fed AFB_1 without or with adsorbents (PC vs TN/UP). Of those DE genes, 49 were common to the comparisons PC vs NC and PC vs TN/UP. These genes represented functional clusters including glycoproteins and milk proteins, secretion, signaling, protein binding, transporter activity, and response to steroid hormones. Protein domains found to be differentially expressed included a- and b-caseins. Furthermore, approximately 20% of the common DE genes in MSC were mammary gland-specific. In summary, daily feeding of 2.8 mg of aflatoxin B_1 to lactating dairy cows resulted in few DE genes in blood leukocytes, but elicited numerous changes in gene expression in milk somatic cells, many of which were modulated in cows fed TN or UP.

Key Words: adsorbent, binder, RNA-sequencing
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446 Hematological variables are influenced by vaccine antigen type and acute or chronic stress model in beef calves.

R. E. Hudson*[1], D. J. Tomczak[1], E. L. Kaufman[1], A. M. Adams[1], J. A. Carroll[2], P. R. Broadway[2], M. A. Ballou[3], and J. T. Richeson[1], *[1]West Texas A&M University, Canyon, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Texas Tech University, Lubbock.*

The objective was to determine the effect of replicating and non-replicating vaccine antigens administered to acutely or chronically stressed beef calves on hematologic and endocrine responses. A total of 48 crossbred beef steers (d 0 BW = 226 ± 6.2 kg) from a single ranch origin were used in a 2 × 2 factorial to evaluate main effects of stress, vaccine type and their interaction; resulting in 4 treatments (n = 12/treatment) consisting of acute stress with killed virus vaccination (ACUKV), ACU with modified-live virus vaccination (ACUMLV), chronic stress with KV (CHRKV), and CHR with MLV (CHRMLV). The ACU treatments were weaned at their origin ranch on d -37 and transported 472 km to the study site near Canyon, TX on d -21 to allow acclimation. The CHR treatments were weaned on d -3, transported 460 km to a facility near Lubbock, TX on d -2, and relocated 164 km to the study site on d -1. Vaccine treatments were administered on d 0 and KV was revaccinated on d 14. Animal was experimental unit and dependent variables were analyzed using PROC MIXED with repeated measures (d). Hematological variables were determined from whole blood collected on d -2, 0, 1, 3, 5, 7, 14, and 21 via automated hemocytometer. Cortisol concentration was determined using ELISA from serum collected on d -2, 0, 1, 3, 5, and 7. Total leukocytes were not different on d -2 ($P = 0.66$), but were lesser for CHR vs. ACU on d 0, 1, 3, 5, 7, 14 and 21 ($P \leq 0.02$). Vaccine type also affected total leukocytes; leukocytes were decreased for MLV on d 5, 7, and 14 ($P \leq 0.04$) compared to KV. Neutrophils (2.01 vs. 3.83 K/μL) and neutrophil:lymphocyte (0.27 vs. 0.67) were markedly increased ($P < 0.001$) for CHR on d -2; conversely, neutrophils were decreased ($P \leq 0.007$) on d 1 and 21 for CHR. Monocytes were decreased on d 1, 5 and 7 for MLV ($P \leq 0.04$) and d -2 to 14 for CHR ($P \leq 0.03$). Eosinophils were reduced ($P = 0.007$) for CHR (0.097) vs. ACU (0.176 K/μL) on d -2; however, a rebound response ($P = 0.03$) was noted on d 0 such that eosinophils were 0.288 and 0.160 K/μL for CHR and ACU, respectively. Serum cortisol was greater ($P \leq 0.04$) for ACU on d -2 to 5, suggesting suppression of endocrine activity in CHR over time. Results indicate this CHR stress model and MLV vaccination may have more profoundly induced immunosuppression in beef calves.

Key Words: Vaccine, Beef calves, Stress
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447 Cellular and antibody mediated immune responses are influenced by sex and pregnancy status in mature Brahman cattle.

C. L. Cook*[1], T. H. Welsh, Jr.[1], T. J. Garcia[1,2], D. G. Riley[1], W. Mwangi[3], J. Bray[3], A. W. Lewis[2], D. A. Neuendorff[2], and R. D. Randel[2], *[1]Department of Animal Science, Texas A&M University, College Station, [2]Texas A&M AgriLife Research, Overton, [3]Department of Veterinary Pathobiology, Texas A&M University, College Station.*

Measures of immune responsiveness are under evaluation as criteria to select breeding bulls and cows. The objective of this experiment was to determine whether cell-mediated immune response (CMIR) and antibody-mediated immune response (AMIR) varied according to sex and pregnancy status in mature Brahman cattle. We hypothesized that sex and pregnancy status would influence CMIR and AMIR. Status groups included 84 sexually mature, non-pregnant Brahman cows, 163 pregnant Brahman cows, and 25 fertile Brahman bulls in the Texas A&M AgriLife Research herd. For CMIR determination cattle were administered a $25x10^3$ protein nitrogen units (PNU)/mL subcutaneous (neck) sensitization dose of Candida

Table 447. Comparison of cell-mediated immune response (CMIR) and antibody-mediated immune response (AMIR) among status groups in Brahman cattle (LSM±SE)

Sex Class	CMIR	AMIR
Non-pregnant cows (n = 84)	5.763 ± 0.591^{b}	1.074 ± 0.07^{a}
Pregnant cows (n = 163)	10.778 ± 0.424^{a}	0.521 ± 0.05^{b}
Fertile bulls (n = 25)	12.136 ± 1.083^{a}	1.371 ± 0.127^{a}

[a,b] Means bearing different superscripts within columns differ at $P < 0.05$.

albicans (CA; Greer Labs, Lenoir, NC) with 750 µg of Quil-A (InvivoGen, San Diego, California) adjuvant in 2.5 mL buffer on d0. On d14 after sensitization, tail skin fold thickness (SFT) was measured using a Harpenden caliper prior to intradermal injection of 5x10^3 PNU/mL of CA in 0.5 mL in the skin fold. On d15 the injection site SFT was measured. Response was determined by the difference of SFT from d15 (post-injection) and d14 (pre-injection). For AMIR determination cattle were administered *Salmonella* Newport Extract vaccine (2 mL subcutaneous; Zoetis, Florham Park, NJ) on d0. Blood samples were collected by jugular venipuncture on d0 and d15. Serum samples were stored at -20C until analyzed for vaccine specific IgG by a double sandwich, enzyme linked immunosorbent assay. Data were analyzed using mixed model procedures of JMP (Cary, NC). Table 447 contains the mean CMIR and AMIR for bulls and non-pregnant and pregnant cows. Mean CMIR was greater ($P < 0.05$) in pregnant cows and bulls than non-pregnant cows. Fertile bulls and pregnant cows did not differ in CMIR ($P > 0.05$). With AMIR, fertile bulls and non -pregnant cows did not differ from each other; however the AMIR of these 2 groups exceeded ($P < 0.05$) that of pregnant cows. A statistical relationship between CMIR and AMIR was not detected as correlation coefficients were near zero. The hypotheses that sex and pregnancy status affect CMIR and AMIR in cattle were accepted. Therefore, physiological status and sex should be considered when evaluating either cellular or antibody mediated immune response in mature Brahman cattle.

Key Words: sex, immune response, pregnancy status
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448 The effects of a novel follicle wave and heat synchronization protocol on the follicles, circulating hormones, and estrus of Aanestrous ewes.

S. B. Turner, B. Malaweera, M. Payne, L. A. Carroll, and D. M. W. Barrett[*], *Faculty of Agriculture, Dalhousie University, Truro, NS, Canada.*

Reproductive performance in seasonally anestrous ewes is poor even after the use of current controlled breeding protocols. Anestrous ewes treated with a medroxyprogesterone acetate sponge, for 12 or 14 d, and estradiol-17β (E_2) have synchronized follicular wave emergence. The objective of this study was to determine the effects of an E_2 injection 6 d after CIDR insertion on follicles, E_2 and LH concentrations, and estrus in seasonally anestrous ewes. Ewes (n = 13) received CIDRs (Day -12) followed by an injection of eCG (500 IU; i.m.; Day 0) at CIDR removal and an injection of sesame oil without (1 mL; i.m.; Control) or with E_2 (350µg; i.m.; Day -6) 6 d before CIDR removal. Treatments were balanced for age, parity, and BCS. Blood samples were collected every 6 h for 48 h after E_2 injection and every 3 h for 60 h starting 18 h after eCG injection to determine LH concentrations. Blood samples were collected on Day -6 and 0 and every 6 h for 60 h starting 18 h after eCG injection to determine E_2 concentrations. Ovarian ultrasonography was done on Day -6 and 0. A ram was introduced on Day 1 to observe estrus. Ewes treated with E_2 had higher LH concentrations (0.37 ± 0.05 ng/mL) than ewes treated with oil alone (0.12±0.05 ng/mL) during the 48 h after E_2 injection ($P < 0.005$). Concentrations of LH were highest at 18 h after E_2 injection (1.11 ± 0.12 ng/mL; $P < 0.001$). Ewes treated with E_2 had higher LH concentrations (2.10 ± 0.18 ng/mL) than ewes treated with oil alone (0.12 ± 0.16 ng/mL) at 18 h after E_2 injection ($P < 0.001$). The interval from eCG injection to the start of the pre-ovulatory LH surge was similar (37.1 ± 4.4 h; $P > 0.05$), but was more synchronized in ewes treated with E_2 (2.3 ± 0.6 h) than ewes treated with oil alone (12.0 ± 5.1 h; $P < 0.01$). Concentrations of E_2 were similar between treatments on Day -6 (2.1 ± 0.3 pg/mL; $P > 0.05$) and Day 0 (2.3 ± 0.4 pg/mL; $P > 0.05$). Concentrations of E_2 tended to be highest at 18 h after eCG injection (3.5 ± 0.5 pg/mL; $P = 0.076$). Maximum follicular diameter was larger on Day 0 (4.8 ± 0.2 mm) than Day -6 (3.4 ± 0.2 mm; $P < 0.001$). There were no differences in the interval from eCG treatment to the start (37.6 ± 2.7 h) or end (74.7 ± 1.9 h) of estrus ($P > 0.05$). Adding an E_2 treatment during a CIDR-eCG estrus synchronization protocol increased LH concentrations after E_2 treatment and stimulated a more synchronized pre-ovulatory LH surge in seasonally anestrous ewes.

Key Words: synchronization, anestrous ewes, CIDR
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449 Effect of early calf-hood nutrition on the hypothalamic-pituitary axis in Holstein-Friesian bulls.

A. M. English[*1,2], S. Fair[2], C. J. Byrne[1,3], S. M. Waters[1], and D. A. Kenny[1,3], [1]*Animal and Bioscience Research Department, Teagasc Grange, Dunsany, Meath, Ireland,* [2]*Department of Biological Sciences, University of Limerick, Limerick, Ireland,* [3]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland.*

Improved early life nutrition can advance age at onset of puberty in bull calves. While the precise biochemical mechanisms have not been fully elucidated the effect is most likely mediated through a direct influence of metabolic status on hypothalamic gonadotrophin releasing hormone (GnRH) pulsatility, ultimately leading to enhanced luteinizing hormone (LH) pulsatility and testosterone synthesis and release. The objective of this study was to examine the effect of nutrition during the first 18 weeks of life on selected genes in the arcuate nucleus of the hypothalamus and anterior pituitary in Holstein-Friesian bull calves. Holstein-Friesian bull calves with a mean (±SD) age and bodyweight of 19 (±8.2) days and 47.5 (±5.3) kg, respectively, were assigned to either a high (n = 10) or low (n = 10) plane of nutrition, with target growth rates of 1.2 and 0.5 kg per day, respectively. At 126 ± 3 days of age, calves were euthanized following intravenous administration of sodium pentobarbitone and the arcuate nucleus region of the hypothalamus together with the anterior pituitary were excised. RNA was isolated and cDNA was synthesised. Quantitative PCR was performed to detect mRNA expression of the selected genes. The following genes were selected for analysis in the arcuate nucleus: *Kiss1R, GPR54, GnRH, AgRP, NPY, POMC, MC4R, IGF1R, IGF1, OBR* and *GHSR* while: *LH*β, *FSH*β, *GHSR, GH1, GnRHR, IGF1* and *IGF1R* were selected for the anterior pituitary. *UBQ* and *RSP9* were selected as stable reference genes. Data were analysed using mixed models methodology (PROC MIXED; SAS). For variables that were not normally distributed, λ and log transformations were used. Only one gene, *GHSR* was upregulated in the anterior pituitary ($P < 0.05$) and tended towards greater transcript abundance in the arcuate nucleus ($P < 0.1$) in the low compared with the high plane of nutrition calves. This is the first study to investigate the effect of early calfhood nutrition on aspects of the molecular regulation of the hypothalamic-pituitary axis of the bull calf. The inverse relationship between nutritional status and transcript abundance for the ghrelin receptor (GHSR) in both arcuate nucleus and anterior pituitary tissue is consistent with the well-defined role of this gene in energy homeostasis and regulation of body weight growth and most likely reflects poorer metabolic status of the calves on the low plane of nutrition. Ghrelin is a known inhibitor of GnRH pulsatility, the magnitude of its receptor is related to precocious puberty in cattle.

Key Words: Cattle, Puberty, GHSR
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450 Effect of sire breed on pregnancy rate of Katahdin ewes after liquid semen vaginal artificial insemination.

D. O'Brien*[1], S. Wildeus[1], D. L. Wright[2], A. R. Weaver[2], and S. P. Greiner[2], [1]*Virginia State University, Petersburg,* [2]*Virginia Polytechnic Institute and State University, Blacksburg.*

Previous work has suggested that sire breed (hair vs. wool) may have a significant effect on pregnancy outcome using liquid semen artificial insemination (AI) in hair sheep. In this experiment, we further evaluated the effect of sire breed on pregnancy rates using a flock of Katahdin ewes. Ewes (n = 88) managed under an annual breeding cycle were estrus synchronized by inserting CIDR devices for 12 d. Ewes were allocated to be bred to one of six Suffolk, Texel or Katahdin rams (n = 2/breed) in equal numbers. Ewes were inseminated in October by simple vaginal timed AI at 48 h after CIDR removal, and again 6 h after initial AI with semen from the same collection. Semen was collected and processed on site using an artificial vagina, extended to 250 million sperm/ml in a simple UHT skim milk and egg yolk (5% v/v) extender, and packaged into 0.5 ml straws. For the initial insemination, straws were kept at processing temperatures (36°C) while straws for the second insemination were cooled to and stored at 4°C. Ewes were exposed to natural mating 5 d after AI to the same sire used for AI. Pregnancy was determined by trans-rectal ultrasonography 40 d after AI. Data were analyzed by Chi-square for the effect of sire breed, ram, and ewe age on pregnancy rates. Pregnancy rate to AI (15.9%) was lower than anticipated and following natural mating was 78.4%. There was no effect ($P > 0.11$) of sire breed on AI or natural mating pregnancy rate. However, differences between sires ($P < 0.02$) were observed following both AI (0%, 20%, 13%, 21%, 43%, and 0% for Kat1, Kat2, Suff1, Suff2, Tex1, and Tex2, respectively) and natural mating (100%, 73%, 47%, 86%, 78%, and 87% for Kat1, Kat2, Suff1, Suff2, Tex1, and Tex2, respectively). Pregnancy rates to AI ranged from 9% in yearling ewes to 22% in mature (2 - 4 yr), and 11% in older ewes (> 4 yr), but were not significantly different between groups ($P = 0.1$). Fetal numbers were not different in pregnancies resulting from AI or clean-up mating (71 and 77% multiples, respectively). Under the conditions of this study, sire breed did not influence the overall outcome of liquid semen AI even though there were differences observed among sires. Semen motility was affected by low ambient temperatures at time of collection and may have contributed to low AI pregnancy rates observed.

Key Words: Hair Sheep, Artificial Insemination, Pregnancy Rate
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451 Effects of maternal nutrient restriction during either the first or second trimester on bovine fetal adipose tissue microRNA at the end of mid-gestation.

N. M. Long*, and S. L. Pratt, *Clemson University, Clemson, SC.*

The objective of this study was to determine the effects of early or mid-gestation maternal nutrient restriction on adipose tissue development and expression of microRNAs. Primiparous Angus-cross cows (n = 22) were synchronized and inseminated with sexed semen (time of AI= d0) from a single Angus sire. Animals were fed at 1.2 x (Control [CON]) or 0.55 x (Nutrient Restricted [NR]) of maintenance energy and protein requirements based on BW (NRC 1996). Animals were blocked into groups by BCS and BW then fed CON (n = 8) from d 30-190 of gestation, NR (n = 7) from d 30-110 followed by CON from d 110-190, or CON (n = 7) from d 30-110 followed by NR from d 110-190. Cows were harvested and fetuses collected on d 190 of gestation. Isolation of total RNA was performed using flash frozen fetal perirenal adipose tissue samples (3 subsamples/treatment) using the *mir*Vana microRNA isolation kit and analyzed using a previously validated bovine miRNA microarray containing 1636 probes. Fetal weights tended to be reduced ($P = 0.07$) in NR/CON and CON/NR vs. CON fetuses (9.05 ± 0.48, 8.91 ± 0.48 vs. 10.34 ± 0.45 kg, respectively). Perirenal adipose weight tended to be increased ($P = 0.09$) in CON fetuses compared to NR/CON and CON/NR fetuses (34.3 ± 1.7 vs 28.3 ± 1.9, and 30.8 ± 1.9 g, respectively). Fetal perirenal adipose tissue from the CON group had bta-miR-376b and PC-5p-8838_20 unregulated ($P < 0.05$) and fourteen down regulated miRNAs ($P < 0.05$) vs NR/CON and CON/NR adipose tissue. The miRNA, mmu-miR-6236-p3 was upregulated ($P < 0.05$) in NR/CON group and no other microRNAs independently down regulated ($P > 0.05$) vs CON/NR and CON animals. Animals in the CON/NR group exhibited 3 upregulated ($P < 0.05$) miRNAs, with bta-miR-361 and bta-miR-2904-3-p5 down regulated ($P < 0.05$) vs. CON and NR/CON fetal perirenal adipose. Nine miRNA were similarly upregulated ($P < 0.05$) in the NR/CON and CON/NR tissues compared to the CON fetuses. Five microRNAs were upregulated ($P < 0.05$) in the CON and NR/CON fetal adipose tissue compared to the CON/NR fetal adipose tissue. Hence, maternal nutrient restriction during early or mid-gestation tends to cause alterations in fetal growth and affects miRNA regulation differently depending on the time of gestation in which the restriction occurs. Interestingly, a majority of miRNA expression patterns are similarly upregulated between the two NR treatments compared to the CON fetuses.

Key Words: fetal adipose tissue, fetal programming, maternal undernutrition
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452 Effects of *Lactobacillus reuteri* LR1 on tight junction proteins expression in Ipec-1 cells during enterotoxigenic *Escherichia coli* K88 infection and its underlying mechanisms.

L. Wang[*1,2], H. Yi[1,2], Z. Wang[1,2], Y. Qiu[1,2], X. Wen[1,2], X. Ma[1,2], X. Yang[1,2], and Z. Jiang[1,2], [1]*Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, China,* [2]*Ministry of Agriculture Key Laboratory of Animal Nutrition and Feed Science in South China, Guangzhou, China.*

Intestinal epithelial barrier damages disrupt immune homeostasis and lead to many intestinal diseases. *Lactobacilli reuteri* strains have probiotic functions in modulation of microbiota and immune system in intestines. In this study, we investigated effects of *L. reuteri* LR1, a new strain isolated from the feces of weaning piglets, on intestinal epithelial barrier damages in IPEC-1 cells caused by enterotoxigenic *Escherichia coli* (ETEC) K88 infection. IPEC-1 cells were cultured in transwell dishes for 21 d until their transepithelial electrical resistance was stable. Monolayers of IPEC-1 cells were incubated for 6 h with serum and antibiotics-free medium, ETEC K88 (1×10^7 CFU), *L. reuteri* LR1 (1×10^8 CFU), or ETEC K88 (1×10^7 CFU) plus *L. reuteri* LR1 (1×10^8 CFU) in the upper layer. The FITC-dextran was used to determine the permeability of IPEC-1 cells monolayers. IPEC-1 cells were collected for colony counting, Real-time PCR and Western blotting analysis. Statistical analysis was performed using one-way ANOVA with SPSS 16.0 software. Our findings showed that *L. reuteri* LR1 effectively attenuated ETEC K88-induced increases of permeability of IPEC-1 cell monolayers ($P < 0.05$), and decreased the adhesion and invasion of ETEC K88 in IPEC-1 cells ($P < 0.05$). In addition, we demonstrated that *L. reuteri* LR1 increased the mRNA and protein levels of tight junction proteins zonula occluden-1 (ZO-1) and occludin in ETEC K88-infected IPEC-1 cells ($P < 0.05$), whereas it had no effects on claudin-1 and F-actin expression ($P > 0.05$). Using Colloidal gold immunoelectron microscopy, we confirmed that *L. reuteri* LR1 visualizedly increases ZO-1 and occludin expression in IPEC-1 cells. To explore the regulatory mechanisms of tight junction proteins by *L. reuteri* LR1, we investigate the effects of *L. reuteri* LR1 on myosin light chain kinase (MLCK) and phosphorylated MLCK in ETEC K88-infected IPEC-1 cells, and selected an inhibitor of MLCK (ML-7). We found *L. reuteri* LR1 treatment effectively attenuated ETEC K88-induced decreases of protein levels of MLCK in IPEC-1 cells ($P < 0.05$). Furthermore, we found that the improvements of ZO-1 and occludin expression by *L. reuteri* LR1 were inhibited by ML-7 in ETEC K88-infected IPEC-1 cells ($P < 0.05$). These data demonstrated that *L. reuteri* LR1's improvements of ZO-1 and occludin could be dependent of MLCK pathway. In conclusion, *L. reuteri* LR1 improved ZO-1 and occludin expression via a MLCK-dependent manner in IPEC-1 cells during ETEC-K88 infection.

Key Words: IPEC-1 cells, *Lactobacillus reuteri* LR1, tight junction
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453 Effects of feeding strategy in early lactation on oxidative stress of primiparous dairy cows.

M. Carriquiry[*1], M. Garcia-Roche[1], A. Casal[1], A. M. Cassina[2], and D. A. Mattiauda[3], [1]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay,* [2]*Facultad de Medicina, Universidad de la Republica, MONTEVIDEO, Uruguay,* [3]*Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay.*

Oxidative stress (OS) is linked to impaired immune and inflammatory responses leading to metabolic and health problems in the transition dairy cow. The aim of the study was to assess the effect of feeding strategy in early lactation on blood and hepatic tissue OS markers in Holstein cows. Eighteen primiparous cows (528 ± 40 kg BW, 3.2 ± 0.2 BCS, fall calving) were used in a randomized block design with two treatments during the first 65 days postpartum (DPP): (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). Both groups consumed 2.2 kg DM/d of a commercial ration at each milking. Cows were milked twice a day and milk yield was recorded daily. Cow BCS was recorded and blood samples and hepatic biopsies were collected at -7 and +42 ± 3 DPP. Production of reactive oxygen substances (ROS; d-ROMs Test, Diacron, Italy) and antioxidant capacity (SAC; OXY-Adsorbent Test, Diacron) were determined in serum and OS index (OSi) was calculated (ROS/SAC). Expression of 4-hydroxynonenal (4-HNE) modified proteins in liver homogenates was analyzed by Western blotting. Data were analyzed as repeated measures with a mixed model including DPP and feeding strategy within DPP as fixed effects and block as random effect. Milk yield was greater (27.5 vs. 25.6 ± 0.60 kg/d; $P = 0.03$) while BCS loss from -7 to +42 DPP was less (-0.50 vs. -0.75 ± 0.03; $P = 0.04$) for G0 than G1 cows. Serum ROS production tended to decreased from -7 to +42 DPP (268.4 vs. 244.6 ± 9.7 CarrU; $P = 0.058$). All cows during the pre and postpartum periods, had SAC values lower than 350 µmol HClO/mL indicating an impairment of serum antioxidant barrier. However, SAC decreased from -7 to +42 DPP only in G1 cows (298.2, 278.8 and 304.4 ± 6.3 µmol HClO/mL for -7 DPP and G0 and G1 at 42 DPP, respectively; $P = 0.011$). Thus, during the postpartum, serum OSi tended to be greater ($P = 0.09$) for G1 than G0 cows (0.92 vs. 0.80 ± 0.05 CarrU/µmol HClO.mL^{-1}). Presence of 4-HNE in the liver increased from -7 to +42 DPP only in G1 cows (0.73 ± 0.21 and 1.31 vs. 0.81 ± 0.16 for -7 DPP and G0 and G1 at 42 DPP, respectively; $P = 0.014$). Oxidative stress increased during the postpartum in G1 cows associated to a more severe negative energy balance.

Key Words: dairy cattle, oxidative stress, nutrition
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454 A high-fat diet expands body fat mass and up-regulates expression of genes involved in adipogenesis and inflammation in a genetically lean pig.

X. Yang*[1,2], X. Ma[1,2], L. Wang[1,2], K. Gao[1,2], and Z. Jiang[1,2], [1]*Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, China,* [2]*Ministry of Agriculture Key Laboratory of Animal Nutrition and Feed Science in South China, Guangzhou, China.*

Pigs have been proved to be desirable models in studying obesity/adiposity as of their (patho-) physiological similarity to humans. The present study aimed to explore the possibility and characteristics of diet-induced obesity/adiposity in genetically lean pigs. Crossbred pigs (Duroc-Landrace × Yorkshire; n = 112; male) were fed a control (4% fat, 13.38 MJ/kg feed) or a high-fat (HF, 11.4% fat, 15.55 MJ/kg feed) diet for 3 months. Body weight, feed intake, and dorsal fat thickness were recorded. Body composition and dorsal fat histology were evaluated. An Automatic Biochemical Analyzer measured plasma lipids and glucose, radioimmunoassays determined plasma insulin, leptin, triiodothyronine, thyroxine, and growth hormone levels, and microarray analysis evaluated gene expression profiles in dorsal fat. Approximately 70% of the pigs fed HF diet developed obesity. Body weight and energy intake did not differ between control and diet-induced obese (DIO) pigs. Fat mass percentage, adipocyte size, plasma lipids, insulin, and leptin concentrations were significantly higher in DIO pigs than controls. HF diet significantly regulated the expression of 576 genes. Of these, 108 genes were involved in 21 pathways, with 20 genes related to adiposity development and 26 to immune responses. The genetically lean pigs were observed for the first time to be induced into obesity/adiposity under a HF diet with body fat mass expansion and adipose-related inflammation.

Key Words: diet-induced obesity, inflammation, genetically lean pig
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456 Residual feed intake in beef cattle and hypothalamic regulation of appetite-related genes.

A. A. Elolimy*[1,2], J. C. McCann[2], D. W. Shike[2], and J. J. Loor[1,2,3], [1]*Mammalian NutriPhysioGenomics, Department of Animal Sciences, University of Illinois, Urbana,* [2]*Department of Animal Sciences, University of Illinois, Urbana,* [3]*Division of Nutritional Sciences, Illinois Informatics Institute, University of Illinois, Urbana.*

Residual feed intake (RFI) describes an animal's feed efficiency independent of phenotypic performance. The objective of this study was to determine expression differences of genes that regulate feeding behavior in the hypothalamus between the most-efficient and least-efficient animals, and any interaction with sex. One-hundred and forty-nine beef cattle were allocated to three groups according to sex and herd origin. Animals were fed a finishing diet in confinement for 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. Hypothalamic tissue was collected immediately after slaughter for gene expression analysis using real-time RT-PCR. Of the 32 genes evaluated, expression of *POMC* ($P = 0.06$) was upregulated in steers and *MTOR* ($P = 0.13$) tended to be upregulated in heifers. The most-efficient cattle tended to have greater *GABBR1* expression ($P < 0.15$), while the least-efficient animals tended to have greater expression ($P < 0.15$) of *CNR1*, *NPY2R* and *GCK*. Results from RFI × sex interactions indicated that responses in gene expression of hypothalamus between steers and heifers were based on differences in RFI. *PMCH* was upregulated ($P < 0.05$) in most-efficient heifers but also ($P < 0.05$) in the least-efficient steers. Among the most efficient cattle, *PMCH* was upregulated ($P =$

0.01) in heifers compared with steers. In most-efficient steers, compared with heifers, there was upregulation of *MC3R* (P = 0.06) and a tendency for upregulation of *FOXO1* (P = 0.12). In least-efficient heifers, compared with least-efficient steers, there was upregulation of *AGRP* (P = 0.05) by 2.1-fold. An RFI × sex also was observed where least-efficient heifers tended ($P < 0.15$) to have greater expression of *FOXO1*, *CNR1* and *MC3R* by 1.2-, 2.0- and 2.3-fold, respectively. These findings indicate that differences in the hypothalamic gene expression that may play a role in feed efficiency in beef cattle could follow sex-dependent gene expression patterns.

Key Words: RFI, hypothalamus, gene expression
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457 Effects of protein supplementation with low to medium quality forage on reproductive parameters in beef heifers in early pregnancy.

A. L. Jones*[1], E. L. Stephenson[2], K. Kruckenburg[2], M. Randall[2], E. Zwiefelhofer[2], J. Stuttgen[2], K. Martin[2], A. E. Radunz[2], P. M. Fricke[3], and J. S. Luther[2], [1]*University of Wisconsin-Madison, Madison,* [2]*University of Wisconsin-River Falls, River Falls,* [3]*University of Wisconsin- Madison, Madison.*

A 2-yr study was conducted to investigate the effects of protein supplementation in low to medium quality forage diets on reproductive parameters during early pregnancy (-7 d to 30 d from TAI; d 0) in yearling beef heifers. Angus, Hereford, and Angus-cross yearling beef heifers (402 ± 42 kg initial BW; n = 79) were stratified by initial BW and BCS and randomly assigned to 1 of 4 supplemental treatments. Supplements were formulated to provide similar CP intake; 1) low-fat dried corn distillers grain (LDG, 7.4% fat; 0.8% BW); 2) high-fat dried corn distillers grains (HDG, 9.5% fat; 0.8% BW); 3) cottonseed meal (CSM, 2.2% fat; 0.4% BW) and 4) no supplementation (CON). The basal diet consisted of low to medium quality chopped grass hay (8% CP; 55% NDF yr 1 and 70% NDF yr 2) fed ad libitum twice daily. Supplements were fed once daily and individual intakes were recorded. Diameter of dominant follicles was measured at TAI via transrectal ultrasonography. Beginning on d 2, blood samples were collected 3x weekly (MWF) to determine plasma progesterone (P4) 4 h after supplementation. Diameter of corpora lutea (CL) was measured on d 13 and 14 after TAI at the same time as Doppler ultrasound analysis of vasculature within the ovarian hilus. Supplemented heifers had greater ($P \leq 0.0001$) total DMI than CON heifers. Total CP intake was greater ($P \leq 0.0001$) for HDG and LDG compared to CON and CSM was intermediate. Follicles from LDG heifers tended (P = 0.06) to be larger than CSM and CON heifers, but did not differ (P = 0.41) from heifers fed HDG. However, CL diameter and plasma P4 did not differ among treatments ($P \geq 0.26$). Ovarian hemodynamics (Pulsatility and Resistance Indices) did not differ ($P \geq 0.35$) among treatments and conception rates at d 30 post TAI did not differ (P = 0.98) among treatments (overall 56%). Supplementing heifers with HDG, LDG, or CSM did not influence reproductive measures such as plasma P4, CL diameter, or ovarian hilus vascular resistance when compared with CON.

Key Words: Protein supplementation, early pregnancy, beef heifers
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458 Assessment of glucose homeostasis in crossbred steer progeny sired by Brahman bulls that experienced prenatal transportation stress.

B. P. Littlejohn*[1,2], N. C. Burdick Sanchez[3], P. R. Broadway[3], J. A. Carroll[3], R. D. Randel[2], T. H. Welsh, Jr.[1], and R. C. Vann[4], [1]*Texas A&M AgriLife Research and Department of Animal Science, College Station,* [2]*Texas A&M AgriLife Research, Overton,* [3]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX,* [4]*MAFES - Brown Loam Experiment Station, Mississippi State University, Raymond, MS.*

The objective of this experiment was to assess glucose homeostasis of crossbred male progeny whose Brahman sires experienced prenatal transportation stress (PS) in utero. Sixteen steers (PNS group) sired by 3 PS bulls gestating dams were transported for 2 h at 60, 80, 100, 120, and 140 ± 5 d of gestation) and 16 steers sired by 3 control bulls (gestating dams were maintained in the same environment as stressed dams but not transported) were evaluated. Fifty-six days after weaning, pen score (PS; 1 = calm and 5 = excitable), exit velocity (EV; m/sec) and temperament score [TS; (PS + EV)/2] were recorded. Sixty days after weaning (d -5 relative to the challenge day), the 32 steers were transported in December from Raymond, MS to Lubbock, TX. Four days later (d -1) steers were fitted with rectal temperature (RT) probes and jugular cannulas, and subsequently placed in individual stanchions. Steers had access to ad libitum water for the full duration of the experiment, but feed was removed 12 h prior to collection of the first blood sample. On collection day (d 0), steers received an i.v. bolus dose of 50% dextrose solution (0.5 mL/kg BW), and serum samples were collected at -60, -45, -30, -15, 0, 10, 20, 30, 45, 60, 90, 120, and 150 min relative to glucose administration (0 min = administration) to assess insulin response. Data were analyzed with a fixed model specific for repeated measures and TS as a covariate. Glucose changed ($P < 0.01$) over time during the hour prior to glucose administration (pre-glucose) and control steers tended to have greater glucose concentrations than PNS steers (P = 0.10). There was a pre-glucose treatment by time interaction (P = 0.03), with PNS steers having greater insulin concentrations 45 min before glucose administration compared to controls. The pre-glucose insulin:glucose (I:G) ratio changed ($P < 0.01$) over time and PNS steers tended (P = 0.06) to have a greater I:G ratio than controls. There was no difference ($P > 0.1$) in circulating concentrations of glucose or insulin in the 150 min period following glucose administration (post-glucose). As expected, there was a post-glucose effect ($P < 0.01$) of time in response to glucose administration for glucose, insulin, and I:G ratio. This appears to be the initial assessment of paternal transgenerational influence of such a prenatal stressor on glucose homeostasis in cattle. Prenatal transportation stress of bulls resulted in altered basal glucose and insulin homeostasis but no effect on insulin response to exogenous glucose in their steer calf progeny.

Key Words: Insulin, Transgenerational Stress, Glucose
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459 Assessment of physiological parameters in response to an endotoxin challenge in crossbred steer progeny sired by Brahman bulls that experienced prenatal transportation stress.

B. P. Littlejohn[*1,2], N. C. Burdick Sanchez[3], P. R. Broadway[3], J. A. Carroll[3], T. H. Welsh, Jr.[1], R. D. Randel[2], and R. C. Vann[4], [1]*Texas A&M AgriLife Research and Department of Animal Science, College Station,* [2]*Texas A&M AgriLife Research, Overton,* [3]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX,* [4]*MAFES - Brown Loam Experiment Station, Mississippi State University, Raymond, MS.*

The objective of this experiment was to assess physiological responses to an endotoxin challenge in crossbred male progeny whose Brahman sires experienced prenatal transportation stress (PS) in utero. Sixteen steers (PNS group) sired by 3 PS bulls (gestating dams were transported for 2 h at 60, 80, 100, 120, and 140 ± 5 d of gestation) and 16 steers sired by 3 control bulls were evaluated. Fifty-six d after weaning, pen score (PS; 1 = calm and 5 = excitable), exit velocity (EV; m/sec) and temperament score [TS; (PS + EV)/2] were recorded. Four d later (d -6), steers were transported from Raymond, MS to Lubbock, TX (1,200 km). On d -2, steers were fitted with rectal temperature (RT) probes and jugular cannulas, and placed in individual stanchions. On d 0, all steers received an endotoxin challenge (LPS; 0.25 μg/kg BW). Physiologic variables included RT, sickness behavior score (SBS; 1 = lowest and 5 = greatest sickness behavior), and complete blood count (CBC). Endocrine and metabolic variables included cortisol, glucose, and insulin. Serum cortisol, glucose, and SBS were assessed at 30-min intervals, RT at 1-h intervals, and CBC at 2-h intervals from -2 to 8 h and at 24 h relative to LPS administration (0 h = administration). Serum insulin was assessed at 30-min intervals from -2 to 6 h. All data were analyzed with a fixed model specific for repeated measures, and TS was a covariate for cortisol, insulin, and glucose. There was a pre-LPS cortisol treatment by time ($P < 0.01$) interaction, with greater cortisol in controls than PNS steers at time 0. There was no influence ($P > 0.1$) of treatment or time on pre-LPS glucose or insulin. Controls had greater ($P < 0.01$) post-LPS cortisol, which changed ($P < 0.01$) over time. There was a post-LPS treatment by time interaction for glucose and insulin ($P < 0.05$). There was a post-LPS SBS treatment by time interaction ($P = 0.02$), with a greater SBS in PNS steers from 0.5 to 3 h. The RT changed ($P < 0.01$) over time in response to LPS but was not affected by treatment ($P > 0.1$). All CBC variables changed over time in response to LPS ($P < 0.01$). The PNS steers had lower hemoglobin and hematocrit counts, but greater platelet, white blood cell counts, and monocyte counts than controls ($P < 0.01$). The PNS steers had lower ($P < 0.01$) eosinophil counts than controls from 4 to 8 h after LPS. Male progeny from prenatally stressed bulls had altered hematologic, endocrine, and metabolic responses to an endotoxin challenge.

Key Words: Transgenerational Stress, LPS, Cattle
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460 Assessment of chromatin damage in bull semen utilizing an Acridine Orange assay adapted for Agilent 2100 Bioanalyzer.

P. Rowan[*], R. Johnston, A. N. DeCarlo, and S. L. Pratt, *Clemson University, Clemson, SC.*

The objective of this study was to assess induced chromatin damage of sperm obtained from bulls consuming ergot alkaloids with an Acridine Orange (AO) staining procedure adapted to flow cytometry procedures using the Agilent 2100 Bioanalyzer Cell Chip technology. The AO staining technique was validated by exposing $\approx 1X10^6$ formalin fixed sperm (100 ml) to UV light at 254 nm, 302 nm, or 365 nm for 0, 30, 60, and 90 minutes, in triplicate, to induce acrosomal damage. Following UV exposure, cell membranes were permeabilized with 500 ml of a 0.1% triton solution. Samples were stained by incubating with 300 ml staining buffer and 2 ml of a 6 mg/ml Acridine Orange stain solution. Cells were pelleted, resuspended in 100 ml Agilent cell chip buffer and then analyzed through the Agilent Cell Chip Assay to evaluate percent gated cells, correlating to cells with chromatin damage. Angus bulls (n = 25), ≈ 12 mo of age and having passed a breeding soundness exam were stratified by BCS and BW and allotted to one of two treatments, non-toxic fescue, Texoma Max Q II (E-), or ergot alkaloid containing, Kentucky 31 (E+). Bulls were allowed to graze for 84 d (January to April). Semen was collected at days -28, 0, 28, and 56 (allotment to treatment = d 0) by electrojaculation. Samples were fixed in formalin until assessment of chromatin damage using the adapted AO assay. Results assessing UV induced chromatin damage were subjected to analysis using JMP (SAS Institute, Cary NC) using LS means procedures where UV wavelength, time of exposure and their interactions were the main effects. Data evaluating the effect on chromatin damage due to the consumption of E+ diets were subjected to LS means procedures where treatment, d, and their interaction were the main effects. Using the adapted AO staining procedure, an increase in chromatin damage was detected with exposure to 302 nm ($P = 0.007$). The highest percent gated was reached in cells exposed to UV for 90 min ($P = 0.007$). When comparing sperm for E+ and E- bulls, no significant differences in number of chromatin damaged cells due to treatment, d or the treatment by d interactions were detected. These data indicate that the AO assay adapted to the Agilent 2100 Bioanalyzer Cell Chip technology can detect sperm chromatin damage and that grazing E+ forage does not negatively impact sperm physiology through induction of chromatin damage.

Key Words: sperm, chromatin damage, Acidine Orange
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461 Clostat® alters the serum metabolome of Holstein steer calves.

P. R. Broadway*[1], J. A. Carroll[1], N. C. Burdick Sanchez[1], T. R. Callaway[2], S. D. Lawhon[3], L. K. Bryan[3], E. V. Gart[3], D. O'Connor[4], and P. W. Rounds[4], [1]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX,* [2]*USDA-ARS, College Station, TX,* [3]*Department of Veterinary Pathobiology, Texas A&M University, College Station,* [4]*Kemin Industries, Inc., Des Moines, IA.*

Probiotics are gaining increased interest in calf feeding operations as some producers seek novel, non-antibiotic technologies to improve health and performance. Therefore, the objective of this study was to evaluate changes in serum metabolomic compounds of Holstein steer calves supplemented with CLOSTAT® (13g/hd/d for 35d; Kemin Industries, Des Moines, IA) following an experimental oral *Salmonella* challenge. Holstein steer calves (n = 40) were assigned to treatments in a 2 x 2 factorial design and either fed CLOSTAT (CLO) or not (CON) and inoculated with *Salmonella* Typhimurium (SAL; 1.1 x 10^6) or not (NOSAL) via milk replacer. Data has previously reported CLO supplementation greatly reduced *Salmonella* concentrations in the gastrointestinal tract of calves after experimental infection and mitigated some of the negative effects of the disease challenge. Additionally, rectal temperature was greatly reduced in calves subjected to the challenge. For this study, serum was analyzed from blood samples collected 48 h after experimental infection representing peak rectal temperature. Serum metabolites were identified and quantified using GC-MS (West Coast Metabalomics Center, UC Davis). Data were log transformed prior to analysis to achieve normality. Data were analyzed using univariate ANOVA, principal component analysis, and partial least squares-discriminate analysis using the fixed effects of metabolite, treatment, *Salmonella*, and their interactions using Metaboanalyst 3.0. Mean separation was determined at $\alpha = 0.05$. A total of 334 compounds were quantified, and 118 were of known identity. Overall, serum metabolome was shifted more due to CLO supplementation (9.6%) as opposed to SAL inoculation (7.1%). Clostat increased the concentrations of leucine and 32 other metabolites ($P < 0.05$). *Salmonella* was responsible for increasing myristic acid, heptadecanoic acid, and other fatty acids ($P < 0.05$) which have known antimicrobial properties. Uric acid was increased ($P < 0.05$) in CLO supplemented calves and may have enhanced macrophage killing capabilities which may correlate to reduced migration, colonization, and translocation observed in the gastrointestinal tract of supplemented calves. This may partially explain the previously reported reduced rectal temperature in CLO supplemented calves. *Salmonella* additionally altered 25 other metabolites ($P < 0.05$). Only 9 interactions existed between supplementation and *Salmonella* infection across 334 compounds. These data suggest that supplementation of calves with CLO may alter serum metabolites and shift metabolic and immune pathways regardless of their *Salmonella* status which may have played a role in reducing the negative effects of a *Salmonella* challenge.

Key Words: Salmonella, Metabolome, CLOSTAT
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462 Fractionated dairy cow milk β-Casein enhances affinity of the jejunal alkaline phosphatase for hydrolyzing ATP in piglets fed liquid formulas.

N. Burello*, N. Rafiee Tari, K. Zhou, T. Archbold, M. Corredig, and M. Z. Fan, *University of Guelph, Guelph, ON, Canada.*

Some bioactive peptides originating from β-casein have been shown to be resistant to enzymatic digestion in the gastrointestinal tract and to influence immunological responses. Intestinal alkaline phosphatase (IAP), a critical anti-inflammatory mediator, can catalyze the hydrolytic dephosphorylation of endotoxin lipopolysaccharides (LPS) and other emblematic members of pathogen-associated-molecular patterns (PAMPs) such as ATP, therefore preventing gut dysbiosis and disorders. Objectives of this study were to determine responses in the enzyme kinetics, including affinity (Km) and maximum activity (Vmax) of IAP in hydrolyzing ATP, in piglets fed liquid formulas with varying levels of β-casein. Three formulas were formulated, including a control formula containing whey protein as the sole source of protein, and two testing formulas containing total casein to whey protein ratio (%) of 40:60, but differing in β-casein at 3.51 and 4.36% (on air-dry basis), respectively. Contents of all other dietary nutrients, including ME, CP, minerals and vitamins, were formulated to be equal among the three formulas. A total of 24 colostrum-suckled 3-d-old piglets were randomly assigned to the three formulas, housed individually in metabolic crates, and fed their assigned formulas for 18 d according to a randomized block design. Piglets were euthanized at the end of their study periods and the proximal jejunal tissue samples were collected. Each kinetic experiment was conducted with homogenized porcine jejunal samples (about 5 μg protein each incubation) and 11 gradient concentrations of ATP, ranging 0 – 1.25 mM in incubation media in 4 replicates at pH 7.4 and 37°C. The kinetics (parameter estimates ± SE, $P < 0.05$, $R^2 = 0.66 - 0.93$ for equations; n = 44) of jejunal IAP in hydrolyzing dephosphorylation of ATP were obtained, including Vmax values (ug/mg protein·min) of 4.39 ± 0.12, 2.90 ± 0.07, and 2.17 ± 0.14; and

Km values (mM,) of 0.070 ± 0.008, 0.056 ± 0.006, and 0.046 ± 0.013 in the control, the 3.51%-β-casein, and the 4.36%-β-casein formulas, respectively. Pooled t-test comparisons showed although the Vmax values were reduced ($P < 0.05$) by dietary β-casein feeding, the Km value of the control group was higher ($P < 0.05$) than the 3.51%-β-casein group by 20%, and the 4.36%-β-casein group by 52%, respectively. Results of this study suggest dietary β-casein affects the jejunal IAP functionality. Dietary inclusion of β-casein at 3.51-4.36% has been demonstrated to increase IAP affinity for dephosphorylation of ATP, potentially protecting neonatal piglets from gut dysbiosis and inflammation.

Key Words: β-casein, intestinal alkaline phosphatase, piglet
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463 Broiler chickens express differential alkaline phosphatase activity and enzyme affinity in hydrolyzing ATP along the small intestinal longitudinal axis.

K. Zhou*, N. Burello, W. Wang, T. Archbold, H. Leung, E. Kiarie, and M. Z. Fan, *University of Guelph, Guelph, ON, Canada.*

Broiler chicken growth rates are rapidly accelerating in the industry, requiring an average of 6 to 7 weeks to achieve market body weight. A possible determinant is intestinal alkaline phosphatase (IAP), a key enzyme which dephosphorylates pathogen-associated-molecular patterns (PAMPs) such as endotoxin lipopolysaccharides (LPS) and ATP, thereby preventing gut dysbiosis and disorders. However, IAP's roles in maintaining gut health have yet to be elucidated in the broiler chicken. Thus, the objective of this study was to determine IAP activity kinetics for hydrolyzing ATP at pH 7.4 and 41°C in the duodenal, jejunal, and ileal segments of young broilers. Ten 28-d old broiler (Ross 708) chickens, maintained on a standard grower corn soybean meal diet, were euthanized for collecting duodenal, jejunal, and ileal tissue samples. Each ATP kinetic experiment was conducted with 20 gradient concentrations of ATP in 4 replicates, ranging 0 – 5 mM in incubation media. All enzymatic incubations were conducted with about 3 μg protein of the homogenized small intestinal segmental tissues. The kinetics (parameter estimates ± SE, $P < 0.05$, $R^2 = 0.82 – 0.93$; n = 80) of the broiler small intestinal segmental IAP activities of hydrolyzing ATP were obtained, including Vmax values (μg/mg protein·min) of 7.59 ± 0.09, 8.60 ± 0.16, and 7.77 ± 0.19; and Km values (mM) of 0.045 ± 0.004, 0.132 ± 0.015, and 0.105 ± 0.015 in the duodenum, jejunum, and ileum, respectively. Pooled t-tests showed that the Vmax was higher ($P < 0.05$) in the jejunum than in the duodenum and the ileum, while the Vmax value was higher ($P < 0.05$) in the ileum than in the duodenum. Furthermore, the Km value was lower ($P < 0.05$) in the duodenum than in the jejunum by 2-fold and the ileum by 1.3-fold, respectively, while the Km value was lower ($P < 0.05$) in the ileum than in the jejunum by 26%. Our results suggest that young broiler chickens express differential alkaline phosphatase activity and enzyme affinity in hydrolyzing ATP along the small intestinal longitudinal axis.

Key Words: ATP hydrolysis, broiler chickens, intestinal alkaline phosphatase
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464 Comparison of follicular and luteal function in two and three follicular wave estrous cycles and their repeatability.

R. A. d'Orey Branco*[1,2], D. A. Neuendorff[2], W. B. Smith[2], T. H. Welsh, Jr.[1], and R. D. Randel[2], [1]*Department of Animal Science, Texas A&M University, College Station,* [2]*Texas A&M AgriLife Research, Overton.*

The objective of this study was to determine if: a) there is repeatability in follicular dynamics between estrous cycles (EC) within a cow, and b) there are differences in follicular and luteal function between cows with two (2FW) or three follicular waves (3FW). We hypothesized that: a) follicular dynamics are repeatable, and b) there are differences in follicular and luteal characteristics between 2FW and 3FW EC. Daily blood collection from the coccygeal vein and a daily three-dimensional ultrasound (3DUS) exam of the ovaries were performed on Brahman cows (n = 13). Ultrasound images were collected using a GE-Voluson I© with a RIC5-9-D H48651MS transducer. Serum samples and 3DUS images were collected from the d after the first estrus behavior and continued throughout two full EC. Data were analyzed using Proc Mix, and Proc Mix specific for repeated measures of SAS v9.3. Within cow, EC 1 (C1) and EC 2 (C2) did not differ ($P \geq 0.77$) in length (d) (C1: 18.7±0.36; C2: 2.46±0.14), number of follicular waves (NFW) (C1: 2.46±0.14; C2: 2.46±0.14), ovulatory follicle volume (FollVol: cm3)(C1:1.23± 0.14; C2: 1.23±0.16), or ovulatory follicle diameter (FollDim; mm) (C1: 17.49±0.70; C2: 17.77±0.77). Antral follicular count (AFC) was not affected ($P \geq 0.68$) by d of EC, nor cycle (C1: 62.80±4.5; C2: 61.96±4.5), and there was no interaction between cycleXd of EC. There were no differences ($P \geq 0.56$) in the length, FollVol, FollDim between 2FW and 3FW (Table 464). AFC was not affected ($P = 0.97$) by d or an interaction between NFWXd of EC. However, 2FW had a greater ($P < 0.0001$) AFC when compared with 3FW. Serum progesterone concentration (P4) during the10 d after estrus was affected ($P < 0.0001$) by d but not ($P \geq$

Table 464. Differences in follicular and luteal function between two (2FW) and three follicular waves (3FW)

Item	2FW(n = 6)	3FW(n = 7)	*P*-value
Length(d)	18.70(±0.36)	18.80(±0.36)	0.82
FollVol(cm3)	1.17(±0.15)	1.29(±0.15)	0.56
FollDim(mm)	17.49(±0.73)	17.77(±0.77)	0.78
AFC	66.91(±1.20)	57.07(1.32)	0.001
P4 10 d after estrus(ng/mL)	2.31(±0.10)	2.12(±0.11)	0.22
P4 10 d before estrus(ng/mL)	3.70(±0.13)	2.84(±0.14)	0.001

0.21) by NFW or an interaction between d afterXNFW. Serum progesterone during the 10 d before estrus was affected ($P < 0.0001$) by d and was greater ($P < 0.0001$) in 2FW compared with 3FW cows (Table 464). In conclusion, these results support the hypotheses that a) there is repeatability in follicular dynamics, such as, length, FollVol, FollDim NFW and AFC across EC within cow, and b) there are greater AFC and P4 during the regression phase of the CL in cows with 2FW.

Key Words: Follicular Wave, Antral Follicular Count , Three-Dimensional Ultrasound
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465 Resynchronization with ovsynch improves cumulative pregnancy and reduces embryonic losses in CIDR-GnRH synchronized Nili-Ravi buffalo.

N. Ahmad*[1], U. Arshad[2], A. Qayyum[1], M. Hassan[3], A. Husnain[2], and A. Sattar[1], [1]*Department of Theriogenology, University of Veterinary and Animal Sciences, Lahore, Pakistan,* [2]*University of Veterinary and Animal Sciences Ravi Campus, Pattoki, Pakistan,* [3]*College of Veterinary and Animal Sciences, Jhang, Pakistan.*

The objective of the present study was to determine the effect of resynchronization on Day 23 either with OVS or CIDR on pregnancy rate, cumulative pregnancy, embryonic and fetal losses in CIDR-GnRH synchronized Nili-Ravi buffalo. For this, buffalo of mixed parity (n = 181), lactating, 181 ± 72.8 days postpartum, having BCS 3.2 ± 0.5 (scale of 1-5) and 400-600 kg weight were subjected to the synchronization as well as resynchronization. All buffalo received CIDR protocol on Day -9.5. In addition, GnRH was injected 36 h after CIDR removal and FTAI was performed 18 h later (Day 0). On Day 23, buffalo were randomly assigned to receive one of the following treatments 1) OVS (n = 63), 2) CIDR (n = 55) and 3) control (CON; n = 63) for resynchronization (2nd AI). Pregnancy rate and embryonic and fetal losses were monitored by serial ultrasonography on Day 30, 45, 60 and 90 after synchronization (1st AI), respectively. The pregnancy retention rate in OVS buffalo remained significantly and consistently higher ($P < 0.05$) than the CON at day 30, 45, 60 and 90 after 1st FTAI. The pregnancy rate in resynchronized open buffalo did not differ ($P > 0.05$) between OVS and CIDR groups. Whereas, cumulative pregnancy rate in OVS group (84%) after first and second FTAI when determined on Day 64 was higher ($P < 0.05$) than CON (59%) group. The embryonic losses were significantly lower ($P < 0.05$) in OVS (18%) buffalo, when compared to CON (42%) buffalo on Day 45 post 1st AI. Fetal losses were fewer and did not differ ($P > 0.05$) due to treatment on Day 60 or 90 post 1st AI. In conclusion, i) the pregnancy rate and cumulative pregnancy rate in OVS buffalo was higher than CON buffalo when determined on Day 64 after resynchronization, ii) embryonic and fetal losses were lower in OVS buffalo when determined from Day 31 - 90 compared to CON buffalo.

Key Words: Cumulative pregnancy, Resynchronization, Nili-Ravi buffalo
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466 Administration of a subcutaneous high concentrate prostaglandin F2α in replacement beef heifers and the effects on estrus response and pregnancy rates.

N. Oosthuizen*[1], L. B. Canal[1], P. L. P. Fontes[1], C. D. Sanford[1], N. DiLorenzo[1], C. R. Dahlen[2], and G. C. Lamb[3], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*Department of Animal Sciences, North Dakota State University, Fargo,* [3]*Department of Animal Science, Texas A&M University, College Station.*

To evaluate the effects of a high concentrate $PGF_{2\alpha}$ (12.5 mg of dinoprost tromethamine/mL, Lutalyse *HighCon*, Zoetis Animal Health) compared with a conventional $PGF_{2\alpha}$ (5 mg of dinoprost tromethamine/mL, Lutalyse, Zoetis Animal Health), 841 *Bos taurus* replacement beef heifers were assigned to treatments in a complete randomized design at 8 locations over the period of April 1 to July 15, 2016. All heifers were exposed to the 7-day CO-Synch + CIDR protocol. On d -7 of the protocol heifers received 100 µg of GnRH, and a controlled internal drug releasing (EAZI-BREED CIDR; 1.38 g of progesterone; Zoetis Animal Health) insert for 7 d. On d 0, at CIDR removal, Estrotect (Rockway Inc., Spring Valley, WI) estrus detection patches were applied to all heifers and, within location, all eligible heifers randomly received one of two $PGF_{2\alpha}$ treatments: 1) CONTROL (n = 417); heifers received a 5 mL injection of conventional Lutalyse, administered i.m.; or 2) HiCON (n = 424); heifers received a 2 mL dose of Lutalyse *HighCon*, administered s.c. A second GnRH injection was administered 54 ± 2 h and heifers were inseminated by fixed-time AI (TAI). Heifers were evaluated for estrus activity prior to TAI. Pregnancy was diagnosed by transrectal ultrasonography between 35 and 55 d after TAI to determine the presence of a viable embryo, thereby assessing AI pregnancy rates. The percentage of heifers exhibiting estrus between CIDR removal and TAI differed ($P < 0.001$) among locations and ranged from 35.5 to 65.0%. The percentage of heifers exhibiting estrus between d 0 (CIDR removal) and TAI on d 2 did not differ ($P = 0.677$) between CONTROL and HiCON treatments (47.9 vs 49.5%). In addition, although pregnancy rates to TAI differed ($P = 0.032$) among locations, pregnancy rates to TAI were similar ($P = 0.647$) between CONTROL and HiCON treatments (46.4 vs 44.7%). Final pregnancy rates did not differ ($P = 0.27$) between treatments. Since the use of a high concentrate $PGF_{2\alpha}$ had similar effects on estrus expression, pregnancy rates to TAI, and final pregnancy rates in beef heifers compared to conventional $PGF_{2\alpha}$, we concluded that high concentrate PGF$_{2\alpha}$ is a suitable alternative for use in beef heifer estrus synchronization protocols.

Key Words: beef heifers, estrus synchronization, prostaglandin F2α
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467 Abstract withdrawn.

468 The application of busulfan to inhibit the spermatogenesis in chicken testis.

A. Vetokh, N. Volkova, E. Tomgorova*, D. Beloglazov, A. V. Dotsev, and N. A. Zinovieva, *L.K. Ernst Institute of animal husbandry, Podolsk, Russian Federation.*

Spermatogonia cells are considered as a valuable genetic material to produce individuals with desired traits in the framework of preservation of animal and poultry gene pool (cryobanks) and genetic modification of their genome (transgenesis). This technology is based on the introduction of donor spermatogonia into the testes of male recipients and the following obtaining the exogenous sperm to produce progeny with desired characteristics. A key step of this technology is the removal of own spermatogenic cells (spermatogenesis inhibition) in the male recipient. We have optimized the method to inhibit the spermatogenesis in chicken testes using alkylating agent busulfan. The multiple injections of busulfan at the concentration from 40 to 100 mg per 1 kg of body weight was performed directly into the parenchyma of testes of six month old chicken males (n = 16). In order to detect the presence of spermatogenic cells in seminiferous tubules, we carried out the histological studies of testes in one month after injection. We observed the decrease in diameters and the number of spermatogenic cells at the cross sectional area of the seminiferous tubules in the experimental group as compared to the control. When using busulfan at concentration of 40 mg/kg the number of cells averaged 35±3 cells per seminiferous tubule, which was 32.8 times less as compared to the control (1149±95). At higher concentrations of busulfan the number of cells decreased and averaged 20±2, 12±0.5 and 9±0.4 cells at concentration of 60, 80 and 100 mg/kg, repectively. Analysis of cell types of the seminiferous tubules revealed that mainly the Sertoli cells and spermatogonia represented the cell population. Moreover, with increasing concentrations of busulfan the ratio of spermatogonia was significantly reduced. The ratio of Sertoli and spermatogonia cells after introduction of busulfan into the testes at a concentration of 40, 60, 80 and 100 mg/kg was 57 and 43%, 75 and 25%, 95 and 5 % and 96 and 4%, respectively. However, the application of busulfan at a concentration 100 mg/kg led to high mortality of chicken. Thus, we demonstrated that the optimal concentration of busulfan to kill the spermatogonial cells was 80 mg/kg. The complete inhibition of spermatogenesis was observed in 9-10 months after introduction of busulfan at this concentration. The study was supported by the Russian Science Foundation within Project no.16–16–10059.

Key Words: spermatogonia, spermatogenic cells, spermatogenesis
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469 Abstract withdrawn.

470 Effects of eCG administration 4 versus 2 days prior to timed AI on Nellore cows.

G. H. L. Marquezini*[1,2], G. F. Santos Junior[2], R. A. Franco[2], and R. A. Souza[2], *[1]Faculdade Marechal Rondon FARON, Vilhena,RO, Brazil, [2]Norte Genética, Vilhena,RO, Brazil.*

The objective of this study was to evaluate growth of the dominant follicle (DF) in multiparous Nellore cows treated with equine chorionic gonadotropin (eCG) either 4 or 2 d prior to timed AI (TAI). We hypothesized that early eCG administration improves follicular growth and increase DF diameter at TAI. Cows (n = 137) had their estrous cycle synchronized with an intravaginal device containing 1.9 g of progesterone (CIDR) and 2.0 mg of estradiol benzoate (d 0), 12.5 mg of PGF$_{2\alpha}$ (d 7), CIDR withdrawal and 0.3 mg of estradiol cypionate (d 9), and TAI 48 h later (d 11). On d 7, ovaries were evaluated by ultrasonography and cows were blocked based on DF diameter (< 9 mm vs. ≥ 9 mm). Within block, cows were randomly assigned to receive 300 IU of eCG either on d 7 (eCGD7; n = 64) or on d 9 (eCGD9; n = 73). Diameter of the DF was evaluated by transrectal ultrasonography on d 7, 9, and 11. Follicular growth from d 7 to 9, 7 to 11, and 9 to 11 was analyzed by ANOVA using the GLIMMIX procedure of SAS. Follicular diameter was analyzed by ANOVA for repeated measures and cow was considered a random effect. Follicular growth from d 7 to 11 tended to be greater ($P = 0.08$) for eCGD7 compared with eCGD9 (4.9 ± 0.2 vs. 4.4 ± 0.2 mm). The overall effect of treatment was explained mostly by DF growth from d 7 to 9 (eCGD7 = 2.6 ± 0.2 vs. eCGD9 = 2.0 ± 0.2 mm; $P < 0.01$) as growth from d 9 to 11 did not differ ($P = 0.44$) between treatments (eCGD7 = 2.3 ± 0.2 vs. eCGD9 = 2.4 ± 0.1 mm). Follicular diameter was affected ($P < 0.01$) by the interaction between treatment and day. Whereas no difference was observed on d 7 (eCGD7 = 9.7 ± 0.2 vs. eCGD9 = 9.6 ± 0.2 mm), DF in eCGD7 cows was larger ($P < 0.01$) on d 9 (12.3 ± 0.2 vs. 11.5 ± 0.2 mm). In addition, DF on d 11 did not differ ($P = 0.12$) between treatments (eCGD7 = 14.5 ± 0.3 vs. eCGD9 = 14.0. ± 0.2 mm). Treatment with 300 IU of eCG 4 d prior to TAI improved follicular growth but did not increase overall mean of DF diameter at TAI compared with eCG administration 2 d before TAI in Nellore cows.

Key Words: Artificial insemination , *Bos indicus*, eCG
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471 Use of doppler ultrasound to evaluate testicular blood flow dynamics in bulls.

P. Favaro*[1], F. A. Barca Junior[1], G. R. Pereira[1], S. R. Menegassi[2], J. O. Barcellos[3], and C. Koetz Junior[1], [1]*UNOPAR, Arapongas, Brazil,* [2]*NESPRO/UFRGS - Federal University of Rio Grande do Sul, Porto Alegre, Brazil,* [3]*NESPRO/UFRGS - Department of Animal Science, Federal University of Rio Grande do Sul, Porto Alegre, Brazil.*

Evaluation of the testicular hemodynamics can significantly contribute to understand the thermoregulatory mechanisms and oxygen supply of the testis in domestic animals. The objective of this study was to evaluate the circulatory dynamics of the testicular arteries in bulls during four consecutive seasons. We evaluated bulls (Hereford n = 24 and Angus n = 29) by means velocimetry parameters (Vel), pulsatility index (PI) and resistance index (RI) using Doppler ultrasonography. All procedures were approved by the Ethical Committee for Care and Use of Experimental Animals (#18656/2014/58). In addition, climate temperature-humidity index (THI) data were collected from an automatic weather station from the National Institute of Meteorology. Data were analyzed using ANOVA (GLM) and Pearson's correlation with significance level of 5%. No differences were observed between breed and breed*season; however, season was difference between evaluated animals. The THI was lower in the fall (46.8) compared to winter (66.9), spring (71.9) and summer (72.7). Blood flow velocity (cm/sec) showed difference between fall (7.44 ± 2.72) compared to winter, spring and summer (12.74 ± 4.30; 12.74 ± 3.87 and 11.33 ± 3.42, respectively; $P < 0.05$). In addition, PI showed difference in the fall (0.45 ± 0.15) compared to winter, spring and summer (0.33 ± 0.20; 0.35 ± 0.17 and 0.27 ± 0.17, respectively; $P < 0.05$). We observed no difference in RI indexes between evaluation periods. In the fall season, we observed a positive correlation (0.87) between PI and RI ($P < 0.05$) indices; however, a negative correlation was observed between Vel x PI (-0.60) and Vel x RI (-0.59). In the fall, when THI is lower, there is a decrease in Vel of the blood flow arteries and an increase of PI in the circulatory dynamics in the pampiniform plexus area. Therefore, there is no need for additional nutrients supply when the testicular blood flow is lower due to the less heat dissipation by the scrotum to maintain an ideal temperature for normal spermatogenesis. We concluded that there is difference in Vel and PI of the supratesticular arteries from animals evaluated in the fall season. Therefore, the Doppler ultrasound can be used to evaluate scrotal blood flow changes of the pampiniform plexus during season and it suggests that differences in Vel and PI dynamics are an important players in the physiological requirements for its normal reproductive performance under different environmental conditions.

Key Words: bulls, thermoregulation, testicular blood flow
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472 Sophorolipids are a potential antimicrobial agent in vitro and in broilers.

K. P. Sung*[1,2], S. K. Lee[2], D. Garnett[3], J. Kim[1], and K. Y. Whang[1], [1]*Department of Biotechnology, Graduate School, Korea University, Seoul, Korea, Republic of (South),* [2]*EASY BIO, Inc., Seoul, Korea, Republic of (South),* [3]*Pathway Intermediates Ltd., Shrewsbury, Shropshire, United Kingdom.*

Recently, the ban of antibiotic growth promoters (AGP) using in animal feeds has been rapidly spread worldwide and the needs for alternative strategies to AGP have increased. Sophorolipids (SPL) are glycolipid biosurfactants produced by non-pathogenic yeast species such as *Candida bombicola*. Previous researches demonstrated SPL has a selective antimicrobial activity toward Gram-positive bacteria. Therefore, two experiments were designed to investigate the possibility of SPL as an alternative to AGP in broilers. An *in vitro* study was conducted to estimate antimicrobial activities with various concentrations of SPL against both of Gram-positive and Gram-negative bacteria. SPL treatment showed antimicrobial activities against *Streptococcus bovis, Stapylococcus aureus, Bacillus cereus, E. coli* K88 and *Pseudomonas aeruginosa*. To confirm the result of the *in vitro* study, an *in vivo* experiment was conducted to investigate the effects of supplemental SPL as an antimicrobial agent in comparison with zinc bacitracin (ZB) in broilers. A total of 540 0-day-old Ross® 308 broilers were randomly allotted to 9 dietary treatments with 6 replicates and fed the experimental diet for 5 weeks. Dietary treatments consisted of control (CON; basal diet), ZB groups (0.025%, 0.05%, 0.10% and 0.20%) and SPL groups (0.025%, 0.05%, 0.10% and 0.20%). At the end of experiment, one bird per pen was sacrificed to collect cecal contents and gut microbiota of the samples were identified by 16S rRNA gene-pyrosequencing. A taxonomy-based analysis of cecal samples revealed that both of ZB groups and SPL groups decreased the microbial diversity and abundance compared with CON. At phylum level, two phyla, *Firmicutes* and *Bacterodetes,* were predominant (over 95%) in broiler ceca of all treatments. The ratio of *Firmicutes* to *Bacterodetes* in the cecal microbiota was greater in ZB groups than SPL groups and CON. At genus level, *Barnesilella* was the most abundant microbiome in CON (25.0% of total cecal microbiota). *Barnesilella* was decreased in ZB groups in a dose dependent manner, as an example, decreased from 25.0% in CON to 2.75% in 0.2% ZB treatment. In contrast, *Barnesilella* were not changed in SPL groups compared with CON. In SPL groups, supplemental SPL tended to decrease Gram-positive bacteria including *Romboutsia, Lactonifactor, Turicibacter and Sporobacter*. These findings indicate SPL inhibits mainly Gram-positive bacteria on both of *in vitro* and *in vivo*. Therefore, SPL and ZB induced less diversity and less abundance of cecal microbiota in broilers but SPL showed more specific and balanced antimicrobial effects than ZB.

Key Words: Sophorolipids, Antibiotics, Gut Microbiota of Broilers
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473 Differences in embryo survival between Bos indicus and Bos taurus females receiving energy restricted diets during early gestation.

P. L. P. Fontes*[1], N. Oosthuizen[1], D. D. Henry[1], F. M. Ciriaco[1], C. D. Sanford[1], L. B. Canal[1], V. R. G. Mercadante[2], S. E. Johnson[3], A. D. Ealy[3], N. DiLorenzo[1], and G. C. Lamb[4], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]Virginia Tech - Animal and Poultry Sciences, Blacksburg, [3]Virginia Tech, Blacksburg, [4]Department of Animal Science, Texas A&M University, College Station.*

To evaluate the impact of energy restriction on embryonic survival in *Bos taurus* and *Bos indicus* genotypes, a reciprocal embryo transfer approach was used in a completely randomized design with a 2 × 2 × 2 factorial arrangement of treatments. Recipient cows were assigned randomly to 1) a diet to meet daily maintenance requirements (MAINT), or 2) restricted intake of nutrients to 70% of energy maintenance requirements (RESTR). Angus (AN) and Brangus (BN) embryo donors were superovulated and artificially inseminated with female sexed-sorted semen from the same breed. Embryos were then randomly transferred 7 d post-insemination (d 7) to either AN or BN recipients fed the respective diets for 20 d to create 8 treatment combinations (AN × AN × RESTR, n =14; AN × AN × MAINT, n = 19; AN × BN × RESTR, n = 16; AN × BN × MAINT, n = 17; BN × BN × RESTR, n = 15; BN × BN × MAINT, n = 19; BN × AN × RESTR, n = 14, BN × AN × MAINT, n = 19). Recipients remained on the dietary scheme until d 91. All cows were then submitted to the same feeding regime until calving. Pregnancy diagnosis was performed at d 28 and 91. Embryo loss was defined as a cow that received an embryo but was diagnosed as nonpregnant. There was an effect of diet ($P < 0.001$) and day ($P < 0.001$) on recipient BW. Similarly, diet altered recipient BCS (diet × day, $P = 0.005$). There was a recipient breed × diet interaction on embryo loss at d 28 ($P < 0.001$), where AN × RESTR recipients had greater embryo loss than AN × MAINT (69.0 vs 28.2%, respectively), and BN × RESTR (69.0 vs 27.9%, respectively). There was also an embryo breed × diet interaction ($P < 0.021$) on embryo loss by d 28, with RESTR recipients that received an AN embryo experiencing greater embryo loss than RESTR recipients receiving BN embryos (64.3 vs 31.9%, respectively). At d 91, AN × RESTR recipients had greater (recipient breed × diet, $P < 0.001$) embryo loss than AN × MAINT (78.4 vs 41.9%, respectively) and BR × RESTR (78.4 vs 41.0%, respectively). These results indicate that *Bos taurus* cattle may be more susceptible to embryonic loss than *Bos indicus* when submitted to a feed restriction scheme during the first trimester of gestation.

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474 Effect of four assisted hatching techniques and two in vitro culture media on embryo hatching rate.

N. C. Negota*, L. P. Nethenzheni, and N. R. Serota, *University of Venda, Polokwane, South Africa.*

The objective of the study were to determine the effect of four assisted hatching (AH) techniques (mechanical, chemical, enzymatic and laser) and use of two *in vitro* culture media (Hams F10 and TCM-199) on hatching rate of blastocyst-stage embryos following 24 hour *in vitro* culture. The C57BL/6-black and BALB/c-white breeds were raised until maturity and naturally bred to produce F1 generation. The light in the breeding house was controlled and the mice were fed without restriction. Superovulation was done using both equine chorionic gonadotropins and human chorionic gonadotropins and the F1 generation was used for collection of the blastocyst-stage embryos at six weeks of age. There was a significant difference ($P < 0.05$) observed between the diameter of ZP diameter before AH and after 24 hours of culture, while no significance difference ($P > 0.05$) among hatching rates and the blastomeres counted after staining. The diameter of the ZP decreased with assisted hatching techniques. Also, the interaction between AH techniques and *in vitro* culture was found to be significantly different ($P < 0.05$) on hatchability, but with highest hatchability in laser AH techniques 85.4 ± 13.30% with TCM-199 culture medium followed by mechanical AH techniques at 79.13 ± 19.50% in the same *in vitro* culture medium. The lowest hatchability (69.36 ± 30.50%) was recorded in the chemical AH technique group The number of blastomeres counted under interaction of AH techniques and culture media was not significantly different ($P > 0.05$), with the values ranging from 69 ± 6.35 to 76 ± 10.92 blastomeres for hatched embryos. Data collected were subjected to analysis of variance using PROC General Linear Model of SAS version 9.4, where samples were randomly collected. Where significant differences between groups was detected and the Tukey's test was used to separate the means. In conclusion, the results of the study indicated that the use of different AH techniques has got varying and increase outcomes towards hatching rate, commonly when they are subjected to different *in vitro* culture.

Key Words: Assisted hatching, Culture media, Embryo
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475 Pregnancy loss associated with timed-artificial insemination using gender-selected semen in cows.

S. L. Pratt*, A. N. DeCarlo, G. S. Sell, L. K. Lewis, and N. M. Long, *Clemson University, Clemson, SC.*

Pregnancy rates are lower for gender selected (GS) than non-selected, industry standard semen (STD) when used in timed-artificial insemination (TAI) protocols; however, lower pregnancy rates could be due to lower fertilization rates or early pregnancy loss post-TAI. The objective of this study was to determine pregnancy rates for GS compared to STD semen when used in combination with TAI between d 30 through 45 of gestation. Multiparous Angus (AN) and AN-cross cows (n = 80) were stratified by BCS, BW, and days post-partum; and assigned to be inseminated with GS (enriched for Y chromosome containing sperm), or STD semen. Cows were synchronized using the 7-day CO-Synch + CIDR procedure and TAI performed between 60 and 66 h post-CIDR removal. Cows were exposed to natural service beginning 14 d post-TAI. Pregnancy status was evaluated by ELISA for pregnancy specific protein B concentration (PSPB; BioPRYN, BioTracking, Moscow, ID) in maternal serum at d 30 and 45 of gestation (TAI = d 0) and by transrectal ultrasound on d 30, 35, 40 and 45 of gestation. Differences in pregnancy rates due to semen source within day of gestation were determined using Chi Square analysis. Pregnancy rates were lower when using GS semen on d 35 (P = 0.04; 35 and 57.5% for GS and STD, respectively) and d 40 (P = 0.04; 35 and 57.5%, for GS and STD, respectively) of gestation as determined by ultrasound. No difference in pregnancy rates due to semen source was observed at d 30 or 45 of gestation. Pregnancy rates as determined by PSPB levels did not differ at d 30 of gestation due to semen source (12.5 vs 15% for GS and STD, respectively); however, pregnancy rates at day 45 of gestation were lower for the GS group compared to STD at day 45 of gestation (P = 0.04; 40 versus 62.5 %, respectively). Of the animals identified as pregnant at d 30 by PSPB concentration, 55% were determined to be open by transrectal ultrasonography at d 45 and 73% did not calve to the TAI date. Increases in pregnancy rates at d 45 observed via ultrasound, compared to earlier dates were due to natural service. Pregnancy evaluation using ultrasonography indicated that GS pregnancies were lost by d 35 post-TAI which was not observed using PSPB ELISA and pregnancy rates at d 30 and 45 were not consistent between the two methods for determination of pregnancy.

Key Words: gender selected semen, pregnancy specific protein B, timed artificial insemination
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476 The presence of prolactin and tyrosine hydroxylase messenger ribonucleic ccid in bovine testis and epididymis.

A. N. DeCarlo*, and S. L. Pratt, *Clemson University, Clemson, SC.*

Examples of the extra-pituitary expression of prolactin (PRL) have been reported in several species, and recently PRL was detected in bovine seminal fluid by using RIA; however, the source of production for PRL present in bovine seminal fluid has yet to be determined. The objectives of these experiments were to identify the presence or absence of the mRNA for bovine PRL (bPRL) and its rate-limiting enzyme, tyrosine hydroxylase (bTH) in bull testis and epididymis. Testis tissues were obtained from bulls 16 to18 months of age at time of slaughter. The tissues were frozen in liquid nitrogen and kept at -80° C until use for analysis. Total RNA was isolated from frozen testis using the *mirVana* mRNA isolation kit (Ambion, Austin, Texas,USA). Copy DNA was generated by reverse transcription reaction using Superscript II Frist-Strand kit (Invitrogen, Carlsbad,CA). Primers for bTH and bPRL were generated through the PrimerQuest Tool (XXIDT, Coralville, Iowa, USA) for use in polymerase chain reaction (PCR), specific for bTH (accession number: NM_173884.2) and bPRL (accession number: NM_173953.2) corresponding to nucleotide positions 146−165 forward primer and 411−431 reverse primer of the mRNA bPRL sequence; 1263−1283 forward primer and 1360 −1381 reverse primer of the mRNA bTH sequence. End-point PCR was performed and the resulting amplified cDNA was subjected to slab gel electrophoresis in 2.5% agarose gels. The PCR products of the predicted size for both bPRL (285 bp) and bTH (118 bp). To further verify the identity of the PCR products, the cDNA for bPRL and bTH was subjected to an overnight ligation reaction at 4°C using the Qiagen PCR Plus Cloning kit and used to transform *E. coli* (EZ competent; Qiagen, Germantown, MD). Transformation reactions were plated on LB agar plates containing Ampicilin (100 mg/ml) and IPTG/Xgal for blue-white screening, and incubated over night at 37°C. Colonies were selected, used to inoculate LB-Broth and grown to saturation overnight at 37°C shaking at 250 rpm. Resulting DNA was purified using the Wizard Mini-Prep Plus (Promega, Madison, WI) and subjected to restriction enzyme digest and dideoxy-sequencing. Plasmid DNA was digested with EcoR1 (Promega, Madison, WI, USA) and products of the expected sizes were released for the putative bPRL and bTH clones. Sequencing confirmed the identity of the subloned cDNA as bPRL and bTH in both testis and epididymis. These data indicate that PRL present in bull seminal fluid could be produced in male reproductive tissues.

Key Words: prolactin, tyrosine hydroxylase, bovine testis
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477 Effects of delayed insemination on pregnancy rates of suckled beef cows enrolled in the 7-d CO-Synch+Cidr estrus synchronization protocol and that were not detected in estrus by the time of fixed-time AI.

N. W. Dias*[1], C. L. Timlin[1], J. F. Currin[2], S. Clark[2], W. D. Whittier[2], and V. R. G. Mercadante[1], [1]*Virginia Tech - Animal and Poultry Sciences, Blacksburg, VA,* [2]*Virginia-Maryland Regional College of Veterinary Medicine, Blacksburg, VA.*

We determined the effects on pregnancy rates of delaying the time of AI of beef cows enrolled in an estrus synchronization protocol that were not detected in estrus by the time of fixed-time AI. At five locations, a total of 546 suckled beef cows were enrolled in the 7-d CO-Synch+CIDR estrus synchronization protocol. Briefly, 100 µg injection of GnRH and CIDR (controlled internal drug release device) insertion (d -10); 25 mg injection of PGF2α, CIDR removal and estrus alert patch attachment (d -3); on d 0 (approximately 66 h after CIDR removal) cows with activated estrus alert patches received AI, but no injection of GnRH (TAI; n = 295); and cows with non-activated patches were randomly assigned to receive either 100 µg injection of GnRH and AI immediately (GnRH+TAI; n = 130); or 100 µg injection of GnRH and delayed AI 8 h later (GnRH+8AI; n = 121). Pregnancy status was determined by transrectal ultrasonography between d 35 to 45. Pregnancy data were analyzed using GLIMMIX procedure of SAS with cows as the experimental unit, including the fixed effects of treatment, location, age of cow, days post-partum (DPP), BCS, and the random effects of sire and AI technician. There were no differences among treatments on BCS (5.6 ± 0.63; $P = 0.579$), DPP (73 ± 15 d; $P = 0.906$), and cow age (5.4 ± 2.6 yr; $P = 0.192$). A total of 295 cows (54%) had activated estrus alert patches on d 0. Overall pregnancy rates differed ($P < 0.001$) among locations, ranging from 30.7% to 66.9%, and no treatment × location interaction was detected ($P = 0.454$). Average delayed between GnRH injection and delayed AI was 7 ± 1.6 h. Pregnancy rate to fixed-time AI differed ($P = 0.018$) among treatments. Cows in the TAI treatment had the greatest pregnancy rate (59.1 ± 0.03%) compared to cows in GnRH+TAI (43.3 ± 0.04%) group, and GnRH+8AI (50.9 ± 0.05%) was intermediate. We conclude that suckled beef cows enrolled in the 7-d CO-Synch+CIDR estrus synchronization protocol that are detected in estrus prior to the time of AI have greater pregnancy rates compared to cows that are not detected in estrus and receive an injection of GnRH and AI at 66 h after CIDR removal. Furthermore, delaying insemination after GnRH injection failed to increase pregnancy rates of cows not detected in estrus.

Key Words: beef cow, estrus synchronization, delayed insemination
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478 Effects of administration of prostaglandin F2α 7 days prior to initiation of the 7-day CO-Synch + Cidr protocol in beef heifers on estrus response and pregnancy rates.

N. Oosthuizen*[1], L. B. Canal[1], P. L. P. Fontes[1], C. D. Sanford[1], N. DiLorenzo[1], C. R. Dahlen[2], G. E. Seidel[3], and G. C. Lamb[4], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*Department of Animal Sciences, North Dakota State University, Fargo,* [3]*Animal Reproduction and Biotechnology Laboratory, Colorado State University, Fort Collins,* [4]*Department of Animal Science, Texas A&M University, College Station.*

To determine the effects of administration of $PGF_{2\alpha}$ (25 mg of dinoprost tromethamine/mL, Lutalyse; Zoetis Animal Health) 7 days prior to the initiation of the 7-day CO-Synch + CIDR fixed-time AI (TAI) protocol, 985 *Bos taurus* beef heifers were enrolled at 9 locations from April 1 to July 15. Within location, all heifers were randomly assigned to one of two treatments: 1) CONTROL (n = 496); 100 µg injection of GnRH (Factrel; gonadorelin hydrochloride; Zoetis Animal Health) and a controlled internal drug releasing (EAZI-BREED CIDR; 1.38 g of progesterone; Zoetis Animal Health) insert for 7 d [d -7], administration of 25 mg of $PGF_{2\alpha}$ (Lutalyse, dinoprost tromethamine; Zoetis Animal Health) at CIDR removal [d 0], followed by a second injection of GnRH and fixed-time AI (TAI) 54 ± 2 h later; or 2) PRESYNCH (n = 489); same as CONTROL but heifers received an additional injection of 25 mg of $PGF_{2\alpha}$ 7 d prior [d -14] to CIDR insertion. Estrotect (Rockway Inc., Spring Valley, WI) estrus detection patches were applied to all heifers on d -14 and were evaluated for estrual activity on d -7. Similarly, estrus alert patches were placed on all heifers on d 0 and evaluated for estrual activity at the time of TAI. Pregnancy was diagnosed via transrectal ultrasonography between 35 and 55 d after TAI to determine the presence of a viable embryo, thereby assessing AI pregnancy rates The percentage of heifers exhibiting estrus between d -14 and d -7 was greater ($P < 0.001$) for the PRESYNCH (70.3%) than the CONTROL (40.0%) treatment, whereas the percentage of heifers exhibiting estrus between d 0 and TAI was significantly ($P < 0.001$) greater for the CONTROL (57.9%) than the PRESYNCH (41.4%) treatment. Estrus response rates differed ($P < 0.001$) among locations. Pregnancy rates to TAI differed ($P = 0.023$) among locations, however, did not differ ($P =0.739$) between CONTROL and PRESYNCH treatments (46.7 vs 45.5%, respectively). Final breeding season pregnancy rates did not differ ($P = 0.811$) between treatments. Therefore, an injection of $PGF_{2\alpha}$ 7 days prior to initiation of the 7-day CO-Synch + CIDR protocol failed to improve pregnancy rates to TAI in replacement beef heifers.

KeyWords: pre-synchronization, prostaglandin F2α, beef heifers
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479 LH Concentration after kisspeptin injection for sexual precocity evaluation in heifers.

G. P. Nogueira*[1], A. F. T. Paiva[2], M. A. Maioli[3], D. M. Pinheiro[3], and T. Arrieiro Rodrigues[4], *[1]FMVA/São Paulo State University, Aracatuba-SP, Brazil, [2]FMVA-UNESP, Araçatuba, Brazil, [3]Unesp, Araçatuba, Brazil, [4]Fazenda Santa Encarnacao, Bataguacu-MS, Brazil.*

In order to research precocious sexual hypothalamic maturation, luteinizing hormone (LH) concentration in response kisspeptin injection in heifers was evaluated monthly, from weaning until the breeding season. The tested hypotheses were that LH secretion in response to kisspeptin increases with age and that at the same age, heifers heavier at weaning secrete more LH, in response to kisspeptin, than lighter weaned ones. The experiment was carried out in a commercial farm, from 184 weaned heifers the 25 heavier and 25 lighter were segregated as groups, but kept in the same pasture. The heifers were challenged monthly with 10 µg/kg (IM) of recombinant bovine kisspeptin (American Peptides) from weaning (8 mo) until 17 months; 20 min after the injection blood sample was collected. At 17 months the heifers were exposed to bulls (25:1) for 60 days, the pregnancy was evaluated 30 d later. Progesterone and LH quantifications were performed by RIA and IGF-I by Elisa. The pregnancy rate of the heavier heifers was 92% (23/25) while in the lighter group it was 62.5% (15/24), gestational time did not differ between groups (88±6 in heavier and 73±8 days in the lighter group). There were no differences on the LH (3.6±0.4; 3.3±0.2ng/mL), IGF-I (460.6±37.6; 450.2±32.2ng/mL) and progesterone (1.4±0.32; 2.3±0.8ng/mL) concentration between lighter and heavier heifers. The same was observed between heifers that became pregnant or not, for LH (3.4±0.1, 3.7±0.2 ng/mL), IGF-I (447.8±32.8, 478.4±42ng/mL) and progesterone (0.9±1.8; 1.04±1.8) concentration. Considering the last weight before the breeding season, pregnant heifers in the heavier group had greater weight than pregnant heifers in the lighter group (319±5; 272±4 kg), even in the lighter group pregnant heifers were heavier than non pregnant (272±4; 254±4 kg). It was concluded that LH concentration after kisspeptin injection was not useful to evaluate hypothalamus sexual maturation and to be used as a screening tool for sexual precocity in Nellore heifers. Acknowledgements: CAPES, UNESP, Fazenda Santa Encarnação- Bataguassu-MS, Brazil.

Key Words: Puberty, GPR54, Nellore heifers
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480 Follicle dynamics and fertility at fixed-time AI of *Bos indicus*-influenced beef cows synchronized with the 5-Day Bee Synch + Cidr protocol with or without GnRH on day 0.

J. O. Scarpa*[1,2], M. M. O'Neil[1,2], R. C. Cardoso[2], R. L. Stanko[1,3], and G. L. Williams[1,2], *[1]Texas A&M AgriLife Research, Beeville, [2]Department of Animal Science, Texas A&M University, College Station, [3]Department of Animal Rangeland and Wildlife Sciences, Texas A&M University-Kingsville, Kingsville.*

The 5-Day Bee Synch + CIDR (Bee Synch) protocol for Bos indicus-influenced cows utilizes a CIDR, GnRH (GnRH-1) and prostaglandin F2α (PGF) on d 0 to eliminate mature corpora lutea, with fixed-time AI (FTAI) and GnRH (GnRH-2) at 66 h after CIDR removal to yield pregnancy rates of ~ 50%. Objectives herein were to test the hypothesis GnRH-1 is not required to optimize follicle synchrony (Exp. 1) or FTAI pregnancy rates (Exp. 2). In Exp. 1, 71 cycling Brangus and Brahman x Hereford (F1) suckled cows were used in 2 replicates (35-36/replicate). Cows were stratified by BW, BCS, and d postpartum, and assigned randomly to a 2 x 3 factorial arrangement involving 2 truncated (no FTAI or GnRH-2) versions of Bee Synch (BS-I and II) begun at 3, 7 and 10 d postovulation (d 3, 7 and 10). Ovulation was pre-synchronized with PGF (Lutalyse; Zoetis). Cows in BS-I received 100 µg GnRH (Factrel; Zoetis) i.m., 25 mg PGF i.m., and a CIDR (Eazi-Breed CIDR; Zoetis) on d 3, 7 or 10 post-ovulation. Cows in BS-II did not receive GnRH-1. On d 5, CIDRs were removed and all cows received 50 mg PGF i.m. Estrus was detected with Estrotect patches (Rockway, Inc.). Daily ultrasonography confirmed ovulation. For Exp. 2, a group of 120 mature cows from spring and fall herds were assigned to full versions (FTAI + GnRH-2 at 66 h) of either BS-I or II in a switchback design over 4 yr. In Exp. 1, synchronized new follicular wave emergence (NFWE; d 1-4) was observed in 68.6 and 38.9% (BS-I vs BS-II; $P = 0.01$) of cows and increased to 93.3 and 72.2%, respectively, if d 0-4 was considered. Size of the large follicle at 66 h (13.5 ± 0.47 mm) did not differ by treatment or d postovulation. Interval from CIDR removal to ovulation was greater ($P = 0.02$) for BS-I (5.2 ± 0.2 d) than II (4.4 ± 0.2 d) and greater ($P < 0.0001$) for d 3 (6.35 ± 0.3 d) than 7 and 10 (4.31 ± 0.3 and 3.7 ± 0.3 d, respectively). A greater ($P = 0.06$) proportion (15.5%) of cows in BS-II ovulated by 72 h than in BS-I. GnRH-1 reduced variation in d to NFWE and incidence of early ovulations. However, pregnancy rates to FTAI (Exp. 2) did not differ (BS-I, 50.2 ± 3.3 and BS-II, 44.7 ± 4.8 %; $P = 0.22$).

Key Words: GnRH, Bee Synch, Bos indicus-influenced
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481 Examining uterine endometrial blood perfusion using a novel laser doppler technique in Angus cows.

M. P. T. Owen*, K. J. McCarty, K. C. Yankey, C. N. McGee, C. G. Hart, and C. O. Lemley, *Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

The objective was to determine endometrial blood perfusion and hormone enzyme activity contralateral and ipsilateral to both the corpus luteum (CL) and developing dominant follicle (DF). Fourteen Angus cows were subjected to an Ovsynch + CIDR estrous synchronization protocol with d 0 corresponding to day of estrus. Equine AI rods were passed through the cervices, which provided a canal for the laser Doppler probe (PeriFlux 5000 LDPM, Perimed Inc., Ardmore, PA) to collect endometrial blood perfusion and microvascular flow of tissue surfaces without traumatizing the endometrium. Optimal perfusion was obtained by selecting 10 s of relatively constant perfusion for measurement, as measured by arbitrary Perfusion Units (PU) following calibration. After perfusion was collected, cattle were subjected to an endometrial biopsy utilizing a mare uterine biopsy punch with a sample collected from each horn and snap frozen. Perfusion and uterine biopsies were collected on d 12, 15, 18, and 21 of the estrous cycle. Data were analyzed using repeated measures ANOVA of the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC), using the Wilcoxon rank sum test, and significance was declared at $P \leq 0.05$. The model statement included day of estrous cycle, CL and DF location (respective to each uterine horn), the respective interactions with day, and CL and DF size with their respective interactions with day as covariants. Cattle were subjected to ultrasonography on d 11 and 19 of the estrous cycle to determine CL and follicular locations and size. Uterine biopsies were homogenized and activity of uridine 5'-diphospho-glucuronosyltransferase (UGT) was determined via luminogenic substrates (expressed per mg of protein). No differences ($P \geq 0.15$) in endometrial perfusion were observed based on the location of the CL. However, endometrial perfusion was greater ($P < 0.01$) on the ipsilateral side to the DF. No differences ($P \geq 0.34$) in endometrial perfusion were observed within day. Finally, no differences ($P \geq 0.38$) were observed for UGT activity. In conclusion, endometrial perfusion relative to location of the DF were different whereas the CL location did not influence blood perfusion or UGT activity. This alteration in endometrial perfusion could be due to an increase in estrogen due to the presence of the DF.

Key Words: endometrial perfusion, dominant follicle, estrous cycle
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482 Age at puberty and pregnancy rate in beef heifer genotypes offered contrasting nutrition levels.

J. Heslin*[1,2], D. A. Kenny[3], A. K. Kelly[4], and M. McGee[5], [1]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland,* [2]*Animal and Bioscience Research Department, Teagasc Grange, Dunsany, Co. Meath, Ireland,* [3]*Teagasc Grange, Dunsany, Co. Meath, Ireland,* [4]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland,* [5]*Teagasc Grange, Dunsany Co. Meath, Ireland.*

The objective was to determine the effect of nutrition and genotype on reproductive performance in beef heifers. A total of 309 spring-born early- (EM) and late-maturing (LM) sired heifers born to dams of dairy (D) or beef (B) origin were used over two successive years. Mean initial age (SD) and BW (SD) were 259 (14.0) days and 256 kg (52.0) kg, respectively. Heifers were blocked according to breed-type, age and weight and from within block, randomly allocated to one of two nutrition treatments; grass silage *ad-libitum* and a barley-based concentrate offered at 1.5 kg/head daily [M] or *ad-libitum* [H] for 141 d (Year 1) or 150 d (Year 2). Heifers were housed in a slatted floor shed in pens of 5 prior to turn out to pasture in mid-April where they rotationally grazed *Lolium perenne* dominant swards. A 12-week breeding programme commenced in late April, in both years, using semen from a single sire. Blood was sampled twice weekly for progesterone analysis. Pregnancy confirmation was carried out 30-40 days post-breeding. Data were analysed using SAS software in accordance with the 2 x 2 x 2 factorial design. Continuous and proportional data were subjected to the MIXED and GLIMMIX procedures, respectively. There were no interactions ($P > 0.05$) between treatments. Compared to M heifers, H had higher ADG indoors (1.03 v. 0.51 kg, $P < 0.001$), were younger at puberty (424 v. 437 d, $P < 0.001$) and had a greater 6-week submission rate (91 v. 79%; $P < 0.01$). However, there was no difference ($P > 0.05$) in pregnancy rates between dietary groups after 6 (H=61%, M=56%) or 12 weeks (H=87%, M=91%) of breeding. Compared to D heifers, B had a lower ADG indoors (0.70 v. 0.84 kg, $P < 0.001$), were of similar age at puberty (429 v. 432 days, $P > 0.05$), tended to have a lower 6-week submission rate (82 v. 90%, $P = 0.08$), had lower 6-week (52 v. 65%, $P < 0.05$) and 12-week (83 v. 93%, $P < 0.01$) pregnancy rates. Compared to EM heifers, LM had similar ADG indoors (0.76 v. 0.78 kg, $P = 0.19$), were older at puberty (438 v. 423 days, $P < 0.001$), had similar 6-week submission rate (83 v. 88%, $P > 0.05$), but a lower 6-week (51 v. 66%, $P < 0.01$). However, there was no effect of breed type ($P > 0.05$) on 12-week, pregnancy rate. In conclusion, age at puberty was reduced by nutrition level and sire, but not dam breed, whereas pregnancy rate was increased by dam and sire breed but not nutrition.

Key Words: Replacement beef heifer, Puberty, Pregnancy
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483 Vasoconstrictive responses of the carotid artery in pregnant ewes to ergot alkaloid exposure.

G. E. Aiken*[1], A. John[2], J. L. Britt[2], M. F. Miller Jr.[2], S. K. Adams[2], and S. K. Duckett[2], [1]*USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY,* [2]*Clemson University, Clemson, SC.*

Color Doppler ultrasonography was used to assess ergot alkaloid-induced vasoconstriction in pregnant ewes (*Ovis aries*) that were fed diets with or without toxic endophyte-infected seed of tall fescue (*Lolium arundinaceum*). A fungal endophyte (*Epicloë coenophialia*)that infects most plants of the standard cultivar of tall fescue, 'Kentucky 31,' produces ergot alkaloids that can cause a persistent constriction of blood flow in grazing ruminants, which incapacitates the animal's ability to thermo-regulate core body temperature. Suffolk ewes were stratified by BCS for random assignment to four treatment groups (n = 15/treatment). Either endophyte-free (E-) or endophyte-infected (E+) tall fescue seed were fed in similar diet concentrations such that the daily consumption of ergovaline and ergovalanine for E+ was 1,772 µg/ewe/d mixed in a TMR (corn, soybean meal, and cottonseed hulls). The ewes were fed the TMR without seed for the first 35 d. On day 35, ewes were fed endophyte-free (E-) or endophyte-infected (E+) seed, and on day 86, half of each group was switched to the opposite treatment (E-E+ or E+E-) and half remained on the same treatment (E-E- or E+E+) to parturition. Ultrasound imaging of left carotid artery was done at the start of lambing and the range in days on fed seed ranged from 50 to 106 days. Color Doppler ultrasonography was performed using a Classic Medical TeraVet 3000 Ultrasound Unit (Classic Universal Ultrasound, Tequesta, FL) with a 12L5-VET (12 MHz) linear array transducer. Cross-sectional area of the left carotid artery was measured for each ewe to determine luminal area, and a Power Doppler image was collected for measuring peak systolic and end diastolic velocities, heart rate, and pulsatility and resistance indices. Luminal areas were similar ($P > 0.5$) between E-E- (28.8 ± 1.98 mm^2) and E+E- (30 ± 1/85 mm^2) treatments, and between E+E+ (17.0 ± 2.06 mm^2) and E-E+ (17.5 ± 2.06 mm^2). Carotid arteries with E-E- and E+E- treatments were relaxed ($P < 0.001$) in comparison to those with the E+E+ and E-E+ treatments. Although there were no treatment effects ($P > 0.10$) on peak systolic and end diastolic velocities or heart rate, pulsatility and resistance indices were greater ($P < 0.05$) for E+E+ and E-E+ than for E-E- and E+E- treatments. Results indicated a vasoconstrictive response of the carotid arteries in pregnant ewes exposed to ergot alkaloids, but vascular recovery was demonstrated for sheep that had been switched from E+ to E- diets.

Key Words: Sheep, Tall fescue, Ergot alkaloids
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484 Effects of ergot alkaloid exposure during gestation on maternal and fetal vasoactivity in sheep.

J. L. Klotz*[1], M. F. Miller Jr.[2], J. L. Britt[2], M. A. Snider[3], G. E. Aiken[1], N. M. Long[2], S. L. Pratt[2], A. John[2], and S. K. Duckett[2], [1]*USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY,* [2]*Clemson University, Clemson, SC,* [3]*University of Kentucky, Lexington.*

Previous research has shown that exposure to ergot alkaloids found in endophyte-infected (*Epichloë coenophiala*) tall fescue (*Lolium arundinaceum*) results in decreased vasoactivity. Little is known regarding the effect ergot alkaloid exposure during gestation may have on vasculature supporting the fetus. The objective of this study was to evaluate contractile responses of uterine and umbilical arteries collected from ewes consuming ergot alkaloids during gestation. On d 35 of gestation, 36 Suffolk ewes (78.24 ±9.5 kg) were randomly assigned to endophyte-infected (E+) or endophyte-free (E-) tall fescue seed treatments that were fed either throughout or switched on d 86 of gestation, creating four seed treatments E+E+, E+E-, E-E+, E-E-. Ewes were fed E+ tall fescue seed to provide 1.77 mg of total ergovaline/head/d with E- ewes receiving the same quantity of E- seed. Gestation was terminated on d 133, and sections of uterine artery and umbilical cord were surgically collected. Only collections from 28 ewes (n = 7/treatment) were of sufficient viability to proceed with the contractility experiments. Arteries were cleaned, sliced into 2-mm cross sections, and suspended in multi-myograph chambers containing 5 mL of continuously oxygenated Krebs-Henseleit buffer. Vessels were exposed to increasing concentrations ($5\text{x}10^{-8}$ to $1\text{x}10^{-4}$ M) of norepinephrine, serotonin, ergotamine, and ergovaline ($5\text{x}10^{-9}$ to $1\text{x}10^{-5}$ M; extract of tall fescue seed) in 15-min intervals. Data were normalized as a percentage of the maximum contractile response induced by a reference dose of 120 mM KCl. Data from each artery were analyzed using mixed models of SAS as a split-plot with seed and myograph treatments as the whole and sub-plot treatments, respectively. Increasing concentrations of norepinephrine generated a moderate contractile response by the uterine artery ($P < 0.05$), but no response in the umbilical artery. Increasing concentrations of serotonin resulted in negligible responses in uterine preparations, whereas umbilical artery preparations were very responsive ($P < 0.05$) to serotonin. Ewes receiving E+E+ and E-E+ treatments had decreased vasoactivity in umbilical arteries to serotonin with a dextral shift in concentrations where the response curve initiated ($P < 0.05$). Interestingly, uterine arteries were not responsive to exposure to ergotamine or ergovaline, whereas umbilical arteries were very responsive.

Umbilical arteries collected from ewes receiving E-E- and E+E- were more vasoactive to ergot alkaloids ($P < 0.05$) than other treatments. These findings indicate that maternal blood supply to the placenta is protected from negative effects of ergot alkaloids; however, umbilical vasculature is not and this could negatively affect fetal growth.

Key Words: gestation, ergot alkaloids, vasoconstriction
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485 Impacts of estrus expression and intensity during a fixed-time AI protocol on parameters associated with fertility and pregnancy success in beef cows.

R. F. Cooke*[1], A. D. P. Rodrigues[2], R. S. Cipriano[3], L. G. T. da Silva[2], R. L. A. Cerri[4], L. H. Cruppe[5], M. Meneghetti[6], K. G. Pohler[7], and J. L. M. Vasconcelos[2], [1]*Oregon State University - EOARC Burns, Burns,* [2]*UNESP - FMVZ, Botucatu, Brazil,* [3]*UniSalesiano, Araçatuba, Brazil,* [4]*Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada,* [5]*Select Sires Inc, Plain City, OH,* [6]*Zoetis, Sao Paulo, Brazil,* [7]*The University of Tennessee, Knoxville.*

*In this experiment (d 0 to 41), 2*90 lactating, primiparous and multiparous non-pregnant Brangus cows received a 2 mg injection of estradiol benzoate and an intravaginal progesterone (**P4**) releasing device (**CIDR**) on d 0, a 12.5 mg injection of $PGF_{2\alpha}$ on d 7, CIDR removal in addition to 0.6 mg injection of estradiol cypionate and 300 IU injection of eCG on d 9, and fixed-time AI on d 11. All cows were inseminated by the same technician with semen from a single bull. On d 7, cows were fitted with a pedometer behind their left shoulder. On d 9, an estrus detection patch was attached to the tailhed of each cow. On d 11, estrus was defined as removal of >50% of the rub-off coating from the patch. Cow activity (total steps) was calculated by subtracting d 7 to 9 results (basal activity) from d 9 to 11 results (expected estrus period). Cows were classified by estrus intensity according to physical activity as: NOESTRUS = cows that did not express estrus; or cows that expressed estrus with physical activity below (LOWESTRUS) or above (HIESTRUS) the population median. Ovarian transrectal ultrasonography was performed on d 11 and 18. Blood was collected concurrently with ultrasonography exams for plasma P4 analysis. Pregnancy status was verified by transrectal ultrasonography on d 41. Only data from cows that ovulated to the synchronization protocol and that were successfully classified according to estrus characteristics were utilized (NOESTRUS, n = 57; LOWESTRUS, n = 87; HIESTRUS, n = 90). Diameter of dominant follicle on d 11, CL volume on d 18, and plasma P4 concentrations on d 18 were greater ($P \leq 0.05$) in HIESTRUS vs. LOWESTRUS and NOESTRUS, and also greater ($P \leq 0.05$) for LOWESTRUS vs. NOESTRUS (14.1, 13.4, and 12.5 mm, SEM = 0.3; 5.5, 4.9, and 3.6 cm^3, SEM = 0.5; and 4.7, 4.0, and 3.0 ng/mL; SEM = 0.2). Plasma P4 on d 11 were greater ($P < 0.01$) in NOESTRUS vs. HIESTRUS and LOWESTRUS, and similar ($P = 0.36$) between HIESTRUS and LOWESTRUS (0.47, 0.30, and 0.25 ng/mL; SEM = 0.07). Pregnancy rates were less ($P \leq 0.04$) in NOESTRUS vs. HIESTRUS and LOWESTRUS, and similar ($P = 0.38$) between HIESTRUS and LOWESTRUS (42.0, 67.3 and 60.5, SEM = 7.1). Hence, estrus expression and intensity, estimated by physical activity after CIDR removal, impacted fertility parameters and pregnancy success in Brangus cows.

Key Words: pregnancy, beef cows, estrus
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486 Effects of late gestational forage system on fetal growth and neonatal calf blood chemistry.

A. M. Meyer*[1], N. B. Duncan[1], J. M. Larson[1], and B. L. Vander Ley[2], [1]*Division of Animal Sciences, University of Missouri, Columbia,* [2]*Great Plains Veterinary Educational Center, Clay Center, NE.*

We have previously reported that grazing stockpiled tall fescue (STF) during late gestation increases cow circulating metabolites and fetal growth compared with feeding poor quality tall fescue hay. Our current objective was to investigate the effects of late gestational forage system on calf size at birth and perinatal nutrient supply, assessed through neonatal blood chemistry. Multiparous spring-calving cows (n = 56; 638 ± 21 [SE] kg initial BW; 5.3 ± 0.1 initial BCS; 5.9 ± 0.4 yr of age; February 16, 2016 average calving date) were allocated by BW, BCS, age, and expected calving date to either strip-graze endophyte-infected STF (n = 4 pastures; 12.5% CP, 59.5% NDF; DM basis) or consume ad libitum endophyte-infected tall fescue hay (n = 4 uncovered drylots; 7.5% CP, 65.3% NDF; DM basis) for the last 75.0 ± 1.7 d of gestation. Cows remained on their respective treatments, but STF cows were moved to drylots on 13.5 ± 1.6 d pre-calving and fed tall fescue haylage (12.6% CP, 61.7% NDF; DM basis) to allow for calf sample collection. Jugular blood samples were obtained from calves at 0 (pre-suckling but after standing), 6, 12, 24, 48, and 72 h postnatally for blood chemistry analysis. Data were analyzed with forage system as a fixed effect and pen as experimental unit. Blood chemistry data were analyzed using a mixed model containing effects of forage system, hour, and their interaction; hour was a repeated effect. Calf birth weight, shoulder-to-rump length, heart girth, and abdominal girth were not affected by forage system ($P \geq 0.23$) in the current study. Calves born to cows grazing STF tended to have longer ($P = 0.09$) gestation length than hay (278.9 ± 0.9 vs. 276.2 ± 1.0 d). Calf serum urea nitrogen was affected by the forage system x hour interaction ($P = 0.009$). Serum urea nitrogen was greater ($P < 0.008$) in calves born to cows grazing STF at 0, 6, 12, and 24 h. Calves born to cows fed hay had greater ($P = 0.04$) serum Ca. Serum aspartate aminotransferase tended to be greater ($P = 0.06$) in calves born to cows grazing STF. No other blood chemistry measures were affected by forage system ($P > 0.10$). An effect of hour ($P < 0.001$) was observed for all serum measures except bicarbonate ($P = 0.26$). These data suggest that late gestational forage quality impacts gestation length and perinatal calf nitrogen supply.

Key Words: developmental programming, metabolism, beef cattle
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487 Effect of melatonin supplementation during mid- to late-gestation on maternal uterine blood flow and calf size at birth.

K. J. McCarty*[1], M. P. T. Owen[1], C. G. Hart[1], K. C. Yankey[1], R. C. Thompson[1], D. D. Burnett[1], E. H. King[2], R. M. Hopper[2], and C. O. Lemley[1], *[1]Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State, [2]Department of Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Mississippi State.*

Melatonin is a strong antioxidant and causes an increase in uteroplacental blood flow when supplemented during gestation. The objective of the current study was to examine the effects of supplemental melatonin on uterine blood flow from mid- to late- gestation in cattle. Commercial beef heifers (n = 32) and cows (n = 25) were artificially inseminated and assigned to one of two treatment groups supplemented with (MEL) or without (CON) melatonin delivered as two-24 mg implants or placebo at d 180, 210, and 240 of gestation. Uterine artery blood flow was determined using color Doppler ultrasonography. At birth, calf body weight, thoracic girth, abdominal girth, curved crown rump (CCR) length, and ponderal index (BW [kg]/CCR $[m]^3$) were determined. Total uterine artery blood flow (summation of left and right arteries) were analyzed using repeated measures of the MIXED procedure of SAS and the model statement included day, treatment, breed, fetal sex and the respective interaction. Calf morphometric measurements were analyzed using the MIXED procedure of SAS and the model statement included treatment, calf sex and the respective interaction with gestation length as a covariant. Heifers and cows were analyzed separately due to a difference in breed between the two groups. In heifers, a treatment by day interaction ($P = 0.01$) was observed for total uterine artery blood flow, whereby total uterine artery blood flow was increased in MEL vs. CON on d 240 of gestation. In cows, total uterine artery blood flow increased ($P < 0.05$) in MEL vs. CON. Gestation length was increased ($P < 0.05$) in MEL heifers gestating male calves vs. female calves, while CON heifers gestating male and female calves were intermediate. In cows, gestation length was not different ($P = 0.15$) between treatments. At birth, calf weight, thoracic girth, abdominal girth, CCR, and ponderal index were not different ($P > 0.05$) between treatments in heifers. In cows, calf weight, thoracic girth, and abdominal girth were not different ($P > 0.05$) between treatments. However, CCR was increased ($P = 0.03$) and ponderal index was decreased ($P = 0.01$) in calves born to MEL treated cows vs. CON. In summary, melatonin supplementation increased uterine blood flow in mid- to late-gestating cattle but this was not accompanied by an increase in calf birth weight. Additional studies regarding the physiological impact of these hemodynamic changes on nutrient transport and offspring development are warranted.

Key Words: Melatonin, Gestation, Uteroplacental Blood Flow
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PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT

488 Enteric methane production and ruminal fermentation from forage Brassica diets fed in continuous culture.

S. L. Dillard*, A. I. Roca-Fernandez, M. D. Rubano, K. R. Elkin, and K. J. Soder, *USDA-Agricultural Research Service, University Park, PA.*

Brassicas provide forage for livestock during the late fall when traditional perennial cool-season forages are not productive. However, little research exists on ruminal fermentation and CH_4 production of brassicas fed as forage. A continuous culture fermentor system was used to assess nutrient digestibility, VFA production and daily CH_4 production of brassicas. 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) 50% orchardgrass (*Dactylis glomerata* L.) + 50% canola (*Brassica napus* L.; CAN); 2) 50% orchardgrass + 50% rapeseed (*Brassica napus* L.; RAP); 3) 50% orchardgrass + 50% turnip (*Brassica rapa* L.; TUR); and 4) 50% orchardgrass + 50% annual ryegrass (*Lolium multiflorum* Lam.; ARG). Feedings (82 g DM/d) occurred 4 times throughout four 10-d periods at 730, 1030, 1400, and 1900 h. Methane samples were collected every 10 min using a photoacoustic gas monitor (LumaSense Technologies, Inc.; Santa Clara, CA) during the last 3 d of the experiment. Effluent samples were collected on d 8, 9, and 10, composited by fermentor within period, and analyzed for VFA and pH as well as DM, OM, CP, and fiber fractions for determination of nutrient digestibility. Data were analyzed using the GLIMMIX procedure of SAS (SAS, Inc.; Cary, NC). Apparent DM, OM, and NDF digestibilities and true DM and OM digestibilities were not different ($P > 0.28$) among treatments (45.1, 63.2, 44.1, 67.1, and 87.2%, respectively). Total VFA (87.2 mol/100 mol), pH (6.47) and acetate (44.6 mol/100 mol) were also not different ($P > 0.20$) among treatments. Propionate was greater ($P < 0.05$) in ARG than CAN and RAP (25.8 vs. 22.0 mol/100 mol). Butyrate was greater ($P < 0.04$) in RAP than ARG (16.8 vs. 11.4 mol/100 mol). Daily CH_4 production was greater (*P*

< 0.01) in ARG than all other treatments (68.9 vs. 11.2 mg/d). Methane, whether expressed as g per g of OM, NDF, digestible OM, or digestible NDF fed was greatest ($P < 0.01$) in ARG but similar ($P > 0.18$) among brassica treatments. Addition of brassicas provided similar nutrient digestibility to ARG while reducing daily CH_4 production, potentially making brassicas a more environmentally friendly alternative for ARG in pasture-based ruminant diets.

Key Words: Methane, Continuous Culture, Brassica
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489 Effects of the inclusion of linseed and increasing concentrations of glycerol as replacement of corn grain on rumen fermentation, methane production and nutrient disappearance in a rusitec system.

C. Gutierrez[1], N. Vera[1], R. Allende[1], P. Williams[2], and J. Avila-Stagno*[1], [1]*Faculty of Veterinary Science, Universidad de Concepción, Chillán, Chile,* [2]*Faculty of Agriculture, Universidad de Concepción, Chillán, Chile.*

The aim of the study was to assess the effects of using linseed and increasing concentrations of glycerol in a forage diet supplemented with corn grain on nutrient disappearance, methane (CH_4) production and fermentation parameters in a Rusitec fermentation system. The experimental diets were: control, (70% ryegrass/clover mixed hay, 30% corn grain); positive control (70% hay, 15% corn grain, 15% linseed); 5% glycerol (70% hay, 10% corn grain, 15% linseed, 5% glycerol); 10% glycerol (70% hay, 5% corn grain, 15% linseed, 10% glycerol). The experiment was a complete randomized design with the four dietary treatments with 2 replicates in an 8 fermenter Rusitec apparatus. Incubations were run twice during 15d. The first 10d were used for fermenter adaptation, followed by 5d of sampling (days 11 to 15). The individual fermenter was the experimental unit. The model included the fixed effects of diet, day and diet/day interactions with the day of sampling from each fermenter treated as a repeated measure. Total VFA concentrations in effluent were increased ($P = 0.005$) in the glycerol added diets as compared to positive control. Acetate concentrations were reduced with increasing glycerol concentration in diets whereas propionate increased with linseed inclusion. Increasing concentrations of glycerol resulted in further increased propionate concentrations ($P < 0.001$), thus leading to important reductions in the acetate/propionate ratio. However, CH_4 production (mgCH_4/g DM digested) was reduced by linseed inclusion in the diet ($P = 0.004$) but not by increasing concentrations of glycerol in the diet. Ammonia nitrogen was increased in all linseed supplemented diets ($P < 0.001$). Total DM and non-fibrous carbohydrates in vitro disappearance were not affected by dietary treatments ($P = 0.411$). However, CP and EE disappearance were increased in linseed supplemented diets ($P < 0.001$) but not further affected by glycerol inclusion. Disappearance of NDF was increased only in the positive control diet as compared to control diet ($P = 0.0185$). In conclusion, the use of linseed as replacement of corn grain reduces CH_4 production in a Rusitec system but increases ammonia nitrogen. Increased propionate concentrations in glycerol supplemented fermenters does not result in reduced CH_4 production despite increases in propionate concentrations. Linseed inclusion increases in vitro disappearance of CP and EE without affecting total DM disappearance.

Key Words: biofuel by products, in vitro techniques, oilseeds
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490 Estimating enteric methane emission from beef heifers with different residual feed intake using greenfeed and respiration chambers.

A. W. Alemu*[1], D. Vyas[1,2], G. Manafiazar[3], J. A. Basarab[4], and K. A. Beauchemin[1], [1]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Dept. of Animal Sciences, IFAS, University of Florida, Gainesville,* [3]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [4]*Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada.*

Greenhouse gas emission from the livestock sector is mainly contributed from enteric methane (CH_4) production. Improving feed efficiency to reduce CH_4 emission while maintaining productivity as well as accurate and robust measurement is of great environmental and economic importance. The objectives of this study were to: compare CH_4 emissions measured using respiration chambers (RC) and the GreenFeed (GF) emission monitoring system and evaluate the relationship between residual feed intake (RFI) and enteric CH_4 production. Sixteen crossbred replacement heifers (8 low-RFI, 8 high-RFI, 377 kg initial BW) were used to measure enteric CH_4 emission. Heifers were group-housed in a pen and fed barley silage ad libitum and their individual feed intakes were recorded by automated feeding bunks. Heifers also received pellets dispensed from the GF emission monitoring system, used to attract and keep the animals in the unit for emission measurement. Enteric CH_4 emission of individual animals was measured over two 25-d periods using RC (2 days/period) and GF systems (all days when not in chambers). Data were analyzed using the mixed procedure of SAS and differences are discussed at $P \leq 0.05$. Estimates of CH_4 (g/d) were greater for GF than RC ($P < 0.001$), but for CH_4 yield the systems only differed for the high-RFI cattle ($P = 0.01$). Average CH_4 emission was 202 and 222 g/d ($P = 0.02$) from the GF system, and 156 and 164 g/d ($P = 0.40$) in RC for the low- and high-RFI heifers, respectively. As expected, high-RFI heifers consumed 6.9% more feed ($P = 0.03$) compared to their more efficient counterparts (7.1 vs 6.6 kg DM/d). However, when adjusted for feed intake, CH_4 yield (g/kg DMI) was similar for high- and low-RFI

heifers (GF: 27.7 and 28.5, $P = 0.25$; RC: 26.5 and 26.5, $P = 0.99$). Intake declined for both groups when they were moved to the RC, and as such DMI was similar ($P = 0.29$) between groups when they were in the chambers. Our study found that the two measurement techniques differ in estimating CH_4 emission, partially due to differences in conditions (lower feed intakes of cattle while in chambers, fewer days measured in chambers) during measurement. Furthermore, high- and low-efficiency cattle produce similar CH_4 yield but different daily CH_4 emission. We conclude that, when intake of animals is known, the GF offers a robust and accurate means of estimating CH_4 emissions from animals under field conditions.

Key Words: Residual feed intake, GreenFeed, Respiration chamber
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491 Impact of sulfur level and source on manure and air emissions from swine diets.

S. L. Trabue*[1], and B. J. Kerr[2], [1]*USDA-Agricultural Research Service, Ames, IA,* [2]*USDA - ARS, Ames, IA.*

Sulfur is a key nutrient associated of H_2S emission and associated with both odor emissions and respiratory distress of animals. Due to potential increases in S levels in swine diets, two experiments were conducted to determine the effect of dietary S level and source on manure slurries chemical properties and gas emissions. Experiment 1 investigated the effects of increasing dietary S level while Exp. 2 evaluated the source of increased dietary S. In Exp. 1, 24 gilts averaging 152 kg BW were fed four different diets ranging between 1,800 and 6,000 mg/kg total S, as supplied by $CaSO_4$, with an ADFI of 3.034 kg/d over the 31 d trial. In Exp. 2, 24 gilts averaging 139 kg BW were fed a diet containing either 1,800 mg/kg total S or diets containing 3,500 mg S/kg diet as supplied by $CaSO_4$, distillers dried grains with solubles (DDGS), or feather meal (FM) with an ADFI of 2.705 kg/d over the 41 d trial. In each experiment, feces and urine were collected after each feeding and added to manure storage containers. At the end of each experiment, manure slurries were monitored for gas emissions and chemical properties. In Exp. 1, regression analysis was used to determine the effects of S in the diet. Sulfur lowered manure pH by 1.36 units, but increased S and sulfide levels in manure by 57% and 0.8%, respectively, for each g of S added to the diet. Sulfur increased emissions of H_2S by 8% and odor by 2% for each g of S increase in the diet. In Exp. 2, ANOVA indicated that S source had a significant effect on excretion of DM, C, N, S in manure. Animals fed FM and DDGS diets had significantly higher levels of VFAs, phenols, and sulfide in manure compared to animals fed CSBM diets. The S levels in the diets significantly increased odor emissions compared to CSBM diets. Animals fed FM and DDGS had a greater percentage of chemical odor associated with VOCs than CSBM diets, and animals fed FM diets had significantly higher levels of odor emissions. In conclusion, dietary S levels and the source of S have a dramatic impact on manure composition and gas emissions.

Key Words: Sulfur, Odor, Diet
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492 Water use intensity of Canadian beef production in 1981 as compared to 2011.

G. Legesse*[1], M. R. C. Cordeiro[2], K. H. Ominski[1], K. A. Beauchemin[2], R. Kröbel[2], E. J. McGeough[1], S. Pogue[2], and T. A. McAllister[2], [1]*Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

The amount of beef produced per animal in Canada has increased significantly from 1981 to 2011 as a result of changes in production efficiency and increases in carcass weight, leading to a decrease in greenhouse gas and ammonia emissions per kilogram beef. This study examined the impact of improvements in production efficiency on water use intensity during the same time frame. The study employed a cradle-to-farm gate life cycle analysis taking into account temporal and regional differences in cattle categories, water use for drinking and feed production, feeding systems, average daily gains, and carcass weight. Water use intensity was defined as the amount of water required to produce one unit of beef. Water use coefficients for each feed crop and pasture type were employed to estimate water consumption associated with feed production for beef cattle. Harvest and feeding losses were also included in the analysis. Estimates of drinking water consumed by a given class of cattle accounted for physiological status, body weight and dry matter intake as well as ambient temperature. Approximately 70% of the drinking water in both years was consumed by the breeding herd (cows, bulls, replacement heifers and calves). In both years, drinking water accounted for less than 1% of total water use when precipitation for feed crop and pasture production were included in the analysis. When precipitation (i.e., green water) was excluded from the analysis, drinking water accounted for up to a 25% of total water use for Canadian beef production. The estimated intensity of blue water use (surface and groundwater) per kilogram of beef at the farm gate was 467 L in 1981 and 395 L in 2011, representing a 15% decline. The observed reduction in water use intensity over the past 3 decades may be attributed to an increase in average daily gain and slaughter weight, improved reproductive efficiency and reduced time to slaughter. Given that feed production accounts for a significant portion of water used in beef production, further improvements can be achieved by increasing feeding efficiencies and reducing water use per unit feed crop and pasture production.

Key Words: beef, Canada, water use intensity
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493 Abstract withdrawn.

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494 Big data analysis of beef production and quality: An example with the Brazilian cattle industry.

V. Cardoso Ferreira*, J. R. R. Dórea, and G. J. M. Rosa, *University of Wisconsin-Madison, Madison.*

‘Big data’ represents the new era in data exploration and utilization in livestock systems. With recent developments in data recording technology and analytics tools, it is now possible to get important insight regarding management practices and environmental effects affecting livestock productivity and product quality on a much larger scale. Even though analyzing Big Data is challenging (as it requires cautious data curation, large computer memory, and specific data mining tools), it can be extremely valuable. In this analysis, data from Brazilian beef cattle was available from two sources: *JBS S.A.* (81,053 farms) and *DSM Produtos Nutricionais* (22,223 farms). After merging, the final dataset comprised information from 7,248 farms and 1,571,023 carcasses slaughtered in the years 2014-2016. Three outcome variables were analyzed: body weight at slaughter (BWS, kg), carcass fat index (FI, 1-5), and age at slaughter (AS, yr). Covariates included in all models were: AS (except when it was an outcome), season (dry or rainy in each year), animal category (steer, bull, cull bull, heifer and cow), frequent technical consulting (FTC, binary), regional sales team (RST, 17 levels), type of feedlot premix (no feedlot premix – NFP, finishing grazing cattle – FGC, feedlot without additives – FWA, and feedlot with additives – FA) and farm (random effect). After extensive data mining, mixed model analyses were performed for all outcomes. The use of FA premix decreased AS, and increased BWS and FI in comparison to NFP (0.55 yr, $P < 0.00$; -1.78 kg, $P < 0.00$; -0.13, $P < 0.00$), FGC (0.34 yr, $P < 0.00$; -3.58 kg, $P < 0.00$, -0.12, $P < 0.00$) and FWA (0.72 yr, $P = 0.04$; -21.09 kg, $P = 0.05$; -0.25, $P = 0.02$). Adopting FTC increased BWS (6.38 kg, $P < 0.01$) and FI (0.07, $P < 0.01$), and reduced AS (-0.13 yr, $P < 0.01$). Bulls presented greater BWS (26.51 kg, $P < 0.01$) and lower AS (-0.46 yr, $P < 0.01$), but presented lower FI (-0.51, $P < 0.00$) in comparison with steers. Differences in BWS were observed for different RST and seasons (most $P < 0.01$). Age at slaughter was reduced and BWS and FI increased for rainy seasons of 2014-2016 ($P < 0.01$). Combining FTC and FA was capable of increasing BWS in 27.4 kg and reducing AS in approximately 10 months in comparison with FWA and non-FTC, suggesting that this approach might be favorable for production. Results presented here provided a wide snapshot of beef production in Brazil under a Big Data perspective never explored before. They provide also useful insight to validate experimental findings and aid decision-making at the farm level.

Key Words: beef cattle, big data, feedlot
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495 Conversion of high-frequency partial body weights to total body weight in feedlot cattle.

D. Benfield*[1], K. Garossino[1], R. D. Sainz[2], M. S. Kerley[3], and C. Huisma[1], [1]*GrowSafe Systems Ltd, Airdrie, AB, Canada,* [2]*University of California, Davis,* [3]*University of Missouri, Columbia.*

Recent technological advances have enabled development of automated data collection systems, e.g., for BW, feed intake, and other performance measures. This study evaluated the use of partial BW data for BW estimation in feedlot cattle. Partial BW (pBW) were collected using the GrowSafe Beef system, consisting of an platform that measures the force applied by the front two hooves while animals are drinking. The animals in this study visited the drinking trough on average 9.2 ± 6.4 times per day with an average visit duration of 69.4 ± 40.2 s. First, variation inherent to traditional chute weighing procedures were assessed by comparing 3,610 consecutive-day chute BW for 1,763 feedlot cattle ranging from 177 to 748 kg (mean 409 ± 98 kg). The mean difference between consecutive-day BW was 0.1 ± 8.8 kg, setting a lower limit to the precision of any estimation procedure. The next step was to compare single-day chute BW and pBW (averaged for the same day). Body weight and pBW data were collected from 7,035 measurements of feedlot cattle (4,130 from bulls, 969 from steers, and 1,936 from heifers) of different origins and biological types (2,316 British breed, 4,387 Continental, 332 Wagyu cross). Three models were used to estimate BW from pBW: (1) slope only, (2) slope + intercept, (3) slope + intercept by sex, (4) slope + intercept by type, and (5) a full model including slope + intercept by sex and type, and all interactions. Results indicate that although inclusion of information in addition to pBW (i.e., sex, breed type, origin) were statistically significant ($P < 0.001$), improvements in precision were not of practical significance (less than 2.3 kg improvement, far lower than the precision of chute BW measurements). Moreover, additional model terms resulted in increased mean bias and slope bias in the error term. Therefore, BW may be

Table 495.

Model	Mean bias	Slope bias	Random error	MSEP[a]	RMSEP[b]	R^2
1	0.1041	2.717	351.0	353.9	18.81	96.4%
	0.029%	*0.77%*	*99.20%*			
2	0.00369	0.00636	351.0	351.0	18.74	96.4%
	0.001%	*0.002%*	*99.20%*			
3	9.755	4.189	320.6	334.5	18.29	96.7%
	2.76%	*1.184%*	*90.60%*			
4	11.35	3.976	306.0	321.3	17.92	96.9%
	3.21%	*1.124%*	*86.46%*			
5	11.37	3.978	257.9	273.3	16.53	97.4%
	3.21%	*1.12%*	*72.90%*			

[a]MSEP, mean square error of prediction; [b]RMSEP, root mean square error of prediction.

estimated as 1.677 x pBW across sexes and breed types with adequate accuracy and precision.

Key Words: body weight, feedlot cattle, data collection
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496 The influence of cow temperament on temperament and performance of offspring.

R. C. Vann*[1], B. P. Littlejohn[2], D. G. Riley[3], T. H. Welsh, Jr.[4], R. D. Randel[5], and S. T. Willard[6], *[1]MAFES - Brown Loam Experiment Station, Mississippi State University, Raymond, [2]Texas A&M University Department of Animal Science, College Station, [3]Texas A&M University, College Station, [4]Texas A&M AgriLife Research and Department of Animal Science, College Station, [5]Texas A&M AgriLife Research, Overton, [6]Department Animal & Dairy Science, Mississippi State University, Starkville.*

The objective was to assess the relationship of cow temperament with calf (n = 3,690) temperament, BW, and ADG at weaning. This study population consisted of predominantly British crossbred cattle. Temperament was assessed by: 1) pen score (PS) the reaction of each calf to an evaluator on a scale of 1 = calm to 5 = excitable; 2) exit velocity (EV) the rate (m/sec) at which a calf exits a cattle chute; and 3) temperament score (TS) the mean of PS and EV. Data were analyzed by mixed linear models. Additive genetic variance was a random effect, and maternal additive genetic variance was 0 for temperament traits. Covariates included d of age at time of record except for ADG and the proportion of *Bos indicus* in each calf. Estimates of heritability were obtained in univariate analyses. Cow age and contemporary group (year-season combinations) had effects on all calf traits ($P < 0.001$). There was a positive relationship ($P < 0.05$) of proportion of *Bos indicus* in the calf with BW and ADG (regression coefficients: 23.99 ± 9.49; 0.08 ± 0.04, respectively). There was a positive relationship ($P < 0.05$) of the proportion of *Bos indicus* in the cow with BW and ADG (regression coefficients: 26.66 ± 6.92; 0.14 ± 0.03, respectively). There was a positive relationship ($P < 0.05$) for dam PS with calf PS, EV and TS (regression coefficients: 0.10 ± 0.05; 0.11 ± 0.05; 0.10 ± 0.04, respectively). There was a positive relationship ($P < 0.05$) for dam EV with calf PS and EV (regression coefficients: 0.06 ± 0.05; 0.07 ± 0.02, respectively). There was a positive relationship ($P < 0.05$) for dam TS with calf EV and TS (regression coefficients: 0.13 ± 0.06; 0.11 ± 0.05 respectively). At weaning, estimates of heritability were 0.42 ± 0.08 for PS; 0.46 ± 0.08 for EV; 0.58 ± 0.09 for TS; 0.52 ± 0.08 for BW; and 0.61 ± 0.09 for ADG. Estimates of maternal additive genetic heritability were 0.20 ± 0.05 for BW; and 0.24 ± 0.05 for ADG; and maternal permanent environmental/phenotypic variance were 0.13 ± 0.03 for BW; and 0.16 ± 0.03 for ADG. Calf temperament, BW, and ADG at weaning were associated with cow age, proportion of *Bos indicus* in the cow and the calf, and contemporary group, and importantly, with temperament of their dams.

Key Words: Temperament, Crossbred Beef Cattle, Heritability
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497 Effects of post-weaning plane of nutrition and estrus synchronization on reproductive performance of *Bos indicus*-influenced beef heifers.

P. Moriel[1], M. Piccolo*[1], P. A. Lancaster[2], G. C. Lamb[3], J. Vendramini[1], and J. D. Arthington[1], *[1]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [2]Missouri State University, Springfield, MO, [3]Department of Animal Science, Texas A&M University, College Station, TX.*

A 3-year study evaluated the effectiveness of estrus synchronization of beef heifers undergoing different post-weaning growth rates. On day 0 of each yr, Angus × Brahman heifers (60 heifers/year; 310 days of age) were stratified by initial BW and age, and randomly assigned, in a 3 × 2 factorial design, to achieve a low (LOW; 0.45 kg/d), medium (MED; 0.73 kg/d), or high (HIG; 1.00 kg/d) growth rate from d 0 to 168 (5 heifers/pasture; 4 pastures/diet/yr). Supplements were formulated to allow LOW, MED, and HIG heifers to achieve 55.0, 62.5, and 70.0%, respectively, of mature weight at initiation of breeding season (d 84). On d 65, all heifers within each pasture (2 pastures/diet) were enrolled (SYNC) or not (NOSYNC) in an estrus-synchronization protocol, which consisted of intravaginal controlled internal drug release (1.38 g P4) insertion on d 65 and removal on d 75, followed by 100-µg i.m. injection of GnRH on d 77, and 25-mg i.m. injection of $PGF_{2\alpha}$ on d 84. Heifers were stratified by diet (1 pasture/diet) and exposed to Angus × Brahman bulls from d 84 to 168 (1 yearling bull/pasture). Pasture was the experimental unit, whereas year, heifer (pasture), and pasture (diet × synchronization) were included as random effects in all analyses. Growth performance, and puberty and calving distribution were analyzed using MIXED and GLIMMIX procedures of SAS, respectively. Interactions among growth rate, estrus synchronization, and time were not detected for any variable ($P \geq 0.26$). Overall heifer ADG achieved only 51 to 56% of targeted ADG, and mature BW on d 84 did not differ between MED and HIG heifers (57.6 vs. 58.6 ± 2.40%; $P = 0.30$), but both were heavier than LOW heifers (53.7 ± 2.40%; $P < 0.0001$). Percentage of pubertal heifers on day 84 was greater for MED and HIG vs. LOW heifers (44.4 and 45.4 vs. 26.5 ± 6.77% $P \leq 0.05$), whereas estrus synchronization increased attainment of puberty on d 84 (23.5 vs. 48.7 ± 4.64% for NOSYNC and SYNC heifers; $P < 0.01$). Pregnancy and calving rates were not affected by diet or estrus synchronization ($P \geq 0.24$), however heifers calved 9 d earlier with the use of estrus synchronization ($P = 0.02$). Estrus synchronization resulted in earlier attainment of puberty and pregnancy in *Bos indicus*-influenced beef heifers; however, at the low rates of BW gain achieved in the current study, estrus synchronization did not impact overall reproductive success.

Key Words: Estrus synchronization, Puberty, Heifers
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498 Virginiamycin increases performance and carcass weight of feedlot cattle under Mexican conditions.

M. A. Gorocica*[1], and L. O. Tedeschi[2], [1]*Phibro Animal Health, Teaneck, NJ,* [2]*Texas A&M University, College Station.*

The objective of this analysis was to evaluate the growth performance and hot carcass weight (HCW) of bulls and heifers fed monensin (MN) alone (400 mg/hd/d) or in combination with virginiamycin (VM) (200 to 250 mg /hd/d) from five Mexican feedlots (trials). There were 224 pens representing 16,197 animals of which 5,072 were heifers (n = 66 pens) and 11,125 were bulls (n = 158 pens). Within each feedlot, animals were blocked by initial BW (< 230, 230 to 300, or > 300 kg) and sex (bulls or heifers), but diet composition and feeding strategies were different among trials. The statistical model for growth performance had block within trial, sex within trial, and trials as random effect variables, and treatments (MN or VM+MN) as a fixed effect variable. The number of pen animals was used as a weight variable. The ADG was adjusted to a common dressing percentage (DP) of 62.1% based on measured hot carcass weight. The initial BW was used as a covariate for the HCW analysis. Overall, animals were fed from 37 to 175 days, the initial and final BW varied from 234 to 351 and 294 to 572 kg, respectively, the ADG varied from 1.026 to 2.150 kg/d, and the DMI ranged from 5.46 to 11.53 kg/d. The MN+VM treatment increased the ADG ($P = 0.0002$) by 4% compared to MN treatment (1.544 x 1.484 kg/d, respectively). The DMI for the MN+VM treatment was not different ($P = 0.797$) from MN treatment (9.01 x 9.03 kg/d, respectively), but the feed conversion ratio (DMI ÷ ADG) was 3.9% less ($P = 0.0003$) for MN+VM than MN treatments (5.88 x 6.12, respectively). The DP was greater ($P = 0.0002$) for the MN+VM treatment than MN alone (60.86 x 60.46%, respectively). Similarly, the unadjusted HCW was also greater ($P = 0.0024$) for the MN+VM treatment than MN alone (306.7 x 302.4 kg, respectively), and the initial BW was a significant covariate ($P = 0.036$). In conclusion, animal performance (ADG, F:G) and HCW were improved when animals were supplemented with the combination of monensin (400 mg/an/d) and virginiamycin (200 to 250 mg/an/d) compared to when the animals were supplemented with monensin alone.

Key Words: Feedlot, Virginiamycin, Growth
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499 Effects of timing of vaccination relative to weaning and post-weaning supplementation frequency on growth and immunity of growing beef calves.

G. M. Silva*[1], P. Moriel[1], M. Piccolo[1], J. Ranches[1], and M. H. Poore[2], [1]*UF/IFAS Range Cattle Research and Education Center, Ona, FL,* [2]*North Carolina State University, Raleigh.*

A 2 × 2 factorial design study evaluated the impact of pre- vs. post-weaning vaccination associated with different post-weaning frequency of energy supplementation (daily vs. 3x weekly) on growth and immunity of beef calves. At 14 d before weaning, 48 Angus-crossbred calves (24 steers and 24 heifers; 244 ± 33 kg; 196 ± 20 d) were stratified by BW, age, and randomly assigned to receive vaccinations against bovine viral diarrhea virus (BVDV-1a) and parainfluenza-3 (PI-3) on d -14 and 0 (PRE) or 7 and 21 (POS), relative to weaning. Calves were weaned on d 0 and offered daily concentrate DM supplementation at 0.5% of BW for 7 d. On d 7, calves were stratified by vaccination scheme, and assigned into 1 of 16 drylot pens (3 calves of same sex/pen; 4 pens/treatment). Pens were randomly assigned to receive similar weekly concentrate DM supplementation (1% of BW multiplied by 7 d) that was divided and offered daily (7X) or 3 times weekly (3X; Mondays, Wednesdays, and Fridays) until d 43. From d 0 to 43, calves were provided ground tall fescue hay ad libitum (57% TDN, 13% CP of DM) and a concentrate mix of 50:50 soybean hulls and corn gluten feed (71% TDN, 15% CP of DM). Blood samples were collected from jugular vein on d 0, 1, 3, 7, and 14, relative to the respective first vaccination, and on d 43 of the study. Effects of sex and vaccination × supplementation frequency were not detected for any variable in this study ($P \geq 0.12$), except for overall ADG from d -14 to 43 ($P = 0.04$), which was less for PRE3X vs. PRE7X, POS3X, and POS7X calves (0.60, 0.70, 0.70, and 0.77 ± 0.04 kg/d, respectively; $P \leq 0.08$). Post-weaning total DMI and G:F did not differ among treatments ($P \geq 0.11$). Pre-weaning vaccination increased plasma concentrations of cortisol and haptoglobin from d 0 to 3, relative to first vaccination ($P < 0.0001$), and decreased serum PI-3 titers on d 42 compared to post-weaning vaccination ($P < 0.0001$). Decreasing the supplementation frequency tended ($P = 0.10$) to increase post-vaccination plasma cortisol concentrations and reduce overall serum BVDV-1a titers. Hence, pre-weaning vaccination associated with reduced post-weaning frequency of supplementation caused the least overall calf growth performance. Post-weaning vaccination and daily concentrate supplementation alleviated inflammatory response and improved humoral immune response compared to pre-weaning vaccination and reduced post-weaning supplementation frequency.

Key Words: timing of vaccination, Immune, supplementation frequency
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500 Appraisal of therapeutic efficacy of antibiotics and prostaglandin based protocol in Holstein cattle suffering from acute puerperal metritis (APM).

A. H. Shahzad*[1], and S. Abbas[2], [1]*Department of Clinical Sciences, College of Veterinary and Animal Sciences, Jhang, Pakistan,* [2]*College of Veterinary and Animal Sciences, Lahore, Pakistan.*

Acute puerperal metritis (APM) is defined as a condition with an abnormally enlarged uterus and fetid, watery, reddish-brown discharge, systemic illness and fever within three weeks of calving. It is one of the major problems faced by dairy enterprises. Incidence rate ranges from 20-40%. Objectives of this field study were to assess a treatment regimen in dairy cow affected with APM and subsequent reproductive performance. Totally 600 cows were routinely examined from day 2-15 postpartum. Thirty cows with APM were enrolled in treatment and 30 healthy in control group. Cows once diagnosed for APM were subjected to a treatment regimen consisted of Ceftiofur@ 2.2 mg/kg BW for 5 consecutive days intramuscularly from day 4-8 postpartum, intrauterine Cephapirin (500 mg) and prostaglandin I/M (25mg) on d-15 postpartum. Therapeutic cure of cows with APM was defined as the absence of fetid, watery, reddish brown abnormal uterine discharge examined on vaginoscopy, and disappearance of loss of appetite, depression, and normal body temperature on day 6 after first ceftiofur administration. Data were analyzed using the SPSS. Independent sample t-test for parametric assumptions and Mann–Whitney test for nonparametric data were used for comparisons between groups.Fisher's Exact and chi-square tests were performed to test the differences between groups of categorical data ($P < 0.05$). Continuous variables were indicated separately according to the groups as means ± SD. Vaginal discharge scores (VDS) for treatment (3.37 ± 0.49, 2.37 ± 0.93, 1.60 ± 1.07, 0.37 ± 0.67, 0.20 ± 20) and control groups (1.40 ± 1.13, 1.00 ± 1.0, 0.27 ± 0.64, 0.13 ± 0.43) cows at different visit days (from V1 to V5) were calculated. Cervical and Uterine sizes (cm) for treatment and control groups cows at different visit days. On visit V1 and V2 cervical diameter was 8.26 ± 1.20 and 6.43 ± 0.85 with corresponding control group having 4.87 ± 0.77. Uterine horn (UH) diameter was 13.42 ± 2.32 vs. 12.51 ± 1.03 in treatment and control group on V2 respectively. On Visit V5 uterine horn diameter was 5.76 ± 0.61 in treatment groups as compared to 2.88 ± 0.24 in positive control group. PMNs percentages on V2 were significantly higher in treatment group (48.17 ± 10.07) as compared to control group (31.73 ± 9.70). On V5 PMNs percentage was 4.10 ± 5.74 in treatment group which was comparable with control one (4.67 ± 6.17). First service conception rate was 40% and 43% in treatment and control group respectively. Pregnancy rate (87%) was comparable in treatment group with control one (90%) after overall inseminations. Results prove that systemic and intrauterine antibacterial therapy combined with prostaglandin has beneficial impact on reproductive performance in dairy cattle with APM.

Key Words: Acute puerperal metritis, Endometrial cytology, Antibiotics

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501 Pre-weaning injections of bovine somatotropin altered liver gene expression, and enhanced puberty attainment and calving rates of *Bos indicus*-influenced beef heifers.

M. Piccolo*[1], P. Moriel[1], G. M. Silva[1], R. F. Cooke[2], G. C. Lamb[3], J. Vendramini[1], and J. D. Arthington[1], [1]*UF/IFAS Range Cattle Research and Education Center, Ona, FL,* [2]*Oregon State University - EOARC Burns, Burns,* [3]*Department of Animal Science, Texas A&M University, College Station.*

A 3-yr study evaluated the effects of three 14-d apart injections of bovine somatotropin (bST) to suckling beef heifers on pre-weaning (yr 1, 2 and 3) and post-weaning growth and reproductive performance (yr 1 and 2 only). On d 0 of each yr, Angus × Brangus heifers (n = 15 heifers/treatment/yr; BW = 147 ± 20 kg; Age = 134 ± 11 d) were stratified by BW and age, and randomly assigned to receive s.c. injections of saline (SAL; 5 mL; 0.9% saline) or 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 (7-8 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 soybean hulls-based concentrate at 1.1% BW (DM basis). Liver samples were collected via needle biopsy on d 0, 42, and at start of breeding season (d 262) of yr 3 only (6 heifers/treatment). Blood samples were collected every 9 to 10 d from d 127 to 346. Heifers were considered pubertal when 2 consecutive plasma samples had P4 $\geq$ 1.5 ng/mL. Resulting interactions among treatment, yr, and day were not detected for any variable measured in the study ($P \geq 0.12$). During pre-weaning phase, bST heifers had greater ADG from d 0 to 42 (1.15 vs. 1.07 ± 0.026 kg/d; $P = 0.03$), but similar BW at weaning compared to SAL heifers (261 vs. 259 ± 1.3 kg, respectively; $P = 0.25$). Liver mRNA expression of GHR-1B and IGF-1 did not differ on d 0 and 42 ($P \geq 0.15$), but was greater for bST vs. SAL heifers on d 262 ($P \leq 0.02$). During post-weaning phase (d 127 to 347), bST heifers had similar ADG (0.17 vs. 0.12 ± 0.07 kg/d; $P = 0.11$), a greater ($P \leq 0.02$) percentage of heifers attaining puberty at initiation of the breeding season (53 vs. 27 ± 7.9%), pregnancy (93 vs. 70 ± 6.6%) and calving rates (90 vs. 53 ± 7.3%) compared to SAL heifers. Calving distribution did not differ between treatments ($P \geq 0.15$). Therefore, three 250 mg injections of bST administered at 14-d intervals, between 135 and 163 d of

age, enhanced reproductive performance of *Bos indicus*-influenced beef heifers.

Key Words: Somatotropin, heifers, puberty
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502 Dissipation of antimicrobials and resistance genes in compost originating from cattle manure after direct oral administration or post-excretion fortification of antimicrobials.

S. Xu*[1], I. D. Amarakoon[2], R. Zaheer[1], S. Sura[3], T. Reuter[4], F. Zvomuya[2], A. J. Cessna[5], F. J. Larney[1], and T. A. McAllister[1], [1]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Department of Soil Science, University of Manitoba, Winnipeg, MB, Canada,* [3]*Cumming School of Medicine, University of Calgary, Calgary, AB, Canada,* [4]*Alberta Agriculture and Forestry, Lethbridge, AB, Canada,* [5]*Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, Canada.*

Our study compared the dissipation of antimicrobials and resistance genes (ARG) during composting of cattle manure fortified with antimicrobials versus manure from cattle administered the same antimicrobials in feed. Manure was collected from cattle fed diets containing (kg^{-1} dry feed): (1) 44 mg chlortetracycline (CTC), (2) a mixture of 44 mg each of chlortetracycline and sulfamethazine (CTCSMZ), (3) 11 mg tylosin (TYL) or (4) Control, no antimicrobials. Fortified treatments were generated by adding antimicrobials to control manure. All manures were composted for 30 d with a single mixing after 16 d. Quantitative PCR (qPCR) measured the concentration of 16S rDNA and genes associated with tetracycline (*tet*), erythromycin (*erm*), and sulfamethazine (*sul*) resistance. Over 95% of antimicrobials dissipated over 30 d of composting, but CTC and SMZ remained higher in fed than fortified treatments, with a reverse trend observed for tylosin. Copy numbers of 16S rDNA decreased ($P < 0.05$) over 30 d, but were not altered by the presence of antimcrobials. Levels of all ARG except *tet*(L) decreased by 0.1-1.6 $\log_{10}$ copies g dry matter^{-1} in the first compost cycle, but some genes [*tet*(B), *tet*(L), *erm*(F), and *erm*(X)] increased ($P < 0.05$) by 1.0-3.1 $\log_{10}$ copies g dry matter^{-1} in the second. This pattern aligned with the positive correlation of these ARG with residue concentrations in the first cycle and the negative correlation in the second. During 30 d of composting, levels of *tet*(M) and *tet*(W) in CTC, *erm*(A), *erm*(B) and *erm*(X) in TYL, and *sul*(1) in CTCSMZ remained higher ($P < 0.05$) in fed than fortified treatments. Our results suggest that dissipation of ARG during composting of manure fortified with antimicrobials differs from manure generated by cattle that are administered antimicrobials in feed and does not always align with the dissipation of antimicrobial residues.

Key Words: Cattle feedlot, Antimicrobials, Composting
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503 Pen location affects thermoregulation and feed efficiency in swine during late summer.

K. R. Kpodo*[1], A. W. Duttlinger[1], and J. S. Johnson[2], [1]*Purdue University, West Lafayette, IN,* [2]*USDA-ARS Livestock Behavior Research Unit, West Lafayette, IN.*

The effects of pen location on swine thermoregulation and productivity were determined for 27 d during late summer. A total of 128 mixed sex pigs ($^1/_2$ Duroc x $^1/_4$ Landrace x $^1/_4$ Yorkshire) were randomly assigned to 16 pens in two grow-finish barns [n = 8 pens/barn; 57.4 ± 1.3 kg initial body weight (BW)]. Pen locations were pre-determined based on initial airflow (m/s) level [n = 4 high airflow (HAF) pens/barn and 4 low airflow (LAF) pens/barn]. High airflow and LAF pen locations were identical between each barn. Two sentinel gilts/pen were selected and vaginal temperature (T_V) was measured daily in 10 min intervals using thermochron temperature loggers. Additionally, whole body skin temperature (T_S) was measured with an infrared camera, and respiration rate (RR) was measured by counting flank movement of the sentinel gilts daily (0800h, 1500h). Pen airflow was measured daily (0800h, 1500h) with a vane anemometer. Ambient temperature (T_A) and relative humidity (RH) within each pen were recorded daily in 10 min intervals. Average daily gain (ADG) and average daily feed intake (ADFI) were determined bi-weekly. Data were analyzed using PROC MIXED in SAS 9.4. Although airflow was lower overall ($P = 0.04$; 11%) in LAF compared to HAF pens, no differences ($P > 0.56$) in T_A (27.63 ± 0.25°C; range 17.80-35.57°C) or RH (68.47 ± 0.46%; range 39.99-98.52%) were detected. An overall increase ($P < 0.03$) in T_V (0.23°C), minimum T_V (0.18°C), and maximum T_V (0.29°C) was detected in LAF versus HAF pens. Similarly, from 0800-1900h and 2000-0700h, T_V was greater overall ($P < 0.02$; 0.22 and 0.25°C, respectively) in LAF compared to HAF pens. A decrease in T_S ($P = 0.04$) was observed in LAF (37.39 ± 0.14°C) compared to HAF (37.61 ± 0.14°C) pens. No RR differences ($P > 0.60$; 76 ± 4 bpm) were detected with any comparison. While no ADG or ADFI differences were detected ($P > 0.16$; 0.75 ± 0.02 kg/d and 2.26 ± 0.07 kg/d, respectively), feed efficiency was decreased ($P = 0.04$; 6%) in LAF compared to HAF pens. No barn differences were detected with any comparison. In summary, pigs located in LAF pens had greater body temperature and reduced feed efficiency despite similarities in T_A and RH. These data have implications towards management of ventilations systems within swine facilities and the impact of pen-to-pen environmental variation on thermoregulation and productivity of pigs during hot summer months.

Key Words: pigs, pen location, airflow
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504 Supplementation with a blend of capsicum and artificial sweetener as a strategy to mitigate the negative heat stress effects on pig growth performance and intestinal physiology.

M. E. Biggs*[1], L. Zhao[1], Z. Zhang[1], E. H. Wall[2], D. M. Bravo[2], and R. P. Rhoads[1], [1]*Virginia Tech, Blacksburg,* [2]*Pancosma, Geneva, Switzerland.*

Pigs exposed to elevated ambient temperatures exhibit reduced average daily gain, alterations in muscle and fat deposition during growth phases, and decreased overall health. Negative aspects of gastrointestinal (GI) function, integrity and permeability also result from hyperthermia. Artificial sweeteners have the potential to ameliorate the negative effects of heat stress (HS) by increasing GI glucagon-like peptide (GLP)-2 production while capsicum oleoresin has been shown to reduce inflammatory response. Study objectives were to examine the effects of a blend of an artificial sweetener and capsicum oleoresin (CAPS-SUC) on growth performance of pigs. Forty-eight pigs (12 weeks of age, 47.3 kg ± 7.6kg) were assigned to six treatments: thermoneutral conditions (21°C) fed ad libitum with (TN+) or without supplement (TN-), heat stress (35°C) fed ad libitum with (HS+) or without supplement (HS-), and thermoneutral conditions pair-fed to HS intake with (PFTN+) or without supplement (PFTN-). Dietary supplementation began 2 days prior to the 3-day environmental treatment period. Body weight was recorded on day -1 and day 3 relative to start of environmental treatment. Body temperature (BT) and respiration rate (RR) were measured thrice daily and feed intake (FI) were recorded daily. Blood samples were collected on day -1 and day 3 to determine metabolite profiles and complete blood count. Following sacrifice, duodenum, ileum, and colon sections were collected for histology. Pigs in HS conditions exhibited increased BT and RR (~2.7-fold) compared to TN and PFTN groups ($P < 0.01$). Irrespective of day, HS+ animals had increased RR when compared to HS- animals ($P < 0.04$). Heat stress decreased FI compared to TN. Regardless of environmental treatment, supplement with CAPS-SUC increased feed efficiency by 0.12kg ($P < 0.04$); in addition, glucose concentrations in the circulation tended to decrease in CAPS-SUC vs. non-supplemented animals ($P = 0.1$). Insulin concentrations in the circulation increased in HS compared to PFTN ($P < 0.04$), but did not differ from TN so was likely linked to altered feed intake. Similarly, monocyte count increased during HS compared to PFTN ($P = 0.01$), but HS and TN did not differ. Lymphocyte count tended to be decreased in HS compared to PFTN and TN ($P = 0.052$). CAPS-SUC increased basophil count ($P < 0.03$), irrespective of environmental treatment. Ileal villus height tended to decrease during HS and PFTN compared to TN ($P < 0.08$), indicating an effect of intake. Duodenal and colon villus height and duodenal, ileal and colon crypt depth did not differ between groups. Overall, CAPS-SUC supplementation increases pig feed efficiency and may improve immune response.

Key Words: Pig, Heat Stress, Growth
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505 Developing heat stress thresholds for sheep.

A. M. Lees, M. L. Sullivan, A. J. Cawdell-Smith, and J. B. Gaughan*, *The University of Queensland, Gatton, Australia.*

Considerable improvements in management of livestock have come about via the development of species specific climate indices. The objective of the study was to define thermal thresholds for sheep. One hundred and forty-four Merino wethers (44.02 ± 0.32kg) were used in a replicated climate control chamber study. Each replicate (n = 2) was conducted over 29 d and consisted of 2 treatments: hot (HOT) and thermoneutral (TN). There were 6 sheep/pen and 3 pens/room. Individual respiration rate (RR) and panting score data were obtained for each animal at 3 h intervals between 0800 h and 1700 h daily for the duration of the study. Ten minute rumen temperature (T_{RUM}) data were obtained using rumen boluses. The development of temperature humidity index (THI) categories were undertaken by determining the THI values at which there were marked increases in RR and T_{RUM}. A backwards regression model (PROC REG, SAS Institute, Cary, NC) was used to determine the relationship between RR, T_{RUM}, ambient temperature and relative humidity. The validity of the thresholds were tested by comparing the RR and T_{RUM} means within each THI threshold category. If the differences between the mean values were different ($P < 0.05$), the thresholds were confirmed. Adjustments to the THI thresholds were then made until best fit was obtained. The statistical validity of the THI categories were then tested. The model included treatment, pen, observation time, day, THI category and the interaction of day × observation time as fixed effects, with animal included as a random effect. These thermal thresholds are an initial categorization of heat stress thresholds, further testing is required to validate their accuracy. Determining the

Table 505. Mean rumen temperature (T_{RUM}, °C) ± standard error (SE) and mean respiration rate (RR, breaths/min) ± standard error (SE) for sheep exposed to thermoneutral (TN) and hot conditions (HOT) under four temperature humidity (THI) heat load categories

Treatment	THI Category	THI Values	Descriptor	T_{RUM}[1]	RR[1]
TNC	1	≤ 24.3	No HL	$39.9^{a} \pm 0.02$	$50.5^{a} \pm 0.46$
HOT	1	≤ 24.3	No HL	$39.7^{a} \pm 0.08$	$93.3^{b} \pm 0.71$
HOT	2	>24.3 ≤ 28.6	Moderate	$40.3^{c} \pm 0.02$	$146.1^{c} \pm 0.63$
HOT	3	>28.6 ≤32.3	High	$40.4^{d} \pm 0.06$	$181.1^{d} \pm 0.79$
HOT	4	>32.3	Extreme	$40.7^{e} \pm 0.02$	$222.4^{e} \pm 5.90$

[1] Means within columns with different superscripts are significantly different ($P < 0.0001$)

thresholds based on climatic variables will provide a management tool to assess the impact of hot conditions on sheep.

Key Words: Heat balance, Heat stress, Temperature Humidity Index
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506 Evaluating the relationship between environment and body temperature of hair sheep ewes in the tropics.

R. W. Godfrey*, A. Nero, G. Roberts, and S. A. Lakos, *Agricultural Experiment Station, University of the Virgin Islands, St Croix, Virgin Islands (U.S.).*

The objective of this study was to evaluate the relationship between environment and body temperature in tropically adapted hair sheep ewes while grazing on pasture. Non-pregnant, non-lactating, multiparous St. Croix White (STX, 5.6 y of age, 43 kg, n = 5) and Dorper x St Croix White (DRPX, 3.8 y of age, 43 kg, n = 5) ewes were evaluated for 96 h d each mo for 1 yr. Temperature data loggers recorded vaginal temperature (VT) at 10-min intervals during each 96-h period. Ambient temperature (TEMP), relative humidity (RH), solar radiation (SOLAR) and THI were measured during the data collections using an onsite weather station (Davis Instruments, Oakland, CA). Data were analyzed using GLM procedures of SAS with breed, time of year and time of day in the model. Over the entire year mean TEMP, RH, THI, and SOLAR were 27.1 °C, 79.0%, 77.9, and 255 W/m^2, respectively. The DRPX ewes had a higher VT than STX ewes between 0900 and 1900 h and 2100 through 0300 h ($P < 0.0001$). There was no difference in VT during 0400 to 0800 h ($P > 0.10$). The minimum VT during the day was not different ($P > 0.10$) between DRPX and STX ewes (38.47 ± 0.07 vs. 38.42 ± 0.06 °C, respectively). The DRPX ewes had a greater maximum VT ($P < 0.0001$; 39.58 ± 0.02 vs. 39.37 ± 0.02 °C, respectively) and range of VT ($P < 0.06$; 1.12 ± 0.07 vs. 0.95 ± 0.06 °C, respectively) than STX ewes did. In STX ewes there was no difference in VT during the afternoon (1300 to 1900 h) during the evening (1900 to 2400 h; $P > 0.10$; 39.08 ± 0.01). In DRPX ewes VT during the afternoon was greater than VT during the evening ($P < 0.0001$; 39.29 ± 0.01 vs. 39.13 ± 0.01 °C, respectively). In DRPX and STX ewes VT was lowly correlated with TEMP measured at 1 h prior (r = 0.28 and r = 0.31, respectively; $P < 0.0001$). In DRPX and STX ewes VT was lowly correlated with SOLAR measured at 1 h prior (r = 0.13 and r = 0.07, respectively; $P < 0.0001$). The lower VT of STX ewes compared to that of DRPX ewes is likely due to their adaptation to the high heat and humidity found in the tropics.

Key Words: Hair sheep, Body temperature, Environment
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507 Milking efficiency in AMS using quarter level milking can be improved by applying a high take off level.

P. D. Krawczel[1], S. Ferneborg[2], R. Black[1], S. Agenäs[2], K. Svennersten-Sjaunja[2], and E. Ternman*[2], [1]*The University of Tennessee, Knoxville,* [2]*Swedish University of Agricultural Sciences, Uppsala, Sweden.*

At the udder level, increasing the milk flow rate at which milking is terminated, shortens milking time and increases milking efficiency in automatic milking systems (AMS). It is hypothesized that this can be improved upon by setting the milk flow rate at the udder quarter level, regardless of feed availability. The objective of this study was to investigate the effect of udder quarter level milk flow rates (0.06, 0.3, or 0.48 kg/min) applied with or without teaser feed on milking time, milk yield, SCC and the degree of udder emptying, of cows in a FeedFirst™ AMS system. Thirty cows were assigned to six groups, balanced by parity (2.9 ± 1.5), days in milk (142 ± 25 d), and production (34.0 ± 11.7 kg/d). All cows had SCC < 115.000 cells/ml when enrolled. Cows were exposed to treatments for 7d using a 3×2 factorial arrangement within a 6×6 Latin square. Data on milk yield, milking time and interval were automatically collected by the AMS. Milk samples for SCC were collected at the udder level during the last 2 d of each period. Udder-level residual milk yield was sampled on the last milking during periods 1, 3, and 5. For harvesting residual milk, cows received an intramuscular injection of oxytocin (70 I.U., Partoxin™ vet) and milking was initiated again 3 min after the injection using a bucket milking machine. The data were analyzed by ANOVA in a linear mixed-effects model using repeated measures in SAS (v9.4). Teaser feed was found non-significant for all response variables. Milking interval for the study was below 8 hours for all treatments and was not affected by take-off level or teaser feed ($P > 0.05$). Milking time was shortest for 0.48 (6.7 ± 0.5 min) and increased with lower take-off levels ($P < 0.05$): 7.2±0.5 min for 0.3 and 7.6 ± 0.5 min for 0.06. Milking time was not affected by teaser feed or the interaction of take-off level × feed. No treatment effect or interaction was evident for milk yield, residual milk yield, residual milk yield as % of total milk, or SCC ($P > 0.05$). In conclusion, milking efficiency in AMS can be improved by applying a take-off level of 0.48 kg/min on udder quarter level without losing milk yield or increase SCC. An effect of teaser feed on udder emptying could not be demonstrated in this study, indicating that teaser feed is less important when cows are directed through the feeding area before milking.

Key Words: Milking management, AMS, Dairy cow
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508 Trend for diurnal temperature variation and relative humidity and their impact on milk yield of dairy cattle in tropical climates.

T. Sae-tiao[1], S. Koonawootrittriron[1], T. Suwanasopee[1], and M. A. Elzo*[2], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

Climate change is expected to adversely affect the agricultural systems principally in dairy farming. Ambient temperature and relative humidity are the main climatic factors that exert influence on dairy production. The diurnal temperature variation in tropical regions (DTV; daily difference between maximum and minimum temperatures) should be considered in conjunction with the relative humidity (RH) due to their large daily variation. The objectives of this study were to characterize the effect of DTV and RH on milk yield of dairy cattle, and their trend in Thailand. The dataset consisted of monthly test-day milk yields (46,444 records) from 5,080 first-lactation cows from 456 farms in Thailand. The climate data consisted of DTV and RH (76,619 daily records) collected from 2002 to 2014 by 17 stations of the Thai Meteorological Department (TMD) located near the dairy farms in this study. The mixed linear model considered herd-year-season of calving (HYS), age at first calving (AFC), days in milk (DIM), days in milk squared (DIM^2), DTV and RH as fixed effects, and animal, permanent environment and residual as random effects. All factors (HYS, AFC, DIM, DIM^2, DTV and RH) had an effect on milk yield ($P < 0.01$). Milk yield increased as DTV increased ($b = 0.029 \pm 0.007$; $P < 0.01$), whereas milk yield decreased as RH increased ($b = - 0.011 \pm 0.002$; $P < 0.01$). The correlation between DTV and RH was high and negative ($r = -0.625$; $P < 0.01$). The yearly LSM ranged from 9.30 °C (2011) to 10.29 °C (2004) for DTV and from 72.57% (2004) to 75.23% (2011) for RH. However, the DTV ($b = -0.005 \pm 0.022$; $P > 0.05$) and the RH ($b = 0.076 \pm 0.056$; $P > 0.05$) trends from 2002 to 2014 were close to zero and not significant. These results confirmed the impact of climate effects (DTV and RH) on milk production of dairy cattle raised under tropical conditions, reiterating the need to account for these factors in both management and genetic selection programs.

Key Words: Dairy cattle, Environment, Tropics
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509 Environmental impact based on life cycle assessment of starting pig production receiving diets with reduced crude protein content.

A. N. T. R. Monteiro[1], M. R. Fachinello[1], L. M. Diaz-Huepa[1], A. V. S. Partyka[2], R. V. Nunes[3], and P. C. Pozza*[2], [1]*Universidade Estadual de Maringá/CAPES, Maringá, Brazil,* [2]*Universidade Estadual de Maringá/CNPq, Maringá, Brazil,* [3]*Universidade Estadual do Oeste do Paraná/CNPq, Marechal Cândido Rondon, Brazil.*

The objective was to evaluate, through life cycle assessment and with experimental data, the impact of producing starter pigs (from 15 to 30 kg) fed diets with different crude protein (CP) levels. In Trial I (performance), 28 crossbred barrow piglets, with an initial average weight of 15.3 ± 1.15 kg were divided up in a randomized block design with four treatments, seven replications and one animal per experimental unit. In Trial II (nitrogen and phosphorus balance), 20 crossbred barrow piglets with an average weight of 21.4 ± 1.62 kg were divided up in a randomized block design with four treatments, five replications and one animal per experimental unit. Four experimental feeds were evaluated in both essays (19.24, 18.24, 17.24 and 16.24% of CP), meeting the requirements of digestible amino acids through industrial amino acid (IAA) addition. From Trial I and II data, the environmental impact was calculated for global warming potential, acidification potential, eutrophication potential, cumulative energy demand, terrestrial ecotoxicity and land occupation (LO). There was a linear reduction in nitrogen ($P = 0.001$) and phosphorus ($P = 0.001$) intake, as well as nitrogen excretion ($P = 0.001$), with the reduction on dietary CP. Total nitrogen excretion decreased by 0.238 g/d for each 1 g of reduction on daily nitrogen intake, due to lower amino acid deamination and, as consequence, lower urea excretion. However, there was no statistical difference ($P > 0.10$) among experimental treatments for the impact categories. For LO, there was a tendency ($P = 0.078$) to reduce the impact with CP reduction, which was 8% lower in the diet with 16.24% of CP, in comparison with 19.24%. This was due to the lower soybean inclusion and higher maize inclusion in low CP diets, because the LO impact for soybean meal more than twice as high as for maize. Besides that, feed production was the main contributor to LO impact. Dietary CP reduction for piglets from 15 to 30 kg, through IAA supplementation, showed a tendency to reduce the environmental impact under LO in a Brazilian context of pig production.

Key Words: nitrogen, environment, carbon emission
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510 Impact of estrus synchronization and fixed-time artificial insemination on calving distribution in *Bos indicus* influenced beef heifers.

N. Oosthuizen*[1], P. L. P. Fontes[1], C. D. Sanford[1], F. M. Ciriaco[1], D. D. Henry[1], L. B. Canal[1], N. DiLorenzo[1], and G. C. Lamb[2], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*Department of Animal Science, Texas A&M University, College Station.*

To determine the effects of estrus synchronization (ES) and fixed-time artificial insemination (TAI) on calving distribution in *Bos indicus* influenced heifers, 751 *Bos taurus* × *Bos indicus* beef heifers were enrolled in a complete randomized design at 2 locations from January to May of 2016. Within location, all heifers were randomly assigned to one of two treatments: 1) SYNCH (n = 371); heifers were exposed to the 5-day CO-Synch + CIDR protocol where they received a 100-µg injection of GnRH (Factrel; gonadorelin hydrochloride; Zoetis Animal Health), 25 mg of $PGF_{2\alpha}$ (Lutalyse; dinoprost tromethamine; Zoetis Animal Health), and a controlled internal drug releasing (EAZI-BREED CIDR; 1.38 g of progesterone; Zoetis Animal Health) insert on d 0, heifers received 50 mg of $PGF_{2\alpha}$ (Lutalyse; dinoprost tromethamine; Zoetis Animal Health) at CIDR removal on d 5, followed by a 100-µg injection of GnRH and TAI 66 ± 2 h later on d 8; or 2) CONTROL (n = 380); heifers were exposed to natural service without any ES or TAI. On d 9, all heifers were exposed to bulls for the remainder of the breeding season at each location. Blood samples were collected on d -9 and on d 0 to determine pretreatment estrous cyclicity (progesterone $\geq$ 1.0 ng/mL). Pregnancy was diagnosed via transrectal ultrasonography 54 d after TAI by determining the presence of a viable fetus. Fetal age was estimated based on fetal size and structural features at the time of pregnancy diagnosis. Pregnancy rates on d 54 differed ($P < 0.001$) between locations, but did not differ ($P = 0.777$) between CONTROL and SYNCH treatments (64.5 vs 65.7%, respectively). Pregnancy rates were greater ($P < 0.001$) in cycling compared with non-cycling heifers (63.9 vs 42.4%). A greater ($P < 0.01$) proportion of SYNCH heifers became pregnant in the first 21 d of the breeding season compared with CONTROL heifers (52.2 vs 46.4%). Overall breeding season pregnancy rates did not differ ($P = 0.982$) between treatments. In summary, ES and TAI increased the percentage of heifers that conceived in the first 21 d of the breeding season, and therefore, potentially altered the calving distribution by ensuring that more heifers calve early during the subsequent calving season.

Key Words: beef heifers, *Bos indicus*, calving distribution
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511 Evaluation of phenotypic and marketing variables that affect the selling prices of Braford bulls using quantile regression.

J. F. Lopes[1], L. A. K. Aguiar[2], D. Paparas[3], I. P. Pereira[1], M. E. A. Canozzi[1], and J. O. Barcellos*[1,4], [1]*NESPRO/UFRGS - Department of Animal Science, Federal University of Rio Grande do Sul, Porto Alegre, Brazil,* [2]*Department of Food Science, Harper Adams University, Newport, United Kingdom,* [3]*Department of Land, Farm and Agribusiness Management, Harper Adams University, Newport, United Kingdom,* [4]*Federal Council of Veterinary Medicine (CFMV), Brasília, Brazil.*

The objective of this study was to evaluate the effects of phenotypic characteristics and marketing factors in prices of Braford bulls using Quantile Regression (RQ). Data about the commercialization process of 1,540 bulls, in thirteen auctions in Rio Grande do Sul State/Brazil, in 2013, 2014 and 2015 were collected. Age (months), scrotal circumference (SC; cm), live weight (kg), frame scores (1 to 3), muscularity (1 to 3), body condition score (BCS; 1 to 5), foreskin size (1 to 3), and presence of horns (yes or no) were the phenotypic characteristics evaluated. The marketing factors of interest were auction, year, sale order, and time of permanence in the ring (seconds). The RQ was used to identify the profiles of bulls on quantiles 10th, 25th, 50th, 75th, and 90th through EViews® software (version 9.5; Irvine, CA, USA). The price was negatively affected by age in all quantiles ($P < 0.01$), except for the 25th. In addition, the magnitude of age effect was greater in bulls in 75th and 90th. SC influenced the price positively from the 25th ($P < 0.01$). The heaviest bulls received higher prices ($P < 0.01$), independent of the quantile. Frame showed a negative impact of 5% in prices in 25th ($P < 0.05$) to each increase in the score unit. Alternatively, muscularity showed an increase of 6 to 7% in all quantiles ($P < 0.05$), except in the 90th. The BCS influenced the prices positively from 25th to 75th ($P < 0.05$); however, in the 50th the effect was 16.5% higher. Foreskin size showed an impact in the 75th ($P < 0.05$), with a reduction of 3.9% in the price to each increase in the score unit. Polled animals positively influenced the prices in all quantiles ($P < 0.05$). The majority of auctions influenced different quantiles. The year of 2014 influenced positively (25th to the 90th; $P < 0.05$), but 2015 negatively impacted the prices in all quantiles ($P < 0.05$). Sale order negatively impacted all quantiles ($P < 0.01$), with discount of 6% to 14% with the entrance of bull in the ring. The time of permanence in the ring negatively influenced prices in the 25th ($P < 0.05$), but influenced positively in the 90th ($P < 0.01$). We concluded that the variables and their impact on prices are different for each quantile, i.e. there are different profiles of bulls buyers.

Key Words: auction, bull marketing, bull price
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512 Preventive effect of nasal lavage with physiologic saline on the colonization with MRSA after working in porcine stable.

C. Heinemann*[1], R. M. Schmithausen[2], E. Sib[2], I. Meyer[1], B. Petersen[1], and J. Steinhoff-Wagner[1], [1]*University of Bonn, Institute of Animal Science, Bonn, Germany,* [2]*University of Bonn, University Hospital, Institute for Hygiene and Public Health, Bonn, Germany.*

Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) are common colonizers of the anterior nares of healthy pigs and pig-workers (farmers, veterinarians or researchers). This potential of zoonotic spread constitutes a serious health risk for both – humans and animals. Researchers working in pig stables were continuously monitored for their MRSA colonization and the probability to leave the stable after working 3 to 6 h with a positive finding were between 30 and 60%. The aim of the study was to identify easy-appreciable prevention procedures that might reduce the risk of MRSA transmission from pigs and stable environment to humans, who are working in pig stables only for a short-time period. A prestudy was performed, where surgical masks failed to have any protection effect on colonization with MRSA (n = 3) in pig herds with high occurrence of MRSA (> 80%). Nasal swab samples were taken from subjects (n = 40, researchers and students) who were working with pigs for 4 to 6 h and analyzed for MRSA by plating onto selective chromogenic MRSA agar, followed by inoculation on Columbia blood agar and processed through MALDI-TOF MicroFlex platform. Sampling was performed before (T0), directly after working with pigs (T1) and after nasal lavage with saline solution (100ml of 0.9% NaCl each side, T3). Occurrence of MRSA in the pig herd was determined by nasal swaps of indicator pigs (n >10/ herd), dust sampling from surfaces (n = 2/ herd) and in air samples (n = 1/ herd). Significant differences were determined with the Mann-Whitney U test using SAS. None of the subjects were colonized with MRSA before, but 22.5% directly after exposure to pigs and stable environment. MRSA colonization of the human subjects tended to be dependent on the proportion of positive MRSA findings in the pigs (*P* = 0.09), but up to now not related to air or dust (*P* > 0.3). None of the subjects were positive for MRSA after nasal lavage. Our results indicate that nasal lavage with physiologic saline solution can minimize the risk of MRSA colonization after working in porcine stable. The study is still ongoing to increase number of observations.

Key Words: preventive measures, one health, resistances

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513 Effect of the number of concentrate feeding places per pen for first two weeks after farm arrival on concentrate consumption and performance in milk-fed Holstein calves.

M. Verdu[1], A. Bach[2,3], and M. Devant*[4], [1]*bonÀrea Agrupa, Guissona, Lleida, Spain,* [2]*IRTA-Department of Ruminant Production, Caldes de Montbui; Balcelon, Spain,* [3]*ICREA, Barcelona, Spain,* [4]*IRTA - Department of Ruminant Production, Caldes De Montbui, Barcelona, Spain.*

Stressors like road transport and commingling cause a transitory anorexia during the first week at farm entrance in milk-fed calves. This circumstance has also negative effects on performance and health, as an inadequate feeding may compromise digestion and immune system. Increasing the number of concentrate feeding places (FP) per pen the first two weeks after arrival could enhance concentrate intake and calves' vitality. Three hundred and fifty Holstein male calves (59 ± 0.6 kg of BW and 30 ± 2.7 d of age), from 2 herds, were used in a randomized design to evaluate the effect of increasing FP on concentrate intake and performance in milk-fed calves throughout a 44-d study. Calves were allocated in 16 pens of 11 animals provided with concentrate and straw feeders, with 5 FP, and one water bowl. Pens were randomly assigned to 1 of the 2 treatments according to the number of FP per pen: 5 vs. 10 FP, where an additional feeder was placed the first two weeks after farm arrival in pens. All calves were fed a milk replacer (23% CP, 19% fat; DM basis) in 1.5 L water as follows: 360 g/d the week 1, 330 g/d during weeks 2 and 3, 300 g/d week 4, and 210 g/d during week 5. Concentrate (2.93 Mcal of ME/kg, 17% CP; DM basis), straw and water were offered ad libitum. Milk replacer intake and health status were recorded daily, and concentrate and straw intake, and BW weekly. Data were analyzed using a mixed-effects model with repeated measures. No effects of the number of FP per pen were observed in concentrate consumption, performance (Table 513), and health outcomes. The temporal increase of FP, the first two weeks after farm arrival, did not have a positive impact on consumption and performance. Thus, this strategy was not effective to facilitate feed access, stimulate the intake,

Table 513. Concentrate intake and performance of milk-fed calves allocated in pens with 5 or 10 FP (11 calves/pen) during the 44-d study

Item	FP 5	FP 10	SEM	*P*-value
Final BW, kg	94.0	94.9	3.95	0.37
Final age, d	74.1	74.9	2.79	0.48
Consumption, kg DM/d				
Milk replacer	0.28	0.28	0.021	0.85
Concentrate	1.68	1.70	0.095	0.63
Straw	0.12	0.13	0.019	0.13
Total	2.00	2.02	0.104	0.49
ADG, kg/d	0.79	0.79	0.032	0.85
Feed efficiency, kg/kg	0.42	0.42	0.022	0.96

and palliate the negative consequences of transitory anorexia after the transportation.

Key Words: milk-fed calves, feeding spaces, concentrate intake
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514 Tracking the movement of hair sheep grazing in pastures in the tropics.

R. W. Godfrey*, A. Nero, G. Roberts, and S. A. Lakos, *Agricultural Experiment Station, University of the Virgin Islands, St Croix, Virgin Islands (U.S.).*

The objective of this study was to monitor the location of tropically adapted hair sheep while grazing in a pasture. Non-pregnant, non-lactating, multiparous St. Croix White (STX, 5.6 y of age, 43 kg, n = 5) and Dorper x St Croix White (DRPX, 3.8 y of age, 43 kg, n = 5) ewes were equipped with global positioning system (GPS) tracking collars (Telemetry Solutions, CA) programed to record location at 10-min intervals for 5 consecutive d each mo for a yr to monitor their movement in a 0.6 ha pasture. A grid overlay of the pasture was developed using longitude and latitude coordinates from a handheld GPS unit (Montana 650t, Garmin Ltd, Olathe, KS) to divide the pasture into 16 sections. Several of the grids received shade from two trees during various times of the day. GPS data within each day was divided into time periods based on time of day (Nite-AM = 0000 to 0600 h, Day-AM 0605 to 1300 h, Day-PM 1305 to 1800 h and Nite-PM 1805 to 2355 h. The GPS coordinates for each ewe within each week of data collection were analyzed between breed and wk using PROC FREG and Chi-squared analysis of SAS to determine frequency of time spent in each pasture grid section. Over the entire year mean THI and solar radiation during the Nite-AM, Day-AM, Day-PM and Nite-PM were 74.8, 79.0, 79.6, 76.1 and 4, 526, 427, 1.8 W/m^2, respectively. During Nite-AM the majority of STX (67.0%) and DRPX (65.7%) ewes were distributed across 4 grids in the center of the pasture ($P < 0.0001$). In the Day-AM period the majority of STX (64.0%) and DRPX (54.5%) ewes were located in three grids to the west of the trees in the shade ($P < 0.002$). During the Day-PM the DRPX and STX ewes were uniformly distributed across the pasture with no concentration of ewes in any grid section ($P > 0.10$). During Nite-PM STX and DRPX ewes spent 50.6 and 53.1% of the time in two central grids, respectively ($P < 0.004$). Hair sheep spent significant time in certain areas of the pasture during the day, perhaps in order to utilize shade provide by trees.

Key Words: Hair sheep, Grazing, GPS
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515 Evaluation of the grazing behavior of hair sheep in the tropics.

R. W. Godfrey*, A. Nero, G. Roberts, and S. A. Lakos, *Agricultural Experiment Station, University of the Virgin Islands, St Croix, Virgin Islands (U.S.).*

The objective of this study was to evaluate the grazing behavior of tropically adapted hair sheep. Non-pregnant, non-lactating, multiparous St. Croix White (5.6 y of age, 43 kg, n = 10) and Dorper x St Croix White (3.8 y of age, 43 kg, n = 10) ewes were evaluated for 5 consecutive d each mo for a yr to monitor grazing behavior in a 0.6 ha pasture. At the start of each wk large numbers were painted on both sides of each ewe to aid in identification from a distance using a spotting scope. Three times each day (0830-0930 h, AM; 1200-1300 h, MID; 1500-1600 h, PM) visual observations were conducted by two observers to record location (sun or shade), activity (grazing, walking, resting, drinking or masticating), proximity to other ewes (within 1 m or >1 m) and posture (standing or laying) of the ewes. The frequency of observed behaviors within time of day, between breeds and across months was analyzed using PROC FREQ and Chi-squared of SAS. Over the entire year mean THI and solar radiation during the AM, MID and PM were 76.3, 80.5, 77.2 and 182, 714, 113 W/m^2, respectively. There were no differences in frequency of any behaviors between breeds or across months of observation ($P > 0.10$). In the AM ewes were observed laying down 86.8% of the time compared to 36.6% and 10.9% in the MID and PM, respectively ($P < 0.0001$). Ewe were within 1 m of another ewe 64.1 and 58.8% of the time in the MID and PM, respectively, and 41.2% of the time in the AM ($P < 0.0001$). Ewes were in the sun 89.5% of the time in the AM and 49.7 and 23.1% of the time in the MID and PM, respectively ($P < 0.0001$). Ewes were observed grazing 63.4 and 87.4% of the time in the MID and PM and 13.2% in the AM ($P < 0.0001$). Ewes were masticating 77.1% of the time in the AM and 36.2 and 11.7% of the time in the MID and PM, respectively ($P < 0.0001$). These results show that these breeds of sheep are adapted to the tropical climate and can graze during the time of day with elevated THI and solar radiation.

Key Words: hair sheep, Grazing, Behavior
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516 Additional excercise among grazing dairy cows and effects on uterine artery blood flow, milk production, and milk quality parameters.

J. E. Larson*, G. R. Dunnam, K. C. Yankey, M. P. T. Owen, M. M. Steichen, K. J. McCarty, A. E. Stone, and C. O. Lemley, *Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

It is expected that grazing animals take more steps per day than those housed in free stall, confinement barns. The aim of this study was to determine if additional exercise in grazing, lactating dairy cows affected milk production, milk quality, and uterine artery blood flow during late gestation. On d 180 of their gestation, 17 (all conceived on 1 of 2 dates within 2 wk and averaged 326 DIM) Holstein cows in a grazing production system were randomly assigned to 1 of 2 treatment groups: an exercise group (WALK; n = 9) which was walked an additional 5.6 km per d and a control group (CON; n = 8) which was not walked more than normal. Cows were fitted with pedometers to record steps; data were collected daily. All animals were housed together on ryegrass pasture with a concentrate supplement. All animals were milked twice daily until the dry off period (d 223 of gestation), milk yield was recorded at each milking, and milk samples (morning and afternoon) were collected on d 180 and 210 of gestation to evaluate milk composition. Ultrasound exams were conducted on d 180, 210, and 240 of gestation to measure heart rate and uterine artery blood flow. The MIXED procedure of SAS (SAS Institute Inc., Cary, NC) was used. Least-square means and pooled standard errors are reported. The number of steps taken were greater ($P \leq 0.0001$) between cows in the WALK group (7,212 ± 208 steps per d) compared to the CON group (5,637 ± 221 steps per d). The number of steps also differed ($P < 0.0001$) between d 210 and d 240 of gestation (7,317 ± 166 and 5,532 ± 166 steps per d, respectively). Treatment did not affect ($P > 0.05$) heart rate or total uterine artery blood flow. Heart rate was greater ($P < 0.0001$) in cows at d 210 of gestation (89.6 ± 1.61 beats per min) compared to d 240 (73.4 ± 1.61 beats per min), although total blood flow did not change ($P = 0.31$) between those time points in gestation. Milk yield as well as concentrations of fat, protein, and lactose were not different ($P > 0.05$) between treatments. Somatic cell counts and milk urea nitrogen did not differ ($P > 0.05$) between treatments. In conclusion, added exercise during late gestation did not impact cardiac or milk measurements in this study.

Key Words: dairy cow, grazing system, milk production
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517 Effect of herbage allowance on forage mass, insulin and IGF-1 concentrations during the gestation and lactation of primiparous beef cows grazing Campos.

M. Claramunt*[1], and P. Soca[2], [1]*Centro Universitario de la Región Este, Universidad de la República, Treinta y Tres, Uruguay,* [2]*Facultad de Agronomia. Universidad de la Republica, Paysandu, Uruguay.*

Our objective was to evaluate the effects of two herbage allowance (HA) on forage mass (FM), Insulin and IGF-1 concentrations of primiparous beef cows. Thirty two spring calving cows were allocated to a completely randomized block design of two blocks and two HA from -150 to 185 days postpartum (DPP). Treatments (ratio between FM and stocking rate) fluctuated throughout seasons: autumn 5 and 3, winter 3 and 3, spring and summer 4 and 2 kg forage DM/kg liveweight for high and low HA, respectively. Put-and-take was employed to adjust HA and FM was measured seasonally via the comparative yield method. Blood samples were collected –90 (autumn), -50, -20 (winter), 20, 50 (spring), 85, 185 DPP (summer). Forage mass, Insulin, IGF-I were analyzed using mixed models and means were compared using Tukey. High HA had greater FM than low ($P = 0.04$; Table 517) and was not affected by HAxDPP ($P = 0.35$). The FM decreased slightly in winter and then increased 3-fold in summer. Insulin was affected by DPP ($P < 0.001$; Table 517) but not by HA ($P = 0.31$) and HAxDPP ($P = 0.21$). Insulin decreased until 20 DPP, increased at 50 DPP and decreased again. Insulin increased 2-fold from 85 until 180 DPP. Seasonal changes in Insulin concentrations can be explained by forage intake associated to FM. The IGF-1 were greater in high than low HA at -90 but no other differences were identified (HAxDPP, $P < 0.007$; Table 517). The IGF-1 decreased from -90 to -20 DPP, then increased to 50 DPP and remained constant until 185 DPP. Forage mass differences between treatments at -90 DPP and the low cow energy requirements could explain the improvement in IGF-1 in high HA. Herbage allowance affected the energy metabolism of primiparous beef cows grazing Campos.

Key Words: grazing management, forage allowance, energy metabolism
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Table 517. Insulin, IGF-1 and FM for high and low HA. L.s.m. ± s.e. are presented

	Insulin µUI/ml			IGF-1 (ng/mL)			FM (kgDM/hectare)		
DPP	High	Low	s.e.	High	Low	s.e.	High	Low	s.e.
-90	15.8^{bc}	11.7^{bc}	1.4	132.6^{a}	89.3^{bd}	8.4	983^{b}	672^{bc}	106
-50	11.5^{cd}	11.5^{cd}	1.4	103.1^{b}	77.1^{bd}	8.4			
-20	13.2^{bc}	12.9^{bc}	1.4	70.5^{de}	52.5^{e}	8.4	613^{c}	464^{c}	106
20	8.5^{d}	7.9^{d}	1.4	57.5^{de}	59.3^{ce}	8.5			
50	16.5^{ab}	15.9^{ab}	1.5	99b^{c}	92.7^{ad}	8.7	962^{b}	796^{b}	106
85	8^{d}	8.8^{d}	1.4	97.2^{bc}	88.4^{bd}	8.1			
185	21^{a}	16.8^{a}	1.5	104.4^{b}	89.8^{bd}	8.8	2499^{a}	2088^{a}	106

$^{a, b, c, d, e}$ different superscripts differ at $P < 0.05$

518 Carcass evaluation of Nellore and Nellore x Angus females recreated in two production system with and without crop-livestock integration.

A. A. Gléria[1,2], L. F. Gonçalves[1], T. D. P. Paim[1], R. Z. Taveira[3], P. V. R. Paulino[4], F. L. Claudio[1], E. M. Alves[1], and R. M. D. Silva*[3,5,6,7], [1]*Goiano Federal Institute, Iporá, Goiás, Brazil,* [2]*Student in the Master in Sustainable Rural Development (MDRS), State University of Goiás (UEG), São Luis de Montes Belos, Goiás, Brazil,* [3]*State University of Goiás (UEG), São Luis de Montes Belos, Goiás, Brazil,* [4]*Nutron Alimentos Ltda, Campinas, Brazil,* [5]*Researcher Professor BIP/UEG, São Luis de Montes Belos, Goiás, Brazil,* [6]*DSc. Professor in the Master in Sustainable Rural Development (MDRS), State University of Goiás (UEG), São Luis de Montes Belos, Goiás, Brazil,* [7]*FAPEG, Goiânia, Goiás, Brazil.*

New technologies that aim to potentiate the productive capacity of the areas currently exploited have been introduced in Brazilian beef cattle. The cross between breeds and the use of integrated production systems are strategies with potential to increase production with an increase in the quality of the final product, the meat. The aim of this research was to evaluate the traits of carcass and meat of Nellore (N) and Nellore x Angus (F1) heifers, recreated in two forage production systems with and without crop-livestock integration (CLI). The experiment was carried out in an area of 9 ha, where were evaluated 36 calves, with initial age of approximately 7 months and live weight of 180 kg, being 18 Nellore and 18 Nellore x Angus, divided into high-investment treatments (HI), pasture of *Urochloa brizantha* cv. Paiaguás, reformed with the maize consortium, *Urochloa* and guandu (CLI), and low investment (LI), pasture of *Urochloa decumbens*. The animals were slaughtered at approximately 19 months. The data collected at slaughter were submitted to analysis of variance, considering the effect of genetic groups and treatments (different pastures), as well as the interaction between them. Correlation analysis was also performed to verify the relationship between meat and carcass variables measured. The F1 animals showed higher carcass weight, round thickness, carcass length and rib eye area (REA) than the Nellore animals. It was observed superiority for REA, fat thickness, marbling, carcass length and hot carcass weight. The interaction between genetic group and treatment was significative only for REA, being that the animals of the treatment HI differed from those LI treatments (72.94 vs 66.89 cm^2). The measure of carcass length and REA showed high and positive correlation with carcass weight, as expected. The shear force showed high and negative correlation with the coloration parameters (L, a, b). It was observed superiority of F1 animals considering the traits of carcass and meat quality. Can be perceived that the CLI system provided increase in the quantity and quality of the meat produced.

Key Words: Crossing, Genetic resources, Urochloa
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519 Effects of different pen lighting Sources on growth, feed efficiency and gene expression in blood and liver of broiler chickens.

L. K. Hirtz*[1], R. O. Rodrigues[1], T. Leiva[2], M. F. Martins[3], M. B. Leigh[1], J. F. Firman[1], L. G. Schumacher[1], and T. B. McFadden[1], [1]*University of Missouri, Columbia,* [2]*Sao Paulo State University, Botucatu, Brazil,* [3]*University of Sao Paulo, Pirassununga, Brazil.*

Several reports suggest use of light-emitting diode (LED) lights of various colors may improve efficiency of broiler production. The objective was to compare effects of different light sources on growth and gene expression of broilers. In a subset of a larger experiment, 48 Cobb 500 strain chicks were assigned to one of six lighting treatments with 8 birds per treatment: 1) incandescent, INC); 2) fluorescent (FL); 3) white LED (WL); 4) green LED (GL); 5) blue LED (BL); or 6) green LED on days 1-9 followed by blue LED on days 10-17 (GB). Treatments were administered by using bulbs that met the above specifications. Feed and water were available ad libitum. At termination on day 17, body weight and feed intake were determined and blood and liver samples were obtained for RNA analysis. Blood RNA was used for RNAseq analysis on a subset of samples (n = 4/treatment for WL, GL and BL) to identify target genes for further analysis. Treatment effects were analyzed by orthogonal contrasts and genes were considered differentially expressed (DE) when $P \leq 0.001$ and FDR ≤ 0.10. Comparing white and colored LED light (WL vs the average of GL and BL) revealed 63 DE genes. Comparing GL to BL identified 107 DE genes. Integrative analysis using DAVID software indicated: Functions including signal, secreted, blood microparticles, extracellular exosomes and plasma membrane; KEGG pathways, including PPAR signaling; and Tissue specificity, indicating liver. Based on those analyses, we selected 12 DE genes for analysis in liver RNA by qPCR. Target genes included AvBD9, APOA4, CAT, CHAC1, FOXN2, HMGCS1, IL15, SCD, SPINK5, TTR, UBAP2, XPA. Target gene expression was normalized to that of a reference gene, RPL4, and data were log2 transformed before analysis using Proc GLM of SAS. Genes were considered DE at $P < 0.05$. There was no effect ($P > 0.05$) of any lighting treatment on expression of the selected genes of interest in liver. Similar to liver gene expression, light treatments had no effect on broiler growth, feed intake or feed efficiency to day 17 ($P > 0.05$). In summary, different light treatments altered gene expression in blood cells but not liver and had no effect on broiler performance. Conflicting gene expression in blood and liver suggests cell type specificity in response to lighting. Similarity of broiler performance under different lighting suggests LED lights of various colors can be used to reducing operating costs without penalizing performance.

Key Words: broiler performance, LED light, RNA-sequencing
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520 Order of loading of ingredients and mixing time on the quality of the diet in bovine's feedlot.

J. R. D. Costa Júnior[1], R. M. D. Silva*[2,3,4,5], R. Z. Taveira[2], J. G. L. Regadas Filho[6], and P. V. R. Paulino[7,8], [1]*Student in the Master in Sustainable Rural Development (MDRS), State University of Goiás (UEG), São Luis de Montes Belos, Goiás, Brazil,* [2]*State University of Goiás (UEG), São Luis de Montes Belos, Goiás, Brazil,* [3]*Researcher Professor BIP/UEG, São Luis de Montes Belos, Goiás, Brazil,* [4]*DSc. Professor in the Master in Sustainable Rural Development (MDRS), State University of Goiás (UEG), São Luis de Montes Belos, Goiás, Brazil,* [5]*FAPEG, Goiânia, Goiás, Brazil,* [6]*Cargill Animal Nutrition, Campinas, Brazil,* [7]*Nutron Alimentos Ltda, Campinas, Brazil,* [8]*DSc. Cargill Animal Nutrition (CAN), Campinas, Brazil.*

The aim of this research was to evaluate the homogeneity of total diet, through the order of loading of the ingredients in wagon mixer and the mixing time of the diet used in a commercial feedlot of cattle. The treatments corresponded to two loading orders and two mixing times, being,: treatment 1 - initiated with forage loading with 5 minutes mixing (FOR5); treatment 2 - initiated with forage loading with 4 minutes mixing (FOR4); treatment 3 - initiated with loading of concentrate with 5 minutes mixing (CON5) and treatment 4 - initiated with concentrate loading with 4 minutes mixing (CON4. The statistical model used was the completely randomized design in factorial scheme 2x2, with four repetitions. Ten diet samples from the trough line were collected after each treatment, being dry matter (DM), crude protein (CP), ether extract (EE) and neutral detergent fiber (NDF) the variables of interest analyzed by portable NIR. A second analysis was performed to evaluate if there was an effect of the sample collection order on the nutrient concentration studied. The results showed that for DM, CP and NDF, there was no evidence of differences in the variability between treatments. For EE, a significant effect was observed in FOR5 and CON5 for the loading time factor. For the effect of the order of sampling on the composition of the diet, there were no indications of changes in the composition of the analyzed variables along the trough lines. Considering the results obtained, it was observed that for the treatments FOR5 and CON5 there was a better mix for the variable EE.

Key Words: Wagon mixer, Homogeneity, Total diet
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521 Pen-shade and morning versus afternoon feeding on feedlot-performance and respiratory rate of growing calves under hot weather.

R. Barajas*[1], B. J. Cervantes[2], B. O. Lopez[3], D. Jimenez-Leyva[4], and L. Avendaño-Reyes[5], [1]*FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico,* [2]*Ganadera los Migueles, S.A. de C.V., Culiacán, Mexico,* [3]*FMVZ-Universidad Autonoma de Sinaloa, Culiacan, Mexico,* [4]*FMVZ Universidad Autónoma de Sinaloa, Culiacán, Mexico,* [5]*Instituto de Ciencias Agricolas, Universidad Autonoma de Baja California, Ejido Nuevo Leon, Baja California, Mexico.*

Sixty four Brahman cross calves (223 ± 18.67 kg) were used to evaluate the effect of pen-shade and morning versus afternoon feeding on feedlot-performance and respiratory rate of growing calves under hot weather. Calves were individually weighed and using initial weight as blocking criteria, in a completely randomized block design, in groups of four calves were assigned to treatments as follows: 1) Placed in ground pen (6 x 12 m) without shade and morning feeding (0700 and 0900); 2) Ground pen without shade and afternoon feeding (1700); 3) Ground pen fitted with central roof (4 m^2 of shade/calf) and morning feeding (0700 and 0900); and 4) Ground pen fitted with central roof and afternoon feeding (1700). Calves were fed ad libitum with a diet (15% CP and 1.34 Mcal NE_m/kg DM) formulated with corn silage, steam flaked corn, soybean meal and mineral premix. Calves were weighed in days 1 and 28. Data was analyzed by ANOVA for a completely randomized block design with a 2 x 2 factorial arrangement. Mean air temperature from 0800 to 1800 was lower ($P < 0.01$) in pen-shade 33.8 vs. 36.7 °C; relative humidity was higher ($P < 0.01$) 62.1 vs. 58.2%; and THI values were lower 85.1 vs. 88.1 ($P < 0.01$). Pen-shade and afternoon feeding increased ($P < 0.01$) average daily gain. An interaction ($P = 0.02$) in ADG was observed, where morning fed calves (shaded and unshaded pens) exhibits similar ADG, but calves allotted in shaded pens fed afternoon have highest gain than calves fed afternoon but placed in unshaded pens (1.56 vs 1.19 kg). Pen-shade increased DMI ($P = 0.02$). Gain/feed ratio was increased both for Pen-shade ($P = 0.05$) as by feeding time ($P < 0.01$). A tendency for interaction ($P = 0.09$) was observed where the lower values were found in calves fed during morning (shaded and Unshaded pens), but inner afternoon fed calves those were provided with pen-shade had higher response ($P = 0.02$) than placed in unshaded pens (0.255 vs 0.220 kg/kg). Serum cortisol values were lower ($P < 0.01$) in shaded pens calves (1.02 vs 3.10 μg/dL). At 0800 h respiratory rate was similar across treatments ($P > 0.15$), but from 1000 to 1800 respiratory rate was lower ($P < 0.01$) in shaded pens calves (56.4 vs 84.9 breaths/minute). Results suggest

providing pen-shade and afternoon feeding contributes to increase feedlot performance of calves under hot weather.

Key Words: feeding time, pen-shade, feedlot calves
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522 Evaluation of oats incorporated into annual ryegrass on performance of beef cattle.

J. D. Rivera*, J. T. Johnson, M. L. Gipson, and R. G. Gipson, *Mississippi State Univ. South Branch Exp. Sta., Poplarville, MS.*

Forty crossbred beef steers (204.1 + 18.9 kg BW) were used in a randomized complete block to determine the effects of incorporating oats (*Avena sativa*) into annual ryegrass (*Lolium multiflorum*) pastures. Ten warm-season perennial pastures (1.21 ha) were killed with glyphosate and then burned, after which pastures were scratched with a disk. Pastures were randomly assigned to 1 of 2 treatments: 1) oats drilled into the pasture at a depth of 2.54 cm, at a rate of 90 kg/ha, after which annual ryegrass was broadcast at the rate of 56 kg/ha (OATS) or 2) annual ryegrass broadcast at the rate of 56 kg/ha (RG). Fertilization rates and application were similar across both treatments. When pastures had sufficient forage to support 4 beef cattle (5 kg forage DM/kg of BW), cattle were weighed and then moved into pastures. Forage biomass was determined weekly with the use of a rising plate reader, and when forage became limiting (less than 5 kg of forage DM/kg of BW), cattle were weighed and then removed. Between forage grazing periods, cattle had access to a commercial feed supplement and dormant forage. Pasture cost of establishment per hectare was greater for OATS ($P = 0.001$; US$332.5 and $219.7 for OATS and RG, respectively). Average daily gain did not differ ($P = 0.90$) between treatments (1.00 vs. 0.99 kg/d for OATS and RG, respectively. Pastures planted with OATS had more grazing days (124 vs. 98) and overall greater gain per pasture ($P = 0.003$; 383.8 kg compared with 291.6 kg for OATS and RG, respectively). Pasture-only cost of gain was similar ($P = 0.24$) for both OATS and RG; however, when the cost of supplementation (when not grazing) was factored into the overall cost of gain, OATS had a more economical cost of gain compared with RG ($P = 0.002$). Results suggest incorporation of a small grain such as oats may increase the winter grazing period and reduce cost of gain.

Key Words: beef cattle , annual ryegrass, small grains
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523 Body condition change and foraging strategy of gestating beef cows in response to herbage allowance and cow genotype.

P. Soca*[1], M. Do Carmo[2], C. Genro[3], and S. Scarlato[2], [1]*Facultad de Agronomia. Universidad de la Republica, Paysandu, Uruguay,* [2]*Universidad de la Republica, Paysandu, Uruguay,* [3]*Embrapa Pecuaria do Sul, Bage, Brazil.*

The objective was to study the effect of herbage allowance (HA) and cow genotype (CG) on BCS and grazing behavior of beef cows during gestation (180 to 0 d prepartum [DPP]). Multiparous beef cows ($n = 24$) were submitted to HA (3 [LO] and 5 kg DM/kg BW [HI]) and CG, purebred [PU] Angus–Hereford (437 ± 53 kg BW and 4 ± 0.5 BCS) and F_1 crosses (CR; 462 ± 29 kg BW and 4 ± 0.7 BCS). Herbage mass and height were 1,300 vs. 1,100 kg DM/ha and 3 vs. 2 cm in HI and LO, respectively, without differences in chemical composition. Body condition was determined monthly. From 88 to 77 ± 11 DPP, probability of grazing (PGT) and rumia (PRT) were visually recorded every 5 min. During the major grazing session, we estimated the time to take 100 prehension bites (bite rate [BR]) and the number of patches (PH) and feeding stations (FS) per hour. Forage intake was estimate based on an internal indicator (*n*-alkanes). Effects of HA, CG, DPP, on BCS and PGT, PRT, BR, PH, and FS were analyzed with repeated measures. The BCS were higher in HI cows (5.3 ± 0.1 vs. 4.2 ± 0.2 and 4.6 ± 0.07 vs. 4.3 ± 0.1 at 90 and 60 DPP, respectively), whereas CR cows had higher BCS than PU cows at calving (4.8 vs. 4.3 ± 0.09 for CR and PU cows, respectively). The HI increased PRT (0.15 vs. 0.05) but did not affect PGT (0.85 for HI vs. 0.87 for LO) PH (14 ± 2 PH/h), and FS (285 ± 25 FS/h). The PGT was reduced for CR cows (0.80 for CR cows vs. 0.85 for PU cows; $P < 0.05$). Patches per hour was lower for CR cows than for PU cows (10 vs. 18 ± 2; $P < 0.05$) but FS per hour was higher for CR cows than for PU cows (320 vs. 263 ± 26; $P = 0.09$). The BR increased in LO–PU with respect to HI–CR, HI–PU, and LO–CR (58 vs. 50 bite/min ; $P < 0.05$). Forage intake was affected by HA (2.6 vs. 2.2% live weight [LW] in HI vs. LO, respectively) but not by CG (2.2% LW). Foraging strategy was oriented to increased energy intake in HI HA cows or improved energy efficiency in CR cows, which could explain improved BCS during gestation.

Key Words: Forage allowance, Cow genetic group, Grazing behavior
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RUMINANT NUTRITION

A1 Early Career Award Speaker: Short-chain fatty acid absorption across the ruminal epithelium: Current knowledge and strategies to modulate absorption.

G. B. Penner*, *University of Saskatchewan, Department of Animal and Poultry Science, Saskatoon, SK, Canada.*

Microbial fermentation in the rumen yields short-chain fatty acids (SCFA) that serve as the primary energy substrate for ruminants. Past research has reported that factors causing a reduction in SCFA absorption predispose cattle to low ruminal pH, and sheep and cattle with greater rates of SCFA absorption are more able to maintain pH. Thus, understanding absorption of SCFA acids across the rumen epithelium can help to stabilize ruminal pH and promote greater energy supply. From a tissue level, SCFA absorption is known to occur via passive diffusion, anion-exchange through a bicarbonate-dependent process, through a nitrate-sensitive mechanism, and via a voltage gated channel. The relative reliance of individual SCFA for each transport pathway differs by chain length of the SCFA and on luminal conditions such as ruminal pH. For example, acetate uptake and flux are primarily mediated through bicarbonate-dependent anion exchange, while passive diffusion accounts for a significant proportion of the butyrate uptake and flux. Interestingly, the inhibitory potential of nitrate on the uptake of acetate and butyrate also differs with less of an inhibitory effect for butyrate. In the presence of low pH, the proportion of acetate transported via bicarbonate-dependent anion exchange increases. Dietary composition can modulate the pathway of SCFA absorption. Increasing dietary sugar with the inclusion of whey permeate has been reported to increase acetate and propionate absorption through bicarbonate-dependent anion exchange. In response to a moderate, but abrupt, decrease in the forage-to- concentrate ratio (92:8 vs. 50:50), uptake of acetate and butyrate via passive diffusion increased. As a strategy to modulate permeability of the ruminal epithelial membrane, we have reported that feeding a diet with a greater supply of saturated fatty acids increased the passive diffusive uptake of propionate and butyrate, but not acetate. Finally, SCFA absorption decreases in response to low feed intake and following induction of rumen acidosis. While the involved pathways responsible for these changes have not been evaluated, intervention strategies using functional nutrients may accelerate recovery of the ruminal epithelium and restore SCFA flux. Understanding the pathways and regulatory mechanisms for SCFA transport is one approach that can be used to develop management strategies to help stabilize ruminal pH and increase absorption of SCFA as an approach to improve the performance of ruminants.

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A3 Early Career Award Speaker: Interactions between trace minerals and growth promoting practices in beef cattle.

S. Hansen*, *Iowa State University, Ames.*

Trace minerals (TM) are necessary to support optimum animal growth. While TM requirements to prevent deficiency were recently updated, the requirements of beef cattle to support optimal performance remain ill defined. Advancements in animal genetics and utilization of technologies to promote growth of feedlot cattle have dramatically advanced production efficiencies in the beef industry. Trace minerals (Co, Cu, Fe, I, Mn, Se and Zn) are integral in a variety of growth processes in the body, including supporting metalloproteins involved in DNA synthesis, collagen production, energy utilization and critical antioxidant enzymes. Over 80% of feedlot cattle are estimated to receive hormone implants to enhance growth and efficiency. Recently, we examined the effect of feeding no supplemental TM, TM supplemented at NRC recommendations, or TM supplemented at industry recommended concentrations (all inorganic sources), fed to Angus cross steers receiving no implant or implanted with Component TE-IS, followed by Component TE-200 on d 56. Harvested on d 124, HCW was, as expected, improved ($P = 0.0001$) by implant, but HCW was also improved by 15 kg ($P = 0.01$) in steers supplemented at industry TM concentrations vs. those receiving no supplemental TM. Additional work is needed to clarify the potentially greater need for TM in cattle receiving hormone implants. Introduction of beta adrenergic agonists revolutionized late stage finishing cattle performance, increasing feed efficiency, ADG, and often HCW of cattle. In a series of studies we have found that increasing supplementation of Zn (from a combination of inorganic and organic sources) to steers fed ractopamine hydrochloride increases cattle performance (ADG, feed efficiency, and HCW in some studies) during the ractopamine feeding period. Zinc is thought to inhibit breakdown of the intracellular signalling molecule, cAMP, perhaps potentiating the growth response. Alternately, demand for Zn and other TM may simply be greater due to increased growth rates. We recently found the retention of Zn and N to be positively correlated and that both ractopamine hydrochloride and Zn increase N retention in steers. It seems likely that growth enhancing technologies influence TM requirements of cattle, and further work is needed to determine TM requirements that optimize cattle performance and maximize producer profitability.

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524 Chemical composition of meat in calves under diferent diets.

A. A. Gomes Lobo*, *University of São Paulo, Pirassununga, Brazil.*

This study was aimed at evaluating the chemical composition of the longissimus dorsi muscle of veal calves. A total of 39 calves with an average initial body weight of 36.0 kg. The animals were distributed according to a completely randomized in a 3 x 2 factorial design, with three levels of milk intake and two levels of concentrate feeding. Treatments included: 1) 2 L of milk per day (2L), 2) 4 L of milk per day(4L), 3) 8 L of milk per day (8L), 4) 2 L of milk per day and ad libitum access to concentrated feed (2 L + C), 5), 4 L of milk per day, and ad libitum access to the concentrated feed (4L + C) and 6), and 8 L of milk per day and ad libitum access to the concentrated feed (8L + C). All animals were slaughtered at the age of 4 mo. The carcasses were kept for 24 hours in the cold chamber at 4°C and after that period the longissimus dorsi muscle was removed from each half carcass. Analysis of dry matter, crude protein, ether extract, and ash were performed. The centesimal composition of the muscle was not affected by the presence of concentrate in the diet ($P > 0.05$). The moisture content was highest in the 2 L treatment (80.63%) and lowest in the 8 L treatment (78.7%). It is worth mentioning that young animals have a higher concentration of water in the body than adult animals. The ether extract content was not influenced by treatment ($P > 0.05$). It is known that the levels of moisture and fat are negatively correlated. Regarding the protein and ash contents, the treatment with highest milk level (8 L) had a higher averages, 19.72% and 0.55%, respectively. It was concluded that both the production of white meat and the pink meat of calves, and the composition of the longissimus dorsi muscle showed no differences among treatments. The amount of milk that the animal ingests during its development phase presents changes in the protein content, ashes and moisture of the meat.

Key Words: carcass, milk, concentrated
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525 Carcass characteristics of Nellore cattle submitted to either nutritional restriction or intake of concentrate feedstuffs prior to adaptation period.

D. D. Millen[*1], M. C. Pereira[2], O. A. Souza[3], A. C. J. Pinto[3], G. P. Bertoldi[3], L. A. Tomaz[2], A. A. Santos[3], and M. D. Arrigoni[2], *[1]Sòao Paulo State University (UNESP) / Dracena Campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil.*

The study, conducted at São Paulo State University feedlot, Dracena campus, Brazil, was designed to evaluate the effects of either nutritional restriction or intake of concentrate feedstuffs before beginning the adaptation period on carcass characteristics of Nellore cattle. The experiment was designed as a completely randomized block, replicated 8 times (4 animals/pen), in which 96 22-mo-old yearling Nellore bulls (365.5 ± 39.2 kg) were fed in 24 pens according to the treatments: Restriction (Tifton hay fed at 1.4% of BW + mineral supplement); Control (Tifton hay fed ad libitum + mineral supplement) and Concentrate (Tifton hay fed ad libitum + 0.5% of BW of a mix of concentrate feedstuffs and mineral supplement). This study lasted 144-d, divided into 2 periods: 32-d of pre-adaptation, in which cattle were submitted to the treatments previously described, and 112-d of feeding high-concentrate diets, where cattle were fed the same diets. The adaptation program consisted of ad libitum feeding of two diets over adaptation period with concentrate level increasing from 72% to 86% of diet DM. The finishing diet contained: 73.5% cracked corn grain, 14.0% sugarcane bagasse, 9.0% cottonseed meal, 1.5% supplement, 1.2% urea and 0.8% limestone (DM basis). Cattle were fed ad libitum three times daily throughout the study. At the end of pre-adaptation period, one animal per pen was slaughtered (n = 24) for carcass evaluations, and the remaining 72 animals were harvested after 112-d of feeding high-concentrate diets. No significant ($P > 0.10$) treatment effect was observed for final dressing percentage, and initial and final marbling scores. Cattle submitted to nutritional restriction had lighter ($P < 0.10$) initial HCW in kg (Restriction = 183.43^{c}, Control= 187.41^{b}, Concentrate= 193.96^{a}), smaller initial LM area in cm^{2} (Restriction = 49.31^{b}, Control= 51.59^{a}, Concentrate= 53.14^{a}), and decreased initial dressing percentage (Restriction = 48.52^{c}, Control= 48.60^{b}, Concentrate= 48.78^{a}) and initial 12th rib fat thickness in mm (Restriction = 2.10^{b}, Control= 2.24^{a}, Concentrate= 2.34^{a}). Nevertheless, cattle submitted to nutritional restriction compensated during the period of feeding high-concentrate diets the negative impact of restriction and presented similar ($P < 0.10$) final HCW in kg (Restriction = 285.35^{a}, Control= 274.10^{b}, Concentrate= 287.30^{a}), carcass ADG in kg (Restriction = 0.92^{a}, Control= 0.77^{b}, Concentrate= 0.83^{ab}) and final 12th rib fat in mm (Restriction = 6.14^{a}, Control= 5.23^{b}, Concentrate= 5.91^{a}) when compared to cattle submitted to intake of concentrate. Thus, cattle should be submitted to nutritional restriction or intake of concentrate feedstuffs before the adaptation period to improve overall carcass characteristics.

Key Words: HCW, Zebu, dressing
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526 Meat quality of feedlot buffalo fed with forage palm+cottonseed replacing high concentrate diet.

V. L. Lima Junior*[1], F. Brandão Pereira[2], J. Nunes Batista[3], L. Rocha Bezerra[4], V. L. F. Santos[5], F. F. da Silva Filho[1], M. dos Santos Menezes[1], L. Andressa da Costa Silva[1], L. Dias do Nascimento Ferreira[1], R. Loiola Edvan[6], A. M. de Azevedo Silva[7], and A. H. N. Rangel[1], [1]*UFRN, NATAL, Brazil,* [2]*University Federal of Piauí, Bom Jesus, CA, Brazil,* [3]*University Campina Grande, Patos, Brazil,* [4]*University Federal of Piauí, Bom Jesus, Brazil,* [5]*Universidade Federal do Piauí, Bom Jesus, Brazil,* [6]*University Federal of Piauí, BOM JESUS, Brazil,* [7]*University Campina Grande, PATOS, Brazil.*

The objective of this study was to evaluate the performance and carcass traits from buffalo (*Bubalus bubalis*) fed with different levels of cactus pear+cottonseed completely replacing high concentrate diet. The research was approved by Ethics Committee on Animal Experiment from Protocol No. 210/16. Twenty-four Murrah buffalos uncastrated males, with age between 8 and 10 mo and BW 300 ± 14.1 kg (mean ± SD) were identified. The treatments consisted of diets with four levels of cactus pear+cottonseed replacing high concentrate diet (0, 33, 66, and 100% replacement based on total DM of the diets). The animals were fed a total mixed ration containing soybean meal, corn grain, and cactus pear+cottonseed to meet the nutritional requirements according to National Research Council (NRC, 1996) for average weight gain of 100 g/d. The diets were offered ad libitum, individually in two equivalent measures at 0800 and 1600 h. The experimental period was 125 d. After the experimental period the animals were fasted for 16 h and slaughtered. The carcasses were divided longitudinally into two carcasses and transferred to a refrigerator at 4ºC for a period of 24 h. longissimus dorsi was removed from the one half of carcass for pH evaluation and the sartorio muscle for physicochemical and sensory evaluation. The data were submitted to linear and quadratic polynomial contrasts using PROC REG procedures implemented in SAS statistical software (version 9.1.2). Differences were considered at $P < 0.05$. Cactus pear+cottonseed replacing high concentrate diets linearly reduced Warner-Bratzler Shear Force ($P = 0.003$) and color indexes, redness a* ($P < 0.001$), yellowness b* ($P = 0.007$) and chrome C* ($P < 0.001$) and presented a negative quadratic effect for the variable luminosity L* ($P = 0.004$). However, there were no effect for cooking weight loss, water retention capacity, pH at 0 and 24 h post-mortem and moisture, DM, protein, lipids and minerals of buffalo's meat. The replacement of high concentrate diets by cactus pear+cottonseed did not change sensorial attributes of buffalo's meat aroma ($P = 0.951$), flavor ($P = 0.296$), softness ($P = 0.418$), succulence ($P = 0.556$) and global acceptance ($P = 0.374$). Inclusion of cactus pear+cottonseed in complete replacement for the high concentrate diets for buffalos in feedlot improves the coloring of the meat without to change the sensorial attributes.

Key Words: *Bubalus bubalis*, meat, supplementation
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527 Liver metabolomics analysis associated with feed efficiency on steers.

V. M. Artegoitia*[1], A. P. Foote[2], R. M. Lewis[3], and H. C. Freetly[4], [1]*University of Nebraska, Lincoln,* [2]*USDA, ARS, US Meat Animal Research Center, Clay Center, NE,* [3]*University of Nebraska-Lincoln, Lincoln,* [4]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

The liver represents a metabolic crossroad regulating and modulating nutrients available from digestive tract absorption to the peripheral tissues. To identify potential differences in liver function that lead to differences in feed efficiency, liver metabolomic analysis was conducted using ultra-performance liquid chromatography, time-of-flight mass spectrometry (MS). Individual feed intake and BW gain was measured on 144 crossbred steers for 105 d on a high concentrate diet. 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 in the least-ADG group (1.57 ± 0.02 kg/d). Liver 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 MS/MS fragmentation patterns with those from authentic compounds. Principal component analysis, fold changes and t-tests on rumen fluid metabolic profile identified 96 metabolites ($P < 0.05$) that segregated with ADG group. These metabolites were primarily involved in taurine and hypotaurine (impact-value 0.75; $P = 0.10$) and glycerophospholipids metabolism (impact-value 0.34; $P < 0.01$), which were up-regulated in the highest-ADG as compared to lowest-ADG group. Conversly, glutathione metabolism (impact-value 0.36; $P = 0.01$) was up-regulated in the least-ADG *vs.* greatest-ADG group. Hepatic levels of 5 metabolites associated with ADG group were quantified and screened by receiver operating curve (ROC) analysis to test their efficacy as biomarkers for ADG. Hepatic concentration of L-glutathione decreased ($P < 0.01$) in the greatest-ADG (4.56 µg/mL) *vs.* least-ADG (8.21 µg/mL) animals while taurocholic acid increased ($P = 0.06$) in the greatest-ADG (5.53 µg/mL) *vs.* least-ADG (2.74 µg/mL) animals. However, hepatic concentration of L-homocysteine, L-methionine and L-cysteine was not affected by ADG ($P > 0.10$). The combination of L-homocysteine and L-glutathione ratio was a good predictor of ADG; area under the curve from the ROC analysis was 0.934 with a 95% CI of 0.78-1.0 representing 87.5% of sensitivity and 87.5% of specificity. From these results, we deduce that the hepatic metabolic profile provides new insight

into the physiological mechanisms of cattle feed efficiency. USDA is an equal opportunity provider and employer.

Key Words: average daily gain, beef cattle, dry matter intake
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528 Metabolic profile in multiple tissues associated with feed efficiency on steers.

V. M. Artegoitia*[1], A. P. Foote[2], R. M. Lewis[3], and H. C. Freetly[4], *[1]University of Nebraska, Lincoln, [2]USDA, ARS, US Meat Animal Research Center, Clay Center, NE, [3]University of Nebraska-Lincoln, Lincoln, [4]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

A study of multiple tissues was conducted to identify potential metabolic differences in cattle differing in feed efficiency. Individual feed intake and BW was measured on 144 steers during 105 d on a high concentrate ration. Steers were selected according to differences in ADG ($P = 0.01$) with those with the greatest ADG (n = 8; 1.96 ± 0.02 kg/d) and least ADG (n = 8; 1.57 ± 0.02 kg/d), yet that did not differ in DMI (10.10 ± 0.05 kg/d; $P = 0.41$), used. Duodenum, liver, adipose, and longissimus dorsi were collected at slaughter. Metabolomics profiles of the 4 tissues were conducted using ultra-performance liquid chromatography, time-of-flight mass spectrometry. Principal components analyses, t-tests ($P < 0.05$) and fold changes in tissue profiles were used to identify differential metabolites between ADG groups (metabolites identified: n = 85 in duodenum; n = 96 in liver; n = 87 in longissimus dorsi; n = 72 in adipose). Of all metabolites identified, none were identified in all 4 tissues. However, some metabolites were found in 3 of the tissues. These were primarily involved in alpha-linolenic metabolism, which were down-regulated in the greatest-ADG as compared to least-ADG group in duodenum, adipose, and longissimus-dorsi (impact-value 1.0; $P < 0.05$). In contrast, taurine and hypotaurine (impact-value 0.75; $P = 0.10$) and glycerophospholipids metabolisms (impact-value 0.34; $P < 0.01$) were both up-regulated in the greatest-ADG compared with least-ADG group in the liver. Despite the distinctive metabolites profile of each tissue, these findings provided evidence of common biochemical pathways across tissues related to difference in cattle feed efficiency. Combining analyses of multiple tissues may offer a powerful approach for defining the molecular basis of differences in performance among cattle for key production attributes. USDA is an equal opportunity provider and employer.

Key Words: average daily gain, metabolomics, UPLC-Q-TOF-MS/MS
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529 Effect of different nutritional strategies on meat quality and fatty acids profile of Nellore bulls finished on pasture.

P. H. Gonçalves[1], M. A. P. Alves[2], I. M. D. Oliveira[3,4], R. M. Fernandes[1], L. F. Prados*[3,5], A. D. Moreira[1], V. A. C. Mota[6], F. D. D. Resende[1,3], and G. R. Siqueira[1,3], *[1]UNESP - Univ Estadual Paulista, Jaboticabal, Brazil, [2]APTA, Colina, Brazil, [3]APTA - Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [4]FAPESP (grant #2016/01961-2 and grant #2013/10340-3), São Paulo, Brazil, [5]Bolsista CNPq, Colina, Brazil, [6]UNESP/FCAV, Jaboticabal, Brazil.*

An advantage of the Brazilian system is the predominant use of animals in pastures, so finishing Nellore in pasture with supplementation can be a strategy in Brazil to obtain meat quality. The objective of this study was to evaluate the effect of different nutritional strategies on meat quality and fatty acids profile of Nellore bulls fed in pasture. Twenty-four Nellore bulls (409 ± 18 kg and 25 mo) were used in a randomized block designed study. The treatments were: mineral-salt (100 g/animal per d during 155 d; MS), supplementation in the amount of 7 g/kg of BW per d (during 155 d; 7g/kg BW) or supplementation in the amount of 20 g/kg of BW per d (70 d fed mineral salt and 85 d fed 20g/kg BW; 20 g/kg BW). These treatments were done to evaluate if the intensity of the supplementation can affect the meat quality of finishing Nellore in pasture. The supplements were fed daily to paddocks (4 paddocks/treatment; 2 animals/paddock). The bulls were harvested on d 155. After 24-h chill, 2 steaks were taken from the longissimus dorsi (12th rib). All data were analyzed using the MIXED procedure of SAS with an alpha = 0.10. There were no differences in pH (5.98 ± 0.11) and cooking loss (31.7 ± 2.21). There was no difference ($P > 0.20$) on meat color ($L^* = 36.9 \pm 1.12$, $a^* = 16.9 \pm 1.07$, and $b^* = 14.1 \pm 0.89$) due to supplementation strategy. The shear force was similar ($P = 0.59$) among treatments (3.89 ± 0.51 kgf/cm^2). Saturated and unsaturated fatty acids were similar ($P > 0.14$) among treatments. Bulls supplemented had greater monounsaturated fatty acids ($P = 0.05$). However, polyunsaturated fatty acids were similar ($P = 0.65$) among treatments. Bulls fed MS had greater ($P = 0.07$) omega-3 compared to bulls fed 20 g/kg (1.41 vs. 0.598). Bulls fed MS and 7 g/kg BW had similar omega-3. Delta 9 desaturase 18 was improved ($P = 0.05$) by 7.7% for bulls supplemented compared to MS. In conclusion, these data suggest that supplementation did not influence on meat quality. However, supplementation influence on fatty acids profile, so meat of bulls fed MS and 7 g/kg BW had greater omega-3 compared to animals fed 20 g/kg BW.

Key Words: fatty acids profile, longissimus dorsi, omega-3
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530 Vitamin A, Zfp423 and intramuscular adipogenesis in beef cattle.

C. L. Harris*[1], M. Du[1], M. L. Nelson[1], and J. R. Busboom[2], [1]*Washington State University, Pullman,* [2]*Department of Animal Sciences, Washington State University, Pullman.*

Marbling, or intramuscular fat, is one of the most important factors in the palatability of beef. Selection for lean muscle and rapid growth in beef cattle has negatively impacted marbling, making it critically important to develop methods to increase marbling and thus palatable beef. Previous studies have shown that vitamin A (VA) promotes the formation of new fat cells in skeletal muscle through an increase in the expression of Zinc finger protein (Zfp) 423, a key regulator of fat cell formation. We hypothesized that VA injection during the critical stage for formation of fat cells in muscle would enhance intramuscular adipogenesis and marbling through the expression of Zfp423. Angus bull calves (n = 26), in a Completely Randomized Design, were randomly allotted to three treatment groups at birth. The first group (n = 9) received no supplemental VA, while the second (n = 7) and third group (n = 10) were given 150,000 IU of VA and 300,000 IU of VA at both birth and one month of age, respectively. After weaning, calves were fed a backgrounding diet until 10 months of age then a high-concentrate feedlot diet until harvested at 14 months of age. Weaning weight and average daily gain during the backgrounding phase were linearly increased ($P < 0.05$) by VA level. Intramuscular fat of steers at 10 months of age, measured by ultrasound, quadratically increased ($P < 0.05$) with VA level from 4.0 to 4.9% 0.26. Similarly, marbling score (small = 500, modest = 600) in the ribeye quadratically increased (584, 674 and 608 21.15 for the 0 IU, 150,000 IU and 300,000 IU treatment groups, respectively). Carcass back fat thickness quadratically increased ($P < 0.05$) with level of VA. However, yield grade quadratically decreased ($P < 0.05$) with VA where the high-level treatment had the lowest, or best, yield grade. Cattle that received VA had greater marbling, though further studies will need to evaluate an optimal amount as the mid-level treatment group had greater fat development and the high-level treatment group had greater muscling and higher average daily gain. Dietary VA enhanced intramuscular adipogenesis and marbling thereby improving meat quality.

Key Words: Vitamin A, intramuscular fat, beef cattle
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531 Effects of dietary concentration of polyunsaturated fatty acids on the carcass traits of feedlot *B. Indicus* and cross-bred *B. taurus* x *B. indicus* cattle.

D. Silva Antonelo*[1], J. Fernando Morales Gomez[1], R. R. S. Corte[1], M. Beline[1], J. Silva[1], H. Bueno Silva[1], G. A. Sene[1], N. Pereira Dias[1], A. R. Cabral[2], and S. L. Silva[1], [1]*University of Sao Paulo/FZEA, Pirassununga, Brazil,* [2]*Texas A&M University, College Station.*

Inclusion of vegetable oils in diets formulation of finishing beef cattle increases the availability of polyunsaturated fatty acids (PUFA) in the diet, which may modulate the carcass traits of lean meat producing animals. This study was carried out to evaluate the effects of PUFA dietary concentration in animals from different genetic predispositions for fat deposition on carcass traits. Thirty Nellore and thirty crossbred Angus x Nellore (368 ± 28 kg bodyweight; 24 mo old) were weighed, tagged and allocated in individual pens according to the initial BW (block) in a block design with a 2 x 2 factorial arrangement (genetic group x diet) and 15 replications per treatment. Animals were fed for 133 d from one of two high concentration diets: control diet (CON; TDN = 78.9%; EE = 3.11%) and soybean oil diet (SBO; TDN = 82.3%; EE = 6.45%), containing corn silage (10%), sugarcane bagasse (5%), corn grain (58% for CON and 54.5% for SBO), citrus pulp (16%), soybean meal (9%), urea (1.2%), mineral salt (0.8%) and soybean oil (3.5% for SBO). Hot carcass weight (HCW), dressing percent (DP), kidney, pelvic and inguinal (KPI) fat weight as a percentage of HCW, and liver weight were evaluated. There was no genetic group x diet interaction for any trait evaluated. No difference was observed between *B. indicus* and cross-bred animals for HCW (316 x 330 kg; $P = 0.1311$), DP (59.1 x 58.8%; $P = 0.7098$), KPI fat (3.0 x 3.1% HCW; $P = 0.3905$), and liver weight (6.6 x 7.0 kg; $P = 0.1075$), respectively. Although no difference was observed between diets for HCW ($P = 0.2469$) and DP ($P = 0.6350$), animals fed SBO diet had a higher KPI fat (3.3 x 2.7% HCW; P = 0.0066) besides tending to have a higher liver weight (7.0 x 5.6 kg; $P = 0.0722$) than animals fed CON diet, respectively. Animals with different genetic predispositions for fat deposition had similar carcass traits, in these study conditions. Higher dietary concentration of PUFA did not change HCW and DP due to the increase of the internal fat deposition and viscera weight.

Key Words: soybean oil, Carcass yield, Fat deposition
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532 Intake, digestibility and ruminal parameters in cattle fed with oil, selenium and vitamin E.

O. R. Machado Neto*[1], M. M. Ladeira[2],
P. D. Teixeira[2], A. V. P. Ferreira[2], A. Cominotte[3],
J. M. Bertocco Ezequiel[4], and E. H. C. B. Van Cleef[5],
[1]*São Paulo State University, Botucatu, Brazil,*
[2]*Universidade Federal de Lavras, Lavras, Brazil,*
[3]*Universidade Estadual Paulista, Jaboticabal, Brazil,*
[4]*São Paulo State University, Jaboticabal, Brazil,* [5]*Sao Paulo State University, Jaboticabal, Brazil.*

This study aimed to evaluate intake, ruminal parameters and digestibility of nutrients in the diets with 6% soybean oil (SO) and with or without supplementation of organic selenium (Se) and vitamin E (E). Five steers cannulated with average initial BW of 398 ± 28.7 kg were subjected to a 5 x 5 Latin Square with 21d periods. Diets consisted of 65% concentrate and 35% corn silage. Steers were assigned to treatments: without additional oil (WAO); SO; SO+E; SO+Se; SO+E+Se. The additives were daily supplemented with 1500 IU vitamin E and 5 g selenium per animal. Rumen contents were collected every two hours after morning feeding to measure SCFA and ammonia nitrogen. Total collection of feces was completed for three days in each period to measure digestibility of nutrients. The data were analyzed using PROC MIXED of SAS. The diet with SO had lower intake (kg) of DM (9.82 and 10.6; $P = 0.02$), DMBW (21.05 g/kg BW and 23.1 g/kg BW; $P < 0.01$), OM (9.96 and 10.8; $P = 0.05$), CP (1.25 and 1.36; $P = 0.02$), NDF (3.20 and 3.52; $P = 0.01$), and NFC (4.22 and 5.11; $P < 0.01$), total protozoa (45 and 380 10^3/mL; $P < 0.01$), total digestibility (g/kg) of DM (726 and 760; $P = 0.05$), OM (725 and 759; P = 0.05), NFC (814 and 845; $P = 0.04$) and NDF (567 and 639; $P < 0.01$), ruminal digestibility (g/kg) of CP (426.50 and 511; $P = 0.05$) and NDF (505.75 and 587; $P < 0.01$), and excretion of N microbial (202 and 156.2 g/day; $P = 0.01$). However, SO had a greater intake (0.85 and 0.33; $P < 0.01$) and total digestibility of EE (897.25 and 826; $P < 0.01$) than WAO. Se reduced ruminal digestibility of DM (475 and 508.5; $P = 0.05$) and OM (475 and 509; $P = 0.05$) and had greater molar proportion (mMol) of acetate (35.6 and 30.45; $P = 0.04$), propionate (19.1 and 16.0; $P = 0.04$), butyrate (9.53 and 8.37; $P = 0.05$) than diet without Se. The diet with SO+E+Se had lower ruminal digestibility of CP (417 and 511; $P = 0.04$) and greater EE (-56.5 and 159; $P = 0.05$). Overall, the study showed that supplementation with soybean oil reduce DM intake and fiber digestibility, while the use of E/Se does not change the total digestibility of nutrients.

Key Words: rumen, selenium yeast, zebu cattle
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533 Selection of white-tot fungi for bioprocessing of wheat straw into ruminant feed.

N. Nayan*[1], W. H. Hendriks[1], J. W. Cone[1], and A. Sonnenberg[2], [1]*Animal Nutrition Group, Wageningen University, Wageningen, Netherlands,* [2]*Plant Breeding Group, Wageningen University, Wageningen, Netherlands.*

White-rot fungi are effective at delignification of agricultural residues, which increase the accessibility to structural carbohydrates and enhance its degradability in the rumen. Fungal pretreatment of lignocellulosic biomass is influenced by various factors including types and conditions of the substrates used, as well as fungal strains/species. Hence, the selection of the best performing fungal strains/species is fundamental for an optimal pretreatment and for future breeding activities to expand the potential in the bioprocessing of agricultural residues. Three white-rot fungi species have been used in this study: *Ceriporiopsis subvermispora* (CS), *Pleurotus eryngii* (PE) and *Lentinula edodes* (LE). Ten to twelve strains from each species were evaluated and selected for their capabilities in improving the in vitro degradability of wheat straw. Wheat straw was inoculated with the spawn of each fungal strains/species under solid state fermentation for 7 weeks. Untreated samples (control) were also run along the treated samples. Weekly samples were analyzed for the total in vitro gas production (IVGP). Data were analyzed as a function of fungal strains (within species), incubation period and their interactions. Out of 32 fungal strains from different species tested, 18 strains showed a significantly higher ($p < 0.05$) IVGP compared to control after 7 weeks of treatment. Three best strains within each species with highest IVGP were selected for further analyses, assessment and comparison across species. Three best CS strains had a mean IVGP of 297 ml/g OM, while PE and LE had mean IVGP of 257.8 and 291.8 ml/g OM, respectively. The total carbohydrate to lignin (C/L) ratio was calculated to exhibit the selectivity of fungi in degrading lignin. There was a good correlation between IVGP and C/L ratio ($r = 0.67$; $P < 0.001$) indicating that a fungus which resulted in a high in vitro degradability, was more selective in degrading lignin. In conclusion, there were considerable variations in the IVGP of the treated wheat straw, not only between species, but also among different strains within each species. Three best performing strains from each species have been selected for further investigation of their benefit in ruminants, and can also be used for future breeding activities.

Key Words: White-rot fungi, in vitro gas production, selection
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534 Effect of *Acacia karroo* leaf meal inclusion level on carcass characteristics, physico-chemical and sensory attributes and histological parameters of pedi goats fed on a *Setaria verticillata* grass hay-based diet.

D. Brown* and J. Ng'ambi, *University of Limpopo, Polokwane, South Africa.*

Pedi goats in communal areas of the Limpopo province depend on *Acacia karroo* leaves, particularly during the dry season. *Acacia karroo* leaves contain high levels of condensed tannins. The objective of the study was to determine the effects of *Acacia karroo* leaf meal inclusion level on carcass characteristics, physico-chemical and meat sensory attributes and histological parameters of indigenous Pedi goats fed a *Setaria verticillata* grass hay-based diet. Thirty indigenous male Pedi goats (16.7 ± 1.26 kg) were randomly divided into five groups consisting of six animals per group, and housed in individual holding pens. The groups were allocated to five treatments in a completely randomized design containing *Acacia karroo* leaf meal inclusion levels of 20% ($S_{80}A_{20}$), 25% ($S_{75}A_{25}$), 30% ($S_{70}A_{30}$), 40% ($S_{60}A_{40}$) and 50% ($S_{50}A_{50}$), respectively, for 90 days. At the end of the study, carcass components were eviscerated and weighed. Samples were also taken from the longissimus dorsi muscle for instrumental color, pH readings, cooking loss, sensory attributes and shear force measurement. Liver and kidney samples from each goat were collected and preserved in 10% neutral buffered formalin for histological parameters. Data on carcass characteristics, physico-chemical and meat sensory attributes and histological parameters were subjected to a one-way analysis of variance. Significance was accepted at probabilities <0.05. All data were analyzed using the general linear model procedures of SAS (2008). Dietary treatments had no effect ($P > 0.05$) on the yields of different carcass components and meat sensory attributes. *Acacia karroo* leaf meal inclusion level had no effect (P > 0.05) on the physico-chemical attributes of goats, except for the meat color at 24 h post-mortem. Goats on a diet having 25% leaf meal had higher ($P < 0.05$) values for meat color lightness than those on diets having 30 or 40% inclusion levels. No histological alterations were found in liver of goats on diets containing 20, 25 or 30% leaf meal. Increased hepatocyte degradation was seen in goats fed 40 or 50% leaf meal. Tubular necrosis was absent in the kidneys of goats fed diets containing 20, 25 or 30% leaf meal while those on diets having 40 or 50% leaf meal showed acute tubular necrosis. It is concluded that *Acacia karroo* leaf meal inclusion levels of 20 to 30% supported moderate productivity of the goats and did not cause any adverse effects. These levels are thus recommended.

Key Words: Acacia karroo, Carcass, Histology
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535 Ruminal planktonic, weakly, and tightly feed-adhered bacterial community as affected by two *Trichoderma reesei* enzyme preparations fed to lactating cattle.

J. J. Romero*[1,2], D. C. Reyes[1], Z. Ma[3], and A. T. Adesogan[2], [1]*Animal and Veterinary Sciences, University of Maine, Orono,* [2]*Dept. of Animal Sciences, IFAS, University of Florida, Gainesville,* [3]*Department of Animal Sciences, University of Florida, Gainesville.*

The objective was to compare effects of 2 *T. reesei* enzyme preparations (EFE) on the ruminal planktonic (LIQ) or the weakly (ASO) or tightly (SOL) feed-adhered ruminal bacterial community (fractions; FRC) of lactating dairy cows. The xylanase activities of the moderate (MIX) and high-xylanase (XYL) EFE tested were 10,549 and 26,926 μmol/min per g, respectively and both improved milk production from a dairy cow diet in a previous study. Three ruminally cannulated dairy cows (159 ± 47 DIM) were assigned to Control (CON), MIX or XYL treatments in an experiment with a 3 × 3 Latin square design with 23-d periods. The MIX and XYL EFE were sprayed on the TMR just before feeding at rates of 3.4 and 1 mL/kg of DM, respectively. Bacterial diversity was determined using the 16S rRNA gene (V1-V3 region) and the Illumina MiSeq platform. The data were analyzed with a model that included effects of EFE, FRC, their interaction and random effects of cow and period. The XYL increased ($P < 0.05$) relative abundance (RA, %) of *Paraprevotellaceae* (5.06 vs. 3.69 ± 0.81), *Spirochaetaceae* (4.25 vs. 2.46 ± 0.48) and tended ($P = 0.11$) to increase those of *Prevotellaceae* (31.8 vs. 24.09 ± 2.82) versus the CON. The MIX decreased ($P < 0.05$) RA of *Ruminococcaceae* (4.61 vs. 9.09 ± 2.23) and unidentified *Clostridiales* (4.48 vs. 6.61 ± 1.43), and tended to increase ($P = 0.06$) that of *Succinivibrionaceae* (1.91 vs. 0.55 ± 3.43) versus the CON. The SOL had higher RA ($P < 0.05$) of *Lachnospiraceae* (13.1 vs. 5.93 ± 1.86), *Veillonellaceae* (8.49 vs. 3.22 ± 1.69), unidentified *Clostridiales* (6.96 vs. 3.53 ± 1.43), and *Spirochaetaceae* (3.40 vs. 1.52 ± 0.48) and lower RA for unidentified *Bacteroidales* (3.48 vs. 9.96 ± 1.49) versus LIQ. The XYL and MIX EFE only tended to reduce the RA of *Veillonellaceae* versus that of CON (6.30 and 5.30 vs. 13.9 ± 2.54) in SOL (FRC × EFE; $P = 0.07$). The MIX EFE had lower phylogenetic diversity versus XYL and CON (48.6 vs. 51.6 and 51.2 ± 1.47; $P = 0.03$). The weighted UniFrac distance showed only community structure differences between FRC ($P < 0.01$). Both XYL and MIX modified the bacterial community profile and diversity of the rumen fractions.

Key Words: Rumen microbiome, Dairy cattle, Enzyme
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536 Biochanin A mitigates rumen microbial changes associated with a sub-acute ruminal acidosis challenge.

B. E. Harlow*, G. E. Aiken, J. L. Klotz, and M. D. Flythe, *USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY.*

Ruminal acidosis is a common digestive disorder in cattle that has significant implications on both health and performance. Sub-acute ruminal acidosis (SARA; pH 5.5 – 5.0), specifically, occurs when highly fermentable carbohydrate (e.g., starch) is introduced into the diet disturbing the microbial ecology of the rumen. Resident starch-utilizing bacteria (*e.g.*, *Streptococcus bovis*, Lactobacilli) rapidly catabolize starch, causing fermentation acids to accumulate in the rumen, reducing environmental pH. Historically, antibiotics (e.g., monensin, MON) have been used in the prevention and treatment of SARA. Biochanin A (BCA), an isoflavone produced by red clover (*Trifolium pratense*), mitigates changes associated with starch fermentation ex vivo. The objective of the study was to determine the effect of BCA on starch-utilizing bacteria and rumen pH during a SARA challenge. Twelve rumen fistulated steers were assigned to 1 of 4 treatments: HF CON (high fiber control), SARA CON, MON (200 mg d^{-1}), or BCA (6 g d^{-1}). Diets consisted of corn silage and dried distiller's grains ± cracked corn ad libitum. The study consisted of a 2-wk adaptation, a 1-wk HF period, and an 8-d SARA step-up challenge (d 1 – 4: 40% corn; d 5 – 8: 70% corn). Samples for pH and enumeration were taken on the last day of each period (4 h). Total starch-utilizing bacteria including, Lancefield group D Gram-positive cocci (GPC; *S. bovis*, enterococci) and lactobacilli, were enumerated. Enumeration data were normalized by log transformation and data were analyzed by repeated measures ANOVA using the MIXED procedure of SAS. During the HF period, pH, and starch-utilizing bacteria were unaffected by MON and BCA treatment ($P > 0.05$). The SARA challenge increased total starch-utilizing bacteria, including GPC, and Lactobacilli ($P < 0.05$). Although BCA had minimal effects on starch-utilizing bacteria during the 40% SARA challenge (inhibited Lactobacilli; $P < 0.05$), BCA decreased total starch-utilizing bacteria, including lactobacilli and GPC, when steers were fed a 70% corn diet ($P < 0.05$). Similar results were observed with MON (excluding Lactobacilli). The SARA challenge decreased pH during both the 40% (pH 5.48) and 70% (pH 5.28) periods in comparison to HF CON (pH 6.11; $P < 0.01$). However, BCA and MON were able to partially mitigate the pH decline (BCA 40%: 5.92, 70%: 5.59; MON 40%: 5.76, 70%: 5.43; $P < 0.01$). These results indicate that BCA may be an effective antibiotic alternative for mitigating SARA in cattle production systems.

Key Words: sub-acute ruminal acidosis, biochanin A, bovine
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537 Intake and ruminal fermentation parameters of beef steers consuming bahiagrass hay treated with calcium oxide.

F. M. Ciriaco*[1], D. D. Henry[1], T. M. Schulmeister[1], P. L. P. Fontes[1], N. Oosthuizen[1], C. D. Sanford[1], L. B. Canal[1], G. C. Lamb[2], and N. DiLorenzo[1], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*Texas A&M University, Department of Animal Science, College Station.*

To determine the effects of CaO treated bahiagrass hay on ruminal fermentation parameters of beef steers, 9 ruminally cannulated Angus crossbred steers (494 ± 145 kg BW) were used in a triplicated 3 × 3 Latin square design. In each of the 3 periods, steers were housed at the University of Florida Feed Efficiency Facility (3 steers/pen), where daily individual intake was recorded via the GrowSafe system. The steers had ad libitum access to bahiagrass hay, and were randomly assigned to 1 of 3 treatments: 1) untreated dry bahiagrass hay ($n = 8$; DH); 2) bahiagrass hay treated with 8.9% $CaCO_3$ (DM basis) + water (to 50% DM; $n = 9$; CC); or 3) bahiagrass hay treated with 5% CaO (DM basis) + water (to 50% DM; $n = 8$; CO). Starting at 0700 h (0 h), ruminal fluid was collected every 3 h for 24 h, and immediately after each collection, ruminal pH was measured. Ruminal fluid was analyzed for concentrations of VFA and NH_3-N. Data were analyzed as repeated measures using the MIXED procedure of SAS and the model included the fixed effects of treatment, time, treatment × time, square, and period. Animal within square and animal within treatment were included as random effects. Average DMI in kg/d ($P = 0.76$) and percent of BW ($P = 0.67$) were not affected by treatment. Ruminal concentrations of NH_3-N tended ($P = 0.06$) to be reduced in steers consuming CO. A treatment effect ($P < 0.001$) was observed for average ruminal pH, where steers consuming CO had the greatest pH when compared to DH and CC. No treatment effects ($P > 0.05$) were observed for molar proportions of acetate, propionate, or branched-chain VFA; however, butyrate molar proportion was lower ($P = 0.002$) in steers consuming CO and CC, when compared to DH. Moreover, no treatment effect ($P = 0.64$) was observed for acetate to propionate ratio; however, total VFA concentration was lower ($P = 0.02$) in steers consuming CO, when compared to DH and CC. Thus, we concluded that bahiagrass hay treated with CaO may reduce ruminal fermentation as indicated by decreased total VFA concentration without altering DMI.

Key Words: bahiagrass hay, beef steers, calcium oxide
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538 Abstract withdrawn.

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539 Evaluation of *Brassica carinata* meal on ruminal metabolism and nutrient digestibility of beef cattle.

T. M. Schulmeister*[1], M. Ruiz-Moreno[1], G. M. Silva[2], M. E. Garcia-Ascolani[1], F. M. Ciriaco[1], D. D. Henry[1], G. C. Lamb[3], J. C. B. Dubeux Jr.[1], and N. DiLorenzo[1], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*University of Florida, Range Cattle Research Center, Ona,* [3]*Texas A&M University, Department of Animal Science, College Station.*

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 (~40% CP) is obtained as a byproduct of oil extraction; however, this meal has not been tested as a potential protein supplement for cattle. A duplicated 4 × 4 Latin square design was used to determine the effects of supplementation with *B. carinata* meal on ruminal fermentation, digestibility, and blood profile in beef cattle consuming bahiagrass hay (*Paspalum notatum*), compared with frequently used protein supplements. Eight Angus crossbred steers (473 ± 119 kg initial BW) were randomly allocated to 8 pens, over 4 periods of 28 d each. Within period, steers were assigned to one of four treatments: 1.62 kg/d cottonseed meal (CSM), 2.15 kg/d dry distillers grains with solubles (DDGS), 1.39 kg/d *B. carinata* meal pellets (BCM), or 1.17 kg/d soybean meal (SBM), supplemented daily, on an isonitrogenous basis. Steers had ad libitum access to bahiagrass hay and water. Intake was measured using the GrowSafe system. Following a 14 d adaptation, feed and fecal samples were collected twice daily for 4 d to determine apparent total tract nutrient digestibility using iNDF as an internal marker. Blood and ruminal fluid samples were collected every 3 h, during a 24 h period, to analyze blood urea nitrogen (BUN) and glucose in plasma, as well as pH, NH_3-N, and VFA concentrations in ruminal fluid. Data were analyzed using PROC MIXED of SAS with repeated measures. Model included the fixed effects of treatment, time, treatment × time, square, and period, and the random effects of steer (square) and steer (treatment). No effect of treatment ($P > 0.05$) was observed for pH, NH_3-N, or glucose concentration. An effect of treatment ($P < 0.01$) was observed for BUN, with steers receiving SBM having greater concentrations. There was no effect of treatment ($P > 0.05$) on total VFA concentrations. Steers consuming CSM had greatest acetate molar proportion, and greater acetate to propionate ratio when compared with DDGS and BCM. Steers consuming DDGS had greatest molar proportions of butyrate and greater molar proportions of propionate compared with SBM and CSM. There was no effect of treatment ($P > 0.05$) on DMI or apparent total tract digestibility of DM, OM, CP, NDF, or ADF. *Brassica carinata* performed similarly to commonly used protein supplements, excluding VFA profile, indicating its viability as a protein supplement for beef cattle.

Key Words: *Brassica carinata*, metabolism, digestibility
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540 Acceptability of *Spondia mombin* Linn Leaves by West African dwarf (WAD) sheep in Ijebu-Ode local government, Ogun State, Nigeria.

A. A. Mako[1], A. O. Mosuro*[2], V. O. Akinwande[1], and A. O. Akinsoyinu[3], [1]*Tai Solarin University of Education, Ijebu-ode, Nigeria,* [2]*University of Ibadan, Ibadan, Nigeria,* [3]*Babcock University, Ilishan, Nigeria.*

Evaluation of nutrient composition of browse forage under utilized as fodder by ruminants was carried out at the Tai Solarin University of Education, Ijagun. Ijebu-Ode. Ogun State. Nigeria. The objective of this work was to study the preference of different leaves (green, yellow and brown) of *Spondia mombin* by West African Dwarf Sheep (WAD). Eight female WAD sheep weighing 10 to 12 kg between the ages of nine months to one year were used in a fourteen day cafetaria feeding to assess the animals' preference profile for the green, yellow and brown leaves of *Spondia mombin*. During the fourteen day preference study, each of the forage (green, yellow and brown laeves) were served in separate container to allow each animal to have free access to each forage. The position of each container was changed every day to prevent animal's adaptation to a particular type of forage. The value of the Coefficient of preference (COP) for each leaf was calculated from the ratio between the intakes of each individual forage divided by the average intake of the forage. The result revealed that the value of COP of different leaf ranged from 1.85 – 2.05 in brown and green leaves respectively. The green leaf was mostly preferred. Samples from the feed refusal were taken to the laboratory to determine the chemical composition of green, yellow and brown leaves of *Spondia mombin*. Data generated were subjected to Analysis of Variance (ANOVA) and means were separated using Duncan's Multiple Range Test. Significance was accepted at 0.05 level of probability. The result showed that dry matter (DM), crude protein (CP), ether extract (EE), Ash, neutral detergent fiber (NDF) and acid detergent fiber differed significantly ($P < 0.5$) among the green, yellow and brown leaves. The highest value (90.22%) of Dry matter was recorded for the brown leaf, while the lowest value (85.05%) was recorded for the green leaf. The Crude protein ranged from 9.59 – 11.25% in brown and green leaves respectively, the green leaf had the lowest value (8.25%) of Ash, while the highest value (10.00%) was obtained in the brown leaf. Same trend was observed in EE, ADF and NDF. The Neutral detergent fiber ranged from 46.48-62.01% in green and brown leaves respectively. It can be concluded that *Spondia mombin* green, yellow and brown leaves has

potential as forage in animal nutrition in this region as all leaf form were acceptable to the animals

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541 Flaxseed containing lipid supplement improves omega-3 concentrations and omega-6-to-omega-3 fatty acid ratios in bovine serum.

K. Swanson*[1], S. Akers[1], R. Wilson[1], M. Keller[1], L. Goddik[1], G. Cherian[1], R. Day[2], and G. Bobe[3], [1]*Oregon State University, Corvallis,* [2]*N3Feed, Tualatin, OR,* [3]*Department of Animal and Rangeland Sciences, Oregon State University, Corvallis.*

In humans, circulating omega-3 fatty acids are associated positively with health outcomes and lower chronic inflammation. To determine whether a flaxseed containing lipid supplement 12BT40 (*N3*Feed® LLC; Tualatin, OR) increases omega-3 content in bovine serum, we fed 6 mid- to late-lactation, pregnant Holstein cows (1 block each for primaparous and multiparous cows) for 6 wk consecutively 0 (Control; 1 week), 0.91 (1 week), 1.81 (2 weeks), and 2.72 kg/d (2 weeks) 12BT40 as top-dressing. Serum samples were collected at the end of each treatment period and analyzed for fatty acid profile. Data were analyzed using PROC MIXED in SAS version 9.4. Fixed effects were supplementation rate (linear, quadratic and cubic) and parity; cow was the random effect. 12BT40 supplementation rates increased linearly (linear $P = 0.01$) total FFA concentrations in serum by 12%. 21%, and 42% for 0, 0.91, 1.81, and 2.72 kg/d of 12BT40. The serum omega-3 concentrations increased from 8.6 to 18.2, 22.3, 28.3±3.2 µg/mL, when 0, 0.91, 1.81, and 2.72 kg/d of 12BT40 was fed (linear $P < 0.0001$; quadratic $P = 0.003$); the serum omega-6 concentrations increased from 35.2 to 38.3, 41.5, and 44.2±4.9 µg/mL (linear $P = 0.10$). As a result, the omega-6-to-omega-3 ratio in serum improved from 4.06 to 2.10, 1.87, and 1.60±0.07 (linear, quadratic and cubic all $P < 0.0001$). Based on these results, we conclude that feeding up to 2.72 kg/d 12BT40 improves omega-3 concentrations and omega-6-to-omega-3fatty acid ratios in bovine serum.

Key Words: Serum, Fatty acid profile, Flaxseed
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542 Calcium, phosphorus, and micro minerals supplementation does not affect nutrient intake and digestibility, and performance of Nellore cattle fed different diets.

D. Zanetti[1], L. A. Godoi[2], T. E. Engle[3], M. V. C. Pacheco[2], B. C. Silva[2], E. B. Ferreira[4], and S. C. Valadares Filho*[2], [1]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil,* [2]*Universidade Federal de Viçosa, Viçosa, Brazil,* [3]*Colorado State University, Fort Collins,* [4]*UFV, Viçosa, Brazil.*

Phosphorus supplementation is commonly reported as unnecessary for beef cattle in feedlots. However, the impact of absence of other macro and microminerals for beef cattle is not frequently reported in literature. The objectives of this study were measure the effects of mineral supplementation on nutrient intake and digestibility, and performance of Nellore beef cattle fed with and without calcium (Ca), phosphorus (P) and micromineral (MM) supplemental sources during the growing and finishing phases. Forty-two Nellore beef cattle (initial BW = 270.4 ± 36.6 kg, age = 8 months) were assigned to one of 6 treatments, aimed to have different Ca:P ratios: Sugarcane (400 g/kg DM) and a soybean meal and soybean hull-based concentrate with (SH100) and without (SH0) Ca, P and MM supplementation; Sugarcane (400 g/kg DM) and a soybean meal and ground corn based concentrate with (SC100) and without (SC0) Ca, P and MM supplementation; and corn silage (600 g/kg DM) with a soybean meal and corn-based concentrate with (CS100) and without (CS0) Ca, P and MM supplementation. The experiment was conducted as a completely randomized design with a 3 × 2 factorial arrangement of treatments. Nutrient intake, digestibility and performance were not affected by mineral factor ($P > 0.10$). Dietary effects were observed ($P < 0.01$) for DM, OM, CP and NDF digestibilities. Sugarcane based diets presented a greater DM and OM digestibility coefficients. It could be related to greater amounts of concentrate in these diets. Neutral detergent fiber presented a reduced digestibility in diets where sugarcane was forage source and the concentrate was ground corn-soybean hulls based. This smaller coefficient may be a consequence of the proportion of indigestible NDF in relationship to dietary NDF. Regarding CP digestibility coefficient, corn silage based diets presented a smaller coefficient than sugarcane based diets. It could be explained by smaller amount of urea in CS diets, and consequently smaller amounts of RDP. Among sugarcane based treatments, SH diets presented greater CP digestibility coefficients than SC diets. With regard to productive performance and efficiency parameters measured, average daily gain, and empty body weight gain, hot and cold carcass yield, carcass length, rib eye area, and subcutaneous fat thickness were not affected ($P > 0.10$) by treatments. The absence of inorganic supplemental sources of Ca, P, Cu, Mn, Zn and Co in diets for Nellore beef cattle during

both the growing and finishing phases does not affect nutrient intake, digestibility and performance.

Key Words: beef cattle, minerals, performance
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543 Supplemental trace minerals (Cu, Mn, and Zn) as sulfates or hydroxychloride sources for beef heifers.

R. H. Burnett*[1], E. B. Kegley[2], J. G. Powell[2], R. W. Rorie[2], J. J. Ball[2], J. A. Hornsby[2], J. L. Reynolds[2], B. P. Shoulders[2], J. D. Tucker[3], D. S. Hubbell, III[3], and S. B. Laudert[4], [1]*Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville,* [2]*Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville,* [3]*University of Arkansas Division of Agriculture Livestock and Forestry Research Station, Batesville,* [4]*Micronutrients, Indianapolis, IN.*

Crossbred-Angus heifers (n = 215, 249 ± 9 kg initial BW, 295 ± 16.5 d of age) were used over a 2-yr period to determine the effects of mineral source on beef heifer development at 2 locations (n = 71, Fayetteville, block 1; n = 72 in each of 2 breeding groups, Batesville, blocks 2 and 3). Within each breeding group, heifers were stratified based on initial BW, age, health, prior research project, and sire; and assigned to 6 groups of 12 heifers, groups were then assigned randomly to 1 of 2 trace mineral treatments. The 2 treatments were trace mineral supplementation (Cu [74 mg/d], Mn [294 mg/d], and Zn [221 mg/d]) as 1) sulfate or 2) hydroxychloride sources. Treatments were delivered through mineral and vitamin supplements provided free choice and formulated for a consumption rate of 113 g/d. Heifers were maintained on fescue-bermudagrass pastures and were rotated monthly to limit pasture effects. Treatments began on d 0, with the breeding season starting on d 112 (block 1, with a synchronization period and A.I for 10 d, followed by a 60 d exposure to bulls); d 130 (block 2, 60 d exposure to bulls); and d 146 (block 3, 60 d exposure to bulls); with the conclusion of the trial on d 224 (block 1), d 252 (block 2), and d 268 (block 3). During the trial, 28-d BW, mineral disappearance, health records, and reproductive efficiency data were recorded. At the end of each trial, pregnancy was confirmed by determining the presence of Pregnancy-Specific Protein B concentrations in blood. There were no treatment differences ($P \geq 0.52$) detected in BW or ADG throughout the trial. There was a tendency for greater mineral disappearance in the sulfate treatment ($P = 0.07$) compared to the hydroxychloride treatment. Pinkeye occurrence was fewer ($P = 0.04$) in the sulfate treatment group compared to the hydroxychloride treatment (1.9% vs. 7.5%). There were no differences in the percentage of heifers treated for bovine respiratory disease ($P = 0.56$) or foot rot occurrence ($P = 1.00$) between sulfate and hydroxychloride treatments. Trace mineral source did not affect reproductive performance ($P = 0.75$). Therefore, supplementing sulfate or hydroxychloride sources of Zn, Mn, and Cu to developing beef heifers resulted in similar performance.

Key Words: trace mineral, source, heifer development
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544 Effect of narasin addition in mineral mixture on gain and intake of feedlot Nellore heifers.

L. G. M. Gobato*[1], R. G. Silva[1], A. A. Miszura[1], D. M. Polizel[1], M. V. C. Ferraz Junior[1,2], G. B. Oliveira[1], A. V. Bertoloni[1], J. P. R. Barroso[1], and A. V. Pires[1,2], [1]*FMVZ/University of São Paulo, Pirassununga, Brazil,* [2]*ESALQ/University of São Paulo, Piracicaba, Brazil.*

Narasin, an ionophore used in poultry, improved BW gain and feed efficiency in cattle fed high forage. However, there is little information about the effect of narasin for cattle fed a high-grain diet. The objective of this study was to determine the effect of adding narasin in the mineral mixture (MM) on gain and intake of feedlot Nellore heifers fed a high-grain diet. Sixty heifers at 12 ± 1 mo of age were assigned to a randomized complete block design, defined by initial BW (244 ± 4 kg), and housed in 20 pens (3 per pen). The experimental treatments were either a control, with no narasin added, or Narasin, with 1,300 mg of narasin per kilogram of MM. The diet was composed of 15.8% (DM basis) sugar cane bagasse, 70.8% ground corn, 12.9% soybean meal, and 0.5% urea. Treatments were arranged in a crossover design (all pens underwent all treatments) with 2 experimental periods of 28 d each, and between periods, there was a 7-d washout. Heifers were weighed at the beginning and at the end of each experimental period to calculate ADG. All days, MM was offered and orts were collected to calculate the MM intake (MMI). The ADG and feed efficiency were submitted to ANOVA by the MIXED procedure (SAS 9.3). The DMI and MMI were analyzed as repeated measures over time using the same procedure. The statistical model was composed by effect of treatments, periods, and pens. The addition of narasin in MM did not affect DMI (6.59 for the control and 6.55 kg/d for the Narasin treatment [SEM 0.25, $P = 0.56$]), MMI (57.6 for the control and 55.6 g/d for the Narasin treatment [SEM 11.9, $P = 0.33$]), and ADG (1.09 for the control and 1.17 kg for the Narasin treatment [SEM 0.04, $P = 0.06$]). However, the addition of 1,300 mg of narasin/kg of MM increased feed efficiency compared with the control treatment (0.165 for the control and 0.179 for the Narasin treatment [SEM 0.01, $P = 0.05$]). Based on DMI and MMI, the narasin intake was 10.6 mg/kg. The inclusion of narasin in MM increased feed efficiency in feedlot Nellore heifers fed a high-grain diet without affecting MMI and DMI.

Key Words: additive, ionophore, feed efficiency
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545 The addition of narasin into a mineral mixture improves performance of grazing Nellore steers.

D. M. Polizel*[1], M. J. P. T. Barbosa[2], B. I. Cappellozza[3], C. N. Lopes[3], M. V. C. Ferraz Junior[1,4], L. G. M. Gobato[1], J. R. S. Gonçalves[5], and A. V. Pires[1,4], *[1]FMVZ/University of São Paulo, Pirassununga, Brazil, [2]CCA/State University of Londrina, Londrina, Brazil, [3]Elanco Saúde Animal, São Paulo, Brazil, [4]ESALQ/University of São Paulo, Piracicaba, Brazil, [5]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, Brazil.*

Previous studies have demonstrated that narasin, a coccidiostatic and antibacterial agent, may improve performance of forage-fed cattle due to rumen fermentation changes. The objective of this trial was to determine the effects of narasin inclusion into a mineral mixture (MM) on performance of grazing steers. Two hundred and forty Nellore steers (12 ± 1 mo of age) were blocked by initial BW (177 ± 0.21 kg), and assigned to 30 lots (8 steers/lot and 10 lots/treatment). Sixty paddocks of *Brachiaria brizantha* with 1 ha each were used and each paddock was continuously grazed by 28 d, followed by 28 d of rest. A paddock rotation among treatments was designed every 28 d to minimize the effect of variation among pastures. Paddocks were assigned to receive 1 of 3 treatments: a control (no narasin; 0N), and an intake of 71.5 (13N) and 110 (20N) mg of narasin (Zimprova®; Elanco, São Paulo, Brazil) per day, corresponding to 13 and 20 ppm considering 2.5% the DMI of steers. Narasin was added in the MM by adjusting their concentration in each period, according to MM intake (MMI) in the previous period. The MMI was evaluated on a weekly basis, starting 28 d before the beginning of the experiment. Forage mass in the paddocks was measured by choosing two points upon entry and exit of the lot from each pasture. All data were analyzed using the PROC MIXED procedure of SAS and evaluated by period (every 28-d) and overall (d 0 to 84). No treatment × period (P = 0.85) or treatment (P = 0.23) effects were observed for daily MMI (64, 61, and 58 g for 0, 13, and 20N, respectively; SEM = 2.19). Conversely, a treatment × period interaction was observed (P = 0.002) for ADG, because ADG was greater ($P \leq 0.01$) for 13N and 20N in the 1st and 2nd periods and also greater (P = 0.03) for 20N vs 13N in the first 28 d of the study, whereas no differences ($P \geq 0.18$) were observed in the last 28 d. Moreover, overall ADG was also greater ($P < 0.01$) for 13N and 20N when compared with cohorts receiving 0N, without differences between 13 and 20N (P = 0.65; 0.493, 0.575, and 0.585 kg/d, respectively; SEM = 0.0150). In summary, narasin inclusion into the mineral mixture did not impact mineral intake and improved overall steers performance during an 84-day period.

Key Words: Grazing, narasin, performance
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546 Inclusion of zeolites(clinoptilolite) in finishing ration of feedlot beef cattle.

N. M. Jones*, T. E. Engle, H. Han, J. J. Wagner, and S. L. Archibeque, *Colorado State University, Fort Collins.*

The objective of this study was to evaluate the inclusion of zeolites (clinoptilolite) on performance of feedlot steers fed a high concentrate, steam flaked corn-based finishing diet for 138 d. It was hypothesized that the ion exchange capacities of zeolites may serve as a buffering agent within the rumen and improve performance in a dose dependent fashion. Crossbred steers (n = 320, initial BW 412 ± 3.2 kg) were evenly distributed in a completely randomized block design with four treatments. Steers were blocked by weight and randomly assigned to one of the four experimental treatments (8 pens per treatment; 10 hd per pen) with pen as the experimental unit. Treatments consisted of zeolite included at 0, 0.5, 1 or 2% of the diet DM. Steers were individually weighed on days 0, 21, 49, 77, 105 and 138. Initial pen BW was used as a covariate in the statistical analysis and significance was determined at $P \leq 0.05$ and tendency level determined at $P \leq 0.15$. Final BW ($P > 0.68$) and feed efficiency ($P > 0.58$) were similar across all treatments. Dry matter intake (P = 0.14) and average daily gain (P = 0.10) tended to be greater for steers fed zeolites at 1% of the dietary DM. There were no differences (P = 0.40) in mortality and morbidity between treatments. These data indicate, that under the conditions of this experiment, the addition of zeolites to steam flaked corn-based finishing diets does not impact final body weight or feed efficiency and tended to improve DMI and ADG of feedlot cattle when zeolites were included at 1% of diet DM.

Key Words: zeolite, clinoptilolite, beef cattle
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547 Fatty acid profile of omasum from cattle fed with soybean oil, selenium and vitamin E.

P. D. Teixeira[1], A. V. P. Ferreira[1], O. R. Machado Neto[2], M. P. Gionbelli[1], L. R. Santos[1], F. F. Moreira[1], A. Cominotte[3], and M. M. Ladeira*[1], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]Universidade Estadual Paulista, Botucatu, Brazil, [3]Universidade Estadual Paulista, Jaboticabal, Brazil.*

The objective of this study was to evaluate the concentration of fatty acid in the omasum when diets with 6% soybean oil and with or without supplementation of organic selenium and vitamin E were fed. Five cannulated steers with an average initial body weight of 398 ± 28.7 kg were subjected to a 5 x 5 Latin Square with 21 days periods: 14 days of adaptation to diets and 7 days of sampling. Diets consisted of 65% concentrate and 35% corn silage formulated to be isonitrogenous (14.4% CP). Steers were assigned to dietary treatments: without additional oil; 6% soybean oil; 6% soybean oil plus vitamin E; 6% soybean oil plus selenium; 6% soybean oil plus vitamin E plus selenium. The additives were offered daily with 1500 IU vitamin E and 5 g selenium per animal. Digesta of the omasum were collected for long chain fatty acids analysis using gas chromatography. The model included the fixed effects of diet and period and animal as a random effect, and was analyzed using PROC MIXED of SAS (SAS Inst. Inc., Cary, NC). The soybean oil diet had lower concentration of lauric acid (C12:0) (0.13 and 0.35; $P < 0.01$), myristic (C14:0) (0.47 and 1.21; $P < 0.01$), pentadecanoic (C15:0) (0.20 and 0.60; $P < 0.01$), palmitic C16:0) (12.75 and 15.6; $P < 0.01$), palmitoleic (C16:1) (0.06 and 0.16; $P = 0.01$), heptadecanoic (C17:0) (0.22 and 0.34; $P = 0.02$), oleic (2.30 and 3.85; C18:1 c9) ($P < 0.01$), and linoleic (C18:2 c9,12) (2.11 and 3.09; $P = 0.01$) than the diet without additional oil. However, the soybean oil diet had higher concentrations of elaidic (C18:1 t9) (0.61 and 0.27; $P = 0.02$), CLA C18:2 t10, c12 (0.04 and not detected; $P = 0.\ 01$) and polyunsaturated fatty acids (PUFA) (2.66 and 3.75; $P < 0.01$) than the diet without additional oil. The supplementation with selenium tended to increase the concentration of C18:2 c9,12 (2.40 and 1.72; $P = 0.07$) and PUFA (3.0 and 2.33; $P = 0.07$) compared to the diet without selenium. In conclusion, supplementation with soybean oil and selenium can contribute to the increase concentration of PUFA in the digesta of the omasum, which may positively impact the concentration of PUFA in the subcutaneous and intramuscular fat of beef cattle.

Key Words: CLA, Lipids, PUFA
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548 Effect of copper supplementation on pre- and postpartum primiparous beef heifer and progeny hematological parameters fed diets with or without supplemental sulfur.

J. Hawley*, E. B. Kegley, and J. G. Powell, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville.*

To assess the effects of Cu supplementation on pre- and postpartum primiparous beef heifer and progeny hematological parameters fed diets with or without supplemental S, 36 primiparous beef heifers (20 ± 0.5 mo of age; initial BW = 398 ± 24.9 kg) 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 study. Pens were assigned randomly 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 $Cu_2(OH)_3Cl$]. Diets were formulated to meet nutrient requirements during late gestation, with the exception of Cu and S. 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 predominantly fescue hay in quantities to ensure ad libitum access to forage. Heifer hematological parameters were assessed from blood samples collected d -113, -85, -57, -29, 0, 56, 85, 113, 142, and 150 ± 16 relative to parturition. Calf hematological parameters were assessed from blood samples collected 0, 31, 59, 86, 115, and 150 ± 6 d relative to birth. Orthogonal contrasts were used to determine the effects of Cu vs. S supplementation. Statistical significance was declared at $P \leq 0.10$. No differences ($P \geq 0.58$) were observed between treatments for heifer hemoglobin, hematocrit, white blood cell count, and red blood cell count. Supplementing heifers additional Cu decreased ($P = 0.10$; Cu main effect) the lymphocyte percentage and increased ($P \leq 0.10$; Cu main effect) the neutrophil:lymphocyte ratio when compared to heifers not supplemented additional Cu. Supplementing heifers 0.55% S decreased ($P \leq 0.10$; treatment × day) basophils at parturition when compared to heifers fed 0.15% S. Heifer pre- and postpartum Cu supplementation with or without supplemental S did not ($P \geq 0.31$) influence progeny hematological parameters. These results suggest that the pre- and postpartum primiparous beef heifer immunity related blood profile (lymphocyte percentage) could be altered with a concomitant increase in inflammatory reaction (neutrophil:lymphocyte ratio) by Cu supplementation at 12 to 14 mg/kg of diet.

Key Words: Beef cattle, Hematological parameters, Mineral supplementation
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549 Influence of commercial yeast products in diets for beef cattle new to the feedlot environment.

E. A. Palmer*[1], J. J. Ball[1], E. B. Kegley[1], P. A. Beck[2], J. G. Powell[1], J. A. Hornsby[1], J. L. Reynolds[1], B. P. Shoulders[1], and A. Boyer[3], *[1]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, [2]University of Arkansas Division of Agriculture SWREC, Hope, AR, [3]University of Arkansas, Fayettville.*

Two truckloads of male beef calves (n = 172; initial BW = 226 ± 24.5 kg) were purchased from regional livestock markets to evaluate the effect of commercial yeast products on health and growth performance during a 28-d receiving period. Within truckload, calves were blocked by initial BW, stratified by gender, and assigned randomly to pen (5 or 6 calves/pen; 15 pens/truckload). Pens within each weight block were allocated to 1 of 3 treatments; an unsupplemented control, or supplementation with 2 commercial *Saccharomyces cerevisiae* yeast products (Y1 or Y2) resulting in 10 pens/treatment. Each day, a mixture (0.14 kg/d for each calf) of 58% ground corn and 42% of the appropriate yeast product, or 100% ground corn (control) was added to the feedbunks immediately after basal diet delivery and hand mixed into the feed offered. The basal diet contained 40% corn, 20% cottonseed hulls, 19% dried distiller grains, 10% corn gluten meal, and 7% soybean meal. Data were analyzed using the MIXED and GLIMMIX procedures of SAS with an alpha of 0.05 for all dependent variables. Final BW at the end of the 28-d trial were 255, 255, and 254 kg ($P = 0.99$) for the control, Y1, and Y2 treatments, respectively. Average daily gain from d 0 to 28 was not different ($P = 0.99$) between control, Y1, and Y2. Supplementation did not affect DMI ($P \geq 0.92$) or gain:feed ratio ($P \geq 0.91$). Morbidity was observed daily at feeding. Percentage morbidity due to bovine respiratory disease (BRD) was not altered ($P = 0.29$) with control, Y1, or Y2 (64.5%, 76.7%, and 63.0%), respectively. The percentage of relapses were 32.7, 38.8, and 51.9 ($P = 0.36$) for the control, Y1, and Y2, respectively. Days until first antibiotic treatment were not different ($P = 0.17$) between the 3 treatments. Antibiotic treatments began on d 2 and by d 5 approximately 50% of calves had been administered their first antibiotic. Antibiotic treatment costs were not different ($P = 0.78$) for control, Y1, and Y2. Given that the cost of antibiotic treatment was not different between groups, the addition of yeast did not provide an economic benefit in prevention against BRD. In high risk calves with over 50% morbidity by d 5, providing yeast products did not have an effect on health and growth performance.

Key Words: yeast, receiving calves, health
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550 The application of *Trichoderma* fermentation extract to growing and finishing rations improved beef cattle performance.

O. AlZahal*[1], A. Waite[2], N. D. Walker[1], T. Byrd[3], and D. Bechtol[2], [1]*AB Vista, Marlborough, United Kingdom,* [2]*Agri Research Centre Inc., Canyon, TX,* [3]*Feedworks USA Ltd, Cincinnati, OH.*

The objective of this study was to evaluate the effect of pre-treating beef cattle rations with a *Trichoderma* fermentation extract (VistaPre-T; AB Vista, UK) on the performance of beef cattle during growing and finishing phases. Predominantly Angus cross heifers (n = 360, BW=248 ± 18 kg) were blocked by their initial BW and assigned randomly to 1 of 4 treatments: 0, 0.5, 0.75, and 1 ml of VistaPre-T/kg of DM. VistaPre-T was applied to the ration during the mixing process. The ration was offered ad libitum and comprised of steam-flaked corn, chopped alfalfa hay, and dried distillers grains. Body weight was measured every 30 d. The offered DMI was measured daily and averaged every 30 d. Animals were shipped to slaughter in two blocks on d 216 and d 238. Statistical analysis was conducted using Proc Mixed of SAS (v. 9.4) with treatment as the fixed effect. Results were presented in Table 550. During the growing phase (d1 to d 60), the application of VistaPre-T linearly increased BW, ADG, and F:G. Additionally, the application of VistaPre-T linearly increased both the final BW and the overall ADG and quadratically increased the overall F:G. In conclusion, the application of *Trichoderma* fermentation extract, VistaPre-T, directly to growing and finishing rations improved the performance and feed efficiency of beef cattle.

Key Words: Beef cattle, Performance, Trichodrma extract
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Table 550.

Item	Trichoderma extract, ml/kg DM 0	0.5	0.75	1	SE	*P*-value Linear	Quad	0 vs 0.5	0 vs 0.75	0 vs 1
BW d 61	330	332	335	336	2	0.00	0.78	0.39	0.03	0.01
Final live BW, kg	563	572	574	576	4	0.02	0.37	0.11	0.05	0.02
ADG, kg/d										
d 1-30	1.27	1.37	1.44	1.46	0.04	0.00	0.25	0.05	0.00	0.00
d 1-61	1.35	1.38	1.43	1.44	0.03	0.00	0.78	0.39	0.03	0.01
d 1-end	1.39	1.44	1.44	1.46	0.02	0.01	0.36	0.05	0.04	0.01
DMI, kg/d										
d 1-30	8.06	7.96	8.16	8.14	0.20	0.63	0.84	0.71	0.73	0.79
d 1-61	8.64	8.44	8.64	8.61	0.20	0.90	0.66	0.48	1.00	0.92
d 1-end	8.72	8.59	8.67	8.81	0.12	0.54	0.28	0.43	0.78	0.63
F:G										
d 1-30	6.47	5.80	5.72	5.62	0.23	0.02	0.22	0.05	0.03	0.01
d 1-61	6.42	6.14	6.13	5.97	0.16	0.06	0.70	0.22	0.19	0.05
d 1-end	6.27	6.02	6.02	6.06	0.07	0.05	0.04	0.01	0.02	0.04

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551 Effect of diet inclusion of tropical fodder trees on digestibility in hair lambs.

R. Castaneda Serrano*[1], M. Sanchez[1], A. Huertas[1], J. Pardo Guzmán[2], V. Díaz[1], R. Piñeros[1], and A. Velez[2], [1]*Universidad del Tolima, Ibague, Colombia,* [2]*Universidad del Tolima, Ibagué, Colombia.*

The objective of this study was to determine the apparent digestibility of diets based on *Dichanthium aristatum* and tropical fodder trees. The experiment was carried at Las Brisas Farm of the University of Tolima – Colombia. Twelve hair lambs (22 ± 2.5) were housed individually in digestion crates in 4 x 4 Latin square design. Each period consisted with 14 d of adaptation and 5 d of sample collection. Treatments were: T1= 100% D. aristatum, T2= 50% *D. aristatum*, 25%

Guazuma ulmifolia and 25% rice bran; T3= 50% *D. aristatum*, 25% *Gliricidia sepium* and 25% rice bran and T4= 50% *D. aristatum*, 25% *Tithonia diversifolia* and 25% rice bran. Tropical tree fodder, rice bran and hay were supplied in total mixed ration twice daily ad libitum. Feeds, orts and feces were collected daily before morning feed during the collection period. Data were analyzed using the PROC MIXED of SAS. It was observed that intake of nutrients were positively affected by the supplementing tree fodder ($P < 0.0001$). Digestibility of dry matter were affected by treatments, T1, T2, T3 and T4, showed values of 45%, 56%; 61% and 62% respectively. Protein digestibility was greater ($P < 0.05$) for T3 (60%) and T4 (59%), respectively. Protein fraction B3 was higher for T2 (80%), T3 (84%) and T4 (71%). It was concluded that supplementation with tropical fodder trees in hair lambs, is an interesting strategy to increase the intake and digestibility of nutrients, contributing to the improvement of performance and mitigate the negative effect of dry season.

Key Words: alternative feed, silvopastoral systems, small ruminants
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552 Effects of fibrolytic enzyme on in-vitro true digestibility of by-products commonly fed to cattle.

L. Barbosa Kondratovich*, J. O. Sarturi, M. A. Ballou, D. Sugg, P. R. B. Campanili, B. Q. Reis, A. C. B. Melo, L. A. Pellarin, and L. A. Ovinge, *Texas Tech University, Lubbock.*

In vitro true digestibility of DM, OM, NDF, and ADF with and without inclusion of a fibrolytic enzymes were evaluated in 12 byproducts. Ruminal fluid inoculum was collected from donors (ruminally cannulated beef steers; n = 4; BW = 463 ± 53 kg) during 4 periods (each period consisted in one in vitro batch [experimental unit]). Donors were fed forage-based diets (high and low quality) for 21 d prior collections (each in vitro batch was inoculated with a mixture of rumen fluid from both high and low quality diet donors). Incubations followed a randomized complete block design (block = in vitro batch). Substrates consisted of: corn cobs (CC), intact sorghum grain (ISG), wheat straw (WHST), cotton burrs (CTBR), corn stalks (CSTK), cotton seed hulls (CSH), grape pomace (GRPM), soybean hulls (SBH), high-quality alfalfa (ALFH), low-quality alfalfa (ALFL), sorghum stalks (SRST), and sorghum dry distillers' grains (SDDGS). Samples were incubated in DAISYII Incubator (Ankom Technology, Macedon, NY) with fibrolytic enzyme (0.75 µl/g of substrate DM; ABVista, United Kingdom) within jar (24 bag plus blank). Quadruplicate samples were incubated according to unit instructions. Following 48-h incubations, analyses NDF, ADF, and ash were performed on bags in sequence. Data were analyzed using the GLIMMIX procedures of SAS, with enzyme, substrate type, and interactions as fixed effect and in vitro batch as random. An enzyme treatment × substrate interaction resulted in a 13.2% increase ($P < 0.01$) in IVTDMD of ISG as well an observed tendency ($P = 0.10$) for greater digestion in CSTK. Similarly, IVTOMD of ISG was enhanced ($P < 0.01$) with addition of enzyme. Sorghum grain also produced an enzyme treatment × ingredient interaction associated with NDF digestibility in which inclusion on enzyme increased ($P < 0.01$) digestion by 16.35% relative to no enzyme. Regardless of substrate type, addition of enzyme increased ($P < 0.01$) disappearance of ADF by approximately 13.6%. Ingredient differences ($P < 0.01$) associated with ADF digestibility resulted in SBHS being the highest (71.78%) whereas CTBR, CSHS, and GRPM had the lowest values (≤ 24.60%). Fibrolytic enzymes positively affected fiber digestion of commonly fed roughage sources in cattle diets, and might have additional benefit when used on sorghum grain-based diets.

Key Words: digestibility, Fibrolytic enzyme, roughages
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553 Effects of pentacyclic triterpenes on in vitro fermentation of bahiagrass hay and a high-grain substrate.

L. Rostoll-Cangiano*[1], D. D. Henry[1], F. M. Ciriaco[1], M. E. Garcia-Ascolani[1], T. M. Schulmeister[1], I. R. Ipharraguerre[2], G. C. Lamb[3], and N. DiLorenzo[1], [1]*University of Florida, North Florida Research and Education Center, Marianna,* [2]*University of Kiel, Kiel, Germany,* [3]*Texas A&M University, Department of Animal Science, College Station.*

Triterpenes are the most representative group of phytochemicals, comprising more than 20,000 recognized molecules. The diversity of triterpenes is highly associated with their broad range of pharmacological effects. Previous studies have demonstrated their anti-microbial potential. Our objective was to determine potential effects of pentacyclic triterpenes (TT) on in vitro batch culture fermentation of bahiagrass hay and a high-grain substrate. A randomized complete block design was used to determine the effects of increasing concentrations of the following TT types: oleanolic acid (OA), ursolic acid (UA) and malsinic acid (MAL) on in vitro fermentation of bahiagrass hay (BGH) or a high-grain substrate (HG) comprised of 43% soybean hulls pellets, 42% corn gluten feed pellets, and 15% peanut hulls (DM basis). Treatments were arranged as a 4 × 3 factorial with 4 doses (0, 4, 25 and 100 mg/L of incubation volume) for each of the 3 TT types. Four ruminally cannulated crossbred steers (362 ± 30 kg BW) were used as ruminal fluid donors. Two steers were fed HG ad libitum, while the other two steers were fed BGH ad libitum for at least 14 d prior to the first incubation day. Each replicate d, 125-mL serum bottles containing 50 mL of a 4:1 buffer:ruminal fluid inoculum and 0.63 g of BGH substrate (DM basis) were incubated for 48 h, and a 2:1 buffer:ruminal fluid inoculum and 0.63 g of HG substrate (DM basis) were incubated for 24 h. Three d (block) of incubation were performed. In vitro OM digestibility (IVOMD) was determined in a separate set of tubes. Data were analyzed using PROC MIXED of SAS with the fixed effect of treatment, and random effect of incubation day. No effect was observed ($P > 0.05$) on total gas production, IVOMD, NH_3-N concentration and H_2S production. There was no effect ($P > 0.05$) of any TT types or doses on concentrations or molar proportions of VFA. No effect ($P > 0.05$) of TT type or dose were observed on acetate:propionate ratio (A:P). In conclusion, the acid form of the pentacyclic triterpenes did not affect ruminal fermentation of either substrate. Future studies should focus on increasing the solubility of these pentacyclic triterpenes by using a sodium salt.

Key Words: in vitro, fermentation, Pentacyclic triterpenes
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554 Effects of *Eucalyptus citriodora* oil on beef cattle ruminal fermentation characteristics on continuous culture system.

B. Q. Reis*[1], R. Ferreira Carvalho[2], J. O. Sarturi[1], P. R. B. Campanili[1], L. A. Pellarin[3], and L. A. Ovinge[1], [1]*Texas Tech University, Lubbock,* [2]*University of Sao Paulo / FZEA, Pirassununga, Brazil,* [3]*USP, Sao Paulo, Brazil.*

The effects of *Eucalyptus citriodra* essential oil on OM digestion, microbial efficiency, pH, and ammonia levels using the continuous culture system technique were evaluated. Three Eucalyptus inclusions (0; 500 and 1,000 mg/kg of DM) were randomly assigned to continuous culture flasks (experimental unit; n = 9; 3 per treatment) following a completely randomized design. Culture flasks (1 L) were equipped with drainage system for effluent (which was collected and kept under refrigeration) and CO_2 plug on the lid. Inoculum (rumen fluid) for culture system was collected from 3 donors (steers; BW = 520 ± 30kg) for all batches (n = 2). Steers were fed diets containing 37% steam-flaked corn, 35% wet corn gluten feed, 25% roughage, and 3% supplement (DM basis). A 7-d incubation period was used for each batch, in which the first 3 d were used for the system adaptation followed by 4 d of collections. Continuous culture substrate was added twice daily, and contents collected at 0, 0.5, 1, 2, and 12 h post-feeding. Data were analyzed using the GLIMMIX procedures of SAS; day was used as repeated measure; and orthogonal contrasts were used to evaluate linear and quadric effects of *Eucalyptus citriodra* inclusion. No interaction treatment x time was observed for in vitro ruminal ammonia and pH ($P = 0.98$ and 0.99, respectively). Eucalyptus inclusion did not affect ($P \geq 0.83$) in vitro ruminal ammonia, while in vitro ruminal pH decreased linearly ($P < 0.01$); in which 1,000 ppm dose showed a more acidic environment compared to other oil inclusions. Regardless of Eucalyptus inclusion, ruminal ammonia concentration peaked ($P < 0.01$) at 0.5 and 1h post in vitro system feeding time, while in vitro pH values reached the least ($P < 0.01$) levels at same collection times. No changes in true digestion of OM ($P = 0.88$), microbial efficiency ($P = 0.31$), NH_3 flow ($P = 0.76$), total N digestibility ($P = 0.95$), and microbial N flow ($P = 0.38$) were observed. Eucalyptus oil does not appear to negatively affect ruminal in vitro deamination or OM digestion. Increased acidity may confer potential positive effects on ruminal energetic load released within the first hour of fermentation post feeding.

Key Words: continuous culture system, essential oil, microbial efficiency
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555 Effect of level of Spirulina supplementation on oxidative stress, immunity, productive performance and reproductive parameters during the transition period by grazing dairy cattle.

C. H. Ponce*[1], D. Vela[2], A. Mullo[2], V. Cabezas[2], and A. Alvear[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.*

Previous data suggested that grazing dairy cattle could have higher levels of oxidative stress compared to confined animals. There is available a spirulina product containing phycocianin which has been characterized as a potent antioxidant. Nevertheless, there is little data available on antioxidant supplementation on grazing dairy cattle during the transition period. Therefore, the objective of this experiment was to evaluate the effects of spirulina supplementation on oxidative stress, immunity and productive performance and reproductive parameters during the transition period by grazing dairy cattle. Twenty-four multiparous gestating cows (BW = 543 ± 57 kg) were enrolled in this experiment, and were stratified by expected calving date. Cows were aleatory assigned to 3 experimental groups; 1) Control; no supplementation of spirulina; 2) Spirulina-15 (15 g of spirulina; 2 g phycocianin); and 3) Spirulina-30 (30 g of spirulina; 4 g phycocianin). Treatments initiated 3 weeks before parturition and were mixed in an energy supplement fed daily in the morning at a rate of 3 kg/cow (DM). Body weight and body condition score were monitored at - 21, 1, 21 d, relative to calving. Blood samples were collected at the same time points (before feeding) to measure oxidative stress indicators. All cows calved within a period of 12 wk, and graze in the same paddock during the experimental phase. The day of parturition colostrum samples and blood samples from calves were collected to measure IgG concentrations. After parturition milk production, milk components and somatic cell count were monitored daily and weekly, respectively. Incidence of postpartum reproductive diseases were also recorded. Body weight, body weight loss, and body condition score were not altered by treatment ($P > 0.46$), nevertheless in average cows had 2.9 and 4% reduction on body weight relative to the beginning of the trial. Total

antioxidative capacity was not affected by spirulina supplementation ($P > 0.31$) at any time point measured. There was a tendency for a quadratic increased on IgG concentration in colostrum as spirulina supplementation increased ($P = 0.10$). Nevertheless, there were no differences on calves serum IgG concentration attributed to treatment ($P = 0.98$). Milk production, milk components, somatic cell count and reproductive postpartum diseases were not altered by treatment ($P > 0.16$). Results from this experiment suggests no positive or negative effects of spirulina supplementation on oxidative stress, productive performance and reproductive parameters during the transition period by grazing dairy cattle. However, IgG response by spirulina supplementation requires further exploration.

Key Words: Dairy cattle, oxidative stress, Spirulina
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556 Effect of feeding isoquinoline alkaloids on biomarkers of inflammation and inflammatory cells in feedlot finishing bulls fed a high-grain diet.

H. Godoi Bertagnon*[1], A. M. Reck[1], M. Neumann[1], and B. Beyer[2], [1]*Universidade Estadual do Centro-Oeste - UNICENTRO, Guarapuava, Brazil,* [2]*Phytobiotics Futterzusatzstoffe GmbH, Eltville, Germany.*

Feeding high-grain rations in feedlots has improved feed efficiency, allowing feedlot cattle to achieve finishing weights faster. However, high-grain diets can lead to metabolic and digestive disorders, as well as to the suppression of the immune system. An impaired immune function predisposes the animals to infectious diseases. In poultry and swine, supplementation with isoquinoline alkaloids (IQs) has demonstrated to modulate the immune response and improve performance. The objectives of this study were to assess the effects of an IQs containing supplementation product on the circulating concentrations of an inflammation biomarker (haptoglobin) and inflammatory cells (leukocytes and neutrophils) in feedlot yearling bulls fed a high-grain diet. Animals were randomly allocated to 2 treatment groups with 16 replicates: (1) no supplementation (CON, n = 16), and (2) supplementation with 4 g/head/d of an IQ containing product (Sangrovit® RS, Phytobiotics Futterzusatzstoffe GmbH, Eltville, Germany; SAN, n = 16) top-dressed at the time of feed delivery. During the study period, all animals were fed the same high-grain diet containing a mixture of 85% whole corn and 15% protein-vitamin-mineral mix as a total mixed ration. Animals received the experimental diet ad libitum for 42 d with an initial adaptation period of 14 d. From study d 21 to 42 daily examination of animals for identification of nasal secretions was performed. On study d 42, blood samples were collected for assessment of serum haptoglobin concentrations and leukocyte and neutrophil counts. Haptoglobin concentrations did not differ ($P = 0.25$) between treatments (CON = 230.1 ± 40 ug/mL; SAN = 181.7 ± 21 ug/mL). Similarly, no differences ($P = 0.45$) in circulating leukocyte count was observed between SAN ($12.76 \pm 1.42 \times 10^6$/mL) and CON ($11.42 \pm 1.1 \times 10^6$/mL) groups. However, circulating neutrophils were elevated ($P = 0.0006$) in the SAN ($3.25 \pm 0.05 \times 10^6$/mL) compared to the CON ($1.18 \pm 0.01 \times 10^6$/mL) group. In addition, less animals ($P = 0.006$) in the SAN group (4.2 animals) presented nasal discharge when compared to the CON group (6.2 animals). Results from this study suggest that supplementation with IQs reduced the negative effects associated with feeding high-grain diets on immune cells. Animals fed IQs had increased circulating neutrophils counts which may help improve the animal response to infectious diseases.

Key Words: isoquinoline alkaloids, Haptoglobin, Neutrophils
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557 Ruminal microbiology from Nellore steers supplemented with additives in the rainy season.

E. E. Dallantonia*[1], J. F. Lage[2], E. San Vito[1], J. A. Torrecilhas[1], P. D. S. Castagnino[1], L. M. Delevatti[1], R. A. Reis[1], and T. T. Berchielli[1], [1]*São Paulo State University (Unesp) School of Agricultural and Veterinarian Sciences, Jaboticabal, Brazil,* [2]*Trouw Nutrition Brazil, Campinas, Brazil.*

The aim of study was evaluate the ruminal microbiology from animals fed supplements with monensin (MN), virginiamycin (VM) or both associated (MNVM), 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 with 0.3% of BW. The diets were: supplement without additives (SUPL), with MN (80 mg/kg), with VM (150 mg/kg) and associated supplement MNVM (80 + 150 mg/kg of MN and VM, respectively). The experiment consisted of four periods of 28 d (27 d of adaptation and 1 d of sampling collection). Animals were housed continuously in the paddocks with animals used in a trial for performance evaluating. The study evaluated the relative proportion of microorganism, *R. albus, R. flavefaciens, F. succinogenes, S. ruminantium* and methanogenic bacteria on 28th and 118th d of the experimental period (1st and 4th period). This design chosen to show the effect in the short and long term antibiotics. Data were analyzed as a completely randomly design with three replicates by treatment on each period, using the MIXED procedure of SAS. In the first period, the *R. albus* and methanogenics groups had no effect ($P > 0.05$) by the use of the two additives. Observed the effect ($P < 0.05$) of VM and MNVM on the relative proportion of *R. flavefaciens, F. succinogenes* and *S. ruminantium* , however, the *R. flavefaciens* bacteria did not differ from the control group to MN. In the 4th period the relative proportion of *F. succinogenes, S. ruminantium* increase when used VM and MNVM. The relative proportion of *R. flavefaciens* did not differ when compared to control group with used MN, however there was decrease the proportion with used VM and MNVM ($P < 0.05$). The methanogenic group showed effect when used VM ($P < 0.05$). In this study, the virginiamycin had greater control over *R. flavefaciens*, it is worth noting that the adaptive effect of bacteria was not conserved when the same additive was used.

Key Words: monensin, pasture, virginiamycin
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558 Feeding behavior of Nellore cattle supplemented with different combinations of sodium monensin and virginiamycin.

A. L. Rigueiro*[1], F. P. Luiz[1], M. C. Pereira[1], G. F. Melo[1], R. A. Rizzieri[1], A. G. Veiga[1], M. M. Squizatti[2], L. V. Toledo[1], D. D. Millen[2], C. L. Martins[1], and M. D. Arrigoni[1], *[1]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [2]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil.*

This study, conducted at Sao Paulo University feedlot, in Botucatu Campus, Brazil, was designed to evaluate the effect of combined use of monensin (MON) and virginiamycin (VM) during the adaptation period and finishing period on feeding behavior of Nellore cattle. Seventy-two 26-mo-old yearling Nellore bulls (388 ± 31.07 kg), backgrounded on pasture were randomly allocated and kept in 24 pens (10 m^2 and 1.67 m bunk space per animal) according to the treatments: MON (30 mg/kg) during the adaptation and finishing period, MON (30 mg/kg)+VM (25 mg/kg) during the adaptation and only VM (25 mg/kg) in finishing, MON (30 mg/kg)+VM (25 mg/kg) during the adaptation and finishing period, and only VM (25 mg/kg) during the adaptation period and MON (30 mg/kg)+VM (25 mg/kg) during the finishing period, thus characterizing a completely randomized block design. Each treatment was composed of 6 replications (pens) in this study. The adaptation program consisted of ad libitum feeding of 3 adaptation diets overa period of 19 d with the concentration level increasing from 69% to 84% of diet DM. Cattle were fed twice daily for ad libitum consumption throughout the study. Two visual appraisals were conducted, 1 at the end of the adaptation period and another at d 60 of the experimental period, every 5 min during 24 h at each observation. At the end of the adaptation period no treatment effects were observed for the time spent resting, ruminating and eating as well as the length and the number of meals per day. Cattle supplemented only with VM during the adaptation period and MON plus VM in the finishing period and those supplemented with MON plus VM during the adaptation period and only VM in the finishing period showed greater ($P < 0.05$) DMI (8.15; 8.10 vs 6.99), eating a rate of DM (20.11; 21.20 vs 26.9, min/kg of DM) and eating a rate of NDF (79.69; 91.39 vs 112.52, min/kg of NDF) compared to those fed only by MON during both adaptation and finishing period. However, at the 60th d of experiment cattle fed with the combination of MON and VM during the adaptation period and only VM during the finishing period showed greater DMI ($P = 0.01$), eating a rate of DM ($P < 0.01$) and NDF ($P < 0.01$) compared to all other treatments. Supplementation with different combination of MON and VM change feeding behavior of Nellore cattle, nevertheless, supplementation with MON and VM during the adaptation period and only VM in finishing period seem to improve the feeding behavior traits of Nellore cattle.

Key Words: Ionophore, Antibiotic, Rumen
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559 Effect of original XPC in receiving diets on newly weaned beef steer performance and response to a *Mannheimia haemolytica* vaccination challenge.

E. L. Deters*, R. S. Stokes, O. N. Genther-Schroeder, and S. L. Hansen, *Iowa State University, Ames.*

The objective was to determine the effects of Original XPC™ (Diamond V, Cedar Rapids, IA), a *Saccharomyces cerevisiae* fermentation product, in the diets of beef steers on total tract nutrient digestibility as well as feeding behavior and acute phase protein (APP) response following a vaccination challenge. Twelve days after arrival, 36 newly weaned crossbred beef steers (323 ± 12 kg) were blocked by BW and randomly assigned to one of three doses of XPC: 0 (CON), 14 (XPC14), or 28 (XPC28) $g \cdot steer \cdot d^{-1}$. Steers were fed via bunks capable of measuring individual intake and received ear tags (Cow Manager, Select Sires, Plain City, OH) that recorded real time ear surface temperature, rumination, and eating behavior. Body weights were collected on d -1, 0, 14, 28, 42, and 56. To determine diet digestibility, titanium dioxide was fed from d 12 to 27. All steers received a *Mannheimia haemolytica* vaccination (One Shot, Zoetis, Kalamazoo, MI) on d 34. Blood was collected prior to vaccination and on d 3, 6, 9, 11, and 14 post-vaccination for analysis of APP. Data were analyzed as a randomized complete block design using Proc Mixed of SAS (experimental unit = steer; 12 per treatment). Post-vaccination eating behavior, APP, and DMI data were analyzed as repeated measures. Digestibility of DM and OM on d 27/28 tended to be greater for XPC14 vs XPC28 ($P \leq 0.07$). Steers fed either dose of XPC exhibited greater CP digestibility compared to CON ($P < 0.0001$). Steers fed XPC14 exhibited greater ADG from d 28 to 56 vs XPC28 ($P = 0.05$) and exhibited greater DMI than CON or XPC28 for the 15 d post-vaccination ($P = 0.001$). Haptoglobin and serum amyloid A concentrations peaked 3 d post-vaccination (day effect; $P < 0.0001$) but did not differ due to treatment ($P \geq 0.14$). Ceruloplasmin concentrations were lesser on d 14 post-vaccination for XPC14 vs CON or XPC28 while treatment did not affect ceruloplasmin concentrations on other sampling days (treatment × day; $P = 0.02$). For the 15 d post-vaccination, CON had more non active min/d than XPC14 or XPC28 ($P = 0.02$). Steers fed XPC14 or XPC28 had lesser average, minimum, and maximum ear surface temperature vs CON ($P \leq 0.01$) during this period. Overall, these data suggest that steers

fed XPC at 14 g/d responded better to a vaccination challenge than steers fed 0 or 28 g/d.

Key Words: Saccharomyces cerevisiae fermentation product, vaccination challenge, cattle
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560 The effect of two additives on ruminal fermentation using a semi-continuous culture system.

M. Capelari*[1], K. A. Johnson[2], B. Latack[1], J. Roth[1], and W. Powers[3], [1]*Michigan State University, East Lansing,* [2]*Washington State University, Pullman,* [3]*University of California, Oakland.*

Seven 37-d trials tested the effect of nitrate (NIT) and monensin (MON) in diets commonly fed to beef (BEEF; 10:90 forage to concentrate; 3 trials) and dairy cattle (DAIRY; 50:50 forage to concentrate; 4 trials) on rumen fermentation and methane (CH$_4$) emissions. Additives (0, 1.25 and 2.5% diet DM of NIT; 0 and 4 mg/L of MON) were tested alone and combined (NIT + MON; 6 total treatments; 3 replicates per treatment). Rumen fluid was pooled from 5 non-adapted lactating cows fed 50:50 forage to concentrate diet 3 h after morning feeding, and 1 L of processed inoculum was transferred to 2.2-L vessels. Treatment diets were added to nylon bags which remained in the anaerobic fermentation system for 48 h. Buffer was infused into vessels at 70 ml/h. Gas production and composition and VFA were measured daily. Ammonia nitrogen (NH$_3$-N) and DMD were measured twice weekly. For BEEF and DAIRY trials, when compared to control, NIT reduced CH$_4$ production (33.5 vs 43.5 and 24.7 vs 32.1 mM/d, respectively; $P < 0.01$; SEM = 1.5) and NH$_3$-N (6.6 vs 8.1 and 17.1 vs 21.0 mg/dL, respectively; $P < 0.01$; SEM = 0.6) while MON reduced CH$_4$ production (26.6 vs 43.5 and 26.3 vs 32.1mM/d, respectively; $P < 0.01$), butyrate (12.6 vs 14.9 and 16.1 vs 19.4 mM/d, respectively; $P < 0.01$; SEM = 0.5), acetate to propionate ratio (1.6 vs 1.9 and 1.6 vs 2.0, respectively; $P < 0.01$; SEM = 0.06) and increased propionate (29.6 vs 26.2 and 26.8 vs 22.2 mM/d, respectively; $P < 0.01$; SEM = 0.6) and total VFA (50.7 vs 48.1 and 38.3 vs 35.4 mM/d, respectively; $P < 0.01$; SEM = 1.9). The combination of NIT+MON in BEEF and DAIRY trials further reduced CH$_4$ (19.3 vs 43.5 and 21.3 vs 32.1 mM/d, respectively; $P < 0.01$) and increased acetate (51.2 vs 49.5 mM/d; P = 0.07 and 53.7 vs 49.9 mM/d; $P < 0.01$, respectively; SEM =0.9). For BEEF only, compared to control, NIT reduced DMD at higher doses (72.3 vs 74.3 g/100g DM; $P < 0.05$; SEM = 1.4) and NIT+MON increased total VFA at lower doses (55.4 vs 48.1 mM; $P < 0.01$). For DAIRY, butyrate was reduced by NIT (16.1 vs 19.4 mM/d; P < 0.01) and further reduced by NIT+MON (15.2 vs 19.4 mM/d; $P < 0.01$). The combination of NIT+MON enhanced CH$_4$ reduction and increased acetate molar ratio. When NIT was present at higher doses, DMD was reduced. The combination of NIT+MON reduced butyrate in DAIRY trials and, at lower doses, increased total VFA production in BEEF trials.

Key Words: Methane, In vitro, volatile fatty acid
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561 Effects of ractopamine hydrochloride on lysine utilization by growing cattle.

A. H. Hussein[1], E. D. Batista[1,2], M. A. Vaughn[1], S. R. Davis[1], E. F. Schwandt[1], E. J. McCoy[3], J. C. Simroth[3], C. D. Reinhardt[1], D. U. Thomson[3], M. D. Miesner[4], D. D. Burnett[1], J. M. Gonzalez[1], and E. C. Titgemeyer*[1], [1]*Department of Animal Sciences and Industry, Kansas State University, Manhattan,* [2]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil,* [3]*Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan,* [4]*Department of Clinical Sciences, Kansas State University, Manhattan.*

Two separate sets of 6 ruminally cannulated Holstein steers (240 kg) were used to study effects of ractopamine on lysine utilization. Steers were housed in metabolism crates and limit-fed 2.52 kg DM/d of a diet (10.1% CP) containing 82% soybean hulls twice daily. Treatments were arranged as a 2 x 3 factorial with 2 levels of ractopamine-HCl (0 and 200 mg/d) and 3 levels of lysine (0, 6, and 15 g/d) continuously infused abomasally. For each replicate of 6 steers, a completely randomized design was used for main-plot treatments (ractopamine-HCl; 0 vs 200 mg/d). Each steer received subplot treatments (lysine; 0, 6, or 15 g/d) in random sequence, such that each replicate contained concurrent 3 x 3 Latin squares, with each Latin square representing either 0 or 200 mg/d ractopamine-HCl. All steers were continuously infused ruminally with 200 g/d acetic acid, 200 g/d propionic acid, and 50 g/d butyric acid and abomasally with 300 g/d glucose to increase energy supply. Urea (10 g/d) was infused ruminally to ensure adequate ruminal ammonia. Steers were abomasally infused with excess of all essential AA except lysine to ensure lysine was solely limiting. Periods were 6 d with N retention measured on d 3 to 6 and longissimus biopsies and blood collected on d 6. Lysine increased ($P < 0.01$) N retention for both control steers (21.3, 28.6, 33.9 g/d) and ractopamine-fed steers (25.5, 33.2, 38.9 g/d); ractopamine tended ($P = 0.07$) to increase N retention. Lysine linearly decreased ($P < 0.01$) plasma urea (2.83, 2.04, 1.88 mM), leucine, and valine, but increased ($P < 0.01$) plasma lysine (34, 51, 76 mM), arginine, and alanine. Ractopamine decreased ($P < 0.05$) plasma lysine and arginine concentrations. In longissimus, ractopamine increased ($P < 0.05$) phosphorylation of RPS6 on Ser-235 and Ser-244, and tended to increase ($P = 0.08$) phosphorylation of AKT on Thr-308 but not Ser-473. Abundance of MAFbx was decreased ($P = 0.01$) and MURF1 was numerically decreased ($P = 0.14$) by ractopamine. Lysine supplementation did not affect phosphorylation of RPS6 or AKT or abundance

of MAFbx or MURF1. The efficiency of lysine use between 0 and 6 g/d supplemental lysine was 49% for control and 51% for ractopamine-supplemented steers. N retention tended to be improved by ractopamine when lysine supply was limiting, but incremental efficiencies of lysine utilization were not affected by ractopamine, suggesting that ractopamine reduced maintenance requirements for lysine.

Key Words: ractopamine, cattle, lysine
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562 Effect of select TC™ on performance and health status of newly received feedlot cattle.

J. R. Pukrop*[1], K. M. Brennan[2], and J. P. Schoonmaker[3], *[1]Purdue University, West Lafayette, IN, [2]Alltech Inc., Nicholasville, KY, [3]Department of Animal Science, Purdue University, West Lafayette, IN.*

A two-part experiment was conducted to determine the effects of Select TC™, a hydrolyzed-yeast based solution for receiving calves, on the health status and performance of steers during the first two months of the feedlot period. Eighty crossbred steers were acquired from commercial sale barns in Mississippi and Georgia, and transported to Purdue University. All animals were fed a corn silage based receiving diet, and were checked and treated daily for respiratory disease as needed following established treatment protocols. In Exp. 1, 64 steers (246.5 ± 4.7 kg initial BW) were blocked by weight and randomly allocated to 2 treatments to determine the impact of Select TC™ supplementation on health, intake and daily gain: Control (CON); and Select TC™ (TC) fed at 13 g/hd/d. Steers in Exp. 1 were housed in bedded pens with 2 animals/pen. Daily DMI was recorded, and steers were weighed every 14 d to determine performance. In Exp. 2, 16 steers (247.1 ± 5.4 kg initial BW) were similarly allotted to 2 treatments (CON and TC), individually penned, and subjected to a lipopolysaccharide (LPS) endotoxin challenge on d 62 or 63 to determine the animal's response to an inflammatory agent. Serum samples and rectal temperatures were taken every half an hour from -2 to 8 h relative to LPS injection from steers in Exp. 2. Data were analyzed as a complete randomized block design using the MIXED procedure of SAS. Performance characteristics from Exp. 1, including weight, ADG, DMI and gain:feed, did not differ among treatments ($P \geq 0.32$). Morbidity and number of animals treated once or twice did not differ in either experiment ($P \geq 0.16$). During the LPS infusion in Exp. 2, there was a treatment x time effect for rectal temperatures ($P = 0.05$) and non-esterified fatty acid (NEFA) concentrations ($P = 0.0002$), where temperature and NEFA were lower pre-LPS, but greater post-LPS in CON compared to TC steers. Decreased NEFA post-LPS in TC steers suggests less break down of the adipose tissue as a source of energy for immune defenses. There were no treatment x time effects in Exp. 2 for blood urea nitrogen ($P = 0.18$), cortisol ($P = 0.96$), or insulin ($P = 0.67$). Results from this experiment indicate that Select TC™ improves health and metabolic status of immune challenged cattle, but this may not result in quantifiable improvements in performance.

Key Words: receiving cattle, yeast cell wall, lipopolysaccharide challenge
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563 Effects of bismuth subsalicylate and calcium-ammonium nitrate on ruminal fermentation of beef cattle.

D. D. Henry*[1], F. M. Ciriaco[1], R. C. Araujo[2,3], P. L. P. Fontes[1], N. Oosthuizen[1], M. E. Garcia-Ascolani[1], C. D. Sanford[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], L. Rostoll-Cangiano[1], G. C. Lamb[4], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]EW|Nutrition GMBH, Visbek, Germany, [3]GRASP Ind. & Com. LTDA, Curitiba, Brazil, [4]Texas A&M University, Department of Animal Science, College Station.*

A duplicated 5×5 Latin square design was used to determine the effects of bismuth subsalicylate (BSS) and encapsulated calcium-ammonium nitrate (eCAN) on ruminal fermentation of beef cattle consuming bahiagrass hay (*Paspalum notatum*) and cane molasses. Ten ruminally cannulated beef cattle were randomly assigned to 1 of 5 treatments as follows: 3.3 g/kg of BW of molasses (CTRL); CTRL + 182 mg/kg of BW of urea (N0B0); CTRL + 538 mg/kg of BW of eCAN (N1B0); N0B0 + 58.4 mg/kg of BW of BSS (N0B1); and N1B0 + 58.4 mg/kg of BW of BSS (N1B1). With exception of CTRL, all treatments were isonitrogenous. Ruminal fluid and rectal temperature was collected 4× per d for 3 d to determine ruminal changes every 2 h from 0 to 22 h post feeding. Ruminal gas cap samples were collected at 0, 3, 6, 9, and 12 h on d 0 of each period followed by 0 h on d 1, 2, 3, and 14. Repeated measures data were analyzed using the MIXED procedure of SAS with the fixed effects of treatment, time, treatment × time, square, period, and animal within square, and the random effect of animal within treatment. For non-repeated data, the model included the fixed effects of treatment, square, period, and animal within square. Orthogonal contrasts were used to evaluate the effects of NPN, eCAN, BSS, and eCAN × BSS. There was no treatment effect ($P > 0.05$) on concentrations of H_2S on d 0, 1, 2, or 14; however, on d 3, concentrations of H_2S were reduced ($P = 0.018$) when NPN was provided. No effect of treatment ($P = 0.864$) occurred for ruminal pH. There was an effect of eCAN on total concentrations of VFA ($P = 0.011$), where a 6% reduction occurred when eCAN was provided. There were effects of NPN ($P = 0.001$) and eCAN ($P = 0.009$) on concentrations of NH_3-N, where cattle consuming NPN had lesser concentrations than those consuming eCAN compared to urea. Total concentrations of VFA and NH_3-N were not affected ($P > 0.05$) by BSS. There was an effect of BSS

($P = 0.009$) on rectal temperature, where cattle not consuming BSS had greater temperatures than those receiving BSS. In conclusion, eCAN does not appear to deliver equivalent ruminal fermentation parameters compared to urea, as indicated by reductions in total concentrations of VFA and NH_3-N.

Key Words: bismuth subsalicylate, fermentation, nitrate
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564 Effects of Biofix® Plus PRO supplemented in liquid feed on the performance of cow-calf pairs in south central Florida.

P. N. Gott*[1], A. Johns[2], A. Stam[3], B. G. Miller[1], B. Bell[1], and T. Weaver[4], [1]*BIOMIN America Inc., San Antonio, TX,* [2]*Seminole Tribe of Florida, Inc., Okeechobee, FL,* [3]*Federally Recognized Tribal Extension Program, Okeechobee, FL,* [4]*Westway Feed Products, Tomball, TX.*

Cattle breeding difficulties across the Southern United States are often attributed to heat stress. Additional factors including mycotoxin consumption may negatively impact reproductive performance. Zearalenone (ZEN) is a mycotoxin associated with reproduction-related effects due to its estrogenic activity. Recent research has identified ZEN contamination in pastures in South Central Florida. A trial was conducted at a commercial ranch in South Central Florida to evaluate the effects of Biofix® Plus PRO (Biomin Holding GmbH, Austria) supplementation in a free-choice molasses-based liquid feed product (Westway Feed Products) on the performance of cow-calf pairs. Cows were randomly assigned to one of two treatment groups: Control (n = 194) or Treatment (n = 206). Liquid feed was provided ad libitum from December 2015 through October 2016 with the formulation adjusted over time to maintain intake goals. Biofix® Plus PRO was supplemented to the Treatment group at an intended rate of 30 gram/head/day during the breeding period (December through April) and reduced to 15 gram/head/day through October. Bulls were with cows from January through early April. Calves from the previous calving season were weaned in June. Treatment group calves weighed on average 24.0 kg more than calves in the Control group. Individual calf weights were not obtained in this commercial facility. All cows were screened for pregnancy status (Control = 91.2% bred; Treatment = 90.3% bred; Z-score $P = 0.741$) at weaning. Every fourth confirmed pregnant cow per group was identified for future pregnancy status evaluation (51 cows per group) and body condition score (BCS) determination (Control = 5.1 ± 0.1 SEM; Treatment = 5.9 ± 0.1 SEM; Unpaired t-test $P < 0.0001$). After 47 days, pregnancy status (Control = 100% bred; Treatment = 96% bred; Z-score $P = 0.162$) and BCS (Control = 5.4 ± 0.1 SEM; Treatment = 6.1 ± 0.1 SEM; Unpaired t-test $P < 0.0001$) were re-evaluated. Two Control cows (1 culled; 1 not caught) were not evaluated. One Treatment cow had calved prematurely and another was estimated to have lost her calf following the first pregnancy screen. Live calf crop from tagged cows (Control = 96% Treatment = 90%; Z-score $P = 0.230$) was determined in February 2017. One Control cow culled during the trial period and two Treatment cows identified as open in August were not included in calf crop calculations. Biofix® Plus PRO supplementation of molasses-based liquid feed significantly increased BCS in cows and increased weaning weights of calves in cow-calf pairs grazing pastures in South Central Florida.

Key Words: liquid feed, zearalenone, cow-calf
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565 Effects of heat load and active dry yeast supplementation on ruminal parameters.

W. L. Crossland*[1], A. B. Norris[1], T. R. Callaway[2], and L. O. Tedeschi[1], [1]*Texas A&M University, College Station,* [2]*USDA-ARS, College Station.*

An active dry yeast (ADY) supplement (Vistacell, AB Vista, UK) was proposed to favorably influence ruminal parameters of heat loaded cattle. Eight British-cross steers (365 ± 27 kg) were fed a 90% concentrate diet (1.8% of BW intake, DM basis) and supplemented with either ADY (3.0 g/d; providing 6×10^{10} CFU/d) or no yeast (0.0 g/d; CON) for 14 d. Rumen boli were inserted through the esophagus on d 0 for continuous monitoring of pH and rumen temperature. On d 13 and 14, steers were housed in an open circuit calorimetry chamber for 48 h in either thermoneutral (TN) (18 ± 0.55°C; 35% RH) or heat loaded (HL) (35 ± 0.55°C; 35% RH) temperature. After 48 h, rumen fluid (500 mL) was extracted via esophageal pump and immediately processed for further analysis and in vitro fermentation using a 2×2 factorial arrangement with the in vitro gas production technique (IVGP). The IVGP revealed an effect of ADY on DMD versus CON (61.7% vs 32.8%, $P = 0.031$) but there was no effect of temperature. No effects were observed on the fermentation dynamics of the DM. There was a significant interaction of supplement and temperature on estimated ME in which ADY+TN, CON+HS, and ADY+HL were greater ($P = 0.0307$) than CON+TN (2.97, 2.84, 2.72 vs 1.95 Mcal/kg, respectively). The IVGP of methane (CH_4) g/L or CH_4 g/L/g of DM digested was not affected. Mean rumen pH of steers tended to be affected by temperature and supplement: HL steers had lower pH than TN ($P = 0.064$), and CON steers had lower pH than ADY ($P = 0.077$). Time spent below pH of 6 was affected by supplement: ADY was much less than CON (390.0 vs 882.5 min/d, $P = 0.05$). Time spent below pH of 5.0 was affected by temperature: TN was much less than HL (1.75 vs 590.75 min/d, $P = 0.034$, respectively). Mean rumen temperature and time spent above 40°C was affected by temperature but not by supplement. As expected HL steers had greater rumen temperature and spent more time above 40°C than TN steers (40.51 vs 39.21 °C, $P = 0.0165$; 1,216.25 vs 27.5 min/d, $P = 0.002$). Our results indicated that supplementation of 3.0 g/d of an ADY in the diets of steers consuming 90% concentrate diets under severe heat loads may increase DMD, increase available ME, and relieve subacute ruminal acidosis.

Key Words: Yeast, Heat load, pH
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566 Isolation of *Fusobacterium necrophorum*, *Trueperella pyogenes*, and *Salmonella enterica* from ruminal, ileal, and colonic epithelial tissues of finishing beef steers receiving different levels of dietary roughage with and without tylosin.

C. M. Meredith[1], C. P. Weiss[1], W. W. Gentry[1], R. G. Amachawadi[2], S. K. Narayanan[2], T. G. Nagaraja[2], F. T. McCollum[1], and J. S. Jennings[*1], *[1]Texas A & M AgriLife Research and Extension Center, Amarillo, [2]Kansas State University, Manhattan.*

To improve our ability to prevent liver abscesses in finishing beef steers, we must evaluate the possibility of pathogens originating from the hind gut as well as the rumen. We hypothesized that pathogens promoting liver abscess formation are located throughout the gut. Furthermore, the increased dietary roughage levels could improve gut integrity overtime. This experiment was conducted to isolate specific pathogens within the ruminal, ileal, and colonic epithelial tissues. Treatment diets were steam-flaked corn-based with 5 or 15% corn stalk inclusion (DM basis) with (5T and 15T) or without (5NT and 15NT) tylosin. Two hundred sixty-four crossbred beef steers (BW = 257 ± 18 kg) were used in a randomized complete block design with 8 hd/pen (8 pens/treatment). Half of the pens for each treatment were designated for serial slaughter while the other half remained on feed the entire experiment for performance evaluation. Steers were fed each day at 0730 h for an average of 220 d (heavy block = 205 d, light block = 234 d). At trial initiation, 8 steers were slaughtered for initial tissue sampling and 1 pen/treatment was slaughtered every 56 d thereafter. During serial slaughter, a dorsal and ventral sample of the rumen was taken for histopathological evaluation along with ruminal, ileal, and colonic tissue for bacterial isolation. Performance data were analyzed using the MIXED procedure of SAS and pen was the experimental unit. Bacterial isolation data were analyzed using the GLMMIX procedure of SAS and animal was the experimental unit. Means were separated using LSMEANS with PDIFF option. There were no differences between treatments for final BW ($P = 0.93$) and feed conversion ($P = 0.17$). The 15NT treatment had the greatest ($P = 0.04$) ADG and 5NT the lowest, with 15T and 5T intermediate. None of the cattle, except one, had abscessed livers. There were no differences in the prevalence of *Fusobacterium necrophorum*, *Trueperella pyogenes*, and *Salmonella enterica* in ruminal, ileal, and colonic epithelial tissues ($P \geq 0.35$). However, this experiment was the first to isolate *F. necrophorum* in ileal and colonic epithelial tissues of finishing beef steers, which suggests that post-ruminal gut tissue could be a source of *F. necrophorum*. With limited efficacy of tylosin in the hind gut, further research is warranted to explore post-ruminal acidosis and its effects on gut epithelial integrity, pathogen prevalence, and liver abscess formation.

Key Words: gut pathogens, roughage, beef finishing diet
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567 Ruminal characteristics and feedlot performance of feedlot steers during accelerated step-up to high-concentrate diets using Lactipro Advance®.

T. J. Ellerman*, L. M. Horton, S. L. Katulski, C. L. Van Bibber-Krueger, C. C. Aperce, and J. S. Drouillard, *Kansas State University, Manhattan.*

Megasphaera elsdenii (ME) is the principal lactate-utilizing bacterium in cattle adapted to concentrates, and is marketed commercially as a probiotic (Lactipro Advance, MS Biotec) to facilitate transition to high-grain diets. In this study, ruminal characteristics and feedlot performance were measured for steers adapted to a high-grain diet using a traditional 22-d step-up program (C), and for steers adapted over 10 d with the aid of ME fresh culture administered as an oral gavage (F), an oral gavage of rehydrated lyophilized culture (R), or R combined with lyophilized culture powder administered daily as a ration top-dress (D). Yearling steers (n = 435; initial BW = 408 ± 5 kg) were blocked by weight and randomly allocated to 64 concrete surfaced pens with 7 steers/pen and 16 pens/treatment. Step-up diets contained 40, 30, and 20% corn silage, and were followed by a finishing diet containing 10% corn silage and 90% concentrate. Ruminal fluid was obtained by rumenocentesis 26 h after steers received their first step-up diet, and inoculated into culture tubes containing lactate medium to determine differences in capacity for lactate metabolism over

Table 567.

Item	C	F	R	D	SEM	*P*-value
G:F	0.1743	0.1733	0.1705	0.1705	0.0028	0.66
HCW, kg	433.9	436.6	438.9	435.3	4.29	0.63
Choice + Prime, %	49.1	51.0	52.7	46.6	5.00	0.82
Absorbance at 600 nm	1.30^{a}	1.50^{b}	1.53^{b}	1.53^{b}	0.04	< 0.01
Lactate, mM	22.6^{a}	7.2^{b}	10.5^{b}	7.8^{b}	3.17	0.01
Butyrate, mM	3.5^{a}	8.8^{b}	7.1^{c}	$7.5^{b,c}$	0.52	< 0.01

[a,b] Means within a row without a common superscript letter are different, $P < 0.05$

24 h. Steers were fed once daily ad libitum for 156 d, then weighed, and transported 450 km to a commercial abattoir for harvest. Hot carcass weight and incidence of liver abscesses were determined at harvest and carcass traits were evaluated after 36 h of refrigeration. No differences were detected for feedlot performance ($P > 0.20$), liver abscesses ($P = 0.45$), or carcass traits ($P > 0.20$). Capacity for lactate utilization was increased with all forms of ME, as evidenced by increases in optical density (absorbance) of ME cultures, disappearance of lactate, and increase in butyrate production (P 0.01). In conclusion, steers dosed with ME can be stepped up to finishing diets in 10 d with no adverse effects on performance.

Key Words: *Megasphaera elsdenii*, feedlot, accelerated step-up
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568 Effects of encapsulated nitrate on growth performance, nitrate toxicity, and enteric methane emissions in feedlot beef steers: Backgrounding phase.

C. Lee*[1], R. C. Araujo[2,3], K. M. Koenig[4], and K. A. Beauchemin[4], [1]*Department of Animal Sciences, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster,* [2]*EW|Nutrition GMBH, Visbek, Germany,* [3]*GRASP Ind. & Com. LTDA, Curitiba, Brazil,* [4]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

A backgrounding feedlot study was conducted to examine the effects of feeding encapsulated calcium ammonium nitrate (EN) on growth, enteric methane production, and nitrate (NO_3^-) toxicity in beef cattle. A total of 108 crossbred steers (292 ± 18 kg) were blocked by BW and randomly assigned to 18 pens. The pens (experimental unit; 6 animals per pen) received 3 dietary treatments: Control, a backgrounding diet supplemented with urea (0.2% NO_3^- and 0.9% urea in dietary DM); 1.25% EN, control diet supplemented with 1.25% EN (1.2% NO_3^-) in dietary DM, which partially replaced urea; or 2.5% EN, control diet supplemented with 2.5% EN (2.3% NO_3^-) in dietary DM, fully replacing urea. Twenty four steers were allocated to additional 4 pens and randomly assigned to 1 of the above 3 dietary treatments plus a fourth treatment: 2.3% UEN, control diet supplemented with 2.3% unencapsulated NO_3^- (UEN; 2.4% NO_3^-) fully replacing urea. Animals in the additional 4 pens were used for methane measurement in respiratory chambers and the pens (except UEN) were also part of the performance study (i.e., n = 7 pens/treatment). The experiment was conducted for 91 d in a randomized complete block design. During the experiment, DMI was not affected by inclusion of EN in the diet. Changes in BW, ADG, and gain:feed were not observed ($P \geq 0.57$) by feeding EN. Methane production (g/d) tended to decrease ($P = 0.099$) by NO_3^- (188, 174, 156, and 152 g/d for Control, 1.25%, 2.5% EN, and UEN, respectively), but yield (g/kg DMI) did not differ ($P = 0.56$) among treatments. Inclusion of EN in the diet increased ($P \leq 0.02$) sorting of the diets in favor of large and medium particles and against small and fine particles resulting in considerable increases in NO_3^- concentrations of orts without affecting DMI. Plasma NO_3^- and NO_2^- concentrations increased ($P \leq 0.05$) for EN compared with Control in a dose response manner, but blood methemoglobin levels were below the detection limit. Nitrate concentration in fecal samples slightly increased (from 0.01% to 0.14%; $P < 0.01$) with increasing levels of EN in the diet. In conclusion, EN can be used as a feed additive replacing urea in beef cattle diets during the backgrounding phase without NO_3^- intoxication or any negative effects on growth performance. In addition, the study confirmed that feeding EN tended to decrease enteric methane production in the long term.

Key Words: encapsulated nitrate, backgrounding feedlot, beef cattle
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569 Feeding tannins to reduce nitrogen losses from feedlot cattle fed high protein diets containing wheat distillers grains: Ruminal fermentation, digestibility, and route of nitrogen excretion.

K. M. Koenig*, and K. A. Beauchemin, *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Four ruminally cannulated and four ruminally and duodenally cannulated beef heifers (476 ± 25 kg, initial BW) were used in a replicated 4 × 4 Latin square to determine the effects of feeding condensed and hydrolysable tannin extracts with a high protein diet containing wheat distillers grains on ruminal fermentation, digestibility, and route of nitrogen (N) excretion. Periods were 4 wk and included a 1-wk washout, 2 wk for adaptation to the tannin extracts, and 1 wk for measurements. Dietary treatments were control (CON, basal diet), 2.5% *Acacia mearnsii* (ACA), 2.5% quebracho (QUE), and 2.5% chestnut (CHE; DM basis). The basal diet was composed of 71% barley grain concentrate, 20% wheat distillers grains and solubles, and 9% barley silage and contained 16.8% CP (DM basis). Diets were fed as total mixed rations once per day for ad libitum intake. Feed offered and refused were measured daily. Total collection of urine and feces were made for 6 d. Plasma was collected at 3 h and rumen fluid was collected at 0, 3, 6, 9, 12, 15, and 18 h after feeding at the end of the collection period. Data were analyzed using a mixed linear model with square, period, and treatment as fixed effects and animal within square as a random effect. Dry matter intake tended ($P = 0.10$) to be lower when heifers were fed the CHE compared to the CON and QUE, and was intermediate for the ACA. Total tract digestibility of DM was similar among heifers fed the tannin extracts (78.1, 77.4, and 77.6% for ACA, QUE, and CHE, respectively), however, all tannin extracts reduced DM digestibility compared to the CON (80.8%, SEM 0.98%; $P < 0.05$). Plasma urea-N and ruminal

NH_3-N were also similar among heifers fed the tannin extracts and were reduced ($P < 0.05$) compared to the CON. There was no effect of the dietary treatments on total N output ($P > 0.05$), but fecal N output was increased ($P < 0.05$) and conversely urinary N output was decreased ($P < 0.05$) for heifers fed ACA and QUE compared to the CON. Fecal and urinary N outputs were intermediate for the CHE. Feeding tannins to beef cattle fed high protein diets containing wheat distillers grains reduced ruminal NH_3-N and plasma urea-N and shifted the route of N excretion from labile forms in urine to feces although there was a 4% decrease in DM digestibility.

Key Words: tannins, wheat distillers grains, nitrogen excretion
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570 Characterization of nutritional values, ruminal and total digestibility of nutrients and predicted metabolizable protein supply to dairy cows: Comparison of tannin and non-tannin faba bean.

H. Xin[1], M. Espinosa[2], and P. Yu*[3], [1]*Department of Animal and Poultry Science, University of Saskatchewan, SASKATOON, SK, Canada,* [2]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada,* [3]*Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada.*

The study was conducted to compare 1) chemical profile; 2) protein and carbohydrate subfractions fractionated by the Cornell Net Carbohydrate and Protein System (CNCPS); 3) energy values; 4) ruminal, intestinal and total digestibility of nutrients; and 5) protein supply predicted by the DVE/OEB system between tannin (var. Fatima) and non-tannin (var. Snowbird) faba beans, with comparison to starchy barley as a reference. The results showed that the brown-seeded Fatima faba bean showed higher contents of CP, ADF, NDICP, SCP and NPN and lower concentrations in EE and starch, compared with the white Snowbird bean. Subsequently, CNCPS protein and carbohydrate subfractions as well as energy values differed between these two beans. Although statistically significant, the differences on RUP, EDCP and TDP were found to be tiny between tannin and non-tannin faba beans. The DVE and OEB values of faba bean with presence of tannin were 6-15% greater than those of Snowbird bean. As a result, feed milk value (FMV) which is estimated from metabolizable protein was higher in Fatima. As for the control starchy barley, it showed significant differences in chemical compositions, CNCPS subfractions and energy values. Remarkable lower DVE and FMV were also found in the barley, compared with faba beans. The optimal OEB value is regarded to be zero or slightly above. In our study, the OEB was determined to be positive in faba beans (118 g/kg DM) and negative in the barley (-6.2 g/kg DM), indicating barley might be better than the beans if used as the unique ingredient in the ration for ruminants.

Key Words: tannin and non-tannin faba bean, degradation and digestion, true nutrient supply
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571 Reduction of the nitrogen excretion and ammonia volatilization from manure of fattening bulls during the finishing phase by reducing the concentrate crude protein concentration.

M. Devant*[1], B. Quintana[2], A. Sole[3], A. Pérez[4], C. Medinya[5], J. Riera[6], J. Grau[7], B. Fernández[8], and F. Prenafeta[9], [1]*IRTA - Department of Ruminant Production, Caldes De Montbui, Barcelona, Spain,* [2]*IRTA-Department of Ruminant Production, Caldes Montbui, Barcelona, Spain,* [3]*IRTA-Department of Ruminant Production, Caldes Montbui, Spain,* [4]*Corporación Alimentària Guissona, Guissona, Lleida, Spain,* [5]*SINUAL, Sallent, Spain,* [6]*NANTA, Tres Cantos, Madrid, Spain,* [7]*Setna Nutrición Animal SAU, Rivas Vaciamadrid, Madrid, Spain,* [8]*IRTA, GIRO, Caldes Montbui, Barcelona, Spain,* [9]*IRTA, GIRO, Caldes de Montbui, Barcelona, Spain.*

The aim of this study was to evaluate the effects of crude protein (CP) on nitrogen (N) excretion (Study 1), performance (Study 2), and manure ammonia volatilization (Study 3) in Holstein beef animals fed with high-concentrate diets during the finishing phase. In Study 1, 24 Holstein heifers (310 ± 5.3 kg of BW and 251 ± 1.4 d of age) were allocated in individual pens and distributed randomly depending on initial BW to 3 dietary treatments (N1: 14.5% CP and 0.6% urea, N2: 12.5% CP and 0.3% urea, N3: 10.5% CP without urea. Concentrate and straw were recorded daily and BW was recorded every two weeks. At days 30 and 58, a N balance was performed. In Study 2, 150 Holstein bulls (344 ± 2.6 kg BW and 252 ± 0.9 days of age) were allocated in 8 pens (18-19 animals per pen). The evaluated treatments were N2 and N3. Concentrate and straw were offered ad libitum, pen intake was recorded daily. The BW was recorded every 2 wks. After d 70, animals were transported to the slaughterhouse where carcass weight and quality was recorded. For Study 3, a fecal and urine sample form each heifer were collected at d 58 of Study 1, mixed at a ratio in 1:1 (wet weight) and pooled by treatment for ammonia volatilization assays under aerobic and anaerobic conditions. Gas samples collected for the analyses of ammonia concentration at day 1, 3, 7 and weekly during 150 days. Data were analyzed with an analysis of variance. In Study 1, urinary N excretion was greater ($P < 0.001$) in N1 (91.5 ± 5.72 g/d) compared with N2 (63.1 ± 5.72 g/d) and N3 (50.4 ± 5.72 g/d). No differences in fecal N excretion among treatments were observed. In Study 2, no significant differences were observed between treatments in average daily gain (ADG, 1.67 ± 0.041 kg/d), concentrate intake (8.1 ± 0.06 kg/d as feed), carcass weight (257 ± 1.7 kg), or dressing percentage (52.3 ± 0.3%). Nitrogen loss from manure estimated from aerobic ammonia volatilization changed significantly during storage (treatment x time interaction, $P < 0.01$); volatilization of N3 was always lower than N1, being N2 an intermediate case. The reduction of CP from 14.5 to 12.5 and 10.5% is an efficient strategy to reduce urinary N excretion by a 20% and manure ammonia volatilization without impairing performance and carcass quality.

Key Words: beef, environmental pollution, nitrogen
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572 Evaluation of *Brassica carinata* meal as a protein supplement for growing beef heifers.

T. M. Schulmeister*[1], M. Ruiz-Moreno[1], J. Benitez[1], M. E. Garcia-Ascolani[1], F. M. Ciriaco[1], D. D. Henry[1], G. C. Lamb[2], J. C. B. Dubeux Jr.[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]Texas A&M University, Department of Animal Science, College Station.*

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 (~40% CP) 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 effects of supplementation with *Brassica carinata* meal (BCM) on animal performance, attainment of puberty, and blood profile in growing beef heifers consuming bermudagrass hay (*Cynodon dactylon*). Sixty-four Angus crossbred heifers (240 ± 39 kg initial BW) were stratified and blocked (2 blocks: light and heavy) by initial BW and randomly allocated into 18 pens over 2 consecutive yr (10 pens in yr 1 and 8 pens in yr 2). 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 were provided ad libitum access to bermudagrass hay and water, and BCM pellets were supplemented daily in the pen. Body weight and blood samples were collected weekly for 70 d, before the daily supplementation. Plasma was analyzed for concentrations of progesterone, triiodothyronine (T3), and thyroxine (T4). Data were analyzed as a generalized randomized block design including the fixed effects of treatment, wk, treatment × wk, block, and block × treatment, and the random effect of year. Repeated measures, with pen within year as subject, were used to analyze T3 and T4 concentrations over time. A survival analysis was conducted to determine time to attainment of puberty. There was a difference ($P < 0.01$) in ADG between CTL (0.14 kg) and BCM (0.42 kg). There was no treatment or block ($P > 0.05$) effect for concentrations of T3 and T4; however, there was a difference in wk ($P < 0.01$). Time to attainment of puberty did not differ between treatments ($P = 0.68$); however, there was an effect of block ($P < 0.01$) where the light block heifers attained puberty earlier compared to the heavy block heifers. Feeding *B. carinata* meal as a protein supplement at 0.3% of BW/d is a viable option for increasing ADG of growing beef heifers, without affecting the attainment of puberty.

Key Words: *Brassica carinata*, performance, protein supplement
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573 Over-feeding metabolizable protein supply in late gestation beef cattle: Effects on DMI, ruminal fermentation, and performance.

K. S. Hare*[1], K. M. Wood[2], C. Fitzsimmons[3], and G. B. Penner[1], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, [2]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [3]Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

The objective was to determine the effect of oversupplying metabolizable protein (MP) pre-partum on DMI, BW, and ruminal fermentation. Twenty-four primiparous crossbred Hereford cows were assigned to a high protein (HP; 140% of MP requirement, n = 12) or control (CON; 100% of predicted MP requirement, n = 12) treatment. Cows were individually fed their treatment diet from d -56 relative to parturition and then were switched to a common diet post-partum. Post-partum cows were individually housed until d 33 following parturition and group-housed by pre-partum treatment thereafter. Dry matter intake was measured throughout the study and summarized by week. Cow BW was measured on d -56, -42, -28, -8, 7, 14, 28, 57, 82, and 112 relative to parturition. Ruminal pH was measured from d -35 to 28, and digesta samples were taken on d -34, -16, 7, and 28 for short-chain fatty acid (SCFA) and ammonia measurements. Data were analyzed as a completely randomized block design using the MIXED procedure of SAS. Fixed included treatment, time, and the two-way interaction, while random effects were cow and block. Time (day or week) was analyzed as a repeated measure. Pre-partum BW of CON did not differ among days; whereas, HP cows increased BW as parturition approached ($P = 0.01$). Post-partum BW did not differ by treatment or day. Treatment did not affect DMI, but DMI decreased by 7.7% from wk -2 to -1 ($P < 0.01$), and, post-partum, cows consumed 14.1 and 8.8% less in wk 3 relative to wk 1 and 4 ($P < 0.01$). Mean ruminal pH was not affected by treatment, but tended to increase ($P = 0.06$) the week prior to parturition. After parturition, mean ruminal pH decreased from wk 1 to 2 (6.67 vs 6.40; $P < 0.01$). Total ruminal SCFA concentration was not affected by treatment during the pre- or post-partum periods, averaging 112 and 120 m*M*, respectively. However, pre-partum concentrations (mol/100 mol) of isobutyric (0.94 vs 0.66, $P < 0.01$), isovaleric (1.03 vs 0.65, $P < 0.01$), and valeric acid (1.35 vs 1.11, $P = 0.02$) were greater for HP than CON. Pre-partum ruminal ammonia

decreased (interaction, $P < 0.010$) as parturition approached for HP (11.1 to 9.37 mg/dL) whereas, ammonia was not affected for CON (0.88 to 1.26 mg/dL). Overfeeding MP during late gestation may improve ruminal fermentation pre-partum without affecting DMI or BW change post-partum.

Key Words: Beef cow, Ruminal fermentation, Metabolizable protein
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574 Effects of protein supplementation with low to medium quality forage on intake and circulating amino acids in beef heifers in early pregnancy.

A. L. Jones*[1], E. L. Stephenson[2], K. Kruckenburg[2], M. Randall[2], E. Zwielfelhofer[2], J. Stuttgen[2], K. Martin[2], P. M. Fricke[3], J. S. Luther[2], and A. E. Radunz[2], *[1]University of Wisconsin-Madison, Madison, [2]University of Wisconsin-River Falls, River Falls, [3]University of Wisconsin- Madison, Madison.*

A 2-yr study was conducted to investigate the effects of protein supplementation with low to medium quality forage diets on yearling heifer performance and plasma AA during early pregnancy. Heifers received timed AI (TAI; d 0) and treatments were fed for 37 d (-7 to +30 from TAI). Angus, Hereford, and Angus-cross heifers (402 ± 42 kg initial BW; n = 79) were stratified by initial BW and BCS and randomly assigned to 1 of 4 protein supplementation treatments formulated to provide similar CP intake; 1) no supplementation (CON); 2) low-fat dried corn distillers grain (LDG, 7.4% fat; 0.8% BW); and 3) high-fat dried corn distillers grains (HDG, 9.5% fat; 0.8% BW); and 4) cottonseed meal (CSM, 2.2% fat; 0.4% BW). The basal diet consisted of low to medium quality chopped grass hay (8% CP; 55% NDF in yr 1 and 70% NDF in yr 2) fed ad libitum twice daily. Supplements were fed once daily prior to hay feeding and individual intakes were recorded. Body weight and BCS was determined at start on (d -9 and -8) and at the end (d 29 and 30). Blood samples were collected 4 h after supplementation d 0, 5, 9, 14, 21, 26, and 30 to determine plasma urea nitrogen (PUN) and AA. Initial BW, initial BCS, and change in BCS did not differ ($P \geq 0.80$) among treatments; however, overall DMI, and ADG were greater ($P \leq 0.0001$) for supplemented heifers than CON heifers. Total CP intake was greater ($P \leq 0.0001$) for HDG and LDG compared to CON and CSM was intermediate. Plasma VAL, LEU, TYR, ILE, TRP, TAUR, total ketogenic AA, and total AA were greater ($P \leq 0.05$) while GLY was less ($P \leq 0.0001$) with protein supplementation versus CON. Concentrations of ALA and LYS were less ($P \leq 0.0001$) from HDG and LDG fed heifers compared to CON and CSM; however, LDG had greater ($P = 0.01$) LYS concentrations than HDG. Heifers fed CSM had greater ($P \leq 0.05$) ARG and ASP. Concentrations of THR were greater ($P = 0.0004$) for LDG and CSM. Protein supplementation increased ($P \leq 0.0001$) PUN in supplemented heifers compared to CON. Protein supplementation during early pregnancy in beef heifers resulted in greater protein intake and increased circulating PUN and total AA.

Key Words: beef heifers, protein supplementation, amino acids
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575 Impacts of balancing feedlot diets for effective energy and predicted amino acid requirement on plasma lysine levels and finishing steer performance.

J. M. Prestegaard*, A. L. Kenny, M. M. Masiero, B. R. McDonald, C. D. Martin, and M. S. Kerley, *University of Missouri, Columbia.*

The objective was to evaluate differences in steer finishing performance and plasma lysine levels when fed diets balanced for predicted lysine requirement to effective energy (EE) ratio using rumen-protected lysine. We hypothesized that finishing steers consuming diets optimized for these parameters would have improved feed efficiency, profitability (defined as when value of gain exceeded cost of gain), and increased plasma lysine concentration. Crossbred steers (n = 120; 451 ± 32 kg) were used in a completely randomized design and stratified by BW and breed type. Animals were sorted into pens of 6 and fed between 112-179 d. Diets were balanced to meet EE requirement and be adequate for non-lysine AAs. Treatments included a lysine-limiting control that contained no rumen-protected products (NEGCON); a lysine-sufficient control (POSCON) that contained rumen-protected soybean meal; and treatments that contained encapsulated lysine at 50% (AJ50), 100% (AJ100) and 150% (AJ150) of the amount of product needed to meet lysine requirement. On d 151 steers were weighed on 2 consecutive days every 14 d and designated to be slaughtered when they were no longer profitable. Jugular blood was collected at 4, 8 and 12 h post-feeding from ruminally cannulated crossbred steers consuming NEGCON, AJ100 and AJ150 in a 3x3 Latin Square metabolism study. Data were analyzed using the LIFETEST procedure of SAS to test profitability and the GLM procedure to test for treatment differences among FBW, ADG, DMI, G:F, and plasma lysine concentration. Steer was used as experimental unit. Steers remained profitable for a greater time (days; $P < 0.01$) for NEGCON (165.6 ± 2.2), POSCON (163.8 ± 2.5) and AJ100 (165.6 ± 2.9) than AJ150 (153.9 ± 1.2). Additionally, AJ100 profitability tended to be greater (P < 0.07) than AJ50 (156.8 ± 1.5 days). Feed efficiency differed across treatments with G:F greater ($P < 0.02$) for POSCON and AJ100 (0.125 and 0.121) than AJ50 and AJ150 (0.108 and 0.103), but no treatment differed from NEGCON (0.110). Steer FBW, ADG or DMI did not differ. For cannulated steers, 8h plasma lysine (µg/mL) was greater ($P < 0.02$) in AJ150 than NEGCON and AJ100 (12.28 vs 8.70 and 10.29 ± 1.05), but did not differ at 4h or 12h. Finishing steers became less profitable sooner when under or over-supplemented encapsulated lysine. Feed efficiency increased with use of rumen-protected products

in diets formulated to meet lysine requirement. Finally, the highest supplemented level of encapsulated lysine resulted in greater plasma lysine concentration 8h post-feeding.

Key Words: rumen protected soybean meal, feed efficiency, rumen protected lysine
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576 The potential benefit of corn dried distillers' grain (co)products (DDG) fed alone or in combination with ionophore and condensed tannin to mitigate methane emission in cattle.

M. Fonseca*[1,2], W. L. Crossland[2], A. B. Norris[2], A. K. Almeida[3,4], and L. O. Tedeschi[2], [1]*University of Nevada, Reno, Reno,* [2]*Texas A&M University, College Station,* [3]*Texas A & M University, College Station,* [4]*UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, SP, Brazil.*

The objective with this trial was to evaluate the potential of ionophore (33 mg of monensin/kg DM) and condensed tannins (offered at 3% of DMI) to mitigate enteric methane production by beef steers fed corn dried distiller's grain (DDG) in finishing diets. Eight British-cross steers, 12 ± 2 mo old weighing 212 ± 11.7 kg, were assigned to two replicated Latin rectangle design (LRD, n = 32) to evaluate four treatments: control (no DDG or feed additive), DDG (40% DDG inclusion), DDGI (40% DDG inclusion + ionophore), and DDGCT (40% DDG inclusion + condensed tannins). Animals were randomly assigned to the diets fed at an intake of 2.5% of BW (DM basis). Animals were adapted to the diets for 14 d prior to collection periods. Enteric methane measurements were collected in two open circuit respiration, pull mode chambers in which animals were fed twice daily 0800 and 1600 h. The data acquisition consisted of a 48-h period of measurements (runs). The statistical analysis was performed using random coefficients model methodology in SAS 9.4 (SAS Inst., Cary, NC) assuming fixed effects of treatment (diet) and random effects of animals and runs. An effect of diet was observed ($P < 0.001$) for CH_4 (L/d) production at 12h, 24h and 36h, but not at 48h. The addition of DDG significantly decreased CH_4 (L/d; $P < 0.001$) at 12h, 24h, 36h, and 48h when compared to the control diet. Additionally, the inclusion of ionophore and condensed tannins decreased CH_4 production (L/d; $P < 0.001$) at 12h, 24h and 36h, but only DDGCT decreased CH_4 production (L/d; $P < 0.001$) at 48h when compared to the control diet, suggesting a more prolonged effect of condensed tannins over enteric CH_4 mitigation. At 24h DDG, DDGI, and DDGCT diets were not different for CH_4 production (L/d; $P < 0.001$), but at 36h DDGI and DDGCT had a significant effect on CH_4 mitigation when compared to the control or DDG. Our results indicated that DDGCT was a prominent CH_4 reducer over 48h followed by the DDGI treatment. The inclusion of ionophore and condensed tannins to DDG-based diets significantly affected enteric CH_4 production (L/d; $P < 0.001$).

Key Words: DDG, feed additives, methane production
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577 In vitro ruminal fermentation and enteric methane production of tropical forages supplemented with nitrogen or the combination of nitrogen and starch.

M. A. Cardozo[1], C. B. Sampaio[2], E. Detmann[3], A. N. Z. Vargas[4], and M. Fonseca*[5], [1]*Universidade Federal de Viçosa, Vicosa, Brazil,* [2]*Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil,* [3]*Universidade Federal de Viçosa, Viçosa, Brazil,* [4]*Universidad Unisarc, Santa Rosa de Cabal, Colombia,* [5]*University of Nevada, Reno, Reno.*

This research was conducted to evaluate in vitro ruminal fermentation parameters (CO_2 emissions, NDF degradability, pH, VFA, and NH_3-N) and enteric methane production of medium quality tropical grass hay (TGH; *Brachiaria decumbens*, 6.8% CP), supplemented with N only (urea:ammonium sulfate), or the combination of N and starch. The 7 treatments evaluated were: control (TGH only, 6.8% CP), N supplementation (TGH + N at 90.1 and TGH + N 130 g/kg), N + starch supplementation (low starch, 10% of forage weight; and high starch, 20% of forage weight). Samples were incubated in serum bottles (50 mL) at 39°C, each run being replicated 4 times. Methane, CO_2, and VFA were evaluated after 24-h incubation. The measurements of NDF degradability, NH_3-N concentration, and pH were performed at 3, 6, 9, 12, 24, 36, 48, 72 and 96 h. Values of pH, NH_3-N, VFA, CH_4, and CO_2 obtained for the different incubation times were evaluated as repeated measures design. Data were analyzed using PROC MIXED of SAS (SAS Inst., Cary, NC) and differences were declared significant at $P \leq 0.05$. Treatment was considered fixed effect whereas treatment within run considered random. When expressed in mL/g DM, no effect was found on CH_4 ($P = 0.498$) and CO_2 ($P = 0.538$) production, potentially degradable fraction of NDF ($P = 0.429$), nondegradable fraction of NDF ($P = 0.429$), and fractional degradation rate of NDF ($P = 0.568$). Yet, compared to control, supplementation did affect total VFA concentration ($P < 0.05$), more specifically, with starch affecting ($P < 0.05$) total acetate production, and decreasing A:P ratio ($P < 0.05$). The pH was found to be higher for supplemented diets ($P < 0.05$). Supplementation also affected NH_3-N, after 36 h, with high starch inclusion being the highest ($P < 0.05$). Overall, the N supplementation alone does not improve TGH fermentation dynamics, and independent of the level of N supplementation, the inclusion of starch onto TGH supplementation strategies is likely to affect only VFA profile rather than total production.

Key Words: supplementation, tropical forage, protein
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578 Effects of roughage removal, rumen modifiers inclusion and post ruminal amino acid supply on growth performance in beef steers.

M. M. Masiero*, A. L. Kenny, J. M. Prestegaard, B. R. McDonald, C. D. Martin, and M. S. Kerley, *University of Missouri, Columbia.*

The objective of this study was to determine the effects of roughage removal, rumen modifiers and diets balanced to meet predicted AA requirement on beef steer growth performance. We hypothesized that growth performance of steers fed different rumen modifiers (monensin, Rumensin 90, Elanco Animal Health vs essential oils [EO], Xtract X60-7065, Pancosma) would not differ, and that diets balanced to meet AA requirements as well as roughage removal would improve G:F and ADG. Crossbred steers (n = 150; 284 ± 23 kg BW) were randomly assigned to one of five diets. Four diets were balanced to meet AA requirements with a common feedlot diet used as control (CON; DM basis; 17% CP, 22% NDF, 12% fescue hay, 58% corn, 27% wet distillers grains with solubles [WDGS]; 300 mg·steer^{-1}·d^{-1} monensin). Two diets contained roughage (R), with monensin (RM) or EO (RE) (DM basis; 17% CP, 17% NDF, 9.4% fescue hay, 70% corn, 9.4% AminoPlus, 9% WDGS, 0.05% AjiPro [Ajinomoto]; and 300mg·steer^{-1}·d^{-1} monensin or 800mg·steer^{-1}·d^{-1} Xtract). Two diets replaced roughage with corn; non-roughage (NR) with monensin (NRM) or EO (NRE). Data were analyzed as a two-factor factorial arrangement plus control, with roughage and rumen modifiers as main effects and steer as experimental unit. Main effects were only considered when interaction was not significant ($P > 0.05$) and data reported as least square means ± SEM. Control was compared only to RM. During the first 21d, steers consuming R had greater ($P < 0.01$) DMI (8.54 vs 6.78 ± 0.22 kg·d^{-1}), ADG (2.81 vs 2.01 ± 0.10 kg) and G:F (0.34 vs 0.30 ± 0.01) than NR. Steers consuming RM did not differ on DMI ($P = 0.08$) and had greater ADG than CON (2.89 vs 2.55 ± 0.09 kg; $P < 0.01$). At 42d, steers consuming R had greater ($P < 0.01$) DMI (9.51 vs 6.98 ± 0.22 kg·d^{-1}) and ADG (2.39 vs 1.90 ± 0.07kg) than NR. When monensin was fed, G:F did not differ regardless of roughage inclusion, however, when EO were added, calves consuming NR were more efficient than R (NRM=0.261, NRE=0.282, RM=0.262, RE=0.245 ± 0.008; $P = 0.02$). Steers consuming RM had greater ($P < 0.01$) DMI (9.52 vs 8.15 ± 0.22 kg·d^{-1}) and ADG (2.47 vs 2.13 ± 0.06 kg) than CON. In conclusion, balancing diets to meet AA requirements improved ADG during early growth. Calves consuming R were more efficient during the first 21d independent of rumen modifier. However, at d42 calves consuming NRE were more efficient than RE, and calves consuming NRM and RM did not differ.

Key Words: monensin, essential oils, non-roughage
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579 In situ and in vitro evaluation of a slow release form of nitrate for ruminants: Nitrate release rates, rumen nitrate metabolism and production of methane, hydrogen, and nitrous oxide.

C. Lee*[1], R. C. Araujo[2,3], K. M. Koenig[4], and K. A. Beauchemin[4], *[1]Department of Animal Sciences, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil, [3]EW|Nutrition GMBH, Visbek, Germany, [4]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

In situ and in vitro experiments were conducted to determine the nitrate (NO_3^-) release rate from encapsulated NO_3^- (EN; 71% NO_3^-) in the rumen and to examine metabolism of EN-NO_3^- in conjunction with methane (CH_4), hydrogen (H_2), and nitrous oxide (N_2O) production. Three ruminally-cannulated beef heifers were used to incubate the following substrates in the rumen for 72 h: soybean meal, EN, and unencapsulated NO_3^- (UEN). Because of immediate solubilization, the soluble nitrogen (N) fraction of UEN was assumed to be 100%. A non-linear regression model fitted to N disappearance of EN ($r^2 = 0.93$, $P < 0.01$) indicated 35.4% and 54.7% of soluble and slowly degradable N fraction, respectively. Two in vitro experiments were conducted where UEN and EN were incubated for 24 h in buffer alone or with buffered-rumen fluid with substrates containing urea, UEN, or EN as sole N sources. When UEN was incubated with buffer, 99.9% of UEN-NO_3^--N was recovered as NO_3^--N in the buffer over 24 h. However, recovery of EN-NO_3^- as NO_3^--N gradually increased over 24 h up to 58%. When urea, EN or UEN were incubated with buffered-rumen fluid, total gas production decreased ($P = 0.022$) for UEN compared with urea and EN. Methane production decreased (10.7 and 13.3 vs 19.6 mL; $P < 0.01$) for UEN and EN, respectively, compared with urea. Hydrogen production increased (0.2 vs 0.07 and 0.08 mL; $P < 0.01$) for UEN compared with urea and EN, respectively. Nitrous oxide production was greater for UEN (20.8, 7.5 and 0.02 μL, respectively; $P < 0.05$) followed by EN and urea. During the incubation with buffered-rumen fluid, 100% of UEN-NO_3^- was recovered as NO_3^--N in the medium until 6 h and then the recovery gradually decreased to 18% at 24 h while recovery as nitrite (NO_2^-)-N increased up to 22% at 24 h. However, recovery of EN-NO_3^--N as NO_3^--N in the medium increased by 20% at 12 h and then gradually decreased to 5% at 24 h without accumulation of NO_2^--N in the medium. In conclusion, EN released NO_3^- comparatively slowly in the rumen and decreased CH_4 production without negatively affecting microbial fermentation. Increases in H_2 and N_2O production and accumulation of NO_3^- and NO_2^- in the medium were not observed for EN compared with UEN, indicating that EN could be a promising NO_3^- source to lower CH_4 production with less risk of NO_3^-/NO_2^- toxicity.

Key Words: encapsulated nitrate, greenhouse gases, hydrogen
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580 Effects of encapsulated nitrate on growth performance, carcass characteristics, nitrate residues in tissues, and enteric methane emissions in feedlot beef steers: Finishing Phase.

C. Lee[*1], R. C. Araujo[2,3], K. M. Koenig[4], and K. A. Beauchemin[4], [1]*Department of Animal Sciences, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster,* [2]*EW|Nutrition GMBH, Visbek, Germany,* [3]*GRASP Ind. & Com. LTDA, Curitiba, Brazil,* [4]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

A finishing feedlot study was conducted with beef steers to determine effects of encapsulated nitrate (EN) on growth performance, carcass characteristics, methane production, and nitrate (NO_3^-) residues in tissues. The 132 crossbred steers were backgrounded in a feedlot and transitioned to the high concentrate diets evaluated in the present study. The steers were initially assigned to 22 pens (6 animals per pen) in a randomized complete block design with BW (18 pens) and animals designated for methane measurement (4 pens) as blocking factors. Five animals in each pen designated for methane measurement were monitored for methane emissions in respiratory chambers twice during the finishing period. Pens received 3 dietary treatments (7 pens each): Control, a finishing diet supplemented with urea (0.03% NO_3^- and 0.9% urea in dietary DM); 1.25% EN, the control diet supplemented with 1.25% EN (1.1% NO_3^-) which partially replaced urea; 2.5% EN, the control diet supplemented with 2.5% EN (2.0% NO_3^-) fully replacing urea. The final pen designated only for methane measurement received a fourth dietary treatment, 2.3% UEN; control diet supplemented with unencapsulated NO_3^- (UEN; 2.0% NO_3^- in dietary DM) fully replacing urea. The cattle weighed 449 ± 32 kg at the start of the finishing period. The 2.5% EN diet decreased DMI (9.9 vs 10.7 and 10.7 kg/d; $P < 0.01$) compared with Control and 1.25% EN. Feeding EN tended to increase ADG (1.41 vs 1.36 kg/d; $P = 0.09$) and increased gain:feed (0.137 vs 0.127 kg/kg; $P < 0.01$) for EN compared with Control. No differences in methane production and yield were observed among treatments. Inclusion of EN in the diets increased ($P \leq 0.03$) sorting in favor of large and medium particles and against small and fine particles. Plasma NO_3^- and NO_2^- concentrations were elevated (0.06 to 3.68 mg/L of NO_3^- and 1.47 to 9.23 μg/L of NO_2^-; $P < 0.01$) with EN in a dose response manner, but blood methemoglobin levels for all treatments were below 1%. Feeding EN increased ($P < 0.01$) NO_3^- concentrations in muscle, fat, liver, and kidney and NO_3^- concentrations of those were similar between 1.25% EN and 2.3% UEN. In conclusion, including up to 2.5% of EN on a DM basis in a finishing diet did not cause NO_3^- toxicity or health problems in a long term study. In comparison with supplemental urea, feeding EN improved feed efficiency despite increases in sorting against dietary EN.

Key Words: encapsulated nitrate, finishing feedlot, beef cattle
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581 Nitrogen utilization of West African Dwarf sheep fed mixtures of Oil Palm Slurry and Cassava Peel in varying proportions.

O. Abiola-Olagunju[*1], A. A. Mako[2], A. O. Mosuro[3], and A. O. Akinsoyinu[4], [1]*Lead City University, Ibadan, Nigeria,* [2]*Tai Solarin University of Education, Ijebu-ode, Nigeria,* [3]*University of Ibadan, Ibadan, Nigeria,* [4]*Babcock University, Ilishan, Nigeria.*

The objective of this study was to evaluate the nitrogen utilization and digestible nutrients by West African Dwarf (WAD) sheep fed mixture of fermented Oil Palm Slurry (OPS) and Cassava Peel (CaP) based diets. A total of twenty four (24) female WAD sheep between the ages of 5-6 months, weighing 9.18 – 11.8 kg were allotted to 6 experimental diets in a completely randomized design as follows; One liter of OPS mixed with 1Kg, 2Kg, 3Kg, 4Kg, 5Kg (Diets A – E) of CaP, respectively while 6Kg (Diet F) of CaP only, served as the control. The experiment lasted fourteen (14) days with feed and water served ad libtum. Data collected were subjected to analysis to ascertain; nitrogen utilization and total digestible nutrients by WAD sheep were also determined. Parameters measured included: Nitrogen intake (N-intake g/d), Fecal Nitrogen g/d (Fecal N), Urinary Nitrogen g/d (Urinary-N), Total Nitrogen excreted g/d (T-N excreted), Nitrogen balance g/d (N-balance) and Nitrogen retention % (N-retention). Digestibility of dry matter, crude protein, crude fiber, ether extract, nitrogen free extracts and total digestible nutrients (TDN) were determined. Results revealed Significant variations ($P < 0.05$) for all parameters measured. Sheep on Diet C (One liter of OPS mixed with 3kg CaP) had the highest values (16.01, 14.0 and 75.05%) for N-intake; N- balance and N-retention respectively, while least values (10.00g/d,1.45 g/d, and 45.60%) respectively, were obtained for sheep on Diet A (One liter of OPS mixed with 1Kg of CaP). Highest value (5.44 g/d) of T-N excreted was recorded for animals on diets C, while the lowest value (2.05 g/d) was recorded for animals on diet A. Significant reduction in values (1.45g/d and 0.60g/d) respectively, were observed for Fecal and Urinary-N in sheep placed on diet C as compared to the increased values of (4.24g/d, 2.50g/d and 1.20g/d, 1.00g/d) respectively, for animals placed on diet A and diet B (One liter of OPS mixed with 2Kg of CaP). Significant observations were obtained for digestible CP, CF, EE ,NFE and TDN, where sheep placed on diet C record highest value of 73.04% and a decreasing value of (58.06%) and (53.90%) were recorded for animals on diets B and A respectively. All the results from these experiments, give strong ground to conclude that sheep placed on Diet C - 1 liter Oil Palm Slurry : 3kg Cassava Peel, showed best results for both parameters measured compared to other diets as sheep feed.

Key Words: Oil Palm Slurry, Cassava Peel, digestible nutrients
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582 Effect of fermenten on nitrogen metabolism and ruminal fermentation profile of Angus crossbred steers.

M. E. Garcia-Ascolani*[1], A. Lopez[2], T. M. Schulmeister[1], M. Ruiz-Moreno[1], D. D. Henry[1], F. M. Ciriaco[1], G. C. Lamb[3], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]INTA EEA Santiago del Estero, Santiago del Estero, Argentina, [3]Texas A&M University, Department of Animal Science, College Station.*

The objective of this study was to assess the effect of two inclusion rates of Fermenten (FER, Church & Dwight Co., Inc., Princeton, NJ) on ruminal fermentation profile, blood urea nitrogen (BUN) and apparent total tract digestibility of nutrients in Angus crossbred steers. Eight steers, fitted with ruminal cannulas, were randomly assigned to treatments in a switchback design. Steers were fed a basal diet (92% of the diet DM) comprised mainly of corn gluten feed, soybean hulls, and peanut hulls, and two different top-dressed premixes (8% of the diet DM) to achieve: 1) a final inclusion rate of FER of 4% in the diet DM (4% FER), or 0% inclusion rate of FER (CTL). Diets were isocaloric (69% TDN) and similar in RDP content (6.5% of diet DM), and were individually fed at 2.8% of BW/d. Individual intake was recorded using the GrowSafe System. Samples of ruminal fluid and blood were collected for 24 h, before feeding (0 h) and every 3 h, to determine ruminal pH, NH_3-N and VFA concentrations, and serum concentrations of BUN. Apparent total tract digestibility of nutrients was measured using indigestible NDF as an internal marker. Data were analyzed using the MIXED Procedure of SAS with steer as the experimental unit. Ruminal pH, VFA and concentrations of NH_3-N and BUN were analyzed as repeated measures using the MIXED procedure of SAS. There was a tendency (P = 0.09) for a treatment × time interaction for ruminal pH. Steers in the 4% FER treatment had increased concentrations of butyrate (P = 0.01) and a tendency (P = 0.06) for decreased concentrations of acetate. Steers receiving 4% FER had decreased intake of all nutrients ($P < 0.05$), as well as a decreased DMI as percent of BW (P = 0.03). Apparent total tract nutrient digestibility was similar between treatments ($P > 0.05$), except for CP, which was greater for 4% FER treatment (P = 0.012). Nitrogen metabolism was similar between treatments; there was no difference on ruminal NH_3-N (P = 0.97) or BUN (P = 0.95) concentrations. Decreased intake may hinder possible effects of FER on ruminal fermentation parameters, N metabolism, and nutrient digestibility.

Key Words: Fermentation, Nutrient digestibility, Fermenten
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583 Effects of lipid intake and degree of saturation on nutrient digestion and nitrogen balance in steers consuming corn-based diets.

E. J. Blom*[1], D. E. Anderson[2], and D. W. Brake[1], *[1]South Dakota State University, Brookings, [2]University of Tennessee-Knoxville, Knoxville.*

Increases in dietary lipid can augment energy density; however, lipids can mitigate ruminal fermentation of feed. We evaluated effects of amount and source of dietary lipid on nutrient digestibility, ruminal fermentation, and N balance in cattle consuming corn-based diets. Five steers (BW = 392 ± 15 kg) fitted with ruminal, duodenal, and ileal cannulas were used in a 5 × 5 Latin square with 12-d periods. Diets contained no added fat, or 4 or 8% added lipid from either a predominantly saturated (i.e., tallow) or predominantly unsaturated (i.e., linseed oil) source. Unsaturated fat decreased (P = 0.01) DMI compared to saturated fat and increasing amount of lipid supplementation tended (*Linear* = 0.14) to decrease DMI. Neither added amounts or source of lipid affected ($P \geq 0.33$) ruminal NDF digestion. However, increased diet lipid decreased ruminal DM digestibility (*Linear* = 0.04) and tended (*Linear* = 0.15) to decrease ruminal starch digestibility. Apparent (*Linear* = 0.03) and truly (*Linear* = 0.05) fermented OM in the rumen decreased in response to increased dietary lipid. Ruminal pH ($P \geq 0.50$), ammonia ($P \geq 0.18$) and total organic acid content ($P \geq 0.31$) were not affected by diet lipid. Additionally, amount and source of lipid had no effect on ruminal acetate ($P \geq 0.21$) or propionate ($P \geq 0.21$) concentrations; however, lipid amount tended (*Linear* = 0.07) to decrease acetate:propionate. Similarly, total tract digestion of DM (*Linear* < 0.01), OM (*Linear* < 0.01), and NDF (*Linear* = 0.02) were decreased by added dietary lipid. Greater lipid intake also tended (P = 0.12) to decrease total tract starch digestion. Unsaturated lipid tended (P = 0.06) to decrease total tract NDF digestibility, but saturated lipid tended to decrease total tract DM (P = 0.12) and OM (P = 0.10) digestion. Microbial N flow to the duodenum was not affected ($P \geq 0.18$) by lipid, but microbial efficiency tended (*Linear* = 0.06) to increase with increased lipid intake. Fecal N excretion was decreased ($P < 0.01$) by unsaturated lipid. Nitrogen balance ($P \geq 0.28$) and N efficiency ($P \geq 0.58$) were not affected by lipid source or amount.

Key Words: Cattle, Lipid, Nitrogen balance
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584 Novel techniques for the extraction of rumen un-degradable amino acids from distiller's coproducts.

Z. Insani Hubi[1], and J. K. Margerison*[2], [1]*Faculty of Animal Science, Universitas Gadjah Mada, Yogyakarta, Indonesia,* [2]*University of Nottingham, Sutton Bonington, United Kingdom.*

Providing adequate and balanced amino acid supply increases nitrogen capture from animal feed into human food products, creating greater food security while lowering environmental impact. New processing techniques allow the extraction of specific protein (SP) from distiller's dried grains and solubles (DDG) resulting in greater rumen un-degradable amino acid (RUAA) supply. The degradation rate and residual RUAA content of two SP extracted from corn (cDDGS) were compared with cDDGS, soya bean meal (SBM) and RUAA processed from SBM and RSM. A Cornell model was applied to thirty-three dried and ground (1 mm) samples of; cDDGS, SBM, RUAA SBM, RUAA RSM, and two SPs (SP2 and SP50), that were combined with a partial mixed ration (PMR), buffered, flushed with CO_2 and incubated for 16 h at 39°C to measure in vitro gas production (IVGP) using Ankom-RFS. Feed composition was analysed pre and post incubation and RUAA profile was estimated using gas liquid chromatography. Data was analysed using general linear modeling, applying feed as a fixed effect and all other factors as random effects, using a confidence interval of 0.95 and differences using Tukey's test (P value <0.05). Gas production was highest from cDDGS and lowest from Hiprosoya, but similar in RUAA from SBM and RSM, SP2 and SP50. RUAA was greatest from SBM, but similar from Hiprosoya, SP2 and SP50 and lowest from RUAA RSM. Liquor pH did not differ. SP50 had the highest total VFA and lowest A:P ratio, while SP2 was similar to RUAA from SBM and/or RSM. In conclusion, results demonstrated the potential of SP2 and SP50 to increase the RUPAA from cDDGS to similar amounts provided by RUAA SBM.

Key Words: Amino acids, Protein, Ruminants
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585 Expression of genes involved in energy metabolism and transport of volatile fatty acids and urea in rumen epithelium of bulls identified for high, medium, and low residual Feed intake.

P. Del Bianco Benedeti[1], M. M. Lopes[1], S. F. M. Bonilha[2], N. V. L. Serão[3], D. R. Lopes[1], H. C. Mantovani[1], M. P. Gionbelli[4], C. J. Newbold[5], E. Detmann[1], and M. S. Duarte*[1], [1]*Universidade Federal de Viçosa, Viçosa, Brazil,* [2]*Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho, Brazil,* [3]*North Carolina State University, Raleigh, NC,* [4]*Universidade Federal de Lavras, Lavras, Brazil,* [5]*Aberystwyth University, Aberystwyth, United Kingdom.*

The objective of this study was to investigate the expression of genes involved in energy metabolism and volatile fatty acids (VFA) and urea transport in rumen epithelium of bulls with high (H-RFI), medium (M-RFI), and low (L-RFI) residual feed intake. Twenty-seven Nellore bulls (BW = 401 ± 42 kg) were identified for L-RFI (n = 9), M-RFI (n = 9), and H-RFI (n = 9) and finished in collective pens. Animals were fed the same diet, formulated to meet the requirements of 1.3 kg daily gain with a target finish weight of 550 kg. After the end of the trial, bulls were slaughtered and ruminal fluid was collected for further VFA analyses. Samples of rumen epithelium from ventral sac were rapidly excised, rinsed with phosphate buffered saline solution (pH = 7.04) and immediately immerged in RNA later solution. After 48 hours, rumen epithelium samples were placed at -80°C until total RNA isolation and qPCR

Table 585. Relative mRNA abundance (Arbitrary units) of target genes

Item	H-RFI	M-RFI	L-RFI	SEM	*P*-value
Oxidative phosphorylation					
NDUFB4	1.65	1.18	1.42	0.16	0.07
UQCR10	1.54^a	0.99^b	1.14^b	0.10	<0.01
Ion pumping					
ATP1B1	1.66	1.70	1.88	0.22	0.76
ATP1B2	1.94	1.57	1.92	0.23	0.45
ATP1B3	1.84	1.55	1.82	0.21	0.56
Protein turnover					
IGF1R	1.81	1.67	1.88	0.18	0.70
MKI67	1.91	1.97	2.29	0.31	0.67
UBA1	1.78	1.58	1.78	0.18	0.67
Heat production					
UCP2	1.53	1.16	1.47	0.13	0.12
Butyrate metabolism					
BDH1	1.81	1.61	1.57	0.17	0.55
HMGCL	1.43	1.34	1.52	0.13	0.65
VFA transport					
DRA	1.82	1.53	2.06	0.23	0.28
MCT1	2.42	2.02	2.26	0.29	0.62
NHE2	1.27	1.21	1.51	0.15	0.32
Urea transport					
AQP10	1.88	1.49	1.56	0.20	0.36
SLC14A1	1.74	1.46	1.86	0.22	0.42

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

analysis. Data were analyzed using SAS 9.4 with $\alpha = 0.05$. Concentrations of total VFA, acetate, propionate, butyrate, valerate, iso-butyrate, iso-valerate, and acetate: propionate did not differ ($P > 0.05$) among treatments. The mRNA abundance of *UQCR10* ($P < 0.01$) and *NDUFB4* (trend; $P = 0.07$) were greater for H-RFI animals (Table 585). The mRNA abundance of genes associated with ion pumping, protein turnover, heat production, butyrate metabolism, and VFA and urea transport did not differ ($P > 0.05$) among treatments. These findings may indicate that L-RFI animals have lower energy expenditure in this tissue, which likely contribute for their better efficiency compared to the M-RFI and H-RFI bulls.

Key Words: Beef cattle, energy expenditure, feed efficiency
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586 Grain processing effects on expression of genes involved in volatile fatty acid transport in rumen epithelium of beef cattle.

P. Del Bianco Benedeti[1], B. C. Silva[1], M. V. Pacheco[1], I. C. Filho[1], M. M. Lopes[1], N. V. L. Serão[2], S. C. Valadares Filho[1], M. P. Gionbelli[3], E. Detmann[1], and M. S. Duarte*[1], [1]*Universidade Federal de Viçosa, Viçosa, Brazil,* [2]*North Carolina State University, Raleigh,* [3]*Universidade Federal de Lavras, Lavras, Brazil.*

This study was conducted with the objective to evaluate the effects of corn and sorghum processing methods on the expression of genes involved in volatile fatty acids (VFA) transport of finishing bulls. Five rumen cannulated Nellore bulls (260 ± 23 kg of body weight) were used in a 5x5 Latin square arrangement with five periods of 23 d, with 14 d for adaptation and 9 d for sample collection. Diets contained 72% concentrate (Dry matter basis) and treatments were four energy sources (Dry-ground corn; dry-ground sorghum; high-moisture corn; high-moisture sorghum), plus a control (55% concentrate diet). Bulls were fed twice daily at 0800 and 2000 h. Total and ruminal digestibilities of organic matter (OM) were determined from day 15 to 19. On day 22, 20 mL of ruminal fluid were sampled and preserved with metaphosphoric acid solution (5 mL, 25% w/v) for later determination of VFA. On day 23, samples of rumen epithelium from ventral sac were rapidly excised and stored at -80°C until total RNA isolation and qPCR analysis. Data were analyzed using SAS 9.4 with $\alpha = 0.05$. Bulls fed high-moisture grains presented greater OM total digestibility and lower OM ruminal digestibility ($P < 0.01$). The concentration of total VFA, acetate, and propionate were greater ($P < 0.01$) for animals fed corn. There was an interaction ($P = 0.03$) between ingredient and grain processing method for mRNA abundance of *DRA*, which was lowest in high-moisture corn treatment (Table 586). The mRNA abundance of *AE2*, *MCT1*, *MCT4*, *NHE1*, *NHE2*, and *PAT1* did not differ ($P > 0.05$) among treatments. These results may suggest that changes in corn processing may impact the VFA transport throughout rumen epithelium of finishing Nellore bulls.

Key Words: Beef cattle, High Moisture, Rumen Tissue
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Table 586. Relative mRNA abundance (Arbitrary units) of target genes

		Dry-ground		High-moisture			*P*-value			
Item	Control	Corn	Sorghum	Corn	Sorghum	SEM	Control x Remain treatments	Ingredient	Grain processing	Ingredient x Grain processing
AE2	3.36	3.67	3.17	2.84	3.07	0.76	0.82	0.83	0.49	0.59
DRA	2.70^a	3.02^a	2.99^a	1.80^b	3.17^a	0.55	0.90	0.04	0.10	0.03
MCT1	1.79	1.97	1.77	1.56	1.62	0.36	0.83	0.78	0.27	0.61
MCT4	1.59	1.82	2.03	1.72	1.95	0.31	0.38	0.46	0.75	0.97
NHE1	1.58	1.84	1.74	1.22	1.68	0.25	0.86	0.39	0.10	0.19
NHE2	2.05	2.24	2.05	1.50	2.07	0.42	0.72	0.36	0.10	0.09
PAT1	3.07	3.25	3.25	2.58	3.17	0.34	0.95	0.13	0.06	0.12

^{a,b} Within a row, different subscripts differ at $P < 0.05$.

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587 The role of diet composition fed during residual feed intake determinations and the impact of the diet on the gene sets associated with efficiency as determined by a gene set enrichment analysis.

J. L. Mutch[1], H. L. Neibergs[2], M. Neupane[1], J. J. Michal[2], D. J. Garrick[3], M. S. Kerley[4], D. W. Shike[5], J. E. Beever[6], S. L. Hansen[3], J. F. Taylor[7], U. S. Feed Efficiency Consortium[7], and K. A. Johnson*[1], [1]*Department of Animal Sciences, Washington State University, Pullman,* [2]*Washington State University, Pullman,* [3]*Iowa State University, Ames,* [4]*Division of Animal Sciences, University of Missouri, Columbia,* [5]*University of Illinois, Champagne,* [6]*University of Illinois, Urbana,* [7]*University of Missouri, Columbia.*

To examine the potential role of diet fed during the residual feed intake (RFI) measurement period on the leading edge genes (LEG) associated with feed efficiency, a gene set enrichment analysis using SNP (GSEA-SNP) was completed using data from 887 Simmental-cross steers. The steers were fed a range of diets during their RFI measurement period with NDF content ranging from 14.40 to 44.73%. To determine if this

NDF range had an impact on the enrichment of gene sets, steers were separated into two groups, one with a diet >40% NDF (n = 611) and one with NDF content <40% (n = 276). Significant SNPs ($P < 0.05$) within the average haplotype block length for the population (8.5 kb) that were associated with RFI by genome-wide association analysis for RFI were used as a proxy for each of 19,723 annotated genes from the UMD3.1 genome assembly. Gene sets from five databases were used for the GSEA-SNP: Panther (n = 165), Kyoto Encyclopedia of Genes and Genomes (KEGG; n = 186), Biocarta (n = 217), Reactome (n = 674), and Gene Ontology (GO; n = 3,147). The null distribution for testing the normalized enrichment score was estimated with GenABEL (R package) and 10,000 permutations. Enriched gene sets (NES > 3.0) and their LEG associated with RFI were identified. Mean DMI and RFI for the steers fed a diet with >40% NDF was 10.67 kg ± 1.36 and -0.39 ± 0.05 and 10.08 kg ± 1.30 and 0.44 ± 0.07 for the <40% NDF. Enriched gene sets for steers fed <40% NDF were GO Behavior (GO:0007610) with 128 LEG and GO Ras Protein Signal Transduction (GO:0007265) with 136 LEG. Four LEG genes were common across the Behavior (GO:0007610) and Ras Protein Signal Transduction (GO:0007265) pathways indicating their importance to the RFI trait. Four gene sets were enriched for steers fed >40% NDF: KEGG Glycerophospholipid Metabolism (map00564) with 65 LEG, GO Ubiquitin Ligase Complex (GO:00001051) with 54 LEG, Reactome Synthesis of Phosphatidic Acid (R-HSA-1483166) with 25 LEG and the Panther Opioid Proopiomelanocortin pathway (P05917) with 18 LEG. The GSEA-SNP analysis based on dietary NDF level resulted in no common gene sets. Steers fed diets containing higher NDF levels had enriched gene sets for lipid metabolism and feed intake while those steers fed diets containing lower NDF levels were enriched for protein transduction and general behavior genes. The diet fed during the determination of RFI had an impact on the gene sets and LEG genes, suggesting differences in metabolic pathways associated with the trait.

Key Words: RFI, Gene Set Enrichment, Beef
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588 Gastrointestinal tract gene expression in ewes under feed restriction.

A. I. Trujillo*[1], C. Febrer[1], A. Casal[1], V. de Brun[2], A. L. Astessiano Dickson[1], M. Carriquiry[1], and J. A. Abecia[3], [1]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay,* [2]*Facultad de Veterinaria, Universidad de la Republica, Montevideo, Uruguay,* [3]*IUCA. Universidad de Zaragoza., Zaragoza, Spain.*

The gastrointestinal tract is known to adapt itself to changes in feed conditions and is the source of various signals that regulate feed intake and energy homeostasis. Therefore, the objective of this study was to assess the effect of a feed restriction period in the mRNA expression of target genes related to feed intake. The study was conducted in a randomized block design with 5 temporal replications (n = 4 or 3 per treatment and replication) in which thirty-five Rasa Aragonesa ewes (BW = 67.1 ± 8.6 kg and BCS = 3.0 ± 0.5) were assigned to two nutritional treatments (3.15 vs 1.05 Mcal per day/1.5 vs 0.5 times the daily requirements for maintenance; Control and Low, respectively) during 30 days. At the end of this period ewes were slaughtered and a total of 12 samples from abomasum and 12 samples from small intestine (6 ewes per treatment selected by embryo presence) were collected. Relative mRNA expression of glucagon-like peptides 1 and 2 (*GLP1*, *GLP2*) and their receptors (*GLP1R, GLP2R*), neuropeptide Y2 receptor (*NPY2R*), ghrelin, insulin-like growth factor-1 (*IGF1*) and its receptor (*IGF1R*) were determined in abomasum while mRNA expression of *IGF1*, *IGF1R*, cholecystokinin (*CCK*), protein kinase AMP-activated-beta 1 (*AMPKB1*), neuropeptide Y1 and Y2 receptors (*NPY1R, NPY2R*), peptide YY (*PYY*), insulin receptor (*INSR*) and ghrelin were determined in the small intestine. The mRNA abundance of target genes was assessed by qPCR using SYBR-Green and normalized by the expression of 3 reference genes. Data were analyzed using a mixed model including nutritional treatment as a fixed effect and block as a random effect. Abomasal expression of *GLP1* mRNA (1.57 vs -1.03 ± 0.45; $P = 0.004$) and *GLP2* mRNA (0.25 vs -1.39 ± 0.37; $P = 0.014$) were greater in Control than Low ewes. Expression of *IGF1R* mRNA in small intestine was greater in Control than Low ewes (-2.01 vs -2.93 ± 0.26; $P = 0.0375$). No other measured genes in abomasum or small intestine showed a differential expression between Control and Low ewes ($P > 0.05$). Results suggest that ewes fed 1.5 times maintenance requirement presented greater expression of genes related to feed intake regulation. The greater expression of *IGF1R* mRNA in small intestine in these ewes may be associated with greater IGF-1 availability in this tissue, while the greater gene expression of *GLP1* and *GLP2* mRNA at abomasal tissue need further investigation.

Key Words: nutritional status, Rasa Aragonesa ewes, mRNA expression
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589 Heat-induced changes in protein molecular structure associated with rumen degradation of oat grains in dairy cows detecting by vibrational molecular spectroscopy.

L. Louzada Prates*, and P. Yu, *Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada.*

Heat processing may simultaneously affect protein rumen degradation and protein intestinal digestion by altering molecular protein structure in seeds. Attenuated Total Reflectance Fourier transform vibrational molecular spectroscopy (ATR-Ft/VMS) is a novel technique that reveals molecular structural features, increasing the understanding of feed structures at cellular level and new level of analytical information. The objective of this study was to reveal the change from heat-related feed processing in the molecular protein structure of oat grains: CDC Nasser and CDC Seabiscuit. Oat grains were sampled from harvested plots (n = 2) grown in 2014 and 2015. Each oat variety was equally divided into 4 portions and performed in one treatment: raw, dry-heating, autoclave heating or microwave irradiation. Samples were rolled (gap size 1.78 mm) for in situ incubation and ground through 0.5 mm screen for molecular spectral analysis. Amide I (1720 – 1577 cm^{-1}) and amide II (1577 – 1486 cm^{-1}) area intensities and peak heights, and secondary protein structures α-helices and β-sheets heights were measured in the region at ca. 1720 – 1486 cm^{-1} were quantified using OMNIC 7.3 software. Rumen degradation was performed using dairy cows equipped with rumen cannulae. Spectral data were analyzed using univariate analysis of recording peak parameters. Spearman correlation was performed after normality test. Multiple regressions were performed using PROC REG of SAS 9.4. Autoclave heating increased ($P < 0.001$) Amide I:Amide II area ratio and heat processing methods increased ($P < 0.001$) Amide I:Amide II height ration comparing to raw. The α-helix and β-sheet heights were lower for autoclave heating comparing to dry heating; however these treatments were statistically similar with raw. Rate of degradation of crude protein (KdCP) was positive correlated with α-helix ($r = 0.54$; $P = 0.028$) and β-sheet ($r = 0.59$; $P = 0.015$); effective degradability (EDCP) was strongly positive correlated with Amide I ($r = 0.75$; $P < 0.001$) and Amide II ($r = 0.67$; $P < 0.001$) areas, β-helix ($r = 0.75$; $P < 0.001$) and β-sheet ($r = 0.86$; $P < 0.001$). Multiple regressions were obtained: KdCP = -22.66 + 205.68 x β-sheet ($R^2 = 0.34$; $P = 0.015$); EDCP = -52.18 + 568.89 x β-sheet ($R^2 = 0.69$; $P < 0.001$). It can be concluded that heat-related feed processing affects molecular protein structures, the difference can be detected by ATR-Ft/VMS and protein molecular structure profile could be used as a predictor to estimate degradation kinetics of CP.

Key Words: ruminants, heat processing methods, structural makeup
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590 Identification of a previously uncharacterized *Ruminococcaceae* bacterial species associated with inclusion of high levels of lipid in the diet of beef steers.

C. Hron*[1], D. W. Brake[1], E. J. Blom[1], and B. St-Pierre[2], [1]*South Dakota State University, Brookings,* [2]*Animal Science Department, South Dakota State University, Brookings.*

The ruminal microbiome remains an enigma, in part, because only 5% of ruminal bacteria have been isolated and cultured. Diet of the host can have large impacts on ruminal microbial composition. Indeed, considerable effort has been dedicated to the identification of fibrolytic bacteria, but understanding of ruminal lipid digestion remains limited. Therefore, we evaluated ruminal microbial composition among 5 ruminally cannulated steers fed a corn-based diet with inclusion of 0, 4 or 8% added saturated (tallow) or unsaturated (linseed oil) lipids. Steers were placed in a 5 x 5 Latin square and treatments were balanced for carry-over effects. Steers were allowed a 14-d adaptation to the diet prior to the collection of ruminal samples. Bacterial composition was determined by next generation sequencing of 16S rRNA amplicons targeting the V1-V3 region for 21 of the 25 possible samples. A total of 422,922 high quality reads were clustered into 37,788 Operational Taxonomic Units (OTUs). In 3 of the 5 steers, a single species-level OTU (OTU-DB-1) was found in much greater abundance when diets included saturated (41.5-44.6%) or unsaturated (32.3-56.3%) lipids. This OTU was, in contrast, found in much lower abundance in controls (<1%). OTU-DB-1 was assigned by Ribosomal Database Project (RDP) classifier to the family *Ruminococcaceae* while database searches using BLAST revealed only one match (99%) to sequences of the NCBI “nt” database. To our knowledge, this is the first report of an OTU associated with greater lipid inclusion in diets to ruminants.

Key Words: Bacteria, Rumen, Lipid
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591 Effect of rumen inoculum on diet utilization and ruminal fermentation parameters of commonly used By-product ingredients in the Rumen Simulation Technique (RUSITEC).

A. K. Kelly*, T. M. Boland, and J. S. Heffernan, *School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland.*

There has been increased interest in the use of by-products (BP) for ruminant feeds, yet a deficit in information regarding nutrient content of these feeds exist. The objective of this study was to assess the effect of different rumen fluid inoculum on in vitro digestibility, including Dry Matter Digestibility (DMD); Organic Matter Digestibility (OMD); Crude Protein Digestibility (CPD); Neutral Detergent Fibre digestibility (NDFd); Acid Detergent Fibre digestibility (ADFd), and fermentation parameters of four commonly used BP feeds: Maize Distillers (MD); Wheat Distillers (WD); Palm Kernel (PK) and Soya Hulls (SH). Rumen inoculum was sourced from six rumen-fistulated continental heifers blocked on weight and age and fed one of two divergent diets vis. 50: 50 silage: concentrate (C, rumen inoculum) on a dry matter (DM) basis or grass only (G, rumen inoculum). In vitro incubation trials were carried out with the rumen simulation technique (RUSITEC). The dietary in vitro treatments consisted of 60% silage (18% DM, 13.37% CP, 51.5% NDF and 37.39% ADF) and 40% of the BP ingredient on a DM basis. These were incubated in one of two rumen inoculum (C or G), replicated three times and distributed evenly among three eight vessel RUSITEC units, resulting in a 2x4 factorial design. No interaction was detected ($P > 0.05$) between rumen inoculum and BP ingredient for any of the parameters examined. Rumen fluid inoculum had no effect on the digestibility of DM, OM, CP, NDF or ADF of concentrate or whole diet; pH; daily gas production; total VFA or molar concentrations of individual VFA proportions ($P > 0.05$). However, ammonia production was higher ($P < 0.05$) in the C compared to G derived inoculum. The DMD of the BP were: WD (70%); MD (60%); PK (53%) and SH (34%) ($P < 0.0001$). By-product ingredient had no effect on gas production, pH or total VFA production. However, concentration of individual VFA varied with by-product ingredient. Palm kernel and SH exhibited the highest acetate: propionate (A: P) ratio of 2.41 and 2.34 respectively. Wheat distillers resulted in the lowest A: P ratio of 2.08. Daily ammonia production was affected by by-product ingredient, resulting in WD > MD > PK >SH ($P < 0.01$). In conclusion, in the RUSITEC culture system the in vitro digestibility and fermentation profile of by-product feeds are consistent and unaffected by rumen inoculum when sourced from divergent diets within a single animal species.

Key Words: By-products, In-vitro digestibiliy, Rumen inoculum
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592 Effects of by-product inclusion and linseed oil supplementation to a pasture based diet on methane production, diet utilization and ruminal fermentation parameters in the Rumen Simulation Technique (RUSITEC).

A. K. Kelly*, T. M. Boland, and J. S. Heffernan, *School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland.*

The objective of this study was to investigate the effects of by-product (BP) inclusion and linseed oil (LO) on diet digestibility, fermentation pattern and methane production using the rumen simulation technique (Rusitec), with perennial ryegrass pasture as the main forage source. Dietary treatment consisted of a supplementary concentrate (factor I) containing either 35% BP (BP35) or 95% BP (BP95) with and without 6% LO inclusion (factor II), thereby culminating in a 2 (concentrate; BP 35 or BP95) x 2 (LO; + or -) factorial arrangement. Dietary in vitro treatments consisted of a 50:50 perennial ryegrass based pasture (PRG) and one the four supplementary concentrates. Treatments were randomly allocated to sixteen fermentation vessels. The in vitro incubation trial involved of a single incubation period lasting 14 d consisting of 10 d adaption and 4 d sampling period. The DM digestibility of the concentrate treatments were: BP35 (68.9%); BP35+oil (68.7%); BP95 (57.4%) and BP 95+oil (54.4%). In general, concentrate that contained lower levels of BP had a higher digestibility parameters (DM, OM, CP, NDF and ADF) than the concentrates that contained a higher BP inclusion ($P < 0.0001$). No significant difference was recorded in pH or NH_3-N production for any treatments examined ($P > 0.10$). Production of volatile fatty acids (VFA) was highest for the low BP diets (BP35; $P < 0.05$) relative to the BP95. Acetic acid proportion ($P < 0.05$) and acetate:proprionate ratio ($P < 0.05$) was greatest in the BP95 concentrate compared to the BP35 diet. Methane production (when expressed as production per day or in terms of production per organic matter digested) was affected ($P < 0.05$) by BP concentrate type and LO supplementation. Addition, of LO reduced methane (CH_4) for both BP concentrate types with BP95+LO having the lowest CH_4 production, BP35+LO and BP95 intermediate and BP35 having the highest CH_4 production, respectively. Under in vitro conditions, the inclusion of BP and addition of supplementary LO to a concentrate supplemented grass based diet of ruminants can effectively reduce CH_4 production.

Key Words: Methane, By-product, Linseed oil
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593 Water intake prediction for beef cattle in Brazil.

D. Zanetti[1], L. F. Prados[2], A. C. B. Menezes[3], J. M. V. Pereira[4], E. Detmann[4], T. E. Engle[5], and S. C. Valadares Filho*[4], [1]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil,* [2]*Federal University of Viçosa, Viçosa, Brazil,* [3]*Universidade Federal de Vicosa, Vicosa, Brazil,* [4]*Universidade Federal de Viçosa, Viçosa, Brazil,* [5]*Colorado State University, Fort Collins.*

Water is the most important nutrient in animal production. Brazil has the largest commercial cattle herd, where the environmental conditions and beef cattle breeds are distinct from those described in the literature and there is no equation to predict water demanded by beef cattle for Brazilian breeds. Our objective was to validate 6 current water intake (WI) equations for beef cattle using water intake data from three experiments conducted in Southeastern Brazil (Nellore beef cattle). Animal performance, diet composition, and environmental data were collected for all experiments. The prediction of WI using the current published WI equations was tested though the regression between predicted and measured WI values. All tested equations did not agree with the measured WI data from the experiments. WI was overestimated by the previously published WI equations when compared to the actual WI observed in Nellore cattle raised in tropical conditions. Several factors can help to explain why the published equations did not predict the actual WI from the 3 experiments. The tested equations were developed in temperate climates using predominantly *Bos taurus taurus*. From the current data we generated new WI equations based on metabolic body weight ($BW^{0.75}$), dry matter intake (DMI), humidity (HU) and temperature-humidity index (THI) for Nellore cattle in Southeastern Brazil, as follow: $-4.315 + 0.205 \times BW^{0.75} - 0.17 \times HU + 0.913 \times DMI + 0.247 \times THI$. We recommended the proposed equation to estimate WI by Nellore cattle in tropical conditions.

Key Words: Equation, beef cattle, Water intake
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594 Feedlot performance of Nellore cattle submitted to either nutritional restriction or intake of concentrate feedstuffs prior to adaptation period.

M. C. Pereira[*1], A. L. Rigueiro[1], A. C. Melo[2], A. M. Silvestre[2], R. R. Ferreira Filho[2], C. H. Soares[3], M. D. Arrigoni[1], and D. D. Millen[4], [1]*São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil,* [2]*São Paulo State University (UNESP), Dracena campus, Dracena, Brazil,* [3]*São Paulo State University (UNESP), Dracena campus, Dracena, BC, Brazil,* [4]*Sòao Paulo State University (UNESP) / Dracena Campus, Dracena, Brazil.*

The study was conducted at the São Paulo State University feedlot, Dracena campus, Brazil. It was designed to compare the effects of nutritional restriction or intake of concentrate feedstuffs before the adaptation period on feedlot performance of Nellore cattle. The experiment was designed as a completely randomized block, which was replicated 8 times (4 animals/pen), in which 96 22-mo-old yearling Nellore bulls (365.5 ± 39.2 kg) were fed in 24 pens according to the treatments: Restriction (Tifton hay fed at 1.4% of BW + mineral supplement); Control (Tifton hay fed ad libitum + mineral supplement) and Concentrate (Tifton hay fed ad libitum + 0.5% of BW of a mix of concentrate feedstuffs and mineral supplement). This study lasted 144-d, divided into 2 periods: 32-d of pre-adaptation, in which cattle were submitted to the treatments, and 112-d of feeding high-concentrate diets, during which all cattle were fed the same diet. The adaptation program consisted of ad libitum feeding of two diets during the adaptation period with the concentrate level increasing from 72% to 86% of diet DM. The finishing diet contained: 73.5% cracked corn grain, 14.0% sugarcane bagasse, 9.0% cottonseed meal, 1.5% supplement, 1.2% urea and 0.8% limestone (DM basis). Cattle were fed ad libitum three times daily throughout the study. No significant treatment effect was observed for days to adapt to the finishing diet (Restriction = 14.6-d, Control = 14.9-d, Concentrate = 14.5-d). Nevertheless, cattle submitted to intake of concentrate tended to have greater ($P < 0.10$) initial BW (Restriction = 376.23^{c}, Control = 384.06^{b}, Concentrate = 397.21^{a} kg) at the beginning of the adaptation period, and also greater final BW (Restriction = 520.17^{ab}, Control = 503.23^{b}, Concentrate = 529.84^{a} kg) than cattle in the control group at the end of the study. Cattle submitted to nutritional restriction had greater ADG (Restriction = 1.29^{a}, Control = 1.06^{b}, Concentrate = 1.18^{ab} kg/d), DMI (Restriction = 9.19^{a}, Control = 8.56^{b}, Concentrate = 8.86$^{ab\ kg/d}$), and DMI expressed as % of BW (Restriction = 2.06^{a}, Control = 1.94^{b} kg, Concentrate = 1.91^{b}) than cattle in gthe control group. Likewise, cattle submitted to nutritional restriction had higher G:F ratios (Restriction = 0.140^{a}, Control = 0.124^{b}, Concentrate = 0.133^{ab}) during the period of feeding high-concentrate diets when compared to cattle on control group. Thus, cattle should be submitted to nutritional restriction or intake of concentrate feedstuffs before the adaptation period to improve overall feedlot performance.

Key Words: adaptation, supplement, Zebu
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595 Does the supplementation during the growing phase and finishing phase influence the performance of Nellore cattle?

I. M. D. Oliveira[*1,2], M. H. Moretti[3], L. F. Prados[1], C. F. Nascimento[4,5], P. H. Gonçalves[5], G. R. Siqueira[1,5], and F. D. D. Resende[1,5], [1]*APTA - Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil,* [2]*FAPESP (grant #2016/01961-2 and grant #2013/10340-3), São Paulo, Brazil,* [3]*Agroceres, Rio Claro, Brazil,* [4]*FAPESP (grant #2015/07046-1 and grant #2016/08867-1), São Paulo, Brazil,* [5]*UNESP - Univ Estadual Paulista, Jaboticabal, Brazil.*

The objective of this study was to evaluate the effect of the supplementation level during the growing and the finishing phase on the performance of Nellore bulls in pasture. Forty calves (172 ± 26 kg, 8 mo) were used in a randomized block designed study with a 2×2×2 factorial arrangement of treatments (2 supplementation levels in the cold, warm season and in the finishing phase). The growing phase comprises all the seasons of the year, so it was subdivided into cold (fall/winter) and warm (spring/summer) seasons. Thus, twenty animals were fed 1 g/kg BW per day (CP = 54%, TDN = 40%) and twenty animals were fed 5 g/kg BW per day (CP = 25%, TDN = 58%) during the cold season. Afterwards, in the warm season, the animals from each supplementation during the cold season were fed either mineral salt ad libitum or 5 g/kg BW. Then, in the finishing phase, the same animals of each supplementation strategies during the growing phase were fed with one of two levels of concentrate (15 or 20 g/kg BW per day, CP = 17% or 14%, TDN = 76 or 77%, respectively). At the end of the experiment (405 days) bulls were weighed and slaughtered. All parts of the body were weighed separately to quantify the empty body weight (EBW). All data (EBW, HCW, no-carcass components [NCC = blood, heart, lung, spleen, liver, kidney, gastrointestinal tract and KPH] and gut fill) were analyzed using the PROC MIXED of SAS with an alpha = 0.05. There were no interactions between supplementation levels during the phases ($P > 0.05$), so the factors were analyzed separated. The cold season supplementation did not affect any variables ($P > 0.05$). In the warm season, animals fed 5 g/kg BW had greater EBW (471 vs 425 kg, $P < 0.01$), HCW (303 vs 269 kg, $P < 0.01$) and NCC (168 vs 156 kg, $P = 0.01$) compared with animals fed mineral. On the finishing phase, animals fed 20 g/kg BW had greater EBW proportion (940 vs 923 g/kg BW, $P < 0.01$) and lower gut fill (30 vs 37 kg, $P = 0.03$) than those fed 15 g/kg BW. In conclusion, supplementation in the cold season does not influence the performance of finishing Nellore bulls in pasture. However, the

greater level of supplementation in the warm season and in the finishing phase produce animals with greater BW.

Key Words: *Bos indicus*, *Brachiaria brizantha*, nutritional strategies
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596 Effects of grinding versus steam-flaking on feeding value of blending barley and corn in low-forage diets fed to dairy cows.

K. Safaei[1], G. R. Ghorbani[1], M. Alikhani[1], A. Sadeghism[1], W. Yang[*2], and M. Saebi-Far[1], [1]*Department of Animal Sciences, Isfahan University of Technology, Isfahan, Iran (Islamic Republic of)*, [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

This study was carried out to evaluate the effects of processing method (grinding vs steam-flaking) on DM intake (DMI), ruminal pH and fermentation characteristics, total digestibility of DM, and milk production of dairy cows fed blended barley and corn-based diets. Eight multiparous mid-lactation Holstein cows (88 ± 12 DIM and 44.0 ± 1.5 kg milk/d) were used in a replicated 4 × 4 Latin square design with 21-d long of each period. Cows were fed ad libitum total mixed diet consisting of 25% corn silage, 15% alfalfa hay, and 60% concentrate with equal portion of barley and corn (DM basis). Treatments were: 1) ground barley and corn (GBGC), 2) steam-flaked barley and corn (SBSC), 3) ground barley and steam-flaked corn (GBSC), and 4) steam-flaked barley and ground corn (SBGC). Data were analysed using the MIXED procedure of SAS with model including treatment as fixed effect and the random effects of square, period within square and cow within square. The PDIFF option adjusted by the Tukey method was included in the LSMEANS statement to account for multiple comparisons among treatments. Intake of DM (kg/d) tended ($P < 0.06$) to be less with SBSC (23.1) than other treatments (averaged 24.2). Digestibility of DM (% of intake) in the total digestive tract was greater ($P < 0.04$) with SBSC (73.9) and GBSC (73.4) than GBGC (70.3) and tended ($P < 0.10$) to be greater than SBGC (71.5). However, yield of actual milk (averaged 44.7 kg/d) and 3.5% fat corrected milk (FCM; 39.9 kg/d) as well as milk composition did not differ among treatments. Milk efficiency (milk yield/DMI) tended ($P < 0.09$) to be improved with SBSC (1.93) vs GBGC (1.85) or SBGC (1.84). Ruminal pH (averaged 6.45), total VFA (averaged 125 mM), and molar proportions of individual VFA were not affected except that molar proportion of acetate tended ($P < 0.06$) to be greater with SBGC (58.8%) than other treatments (averaged 56.0%). Cows fed GBGC diet had sorting index below 100 for the particles retained on 19- and 8-mm sieves, indicated that cows sorted for these particles. In contrast, cows fed SBSC diet had sorting index superior to 100 for the particles retained on 19 and 8-mm sieves, thus, cows sorted against these particles. These results suggest that feeding cows with blend of steam-flaked barley and corn is beneficial to improve DM digestibility and milk efficiency.

Key Words: digestibility, grain processing, dairy cow
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597 Nutrient profiles, sub-fractions, energy values and degradation and digestion kinetics and their relationship with inherent molecular structures in chickpeas.

B. Sun[1,2], and P. Yu[*1], [1]*University of Saskatchewan, Saskatoon, SK, Canada*, [2]*SouthChina Agricultural University, Guangzhou, China.*

The objectives of this study were to (1) study chemical and nutrient profiles of CDC developed Chickpea variety (cv. Frontier Kabuli and Corinne Desi, with multi-year samples) in comparison with and a common CDC barley variety (cv. Cowboy) for ruminants in term of chemical profiles, protein and carbohydrate (CHO) sub-fractions, total digestible nutrients, and energy values, rumen degradation kinetics, and (2) quantify relationship between molecular structure spectral profiles and nutrient availability. The molecular spectral profile was carried out using Globar sourced-Fourier transform infrared vibrational spectroscopy (GS-FT/VIR). The nutritive value for ruminants (nutrient profiles, CHO and Protein subfraction and rumen degradation) were determined using conventional rumen in situ and in vitro methods and CNCPS6.5 system. The results showed that: 1) chickpea had higher ($P < 0.05$) crude protein (CP), non-protein nitrogen, truly digestible CP, soluble CP, water-soluble carbohydrates, energy values, rumen degradable, bypass and intestinal digestible protein, lower ($P < 0.05$) carbohydrates, truly digestible non-fiber CHO, hemicelluloses, lignin, neutral detergent insoluble CP, and rumen bypass CHO compared with the CDC cowboy barley. CDC Frontier Kabuli chickpea had greater ($P < 0.05$) soluble CP, non-fiber CHO, total rumen degradable CHO, rumen degradable, bypass and intestinal digestible soluble protein, total digestible nutrients, truly digestible non-fiber CHO, energy values, and lower ($P < 0.05$) acid detergent fiber, acid detergent insoluble crude protein, cellulose than the Corinne Desi. 2) Molecular structure spectral profiles had a significant relationship with carbohydrate profiles, sub-fractions and rumen degradation, bypass, total digestible carbohydrate and protein. 3) Multiple regression study with parameter model selection indicated that molecular structure spectral profile could be applied to predict nutrient profiles and degradation characteristics for CDC chickpea and barley. In conclusion, CDC chickpea could be used as protein and energy source and Kabuli chickpea was better than Desi. Molecular structure spectral parameters had relationship with nutrient digestive features, could be used to predict nutrient availability in ruminants.

Key Words: Nutrient degradation and digestion, Molecular structure, Non-conventional feed
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598 Effect of amount of milk replacer for first two weeks after farm arrival on concentrate consumption and performance in milk-fed Holstein calves.

M. Verdu[1], A. Bach[2,3], and M. Devant*[4], [1]*bonÀrea Agrupa, Guissona, Lleida, Spain,* [2]*IRTA-Department of Ruminant Production, Caldes de Montbui; Balcelon, Spain,* [3]*ICREA, Barcelona, Spain,* [4]*IRTA - Department of Ruminant Production, Caldes De Montbui, Barcelona, Spain.*

One of the most important productive difficulties in milk-fed calves after farm arrival is a transitory anorexia for first week of adaptation. This feeding disorder affects performance and health because underfed cattle may undergo a deterioration of digestive and immune functions with deleterious consequences on health. Increasing amount of milk replacer the first two weeks after arrival could enhance concentrate intake and calves' vitality. Three hundred and fifty Holstein male calves (56 ± 1.5 kg of BW and 29 ± 9.3 d of age), from 2 herds, were used in a randomized design to evaluate the effect of increasing amount of milk replacer on concentrate intake and performance in milk-fed calves throughout a 47-d study. Calves were allocated in 16 pens of 11 animals provided with concentrate and straw feeders, and one water bowl. Pens were randomly assigned to 1 of the 2 treatments according to the amount of milk replacer (23% CP, 19% fat; DM basis) received for first two weeks after arrival: a conventional program (CON) vs a rescue program (RES). CON program consisted of 360 g/d on week 1, 330 g/d on weeks 2 and 3, 300 g/d on week 4, and 210 g/d on week 5. RES program provided 600 and 500 g/d on weeks 1 and 2, and 300 and 150 g/d on weeks 3 and 4, respectively. Starter (2.93 Mcal of ME/kg, 16% CP; DM basis), straw and water were offered ad libitum. Milk replacer intake and health status were recorded daily, and concentrate and straw intake, and BW weekly. Performance data were analyzed using a mixed-effects model with repeated measures, and health status data with a Chi-square test. RES calves tended ($P = 0.09$) to have a greater final BW than CON at d 47 of study. An interaction between treatment and week was observed in concentrate consumption and ADG. RES calves had a greater ($P < 0.01$) concentrate consumption compared with CON at weeks 5 and 6 (2.0 vs 1.6 and 2.5 vs 2.3 ± 0.08 kg/d, respectively). RES calves exhibited a greater ($P < 0.01$) ADG than CON at weeks 1 and 6 (0.57 vs 0.31 and 1.07 vs 0.95 ± 0.056 kg/d, respectively). In conclusion, increasing the amount of milk replacer during the first two weeks after arrival improved the final BW, ADG at first week, and increased concentrate consumption the weeks 5 and 6.

Key Words: milk replacer program, performance, milk-fed calves
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599 Energy requirements for maintenance of growing Korean indigenous goats (*Capra hircus coreanae*).

S. Moon* *Konkuk University, Chungju, Korea, Republic of (South).*

This study was conducted to determine the energy requirements for maintenance of growing Korean native goats (black goat: *Capra hircus coreanae*). The experiment had a replicated 5×5 Latin square design, using five growing wethers [24.13±2.55 kg body weight (BW)]. Each wethers was individually housed in a metabolic cage and first given 10 days for diet adaptation prior to 7 days of experimental measurements. The goats received timothy (12%), tall fescue (28%), cornflake (30%), concentrates (20%) and one of the following five energy level treatments that were based on recommended metabolizable energy for maintenance, Mem (NRC, 2007): MEm-7% (trial 1), MEm (trial 2), MEm+10% (trial 3), MEm+20% (trial 4), MEm+30% (trial 5). Intakes of dry matter were similar across all diets by restricting feed supply at 2% of BW for all wethers. Average daily gains (ADG) were -14.22, 3.06, 18.06, 31.62, and 37.16 g/day for each treatment. Higher maintenance energy intake (MEI) led to higher ADG. By simple regression analysis, the following equation was defined between ADG and MEI: Y(MEI)=0.2735X(ADG)+112.19. The findings indicate that the estimated maintenance energy requirement for growing black goats is 112.19 kcal/kgBW$^{0.75}$. The estimated value of MEm can be further managed and improved with precision feeding system for black goats.

Key Words: Goat, Energy requirement, Daily gain
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600 Performance and carcass traits of feedlot Murrah buffalos fed with forage palm associated at cottonseed replacing high concentrate diets.

V. L. Lima Junior*[1], F. Brandão Pereira[2], J. Nunes Batista[3], L. Rocha Bezerra[4], V. L. F. Santos[4], F. F. da Silva Filho[1], L. Dias do Nascimento Ferreira[1], W. alves Saraiva[1], R. L. Oliveira[5], R. Loiola Edvan[6], M. Jácome de Araújo[6], and A. M. de Azevedo Silva[7], [1]*UFRN, NATAL, Brazil,* [2]*University Federal of Piauí, Bom Jesus, CA, Brazil,* [3]*University Campina Grande, Patos, Brazil,* [4]*University Federal of Piauí, Bom Jesus, Brazil,* [5]*UFBA, SALVADOR, Brazil,* [6]*University Federal of Piauí, BOM JESUS, Brazil,* [7]*University Campina Grande, PATOS, Brazil.*

The objective of this study was to evaluate the performance and carcass traits from Murrah buffalo (*Bubalus bubalis*) fed with different levels of cactus pear + cottonseed completely replacing high concentrate diets. The research was approved by Ethics Committee on Animal Experiment from Protocol No. 210/16. Twenty-four Murrah buffalos male, uncastrated with age between 8 and 10 months and body weight 300 ± 14.1 kg (mean ± SD) were identified. The treatments consisted

with four levels of cactus pear + cottonseed (0, 33, 66 and 100% in total DM) replacing completely high concentrate diets. The animals were fed with total mixed rate containing soybean meal, corn grain, and cactus pear and cottonseed to meet the nutritional requirements according to National Research Council (NRC, 1996) to average daily weight gain of 100 g/day. The diets were offered ad libitum, individually in two equal portions daily (08:00 and 16:00). During 125 days, Murrah buffalo performance growth was evaluated and the animals were fasted for 16 hours, then weighed and sent to slaughter and determination of the qualitative characteristics of the carcasses. Data were submitted to linear and quadratic polynomial contrasts using PROC REG procedures implemented in the SAS® statistical software (version 9.1.2, Cary, NC, USA). Differences were considered at $P < 0.05$. There was a quadratic increment ($P < 0.001$) of the dry matter intake with different levels of cactus pear + cottonseed replacing high concentrate diets. The substitution of high concentrate diets by cactus pear + cottonseed reduced linearly the final body weight ($P < 0.001$), total weight gain ($P < 0.001$), average daily weight gain ($P < 0.001$), cold carcass weight and yield (P <0.001), hot carcass weight and yield ($P < 0.001$), cold carcass weight and yield (P <0.001). There was effect of completely replacing high concentrate diets cactus pear + cottonseed on cooling losses ($P = 0.821$) of buffalos meat. The use of cactus pear associated at cotton seed replacing to high concentrate diets is not recommended because decrease performance and carcass traits of Murrah buffalos in feedlot.

Key Words: carcass, dry matter intake, *Bubalus bubalis*
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601 Changes in body composition of primiparous Holstein cows with different feeding strategies during early lactation.

A. Jasinsky*[1], A. Casal[2], M. Ceriani[1], A. L. Astessiano Dickson[2], D. A. Mattiauda[1], and M. Carriquiry[2], [1]*Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay,* [2]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay.*

The objective of this study was to estimate changes in body composition during the transition period of dairy cows with different feeding strategies during early lactation. Primiparous Holstein cows calved in autumn were used (n = 18; 528 ± 40 kg BW; 3.2 ± 0.2 BCS) in a randomized block design with two nutritional treatments. At calving and during the first 65 days postpartum (DPP), cows were assigned to either: (G0) total mixed ration (TMR) ad libitum (17kg DM/d offered; 70% forage, 30% concentrate) or (G1) grazing of alfalfa (*Medicago sativa*; 6-h am grazing in 3-d strips; pasture allowance=20 kg DM/d) + TMR (70% of ad libitum TMR; 12 kgDM/d offered). Cows were milked twice a day, milk yield was recorded daily, and all cows consumed 2.2 kgDM/day of a commercial concentrate at each milking. Cow BW and BCS were determined every two weeks from -21 to +60 DPP. At -7 and +42 ± 3 DPP, body composition was determined using the urea dilution technique. Data were analyzed as repeated measures with a mixed model including DPP and feeding strategy within DPP as fixed effects and block as random effect. Means were considered to differ when $P < 0.05$. Milk energy output during the first 42 DPP was greater ($P = 0.05$) for G0 than G1 cows (20.1 vs 18.3 ± 0.6 Mcal NEL/d) but loss of BCS from -7 to +42 DPP was greater ($P = 0.04$) for G1 than G0 cows. Cow body fat mass and retained gross energy (GE) decreased ($P = 0.001$) from pre to postpartum and these decreases were greater ($P \leq 0.20$) for G1 than G0 cows (64.4503, and 59.4043 ± 2.5kg fat and 4007.65, and 4266.14 ± 129 MJ GE for -7 DPP and G0 and G1 at +42 DPP, respectively). In contrast, body protein and water mass were not affected by DPP or treatment. Relative to cow empty BW, body fat and GE content decreased ($P \leq 0.014$) while body water and protein increased ($P \leq 0.04$) from pre to postpartum. Although during the postpartum there were no differences in relative water and protein mass, relative body fat and GE content were less ($P \leq 0.001$) for G1 than G0 cows (136.69 and 147.17± 5.2 kg fat and 9.2,and 9.7± 0.2 MJ GE for -7 DPP and G0 and G1 at +42 DPP, respectively). Negative energy balance during the transition period was more severe for G1 than G0 cows, probably associated to decreased DMI and increased maintenance requirements.

Key Words: dairy cattle, grazing, TMR, urea dilution technique
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602 The impact of time on feed and partial replacement of high-moisture corn with a high-lipid high-fiber pellet on steer performance, visceral organ weight, fat deposition, and carcass composition.

K. M. Wood*[1], and G. B. Penner[2], [1]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The objective of this experiment was to determine the impact of time on feed and the partial replacement of starch with a high-fat, high-fiber by-product based pellet. Angus crossbred steers (n = 97; initial BW 469.3 ± 45.8 kg) were randomly assigned to one of two isocaloric dietary treatments: control (CON; n = 48) steers were fed a finishing diet consisting of 10% haylage, 77% high-moisture corn, 11% soybean meal, and 2% of a salt, vitamin, and mineral pre-mix including monensin; or high-fat, high-fiber pellet (HLHF; n = 49). The HFHF contained 29.8% wheat shorts, 26.2% corn DDGS, 18.8% soy hulls, 19.2% corn gain, and 6% tallow and replaced 30% (DM basis) of the high moisture corn in CON. Steers were randomly assigned to pens equipped with Insentec feeders to record individual feed intake. Steers were randomly split into two blocks in order to facilitate sample collection at the abattoir. On d 1 of the feeding period and every 6 wk thereafter, 10 steers from each treatment were selected at random and slaughtered. Organ and visceral fat weights were recorded, and rib sections were cut into muscle, fat, and bone in order to estimate carcass composition. Data were analyzed as a randomized complete block using PROC MIXED in SAS and included the fixed effects of diet, time on feed, and random effects of pen and block. Contrasts between diet and linear effects of time on fed were used for mean separation and significance was declared at $P \leq 0.05$. Steer initial BW did not differ ($P \geq 0.43$); however, final BW increased linearly ($P < 0.001$), but did not differ with dietary treatment ($P = 0.55$). Overall ADG did no differ with dietary treatment ($P = 0.63$), but decreased linearly with increasing time on feed ($P = 0.015$). Empty rumen mass was 12.4 and 11.4 ± 0.24 for CON and HLHF ($P = 0.004$). Abomasum weight tended to be heavier for HLHF than CON steers ($P = 0.06$). Carcass traits did not differ with dietary treatment ($P > 0.51$). Rib dissection indicated that rib section weights of lean, bone, intermuscular, body and subcutaneous fat did not differ with dietary treatment ($P \geq 0.24$). Overall these data indicate that partially replacing starch with a high-lipid, high-fiber pellet had limited impacts on growth performance and carcass traits and energy partitioning in steers.

Key Words: Beef cattle, Byproduct feeding,
Visceral organ mass
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603 Replacement of rolled barley with citrus pulp in a concentrate supplement for finishing beef cattle offered grass silage.

M. J. Kelly[1], A. P. Moloney[2], A. K. Kelly[3], and M. McGee*[4], [1]*Teagasc Grange, Dunsany Co Meath, Ireland,* [2]*Teagasc, Grange, Dunsany, Meath, Ireland,* [3]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland,* [4]*Teagasc Grange, Dunsany Co. Meath, Ireland.*

A variety of feedstuffs of varying carbohydrate composition are available to rectify deficiencies in nutrient supply for growing cattle fed grass silage-based diets. The objective was to examine the effects of replacing rolled barley (starch) with citrus pulp (digestible fiber) in a supplement on intake and performance of young growing cattle offered grass silage ad libitum for 135 days. Weaned, late-maturing breed, steers (n = 34, initial live weight 446 kg, SD 38.0) were blocked by sire breed and weight and from within block randomly assigned to one of three concentrate treatments. The control concentrate, based on rolled barley (starch), comprised of 865 g rolled barley, 60 g soya bean meal, 50 g molasses, and 25 g minerals and vitamins/kg (BAR). In the other two concentrates, barley was replaced with 400 (CIT40) or 800 (CIT80) g/kg (digestible fibre) plus 10 and 20 g soya bean meal, citrus pulp respectively. Concentrates were formulated to have similar concentrations of PDIE (true protein digestible in the small intestine when energy limits microbial protein synthesis) per kg DM (106 g). Steers were individually offered 4.0 kg DM of the respective concentrates, in two feeds daily. Data were statistically analyzed using ANOVA with terms for treatment and block in the model. Supplement type did not affect ($P > 0.05$) daily grass silage intake (5.05 kg DM). Live weight gain (kg/day) was lower (0.88) and G:F (kg/day) was poorer (10.4) for CIT 80 ($P < 0.01$) compared to BAR (1.03 and 9.2, respectively) and CIT 40 (1.05 and 8.6, respectively), which did not differ ($P > 0.05$). Ultrasonically assessed body fat depth or gain did not differ ($P > 0.05$) between treatments, but muscle depth gain was higher ($P < 0.01$) for BAR compared to CIT80, with CIT40 being intermediate ($P > 0.05$). Carcass weight, carcass conformation and fat score, carcass fat depth, kill-out proportion, ultimate pH and temperature of M. longissimus muscle, and drip loss did not differ ($P > 0.05$) between treatments. Subcutaneous fat lightness (‘L’ value) was higher ($P < 0.01$) for CIT80 than BAR, with CIT 40 being intermediate, whereas redness (‘a’ value) and yellowness (‘b’ value) did not differ ($P > 0.05$) between treatments. In conclusion, citrus pulp can replace barley at inclusion rates up to 400g/kg when offered as a supplement to grass silage without negatively affecting performance or selected meat quality traits.

Key Words: beef cattle, citrus pulp, supplementation
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604 Effect of milk replacer fat content during calfhood and cereal type and supplemental saturated fat inclusion in the finishing ration on the performance and carcass composition of young Holstein Friesian bulls.

N. Ferguson[1], A. K. Kelly[2], A. P. Moloney[3], and D. A. Kenny*[4], [1]*School of Agriculture and Food Science, University College Dublin, Ireland, Dublin 4, Ireland,* [2]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland,* [3]*Teagasc, Grange, Dunsany, Meath, Ireland,* [4]*Teagasc Animal and Bioscience Department, Dunsany, Co Meath, Ireland.*

The objective of this study was to evaluate combined effects of (i) milk replacer (MR) fat content during rearing and (ii) cereal type and (iii) fat supplementation of the finishing ration on performance and carcass composition of young dairy bred bulls. Holstein-Friesian bull calves (n = 120) offered a high (30%) or low (18%) fat content MR from 2 to 10 weeks of age after which were weaned and offered a common diet based on grazed grass and 2 kg of supplementary concentrate. At 10 months of age bulls were blocked, on their original calf rearing regimen and bodyweight, and within block randomly allocated to one of four concentrate based finishing rations composed of (i) maize (M) or barley (B) included at 70%, as fed); (ii) supplemented (PF+; 5% as fed) or not (PF-) with a rumen inert palmitate rich supplement. This resulted in eight treatment groups, arranged in 2 x 2 x 2 factorial arrangement. Animal performance and live weight measurements were recorded on fortnightly basis. Bulls were slaughtered at 16 months of age. Carcass weight (CW), kidney fat (KF), rumen fat (RF), carcass conformation (CC), fat classification (CF) and subcutaneous fat-depth (FD) were recorded at slaughter. At 48hr post-mortem subcutaneous fat color (FC) was measured and the cube roll partitioned into fat, lean and bone components. Performance and carcass traits were analyzed in accordance with the factorial nature of the design using mixed models ANOVA (PROC MIXED, SAS v 9.3) with calf rearing, cereal type and palmitate supplement as fixed effects. There were no biologically significant interactions ($P > 0.10$) amongst the main effects for any performance, or carcass related variables viz CW, KF, RF, CC, CF, FD or FC respectively. There was no latent effect ($P > 0.10$) of calf rearing regimen on carcass measurements. Similarly, no effect of cereal type in the finishing ration was recorded. Inclusion of supplemental fat significantly reduced slaughter weight (PF+ 536 kg vs PF-517kg; $P = 0.004$), ADG (PF+, 1.07 kg vs PF-1.20kg; $P = 0.001$), CW (PF+, 267.8kg vs PF-, 280 .1kg; $P = 0.002$), CC (PF+, 4.40 vs PF-, 4.91; $P = 0.006$) and CF (PF+, 5.52 vs PF-, 6.00; $P = 0.04$). Subcutaneous FD, KF, RF and cube roll fat proportion were all reduced ($P < 0.05$) in bulls offered supplemental fat. In conclusion, supplemental fat in the finishing diet reduced animal performance and economically important carcass traits. Additionally, no evidence of latent effects of MR fat content during calfhood on any carcass trait measured.

Key Words: Cereal, Milk Replacer, Fat supplementation
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605 Effects of residual feed intake phenotype and dietary glycerin on growth and carcass composition of feedlot Nellore bulls.

R. S. Barducci*[1], J. M. B. Ezequiel[1], M. T. C. Almeida[1], E. H. C. B. Van Cleef[1], J. N. S. G. Cyrillo[2], M. E. Z. Mercadante[2], G. V. Silva[2], R. O. Rodrigues[3], T. B. McFadden[3], M. M. Masiero[3], and M. S. Kerley[3], [1]*Sao Paulo State University, Jaboticabal, Brazil,* [2]*Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertaozinho, Brazil,* [3]*University of Missouri, Columbia.*

The objective of the study was to determine the effects of residual feed intake (RFI) phenotype and addition of crude glycerin as a partial substitute for dietary corn on feedlot performance and carcass traits of Nellore bulls. The experiment was conducted as a completely randomized design in a 2 × 2 factorial arrangement, in which treatment groups were initially balanced for body weight (BW) of animals. The main treatment factors were RFI phenotype (Low or High) and diet (corn-based or corn-based with glycerin substituted for 20% of the corn in the diet). Twenty-five Nellore bulls (15 ± 0.6 months of age; 311 ± 36 kg) were individually fed ad libitum once daily at 0900 and weighed every 32 d until slaughter at 96 d. Residual feed intake was calculated at the end of the experiment as the difference between observed and expected dry matter intake (DMI) based on a linear regression of mid-test metabolic BW and average daily gain for the trial. Then, RFI phenotypes were retrospectively assigned to each experimental unit for the specific treatment factor. Residual feed intake was significantly different between RFI phenotypes (-0.92 vs 0.52 ± 0.21 kg/d for Low and High RFI groups, respectively; $P < 0.001$). Final BW and BW gain were not different between RFI phenotype groups. However, DMI and DMI as a percentage of BW were lower for Low compared to High RFI groups (6.3 vs 7.8 ± 0.3 kg/d for DMI, and 1.4 vs 1.8 ± 0.05% for DMI as percentage of BW, respectively; $P \leq 0.003$). High RFI bulls had lower feed efficiency than Low RFI bulls (0.22 vs 0.18 ± 0.01 kg/kg, respectively; $P = 0.02$). Hot carcass weight and carcass yield did not differ between RFI phenotypes. Next, substitution of 20% of dietary corn with glycerin did not affect ($P \geq 0.11$) performance or carcass traits. Interaction of RFI phenotype and diet was not significant. In conclusion, feedlot Nellore bulls of negative RFI phenotype had lower DMI but maintained growth and carcass traits compared to positive RFI phenotype bulls. Furthermore, performance and carcass traits of yearling Nellore bulls in feedlot for 96 days was maintained when crude glycerin was substituted for 20% of dietary corn. This project was funded by São Paulo Research Foundation (FAPESP), São Paulo, Brazil.

Key Words: corn, feed efficiency, by-product
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606 Dry-rolled corn reconstitution ssing sorghum silage.

A. Alrumaih, J. O. Sarturi, M. A. Ballou, B. J. M. Lemos, J. D. Sugg*, P. R. B. Campanili, L. A. Ovinge, and L. A. Pellarin, *Texas Tech University, Lubbock.*

Three levels of dry rolled corn (DRC) were reconstituted on sorghum silage to determine fermentations characteristics, losses profile, and the nutritional value of blends post fermentation phase. Laboratory experimental silos, the experimental units, (n = 49; 3/treatment; 18.93 L units with sand in bottom for effluent collection and gas valve on top for gas release) were treated for the three DRC levels (0%, 25%, and 50%, DM basis) on three sorghum hybrid harvesting sites. Experimental silos were assigned in a randomized complete block design and ensiled for 108, 114 and 115 d; silos were opened together and measured for gas and effluent losses. Samples taken post storage period were analyzed for DM, ash, in vitro true dry matter digestibility (24h and 30h), pH, and total starch. An aerobic stability measurement phase (5, 10, and 15d post silo opening) in which, DM losses and pH was evaluated. Data were analyzed using the GLIMMIX procedures of SAS; orthogonal contrasts were used to test for linear and quadratic effects of DRC inclusion of measured variables. Total DM loss of silos for 50% DRC inclusion had the least ($P < 0.01$) loss (5.96%) compared both DRC at 0 and 25% inclusion. Gas loss linearly decreased ($P < 0.01$) by 7% as DRC was included. Volume of effluent, L/ tonne of DM ensiled linearly decreased ($P < 0.01$) as DRC 50% was included by 27 L compared to DRC 0%. The 50% DRC inclusion showed linear increase ($P < 0.01$) in vitro DM digestibility, in both 24 and 30 h; while corn inclusion linearly increased ($P < 0.01$) digestibility of OM of materials. Silages containing corn were on average 24h more stable ($P < 0.01$) than control treatment, in which a quadratic effect showing silages containing 25% corn with the greatest ($P < 0.01$) stability (130 h). Losses post opening tended ($P = 0.10$) to be decrease in corn treated silages. Current results show the potential for such strategy, since dry-rolled corn reconstitution in sorghum silages not only improved nutritional value of silages, but also minimized losses related to fermentation process, as well as improved stability of material during the silage post-opening aerobic phase.

Key Words: dry-rolled corn, reconstitution, sorghum
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607 Effects of irrigation levels of corn silage hybrids on nutrient profile and in vitro disappearances.

A. Alrumaih[1], J. O. Sarturi[1], W. Xu[2], M. A. Ballou[1], B. J. M. Lemos[1], J. D. Sugg[*1], P. R. B. Campanili[1], L. A. Ovinge[1], and L. A. Pellarin[1], [1]*Texas Tech University, Lubbock,* [2]*Texas AgriLife Extension, Lubbock.*

Corn hybrids designed for silage were evaluated under different irrigation regimens effects on nutritional composition, fermentation losses, and aerobic stability. Corn silage hybrids (n = 6) were randomly assigned into plots (n = 8 per hybrid) divided under two irrigation systems (50 and 100 ET), totaling 48 experimental units (field plots). Forages for all plots were mechanically harvested on the same day, sampled, and ensiled into laboratory experimental silos (18.93 L units with sand in bottom for effluent collection and gas valve on top for gas release) and stored for 98 d. An aerobic stability test was conducted during post silo opening period, with measurements taken at 5, 10, and 15 d. A complete randomized design was used to compare the effects of irrigation level, hybrids, and potential interactions on variables of interest. Data were analyzed using the GLIMMIX procedures of SAS. Upon forage harvesting, DM content of hybrids tended ($P = 0.08$) to interact with irrigation level, where most of the hybrids under irrigation 50ET had 2 to 6 percent units of DM greater than those under 100 ET. Still at ensiling moment, lower ($P = 0.01$) pH and greater ($P = 0.01$) particle size were observed for forages under irrigation 50 ET compared with 100 ET, respectively, regardless of hybrid type. After fermentation period, only subtle differences ($P = 0.05$) on silage pH were observed, in which all of hybrids and irrigation levels showed desirable pH averages for silage. Hybrids submitted to 50 ET irrigation treatment tended ($P = 0.10$) to provide drier silages than those at 100 ET. Tendencies ($P = 0.08$) were also observed for hybrids fermentation losses (DM and gas), regardless of irrigation level ($P \geq 0.81$). Silage time to break aerobic stability was not affected ($P \geq 0.14$) by treatments; whereas regardless of hybrid type, silages that passed by hydric-stress showed lower pH during post-opening compared to 100 ET treatments. In vitro true digestibility of silages were not affected ($P = 0.22$) by treatments, averaging 78%. Corn silage hybrids assessed appear to preserve high nutritional value even when submitted to hydric stress. Corn crops assessed under restricted irrigation may require earlier harvesting time due to drier plants; whereas fermentation losses may be more dependent of hybrid type rather than irrigation level. Imminent post-opening of silos (0 to 5 d) appears to be more stable for hybrids that passed by water restriction.

Key Words: irrigation, corn silage, in vitro
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608 Replacing corn grain by crude glycerol in diets of grazing dairy cows: Feed intake, pasture degradability, and milk production.

M. D. L. A. Bruni[*1], M. Carriquiry[2], A. Delgado[3], and P. Chilibroste[4], [1]*Facultad de Agronomia Universidad de la Republica, Paysandu, Uruguay,* [2]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay,* [3]*Instituto de Ciencia Animal (ICA), San José de las Lajas, Mayabeque, Cuba,* [4]*Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay.*

Eighteen Holstein cows (6 ruminally cannulated) were used in the first 60 days of lactation to evaluate the effect of the replacement of corn grain (CG) by crude glycerol (CGly) on organic matter intake (OMI), pasture degradability and milk yield (MY). Cows were blocked [by parity (3.17±1.42), body condition score (3.0±0.3), expected caving date], and assigned randomly to two treatments (T). T1= partially mixed diet (PMR) containing sorghum silage (SS) plus concentrate (CG, wheat grain, soybean expeller, minerals and vitamins) and T2= PMR containing SS plus concentrate where CGly -76.5% glycerol, ALUR Uruguay- replacing the CG. Both groups received PMR in individual feeders and grazed during afternoon in a temperate pasture with herbage allowance-above the ground level- 60 kg $\text{DM.cow}^{-1}\text{.day}^{-1}$. Chemical composition of PMR (OM, CP, NDF, and EE in g/kgDM) respectively was for T1 [934, 117, 317, and 5] and [927, 106, 297 and 46] for T2. OMI and the ruminal degradation kinetics of DM of pasture were measured *in situ* in two periods. PMR intake (OMI-$_{\text{PMR}}$) was measured individually as the difference between the amounts offered and refused. OMI-forage was determined with chromium oxide (Cr2O3) and indigestible acid detergent fiber as external and internal marker respectively. *In situ* data was fitted to nonlinear model

$D(t)=a+b(1-e-^{ct})$, where D= disappearance of DM , (a) soluble fraction, (b) degradable fraction, and (c) degradation rate. MY was Individual measured daily. Intake, degradability parameters, and MY were analyzed with a mixed model whit repeated measures. The model included fixed effects: T, period/week, interaction T*period and cow as a random effect. The statistical analyzes were performed with SAS (2010), data are expressed as lsmeans (s.e) and were considered to differ when $P < 0.05$. Treatment or interaction did not affect Total organic matter intake, OMI-$_{PMR}$ or OMI-f and was [23.6$_{(1.4)}$, 12.7$_{(0.5)}$ and 10.9 $_{(1.0)}$] kgOM.d^{-1} for T1 and [20.8$_{(1.3)}$, 10.9$_{(0.5)}$ and 9.8 $_{(0.9)}$] kg OM.d^{-1} for T2 respectively. The parameters "a", "b" "c" of pasture were not affected by T, period or interactions and averaged 20$_{(3.1)}$ g/kgDM 602 $_{(3.6)}$ g/kgDM, 0.04$_{(0.007)}$ h^{-1}. Milk yields was not affected by treatment (30.6$_{(1.0)}$ kg.día^{-1}) or interaction T*week of lactation (WOL) but as expected it was affected for WOL. The absence of negative effects related to the use of CGly in substitution of CG in these conditions allows its use up to 10% DMI for dairy cows without altering the efficiency of the milk production process.

Key Words: crude glycerol, corn grain, dairy cow
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609 Feeding behavior and particle sorting of Nellore cattle submitted to either nutritional restriction or intake of concentrate feedstuffs prior to adaptation period.

J. V. Dellaqua[*1], M. C. Pereira[2], D. H. Watanabe[1], A. L. J. Lelis[1], A. F. Toledo[1], A. H. Assumpção[1], M. D. Arrigoni[2], and D. D. Millen[1], [1]*São Paulo State University (UNESP), Dracena campus, Dracena, Brazil,* [2]*São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil.*

The study, conducted at São Paulo State University feedlot, Dracena campus, Brazil, was designed to evaluate the effects of either nutritional restriction or intake of concentrate feedstuffs before beginning the adaptation period on feeding behavior and selective consumption of Nellore cattle. The experiment was designed as a completely randomized block, replicated 8 times (4 animals/pen), in which 96 22-mo-old yearling Nellore bulls (365.5 ± 39.2 kg) were fed in 24 pens according to the treatments: Restriction (Tifton hay fed at 1.4% of BW + mineral supplement); Control (Tifton hay fed ad libitum + mineral supplement), and Concentrate (Tifton hay fed ad libitum + 0.5% of BW of a mix of concentrate feedstuffs and mineral supplement). This study lasted 144 d, divided into 2 periods: 32 d of pre-adaptation, in which cattle were submitted to the treatments previously described, and 112 d of feeding high-concentrate diets, where cattle were fed the same diets. The adaptation program consisted of ad libitum feeding of two diets over the adaptation period with concentrate level increasing from 72% to 86% of diet DM. The finishing diet contained 73.5% cracked corn grain, 14.0% sugarcane bagasse, 9.0% cottonseed meal, 1.5% supplement, 1.2% urea, and 0.8% limestone (DM basis). Cattle were fed ad libitum three times daily throughout the study. Visual appraisal was made on day 102 of the period of feeding high-concentrate diets, every five minutes during 24 hours. Samples of diets and orts were collected for determination of particle sorting by using the Penn State Particle Separator [>19 mm (long), >8 mm (medium), >1.18 mm (short), and <1.18 mm (fine)]. No significant ($P > 0.10$) treatment effect was observed for time spent resting, ruminating, and eating, as well as for meal length and DMI. However, cattle submitted to either nutritional restriction or intake of concentrate had similar ($P < 0.10$) meals per day (Restriction = 13.38^{ab}, Control = 14.83^{a}, Concentrate = 11.98^{b}), DMI per meal in kg (Restriction = 0.82^{a}, Control = 0.70^{b}, Concentrate = 0.87^{a}), and intake of short (Restriction = 1.02^{b}, Control = 1.03^{a}, Concentrate = 1.02^{b}) and fine particles (Restriction = 0.97^{a}, Control = 0.96^{b}, Concentrate = 0.97^{a}). Nevertheless, cattle subjected to intake of concentrate had greater intake ($P < 0.10$) of long (Restriction = 0.77^{b}, Control = 0.94^{ab}, Concentrate = 1.02^{a}) and medium particles (Restriction = 0.98^{b}, Control = 1.08^{a}, Concentrate = 1.05^{a}) than animals subjected to nutritional restriction. Thus, cattle should not be subjected to nutritional restriction before the adaptation period to avoid sorting against long and medium particles.

Key Words: intake, sorting, zebu
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610 Effects of ambient temperature and glycerol supplementation on growth performance in Korean cattle steers.

H. J. Kang[*], M. Y. Piao, H. J. Kim, and M. Baik, *Department of Agriculture Biotechnology, College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea.*

Glycerol may be used as a glucogenic source for glucose synthesis in the liver to provide an increased requirement of energy due to heat stress. This study was performed to evaluate whether ambient temperature and dietary glycerol supplementation affect growth performance in beef cattle. In experiment 1 (Exp1), fourteen Korean steers (average 23.5 months of age and 466.9 kg of BW) were divided into a control diet group (n = 7) and a 3% glycerol supplementation group (n = 7). Steers were allowed to receive daily a concentrate of middle fattening stage (1.5% of BW) and rice straw (0.3% of BW). Feeding trial was performed at a barn with a roof for three months [two months of hot temperature (July and August) and one month of temperate climate (September)] in 2016. Climate data were analyzed by ANOVA, and growth performance data were analyzed by repeated-measured two-way (month, diet) ANOVA. Maximum temperature-humidity index (THI) was higher ($P < 0.01$) in July (88.5) and August (90.5) than in September (83.1). No month × diet interaction was detected for all parameters. Neither month nor diet affected concentrate and roughage intake. Month did not affect average daily gain (ADG) and feed efficiency (FE: gain/feed). Glycerol supplementation increased ($P < 0.05$) both ADG and FE. In experiment 2 (Exp2), six Korean steers (average 23.5 months of age and 478.2 kg of BW) were raised in metabolic cages in a temperature-controlled room. Animals were divided into a control diet group (n = 3) and a 3% glycerol supplementation group (n = 3). Steers were allowed to receive the same amount of concentrate and roughage as in Exp1. A feeding trial was performed for every 20 days at normal (mean 21°C) and hot ambient temperature (mean 30°C). Statistical analyses were performed using the same method as in Exp1. Maximum THI values of the hot temperature period (88.2) were higher ($P < 0.01$) than those of the normal temperature period (73.6). Hot temperature decreased ($P < 0.05$) both concentrate and roughage intake, and it tended to decrease ($P = 0.07$) ADG. Glycerol supplementation increased roughage intake without affecting concentrate intake and ADG and FE. In conclusion, the hot temperature month did not affect growth performance, but glycerol supplementation improved growth performance in a barn trial. In a feeding trial in metabolic cages with a temperature-controlled room, hot temperature decreased growth performance, but glycerol supplementation did not affect it.

Key Words: ambient temperature, beef cattle, glycerol supplementation
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611 Varying levels of low quality grass hay NDF in finishing diets for Nellore cattle.

F. A. P. Santos*[1], J. J. D. R. Fernandes[2], J. S. Drouillard[3], L. G. Oliveira[4], and L. S. Leite[5], [1]*University of São Paulo, Piracicaba, Brazil,* [2]*UFG, Goiania, Brazil,* [3]*Kansas State University, Manhattan,* [4]*Nutripura Nutrição Animal Ltda, Goiânia, Brazil,* [5]*Nutripura Nutrição Animal Ltda, Rondonópolis, Brazil.*

Roughage is included in feedlot diets primarily for maintaining rumen health and increasing dry matter and energy intakes. The objective of this trial was to evaluate the effects of varying levels of low quality tropical grass hay NDF (4, 7, 10, and 13%) in finishing diets for Nellore bulls. Seven hundred and twenty (720) Nellore bulls (425.9 kg ± 29.9 IBW) were blocked by IBW and randomly allotted to 24 pens. Animals were adapted gradually to the final diets for 14 days, and the experimental period lasted 96 days. Experimental diets contained 4, 7, 10, or 13% grass hay NDF (5.7 to 18.5% grass hay), ground corn (64.7 to 52.5%), soy hulls (14.5 to 13.8%), 8% whole cottonseed, 3% cottonseed meal, 1% urea, and 3% minerals/vitamin mix with monensin. Data were analyzed using R statistical software. Increasing grass hay NDF content of the diets caused a quadratic response in DMI, TDN intake, ADG, FBW, and HCW. Dressing and G/F decreased linearly, while kg of DMI/15 kg of carcass increased linearly as roughage NDF was increased in the diet. Due to the small differences in HCW among treatments, no differences were observed for BFT and REA. In conclusion, for zebu cattle fed typical Brazilian finishing diets containing ground corn plus by-products, inclusion of 7% grass hay NDF in the diet increases DMI and optimizes energy intake, ADG, FBW, and HCW, while feed efficiency is greater with 4% grass hay NDF in the diet.

Table 611. Effects of varying levels of low quality grass hay NDF in the diet on performance of finishing Nellore cattle

	Dietary grass hay NDF					
	4%	7%	10%	13%	SEM	*P*-value
IBW, kg	427.2	427	425.7	424.5	1.952	0.742
FBW, kg**	554.5	569.3	569.1	568.1	2.665	0.003
DMI, kg**	9.722	11	11.318	11.604	0.16	<0.001
TDN intake, kg**	7.603	8.429	8.487	8.513	0.151	0.002
ADG, kg**	1.342	1.483	1.503	1.484	0.034	0.016
HCW, kg**	319.3	326.8	324.7	321.4	1.419	0.01
Dressing, (%)*	57.61	57.42	57.2	56.75	0.173	0.019
BFT, mm	4.99	4.92	5.31	5.36	0.23	0.468
REA, cm^2	74.51	73.48	75.36	74.46	1.071	0.68
G/F*	0.138	0.135	0.133	0.128	0.003	0.083
DMI/15 kg of carcass, kg*	138.8	148.7	158	164.4	3.019	<0.001

*Linear effect; **Quadratic effect.

Key Words: beef cattle, feedlot, roughage level
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612 Effects of the seaweed *Ascophyllum nodosum* on the rumen microbiome and fecal pathogenic *Escherichia coli* serotypes in sheep.

M. Zhou*[1], M. Huenerberg[2], Y. Chen[1], T. Reuter[3], T. A. McAllister[4], F. D. Evans[5], and L. L. Guan[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Alberta Agriculture and Forestry, Lethbridge, AB, Canada,* [4]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [5]*Acadian Seaplants Limited, Dartmouth, NS, Canada.*

Feeding rams Tasco® (SW), a high quality, sun-dried seaweed meal produced from the brown macroalga *Ascophyllum nodosum*, reduced *Escherichia coli* O157:H7 shedding in feces without affecting rumen fermentation. The effects of SW on the microbiota and other pathogenic *E. coli* O-serotypes in the rumen have not been extensively studied. The current study aimed to evaluate the effects of Tasco® at different feeding levels on the rumen microbiome as well as the presence of non-O157 *E. coli* serotypes. A 4 × 4 Latin square design used 8 ram lambs randomly allocated to diets containing 0%, 1%, 3%, or 5% of the diet DM as SW. Rumen contents and feces were collected, DNA was extracted, and 16S rRNA was sequenced to study the ecology of bacterial and archaeal communities using QIIME. Functional pathways were predicted using PICRUSt, and seven *E. coli* serotypes were measured using multiplex PCR. Feeding SW linearly ($P < 0.001$)

lowered the total rumen bacterial population ($\log_{10}$ 16S rRNA gene copies/g) from 11.63 in Con to approximately 10.50 and linearly reduced ($P < 0.001$) the total archaeal population from 8.70 to 8.13. Different SW levels did not affect the overall bacterial and archaeal profiles or the microbial diversity indices, with substantial variation in these parameters among individual rams. Relative abundance of three bacteria phyla, five bacteria families, and seven species differed among SW levels. There were 14 enriched metabolic pathways in SW-fed rams, while only 3 pathways were suppressed by SW feeding. A VFA profile with a higher acetate molar portion ($P < 0.001$) and a lower propionate ($P < 0.001$) and butyrate ($P < 0.001$) molar portion was seen with SW supplement, and the lower butyrate can be associated with the enrichment of the "Butanate metabolism' pathway in the SW-fed rams. Total *E. coli* population within the rumen was linearly reduced ($P < 0.001$) by SW from 6.82 ($\log_{10}$ 16S rRNA gene copies/g) in Con to 6.27, 5.86, and 5.90 with the three SW levels. Including SW only completely eliminated O121 in the rumen and the feces, but O45, O103, and O111 were also eliminated in the feces, although they were detected in the rumen.

Key Words: *E. coli*, rumen microbiota, Tasco®
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613 Humic substances supplementation reduces ruminal methane production and increases the efficiency of microbial protein synthesis in vitro.

P. Sheng*[1,2], G. O. Ribeiro Jr.[2], Y. Wang[2], and T. A. McAllister[2], [1]*Institute of Biological Resources, Jiangxi Academy of Sciences, Nanchang, China,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

The effects of humic substances (HS) on rumen fermentation and methane (CH_4) production were investigated using an in vitro rumen batch culture technique. HS was included in cultures with a 60% barley silage: 40% concentrate diet (dry matter (DM) basis) at 0, 108, 216, 324, or 432 mg HS/g of substrate incubated. Rumen in vitro batch cultures were conducted as a completely randomized design with three runs. Gas (GP) and CH_4 production were measured after 3, 6, 9, 12, 24, and 48 h of incubation. Total volatile fatty acid (TVFA), microbial nitrogen (MN), and ammonia nitrogen (NH_3-N), as well as disappearances of true dry matter (TDMD), neutral detergent fiber (NDFD), starch (SD), and nitrogen (ND) were determined after 12 and 48 h. Total GP was linearly increased ($P < 0.05$) with increasing HS inclusion during the first 12 h of incubation, but it was not affected ($P > 0.05$) after 24 and 48 h. Increasing HS linearly decreased ($P < 0.05$) CH_4 production (expressed as ml/g DM) at all time points evaluated. After 48 h of incubation, CH_4 production was reduced by 12.83% at the highest HS dose compared to control. Increasing HS linearly decreased NH_3-N concentration, and the molar proportion of acetate ($P < 0.05$) at 12 h of incubation, while MN, TDMD, and the molar proportion of butyrate linearly increased ($P < 0.05$) and SD responded quadratically ($P < 0.05$). After 12 h, ND, NDFD, TVFA, the molar proportion of branched-chain VFA, and A:P ratio were not affected ($P > 0.05$) by increasing HS. After 48 h, HS linearly increased ($P < 0.01$) MN (35.15%), TDMD (7.31%), and the molar proportion of butyrate but did not affect ($P > 0.05$) ND, SD, the molar proportion of acetate, propionate and branched-chain VFA, A:P ratio, or NH_3-N concentration. Increasing HS resulted in quadratic response ($P < 0.05$) in NDFD after 48 h. Overall, inclusion of HS effectively reduced CH_4 production and increased in vitro substrate disappearance and the efficiency of microbial protein synthesis. Further studies are needed to evaluate the effects of HS on in vivo ruminal fermentation, CH_4 production, the microbiome, and its consequent effect on growth performance.

Key Words: batch culture, humic substances, methane
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614 Effects of synbiotics on rumen fermentation.

U. Y. Anele*[1], C. L. Engel[1], K. C. Swanson[2], and D. Baines[3], [1]*Carrington Research Extension Center, North Dakota State University, Carrington,* [2]*Department of Animal Science, North Dakota State University, Fargo,* [3]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

A metabolism study was conducted to evaluate the effects of synbiotics on ruminal fermentation in steers fed high grain diets. Three synbiotics (hydrolyzed yeast/live yeast (LYHY)), Celmanax (prebiotics)/live yeast (CLY), and Synerall (a commercial pre- and probiotics product, SYN) were selected for a rumen fermentation study. Prior to this, seven different synbiotics were evaluated using the batch culture technique to measure in vitro gas production, DM disappearance, and VFA concentrations. There was no difference in asymptotic gas volume and VFA concentrations, but LYHY, SYN, and CLY had numerically higher DM disappearance values compared with the other treatments. For the ruminal fermentation study, treatments consisted of these three synbiotics and a control. Four rumen cannulated steers were randomly assigned to the following 4 dietary treatments: 1) Control – high grain finishing diet, 2) Control + CLY, 3) Control + LYHY, 4) Control + SYN. Cannulated steers had ad libitum access to the dietary treatments. Steers were housed individually and fed once daily in a 4 × 4 Latin square design with 4 periods of 21 days. In each period, the steers were adapted to the diet for 14 days, and ruminal fluid samples were collected from day 15 to 21 to determine pH, lactic acid, and volatile fatty acid (VFA) concentrations. Addition of synbiotics had no effect ($P > 0.05$) on ruminal pH, although values for the synbiotics treatments were numerically higher compared with the control treatment. For beef cattle in the feedlot, higher pH is desirable to minimize incidences of acidosis. Typically, ruminal pH of 5.6 is regarded as the reference point for chronic acidosis. Ruminal pH value for the control treatment was below this reference point (5.56) compared with higher pH values (5.62) for the synbiotics treatments. With the exception of valeric and isovaleric acid concentrations, no differences were noted in total and individual VFA concentrations. Inclusion of synbiotics resulted in a greater ($P = 0.019$) acetate-to-propionate ratio compared with the control (1.41 vs. 1.23). The LYHY treatment had the lowest numerical acid load (total VFA + lactic acid) compared with the other treatments. Considering that LYHY had the highest numerical in vitro DM digestibility, a lower acid load could be interpreted as LYHY partitioning more energy into microbial mass, which will benefit the animals. The LYHY treatment was selected based on lower acid load compared with the other treatments and is currently being used in a feedlot finishing study.

Key Words: beef cattle, rumen fermentation, synbiotics
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615 Rumen morphometrics of Nellore cattle submitted to either nutritional restriction or intake of concentrate feedstuffs prior to adaptation period.

B. Q. Reis[*1], M. C. Pereira[2], P. F. Santi[1], M. M. Squizatti[1], S. C. Dondé[1], M. M. Ferreira[1], L. F. Oliveira[1], and D. D. Millen[1], [1]*São Paulo State University (UNESP), Dracena campus, Dracena, Brazil,* [2]*São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil.*

The study, conducted at São Paulo State University feedlot, Dracena campus, Brazil, was designed to evaluate the effects of either nutritional restriction or intake of concentrate feedstuffs before beginning the adaptation period on rumen morphometrics and rumenitis of Nellore cattle. The experiment was designed as a completely randomized block, replicated 8 times (4 animals/pen), in which ninety-six 22-mo-old yearling Nellore bulls (365.5 ± 39.2 kg) were fed in 24 pens according to the treatments: Restriction (Tifton hay fed at 1.4% of BW + mineral supplement), Control (Tifton hay fed ad libitum + mineral supplement), and Concentrate (Tifton hay fed ad libitum + 0.5% of BW of a mix of concentrate feedstuffs and mineral supplement). This study lasted 144 d, divided into 2 periods: 32 d of pre-adaptation, in which cattle were submitted to the treatments previously described, and 112 d of feeding high-concentrate diets, where cattle were fed the same diets. The adaptation program consisted of ad libitum feeding of two diets over the adaptation period with concentrate level increasing from 72% to 86% of diet DM. The finishing diet contained 73.5% cracked corn grain, 14.0% sugarcane bagasse, 9.0% cottonseed meal, 1.5% supplement, 1.2% urea, and 0.8% limestone (DM basis). At the end of pre-adaptation period, one animal per pen (n = 24) was slaughtered for rumen evaluations. The remaining 72 animals were harvested after 112 d of feeding high-concentrate diets. At harvest, rumenitis was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative lesions). A 1-cm^2 fragment of each rumen was collect from the 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) was calculated as follows: 1 + (NOP*MPA) - (NOP*0.002). No significant ($P > 0.10$) treatment effect was observed for rumenitis (Restriction = 1.65, Control = 1.79, Concentrate = 1.55). Cattle submitted to nutritional restriction had greater ($P < 0.10$) NOP (Restriction = 72.76^{a}, Control = 63.28^{b}, Concentrate = 62.99^{b}) and larger ASA in cm^2 (Restriction = 26.89^{a}, Control = 22.29^{b}, Concentrate = 22.30^{b}). Also, a significant ($P = 0.05$) interaction between treatment and period was observed for MPA, where no differences were observed at the end of the pre-adaptation period, but cattle submitted to nutritional restriction presented larger MPA than animals in a control group after 112 d of feeding high-concentrate diets. Thus, cattle should be submitted to nutritional restriction prior to a period of feeding high-concentrate diets because it led to greater rumen epithelium development.

Key Words: area, papillae, zebu
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616 Effect of conservation method on in vitro ruminal fermentation of purple prairie clover (*Dalea purpurea* Vent.) in batch culture.

K. Peng[1,2], Z. Xu[2], L. Jin[2], T. A. McAllister[2], S. Acharya[2], S. Wang[1], and Y. Wang[*2], [1]*College of Engineering, China Agricultural University, Beijing, China,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Little information about the effects of the forage conservation method on the biological activity of condensed tannins (CT) in the rumen is available. The objective of this study was to determine the effects of the forage conservation method and CT in conserved forage on rumen fermentation. Purple prairie clover (PPC; *Dalea purpurea* Vent.) containing 84.5 CT/kg DM was harvested at full flower and preserved as freeze-dried forage (FD), hay (H), or silage (S). Batch culture incubations were conducted using conserved forages as a substrate with and without inclusion of polyethylene glycol (PEG) which inactivates CT. The treatments were arranged as a 3 × 2 factorial design, and the incubation was repeated twice with quadruplicate fermentation vials for each treatment in each incubation. ^{15}N labeled ammonium sulfate was used as a microbial N marker, and headspace gas was sampled to determine methane production. Concentrations of NDF and ADF were lower ($P < 0.01$) in FD than in H and S. Ensiling decreased ($P < 0.001$) total phenolics and extractable CT content but had no effect on total CT. Hay did not affect either extractable or total CT content. Hay and silage had lower ($P < 0.01$) true DM disappearance (TDMD) and NDF disappearance (NDFD) than S and FD, whereas inclusion of PEG did not affect TDMD or NDFD at 8, 24, or 72 h of incubation. Hay had lower microbial protein (MP) production ($P < 0.001$) than FD and S, and inclusion of PEG decreased ($P < 0.001$) MP at 24 or 72 h of incubation. Productions of total gas, methane, and total VFA and the rate of gas production were similar, but ammonia accumulation was higher ($P < 0.05$) for PEG than non-PEG treatments during 72-h incubation. Incubation with S produced VFA with a lower ($P < 0.001$) proportion of acetate but higher ($P < 0.05$) proportion of propionate, resulting in a lower ($P < 0.001$) acetate:propionate ratio as compared to that of FD or H after 8 h of incubation. No difference was observed between H and S in the VFA profile. Condensed tannins in PPC decreased protein degradation in the rumen but had minimal effects on overall rumen fermentation, and conservation of PPC as hay or silage had little effect on the efficacy of CT in modulating rumen fermentation.

Key Words: condensed tannin, purple prairie clover, ruminal fermentation
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617 Microbial community structure of conventional and brown midrib corns ensiled at low dry matter concentrations with and without a combo inoculant.

J. J. Romero*[1,2], J. Park[3], Y. Zhao[4], Y. Joo[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, Institute of Agriculture & Life Science), Gyeongsang National University, Jinju, Republic of Korea,* [4]*Department of Animal Nutrition and Feed Science, China Agricultural University, Beijing, China,* [5]*Department of Food, Bioprocessing, and Nutrition Sciences, North Carolina State University, Raleigh.*

We evaluated the effects of an inoculant on the microbial community structure of 4 corn hybrids ensiled at low DM concentration. Treatment design was the factorial combination of 4 corn hybrids (HYB) ensiled with (INO) and without (CON) inoculant. HYB were TMF2R737, F2F817 (A and B, 30.5 and 26.3% DM, respectively), P2089YHR, and P1449XR (C and D, 31.1 and 31.5% DM). B and D were brown midrib mutants. The inoculant 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 treatments replicated 6 times. Corn was chopped, treated or not with inoculant, packed into 7.6L bucket silos, and stored for 100 d. At d 0, bacterial relative abundance (RA, %) of Enterobacteriaceae was lower in D vs. the other hybrids (~51.3 vs. 58.4, respectively) and lower for CON vs. INO (54.8 vs. 58.5 ± 1.83, respectively; $P < 0.04$). For fungi, A and C had a higher RA vs. B and D for *Tremellales* (~25.8 vs. ~13.9 ± 3.91) and lower RA for Mucoraceae (~3.64 vs. ~7.51 ± 1.18; $P < 0.04$). At d 100 for bacteria, INO had higher RA vs. CON for Lactobacillaceae (99.2 vs. 75.7 ± 3.08) and lower RA for Enterobacteriaceae (0.28 vs. 9.93 ± 1.32) and Lachnospiraceae (0.03 vs. 1.71 ± 0.60; $P < 0.05$). INO had a lower RA of Leuconostocaceae vs. CON only for D (0.21 vs. 14.5) but not for other HYB (~0.21 vs. ~2.70 ± 1.87; HYB × INO, $P < 0.05$). For fungi, INO had a lower RA vs. CON for Monascaceae (12.6 vs. 44.7 ± 7.30) and increased incertae sedis *Tremellales* (8.0 vs. 1.2 ± 2.31) and Saccharomycetales (6.4 vs. 0.3 ± 1.72). INO had less OTUs for bacteria (66 vs. 226 ± 10.7) and more for fungi (45.6 vs. 20.1 ± 3.59; $P < 0.01$; d 100) vs. CON. PCoA plots showed a separation in the structure of bacterial and fungal communities at d 0 and 100 and within d 100 between the CON and INO. The results indicate that epiphytic microbial composition differs depending on HYB. In addition, INO favored the dominance of the Lactobacillaceae, compared to a more diverse CON, and reduced the dominance of Monascaceae, increasing fungal diversity relative to CON.

Key Words: corn silage, inoculant, microbial diversity
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618 Identification of six uncultured rumen bacteria from different phylogenetic lineages using cellulose as a selection agent.

Lee J. Opdahl*, Michael G. Gonda, and Benoit St-Pierre, *Department of Animal Science, South Dakota State University, Brookings.*

The microbial-driven process of converting cellulosic biomass into utilizable energy is a defining feature of ruminant animals. Due to the complexity of rumen microbial communities, the vast majority of these rumen microorganisms remain uncharacterized. In order to gain further insight, selection-based batch culturing from bovine rumen fluid was used to identify previously uncharacterized rumen bacteria capable of metabolizing cellulose. Each independent trial consisted of 3 replicate cultures supplemented with cellulose (Sigma, cat# C8002) and 2 replicate cultures with no added substrate. 16S rRNA-based population analysis was used to identify rumen bacteria enriched within 14 days of culturing. A total of 116,111 to 336,246 high quality, non-chimeric sequence reads per trial were used for operational taxonomic unit (OTU) clustering. As a result of 3 trials, seven different candidate cellulose-utilizing species-level OTUs were identified. Six of the enriched OTUs showed increased levels ranging between 140 and 500-fold increases compared to their respective rumen inocula, representing 14.1% to 41.3% of reads in samples supplemented with cellulose. One OTU corresponded to a known species (*Ruminococcus flavefaciens*), four were predicted to be uncultured species of known genera (*Rummeliibacillus* sp., *Ethanoligenens* sp., and 2 *Prevotella* spp.), and one was assigned to the family Ruminococcaceae. The remaining OTU (*Prevotella* sp.) was found in moderately high abundance in the rumen inoculum (5.8%) and was enriched 2.5-fold

(15.6%). While future research is necessary to further characterize their involvement in cellulose metabolism, identification of these bacteria will provide additional insights towards a better understanding of ruminal cellulose metabolism.

Key Words: 16S rRNA, bacteria, cellulose
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619 Rumen microbial population dynamics driven by the interactions between the host and diet in cattle with different feed efficiencies.

A. L. A. Neves*[1], F. Li[1], B. Ghoshal[1], T. A. McAllister[2], J. A. Basarab[3], K. H. Ominski[4], and L. L. Guan[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [4]*Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada.*

Current understanding regarding the impact of interactions between diet and host on the rumen microbiome is limited. The objectives of this study were to (i) investigate rumen microbial population dynamics in beef cattle fed grain-based (high starch content) and/or forage-based diets (rich in neutral detergent fiber, NDF) over two 80-day feeding periods (with a 20-day adaptation in between) and (ii) evaluate the rumen microbiota of cattle exhibiting different feed efficiencies. Sixty purebred Angus bulls (mean age: 249 ± 22 days; average body weight: 313.9 ± 32 kg; mean ± SD) were raised in confinement at the Glenlea Research Station (University of Manitoba, CA) and randomly assigned into four pens fed the following diets in periods one and two, respectively: pen 1, forage/forage; pen 2, forage/grain; pen 3, grain/forage; and pen 4, grain/grain. Microbial populations were estimated using quantitative PCR (qPCR) for bacteria, archaea, fungi, and protozoa from two rumen fluid samples collected per period using a Geishauser oral probe. Thereafter, individual hosts were classified into three groups based on the magnitude of the microbial population shift between each feeding period using $\log_2$-fold change ($\log_2$fc < -1, low; -1 < $\log_2$fc < 1, stable; and $\log_2$fc > 1, high) in 16S rRNA gene copy number for bacteria/archaea and 18S rRNA/ITS (internal transcribed spacer) for protozoa/fungi. The effects of starch/NDF intakes, feed conversion rate (FCR), and CH_4 on the rumen microbes and their interactions with the three groups of host-microbial abundance variation were analyzed through log-normal generalized linear mixed models. Starch intake was associated with a marked decline in bacteria and fungi in the low group ($P < 0.001$ and $P = 0.012$, respectively), and NDF consumption increased bacteria and fungi only in the high group ($P < 0.011$), while no relationship was observed for archaea and protozoa across groups. Cattle in the low group produced more CH_4 as bacteria density increased ($P = 0.028$), whereas bacterial abundance and CH_4 remained constant in the stable and high groups. Bulls in the stable group were more efficient when linked to a higher bacterial abundance while bulls categorized in the low and high groups utilized the diet more efficiently when associated with the lowest bacteria densities. These findings suggest the potential use of the individualized rumen microbiota in host-tailored precision feeding systems, specially designed to improve feed efficiency in cattle.

Key Words: beef cattle, feed efficiency, rumen microbiota
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620 Estimating gas volume from headspace pressure in a batch culture system.

A. Romero-Pérez* and K. A. Beauchemin, *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Estimation of headspace gas volume (G_V) from headspace pressure (G_P) in in vitro batch culture experiments conducted at our lab is currently done using equations obtained overseas (Mauricio et al., 1999). Thus, the objective of the present work was to generate an equation to estimate G_V from G_P based on data obtained under our own experimental conditions. Two independent batch culture runs were conducted on different days. Twelve different feed ingredients including forages, grains, and by-products were utilized. Headspace G_P and G_V were measured after 3, 6, 9, 12, 18, 24, 48, 60, and 72 h using a pressure transducer and graduated plastic syringes (20 or 50 mL) connected to a three-way stopcock, respectively. A total of 1811 pairs of headspace pressure-volumes were obtained. One half of the data set was used to generate linear, quadratic, and cubic equations with intercepts set to zero or not (six equations in total). The second half was used to evaluate estimated G_V from obtained equations. The best equation (equation 1) was then compared against equations reported by Mauricio et al. (1999; equation 2) and Lopez et al. (2007; equation 3). Boyle's law adapted to our lab conditions was also evaluated (equation 4; 63 mL headspace volume; atmospheric pressure 13.15 PSI). Equations were evaluated using the r^2 between the observed and predicted values, root mean square prediction error (RMSPE), concordance correlation coefficient (CCC), and error due to the disturbance or random variation (ED). A quadratic equation was the most precise and accurate among the 6 equations obtained ($G_V = -0.2232 + 4.8021G_P + 0.0422G_P^2$; $r^2 = 0.995$; RMSPE = 0.64 mL; ED = 99.9%; CCC = 0.99). When compared with equations 2, 3, and 4, equation 1 ranked first, followed by equation 4 ($G_V = 4.79G_P$; $r^2 = 0.994$; RMSPE = 1.10 mL; ED = 39.3%; CCC = 0.99), equation 3 ($G_V = 5.385G_P$; $r^2 = 0.994$; RMSPE = 1.85 mL; ED = 13.8%; CCC = 0.98), and equation 2 ($G_V = 0.18 + 3.697G_P + 0.0824G_P^2$; $r^2 = 0.994$; RMSPE = 3.33 mL; ED = 4.23%; CCC = 0.93).

In conclusion, the quadratic equation obtained in the present study estimates G_V precisely and accurately and can be used in further experiments conducted under similar conditions.

Key Words: batch culture, equation, gas volume
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621 Effects of different forages and kenaf silage on in vitro rumen fermentation and growth performance of Hanwoo steer.

C. Ryu*[1], M. Park[1], E. Jeon[1], Y. Kim[1], H. S. Lee[1], S. Cho[2], and N. J. Choi[1], *[1]Chonbuk National University, Jeonju, Republic of Korea, [2]CALSNBT, Seoul, Republic of Korea.*

The present study evaluated the feed value of a new forage resource, kenaf, for the ruminant animal. Rumen fermentation characteristics and digestibilities of kenaf (K) and its silage (KS) were compared with those of rice straw (RS) and ryegrass (RG) in an in vitro study. The effects of KS feeding on growth performance of Hanwoo steer were also investigated. In vitro rumen fermentation using 0.5 g of dried and ground forage and 50 mL of rumen inoculum was performed for 72 hours. For rumen fermentation characteristics, total gas production of KS was significantly higher than that of others at 48 h. Gas productions of RG and K were significantly higher than others at 72 h. Ammonia nitrogen did not differ among groups at both of 48 and 72 h. For IVDMD, K showed significantly higher values than others at 48 h ($P < 0.05$). At 72 h, RG and K showed significantly greater IVDMD than the others treatments ($P < 0.05$). No difference between RG and K for IVDMD was found. Total volatile fatty acid and acetate production were significantly higher in the order of K > RG > KS > RS, regardless of incubation time ($P < 0.05$). In propionate production, RG was significantly higher than others at 48 and 72 h ($P < 0.05$). Thirty-six Hanwoo steers were assigned into three groups (RS, RG, and KS) based on a complete randomized design for a feeding trial. Growth performances were measured for 172 days. During the early period (0 ~ 43 days), average daily gain (ADG) of K was significantly lower than that of other treatments ($P < 0.05$). However, during the following days, no significant differences in ADG between groups were detected. At the end of trial, a significantly decreased feed requirement (feed/gain) was found in the KS group ($P < 0.05$). In conclusion, results of ruminal fermentation characteristics and feeding trial showed that kenaf and its silage can be used as forage resource for ruminants, and these resources could be beneficial for farm in terms of nutrition for animal and economics for farm.

Key Words: growth performance, kenaf silage, rumen fermentation
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622 Relation between organic acids in total mixed ration and rumen volatile fatty acids.

C. Ryu*[1], M. Park[1], E. Jeon[1], Y. Kim[1], H. S. Lee[1], N. J. Choi[1], and S. Cho[2], *[1]Chonbuk National University, Jeonju, Republic of Korea, [2]CALSNBT, Seoul, Republic of Korea.*

The present study investigated the relationship between organic acid contents in total mixed ration (TMR) and rumen volatile fatty acid production. TMR for lactating dairy cow was used. Organic acid production in TMR was modified by inoculation of different starter cultures. Five lactic acid bacteria (LAB) were used as a starter culture, and 12 different blends of those strains were designed based on Plackett-Burman experimental design. TMRs with different inoculants were fermented for 3 days at room temperature, and organic acid profiles (lactate, acetate, propionate, butyrate, and valerate) were examined. Fermented TMR was then air-dried at 60°C and ground for in vitro rumen fermentation. Rumen fluid from a cannulated Holstein cow was mixed with McDoughal solution. In vitro rumen fermentation with TMR was performed for 24 hours, and volatile fatty acid (VFA) production was measured. Significant effects of LAB were found for lactate, propionate, and butyrate of TMR ($P < 0.05$). On lactate, *L. paracasei* HNB34 showed a significant positive effect (PE) ($P < 0.05$). A significant PE on propionate was detected for *L. paracasei* HNB31 ($P < 0.05$). On butyrate, HNB34 and *L. parabuchneri* HNB35 showed a significant PE ($P < 0.05$). Significant alterations of nutrients (DM, CP, EE, NDF, and ADF) in TMR by LAB were not found. Then, the correlation between volatile fatty acid profiles from in vitro rumen fermentation with TMRs and organic acids used in TMR was investigated. Lactate in TMR showed a significant positive correlation (PC) with propionate in the rumen fluid ($P < 0.05$). Ruminal propionate was found to be negatively correlated with acetic acid in TMR, significantly ($P < 0.05$). Propionate in TMR showed significant correlation with all ruminal VFAs ($P < 0.05$). All ruminal VFAs, except valerate, showed PC with propionate in TMR. Butyrate in TMR showed a significant PC with valerate ($P < 0.05$) and significant negative correlations with acetate and propionate ($P < 0.05$). In conclusion, propionate and butyrate were detected as influencing factors toward rumen VFAs profiles. More propionate and less butyrate production in TMR could be beneficial in terms of more propionate production in the rumen.

Key Words: correlation, organic acids, rumen volatile fatty acid
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623 Identification of novel rumen bacteria using starch as a selective nutrient in batch cultures.

V. Bandarupalli*, *South Dakota State University, Brookings.*

The rumen is a complex and diverse microbial ecosystem composed of bacteria, methanogens, protozoa, and fungi. Among these diverse and complex microbial communities, bacteria are a predominant component in terms of cell densities, taxonomic diversity, and metabolic potential that play a vital role in the fermentation of feedstuff. Since the specific role of most rumen bacteria in the digestion of feedstuff remains to be determined, the primary objective of this research was to identify uncharacterized bacteria that are involved in metabolizing starch. Our general approach consisted of culturing rumen fluid under anaerobic conditions and at a constant temperature, using laboratory-scale bioreactors in the presence of starch. For each experiment, three replicate cultures were supplemented with starch (ADM Corn processing, Clinton, Iowa) as substrate, while two replicate cultures received no supplementation. Candidate starch utilizing bacteria was identified using amplicon sequencing for the V1-V3 region of the 16S rRNA gene, by comparing OTU profiles of starch-enriched cultures to non-supplemented cultures. For trial 1, combined 351,356 high quality sequence reads were used to determine the bacterial composition in control and treatment groups, ranging between 14,460 and 84,655 per sample. Our results showed that one species-level operational taxonomic unit (OTU), named OTU-SD1, corresponding to an uncultured species of *Prevotella*, was enriched on days 7 (15.6 ± 3.22) and 14 (17.7 ± 5.02) in treatment groups when compared to control cultures (0.17 ± 0.08). For trial 2, combined 309,387 high quality sequence reads were obtained ranging between 4691 and 77,984 per sample. Our results showed that two species-level operational taxonomic unit (OTUs), named OTU-SD2, and OTU-SD3, corresponding to an uncultured species of *Prevotella*, were enriched on day 7 (36.7 ± 31.7) and *Acetobacter* was enriched on day 14 (27.4 ± 26.2) in treatment groups when compared to control cultures (1.90 ± 1.39). Metagenomic sequence analysis for OTU-SD1 revealed the presence of genes for sugar utilization, including an α-amylase enzyme predicted to be involved in hydrolyzing starch. A better understanding of the role of novel bacteria in feed digestion will provide new avenues for developing supplements or feed additives that support animal health and increase production efficiency of the livestock industry.

Key Words: bioreactors, metagenomics, OTU
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624 Effects of replacing mushroom by-product with tofu by-product on chemical composition, microbe and rumen fermentation indices of the fermented diet.

H. J. Lee*[1], Y. H. Joo[1], S. S. Lee[1], D. H. V. Paradhipta[1], S. B. Kim[2], I. H. Choi[3], and S. C. Kim[1], [1]*Division of Applied Life Science (BK21Plus, Institute of Agriculture & Life Science), Gyeongsang National University, Jinju, Republic of Korea,* [2]*National Institute of Animal Science, RDA, Cheonan, Republic of Korea,* [3]*Department of Companion Animal & Animal Resources Science, Joongbu University, Geumsan, Republic of Korea.*

This study was aimed to estimate the effect of replacing mushroom by-product (MBP) with tofu by-product (TBP) on chemical compositions, microbes, and rumen fermentation indices of the fermented diet. The basal diet was formulated with MBP, TBP, rice bran, molasses, and inoculant at 32, 27, 37.5, 2.0, and 1.5% on a dry matter (DM) basis, respectively. The inoculant mainly contained *Lactobacillus acidophilus* (1.2 × 10^{10} cfu/g), *Bacillus subtilis* (2.1 × 10^{10} cfu/g), and *Saccharomyces cerevisiae* (2.3 × 10^{10} cfu/g). The MBP of basal diet was replaced with TBP at 0, 5, and 10% (DM basis) to mix the experimental diets. The experimental diets were ensiled into a 10 L mini silo with 5 replications and incubated at 39°C for 48 h. After incubation, the fermented diets were subsampled for the chemical compositions, pH, microbes, and rumen fermentation indices. For rumen fermentation indices, the subsampled diets (0.5 g) were placed into the incubation bottles and mixed with rumen fluid mixture (40 ml) composed of Van Soest medium and rumen fluid collected from two cannulated Hanwoo heifers at a 2:1 ratio. The mixtures were incubated in a CO_2 incubator at 39°C for 48 h with 5 replications and 3 blanks. The bottle content was centrifuged at the end of incubation. The supernatant was used for rumen pH, ammonia-N, and volatile fatty acid, and the residue was used for DM and neutral detergent fiber digestibilities. With increasing TBP replacement levels, crude protein of fermented diet increased (L, $P < 0.001$), while crude ash decreased (L, $P = 0.002$). The pH (L, $P < 0.001$) and mold (Q, $P < 0.001$) of fermented diets decreased by increases of TBP replacement levels, whereas lactic acid bacteria (L, $P = 0.020$) increased. However, *Bacillus subtilis* and yeast were not affected by TBP replacement levels. In vitro rumen digestibility of DM ($P = 0.053$) and neutral detergent fiber ($P = 0.024$) increased linearly by increases of replaced TBP levels, while rumen pH changed quadratically ($P = 0.026$). Rumen total volatile fatty acid decreased (L, $P = 0.001$) by increases of TBP replacement levels, but rumen ammonia-N was not affected. With increasing TBP replacement levels, the contents (% of molar) of iso-butyrate ($P = 0.003$) and butyrate ($P = 0.080$) increased quadratically. However, the contents of acetate, propionate, valerate, and iso-valerate were not affected by TBP replacement levels. In conclusion, this study indicated that the replacement of MBP with TBP up to 10% could improve the quality of fermented diets by the results of increased crude protein, nutrient digestibility, and lactic acid bacteria but decreased pH and mold.

Key Words: fermented diet, mushroom by-product, tofu by-product
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625 Effects of bacterial inoculation on the fermentation and aerobic stability of ensiled avocado (*Persea americana*) pulp.

B. D. Nkosi*[1] and V. N. Johan[2], [1]*ARC-Animal Production Institute, Irene, South Africa,* [2]*University of Free State, Bloemfontein, South Africa.*

The objective of the present study was to evaluate the effects of bacterial inoculation on the fermentation characteristics and aerobic stability of avocado (*Persea Americana*) pulp silage. Avocado pulp (332 ± 1.026 g dry matter, 119 ± 1.282 g extracted ether, 5.68 ± 0.481 pH, and 20 ± 1.531 MJ/kg DM gross energy) is a by-product of oil production. An amount of 80% avocado pulp was mixed with 15% grape pomace and 5% sugarcane molasses. The mixture was treated with i) control (no additive), ii) emsilage (lactic acid bacterial inoculant), and iii) Sil-All (lactic acid bacterial inoculant). The treatments were ensiled in 1.5l jars and kept at room temperature for 90 days. After 90 days of ensiling, three jars per treatment were opened and sampled for fermentation characteristics. Further, the silage samples were subjected to an aerobic stability test (CO_2 production) that lasted for 7 days. The dry matter (DM) and the terminal pH were not affected by treatments. However, Sil-All treatment reduced ($P < 0.05$) the water-soluble carbohydrate (WSC) content (17.7 ± 1.35 g WSC/kg DM) while increasing ($P < 0.05$) the lactic acid (47.8 ± 2.48 g LA/kg DM) content of the silage compared to the other treatments. However, the aerobic stability of the silage was reduced ($P < 0.05$) with Sil-All inoculation as indicated by higher CO_2 production (20.6 ± 1.47 g CO_2/kg DM) compared to other treatments. It was concluded that good quality avocado pulp silage was produced with Sil inoculation, and work to test this silage on animal feeding experiments is needed.

Key Words: acids, by-product, silage
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626 Maternal nutrition during the first 50 days of gestation alters bovine fetal hepatic metabolic transcriptome.

M. S. Crouse*[1], J. S. Caton[1], R. A. Cushman[2], K. J. McLean[3], C. R. Dahlen[1], P. P. Borowicz[1], L. P. Reynolds[1], and A. K. Ward[1], [1]*Department of Animal Sciences, North Dakota State University, Fargo,* [2]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE,* [3]*Department of Animal and Food Sciences, University of Kentucky, Lexington.*

We hypothesized that maternal nutrition during the first 50 d of gestation would alter the metabolic transcriptome of the bovine fetal liver. Fourteen beef heifers were estrus synchronized and assigned to 2 treatments at breeding (CON, 100% of requirements to gain 0.45kg/d; RES, 60% of CON). Heifers were ovariohysterectomized on d 50 of gestation, and fetal livers were dissected and flash frozen, RNA was extracted, and RNA-Sequencing was conducted. Transcriptome analysis was run via the Tuxedo Suite, and KEGG Pathways were analyzed with DAVID 6.8. A total of 548 genes ($P < 0.01$) were used for pathway analysis, of which 201 were false discovery rate protected ($q < 0.10$). Fetal hepatic metabolic KEGG pathways resulted in 45 genes that were differentially expressed and grouped by function: amino acid metabolism (n = 10), purine and pyrimidine metabolism (n = 7), carbohydrate metabolism (n = 10), reducing equivalent (NAD/FAD) metabolism (n = 5), steroid and lipid biosynthesis (n = 9), cytochrome and heme metabolism (n = 2), and 2 remaining unrelated genes. Five genes involved in amino acid metabolism were upregulated in CON vs. RES fetal liver (Min = 1.73; Max = 2.46; Avg = 1.99-fold). Five genes involved in amino acid metabolism were upregulated in RES vs. CON (Min = 1.63; Max = 2.36; Avg = 1.85-fold). Genes involved in purine and pyrimidine metabolism were upregulated in RES vs. CON (Min = 1.72; Max = 2.50; Avg = 1.94-fold). Five genes involved in carbohydrate metabolism were upregulated in CON vs. RES (Min = 1.61; Max = 3.50; Avg = 2.08-fold). Five genes involved in carbohydrate metabolism were upregulated in RES vs. CON (Min = 1.69; Max = 2.13; Avg = 1.92-fold). Genes involved in reducing equivalent metabolism were upregulated in RES vs. CON (Min = 1.63; Max = 1.92; Avg = 1.74-fold). Eight genes involved in steroid and lipid biosynthetic pathways were upregulated in RES vs. CON (Min = 1.61; Max = 2.07; Avg = 1.82-fold), and 1 gene was upregulated in CON vs. RES (1.70-fold). The two genes involved in cytochrome and heme metabolism were upregulated in RES vs. CON (Min = 2.53; Max = 3.18; Avg = 2.9-fold). These data are interpreted to support our hypothesis that a moderate maternal nutrient restriction during the first 50 d of gestation 'programs' the bovine fetal hepatic metabolic transcriptome primarily reflected

by upregulation in RES offspring. USDA is an equal opportunity employer and provider.

Key Words: developmental programming, metabolism, nutrient restriction
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627 BeefTrader: Optimal economical endpoint decision support system for feedlots and meat packers.

T. Z. Albertini*[1], A. G. Biase[1], M. Barbosa[1], A. G. Cerqueira[1], H. C. Gonçalves[1], L. G. Barioni[2], J. V. Caixeta-Filho[3], T. G. Péra[3], C. T. D. S. Dias[4], S. R. Medeiros[5], J. W. Oltjen[6], N. H. C. Nepomuceno[7], and D. P. D. Lanna[8], *[1]@Tech - Innovation Technology for Agriculture, Piracicaba, Brazil, [2]Embrapa Informatica Agropecuaria, Campinas, Brazil, [3]Department of Economics, Management and Sociology, Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, Brazil, [4]Department of Exact Sciences, Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, Brazil, [5]Embrapa Gado de Corte, Campo Grande, MS, Brazil, [6]University of California, Davis, [7]Integra Software, Brasília, Brazil, [8]Department of Animal Science, Animal Nutrition and Growth Lab., Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, Brazil.*

This study aimed to identify the most profitable feeding endpoint for feedlot cattle based on each individual animal's optimal economical endpoint (OEE) using the BeefTrader Decision Support System (DSS). The hypothesis was that the traditional slaughter endpoint (TSE, currently used in commercial feedlots) would have different profitability than the OEE which is determined when the marginal net profit (MNV = daily change in revenue – expense) becomes negative. Using Monte Carlo simulations, MNV curves for 280 Nellore breed cattle were generated for 14 feedlots, using the Davis Growth Model reparametrized for Nellore. These simulated animals were sold by the model to 83 meat packers in Brazil. The constraints used were feedlot period ≥ 1 d, shrunk BW ≥ 390 kg, and empty body fat ≥ 16%. The optimized method considered the most suitable time for sale. From 280 animals simulated, 258 were sold by optimization process. The integrated MNV increased up to 74% ($P < 0.05$) for OEE compared to TSE. On average, an animal sold by OEE had a net profit of R$ 202.64 ± 6.35 (± SD) and for TSE R$ 116.54 ± 34.80. The variability of the animal's sale to OEE was significantly lower (about 3 times) in relation to the TSE, showing that BeefTrader can determine the time of slaughter based on both the chemical and physical body composition. At present, TSE is determined by visual inspection by trained technicians, resulting in greater variability and increased risk, since it is a non-optimized process. BeefTrader changes this scenario using an individual animal's dynamic growth and chemical composition, along with internal and exogenous economic information. The next step for this DSS is to be tested in a real farming situation, because the results presented here are encouraging. Acknowledgements: Grant #2015/07855-7 [BeefTrader PIPE Project and scholarships (16/02347-6; 16/02451-8; 16/07154-1; 16/12825-2; 16/12709-2)].

Key Words: mathematical, modeling, ruminant
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628 Short-term herbage intake of grazing multiparous and primiparous Holstein cows.

J. P. Soutto*[1], P. Gauthier[1], P. Pellaton[1], M. Carriquiry[1], P. Chilibroste[2], and A. I. Trujillo[1], *[1]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay, [2]Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay.*

Differences in the grazing harvest process between multiparous (MUL) and primiparous (PRIM) dairy cows could be explained by short-term grazing behavior (i.e., instantaneous herbage intake rate, bite mass, length of the grazing bouts). Therefore, this study was conducted in a randomized block design (3 blocks; n = 9 cows per parity) to assess the effect of parity on herbage intake (HI), HI rate, length of grazing bout, bite rate, and bite mass during the first grazing bout in the am grazing session. Cows (days in milk = 73 ± 7 d; BW = 521 ± 32 kg; BCS = 2.75 ± 0.25; milk yield = 26 ± 3 kg) grazed a vegetative oat pasture (8 h of access to pasture from 8:30 to 16:30 h; pasture allowance = 30 kg DM/d; DM = 14%, CP = 23%, NDF = 46%, DM basis) and were individually fed 6 kg DM/d of a mixture (70:30 forage to concentrate ratio, as-fed basis) after pm milking. Herbage intake was estimated by weighing animals before and after grazing with correction for insensible weight loss (2 consecutive d). The HI rate (kg DM/min) was estimated by dividing HI by the length of the grazing bout, bite rate (bite/min) by counting prehension bites during 1 min every 2 min, and the bite mass (g DM/bite) by dividing HI by the number of bites. Data were analyzed using a mixed model with parity as a fixed effect and block as a random effect. Cow HI (5.6 vs. 4.5 ± 0.35 kg DM/d; $P = 0.043$ and 0.096 vs. 0.087 ± 0.005 kg DM/kg BW; $P = 0.088$), HI rate (0.051 vs. 0.043 ± 0.003 kg DM/min; $P = 0.008$), and bite mass (0.98 vs. 0.79 ± 0.07 g DM; $P = 0.013$) were greater for MUL than PRIM while bite rate and the length of the grazing bout did not differ ($P > 0.10$) between parities. Results indicate that bite mass plays a central role in the short-term intake behavior when MUL and PRIM dairy cows were compared. Differences in bite mass could be explained by grazing adaptability, hierarchical relationships, or physical factors (i.e., mouth dimension).

Key Words: bite mass, grazing behavior, herbage intake
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629 Effects of strategic supplementation of low quality diets and residual feed intake classification to optimize performance in gestating beef cattle.

K. M. Spence*[1], C. P. Campbell[1], J. P. Cant[1], A. Cánovas[1,2], I. B. Mandell[1], [1]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

A wintering beef cow study was conducted to evaluate strategic supplementation of a straw-based diet with an energy-protein supplement during the last 75 days of gestation on beef cow performance and feed efficiency during gestation and subsequent pre-weaning calf performance. Gestating crossbred beef cows (predominantly Angus × Simmental; n = 118, 128 ± 31 days in gestation, 691.5 ± 235 kg BW) were evaluated on one of five nutritional regimens: 1) 70% haylage, 30% millet straw on a dry matter basis (DMB) fed ad libitum (HAYL), 2) millet straw fed ad libitum along with haylage at 0.8% DMB of cow BW (WSHAYL), 3) WSHAYL along with an energy-protein supplement once/week, 4) WSHAYL with supplementation twice/week, and 5) WSHAYL with supplementation three times/week. The supplement contained 54.6% corn gluten meal, 23.4% soybean meal, 21.0% calcium propionate, and 1.0% tallow and was fed at 0.32 g/kg of BW per day DMB. Cows were allocated to ensure similar days in gestation, age, residual feed intake (RFI) classification and breed composition across nutritional regimens. Cows were evaluated throughout second and third trimesters of gestation for feed intake, BW, average daily gain (ADG), residual feed intake (RFI), body condition score (BCS), ultrasound measurement of rib fat depth, serum blood metabolite concentrations, and pre-weaning calf performance traits. Cows were classified into low, medium, and high RFI groups (<0.5 SD; ±0.5 SD; >0.5 SD, respectively, based on a mean RFI of 0). Statistical analysis to examine differences in nutritional regimens and RFI classification was performed using PROC GLIMMX in SAS. Cows fed the HAYL diet had a higher percentage of high RFI cows and greater DMI vs. all other nutritional regimens ($P < 0.001$). Serum NEFA concentrations were lower in low RFI cows ($P = 0.003$) while urea concentrations tended to be greater in low RFI cows ($P = 0.069$). Serum AST concentrations were greater in HAYL cows vs. all other diets ($P = 0.001$). ADG was highest in HAYL cows vs. all other nutritional regimens ($P < 0.001$), while ADG was greater in low vs. high RFI cows ($P < 0.001$). Rib fat depths increased the most over gestation in HAYL vs. all other nutritional regimens ($P < 0.001$). Pre-weaning calf performance traits were not significantly affected by nutritional regimen or RFI classification. RFI classification was affected by nutritional regimen while wintering cow performance was related to individual cow RFI classification.

Key Words: beef cow, low-quality diets, RFI
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630 Bicarbonate supplementation as a strategy to mitigate effects of endophyte-infected tall fescue on replacement heifer development.

K. N. Hardin*[1], N. W. Dias[1], D. A. Fiske[1], V. R. G. Mercadante[2], M. L. Rhoads[1], A. D. Ealy[1], T. B. Wilson[1], and R. R. White[1], [1]*Virginia Tech, Blacksburg,* [2]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg.*

Endophyte-infected tall fescue occupies most grazing lands in the Southeastern U.S. and is associated with poor growth and reproductive performance. Supplementing bicarbonate to cattle grazing endophyte-infected tall fescue was hypothesized to be a strategy to alleviate these negative performance outcomes. The objective of this study was to evaluate growth and reproductive characteristics of heifers consuming endophyte-infected tall fescue with or without sodium bicarbonate supplementation. Forty-eight heifers (8 mo; BW = 589 ± 53 kg) were blocked by BW and assigned to pens and treatments. Heifers were group-housed and fed individually using Calan gates. Treatments were arranged as a 2 × 2 factorial design with heifers receiving either high- or low-endophyte fescue seed with (E+B, E-B) or without (E+, E-) sodium bicarbonate supplementation. Heifers were fed a corn silage diet; seed and bicarbonate were supplemented at 1.5 kg/day and 0.25 kg/day, respectively. Heifer BW was recorded on sequential days at the start and end of the 84 d experiment and every 14 d. Feed intake and refusals were collected daily. The BW and DMI data were used to estimate ADG and G:F. Reproductive tract scores (RTS) were performed every 28 d via transrectal palpation and ultrasonography. Results were analyzed after the 2nd ultrasound (56 d) and at the end of the experiment. At d 56, RTS ($P = 0.005$) was affected by the interaction of bicarbonate supplementation and fescue seed type, and G:F ($P = 0.061$) and ADG ($P = 0.058$) tended to be affected. In general, RTS, G:F, and ADG of all other treatments were improved compared with the E+ treatment. Neither factor affected DMI at d 56 ($P > 0.10$). By d 84, bicarbonate supplementation tended to decrease ADG ($P = 0.051$) and decreased G:F ($P = 0.016$), and infected fescue consumption tended to decrease DMI ($P = 0.060$). On d 56, bicarbonate showed promise as a strategy to ameliorate the negative effects of endophyte-infected fescue consumption; however, by the end of the study, no effects of fescue seed type on ADG or G:F were observed. Short-term bicarbonate supplementation appears to be a promising strategy to eliminate negative production responses associated with endophyte-infected fescue consumption; however, additional research is needed to fully understand why this benefit was not sustained over the full experimental period and how the strategy would translate to traditional pasture systems where animals can self-select a bicarbonate supplementation level.

Key Words: fescue toxicosis, replacement heifer, sodium bicarbonate
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631 Effect of increasing protein and fat inclusion in the diets of beef cows during gestation and lactation on progeny performance, carcass characteristics, and plasma nonesterified fatty acids.

A. J. C. Nuñez and J. P. Schoonmaker*, *Department of Animal Science, Purdue University, West Lafayette, IN.*

This study was conducted to evaluate the effects of increasing CP and fat inclusion in the diets of Angus × Simmental cows during late gestation through mid lactation on progeny feedlot performance, carcass characteristics, and plasma NEFA concentration. Forty-eight cows (610 ± 16.8 kg BW), pregnant with male progeny, were allotted by BW and BCS to 4 treatments arranged in a 2 × 2 factorial, with 2 CP (11.9 and 17.1%) and 2 fat (2.0 and 4.8%) concentrations in the diet DM. Treatment diets were formulated to be isocaloric and were fed to cows in individual pens for 178 d. The average calving date was on d 85 ± 7.2 from treatment start. After the treatment period, cow-calf pairs were placed on pasture and managed as one group until weaning (d 279). Steers were then transitioned to a common backgrounding diet, fed until d 414 (329 d of age), and placed in an indoor feedlot in individual pens. Steers were fed a feedlot diet for 142 d composed of 57% dry-rolled corn, 22% dried distillers grains with solubles, 10% corn silage, 5% rye silage, and 6% vitamin/mineral supplement in the diet DM. Jugular blood samples were collected at the beginning and end of the feedlot period to determine plasma NEFA concentration using a commercial kit. Steers were slaughtered at a target BW of approximately 648 kg, and carcass characteristics were determined after a 24-h chill. Data were analyzed using the MIXED procedure of SAS. No interactions among dietary CP and fat concentrations were observed ($P \geq 0.31$). Initial and final BW, as well as ADG, DMI, and gain:feed of the steers throughout the feedlot period, were not affected by CP ($P \geq 0.26$) or fat ($P \geq 0.70$) in the maternal diet. Similarly, increasing CP or fat inclusion in the diets of dams had no effects ($P \geq 0.25$ and $P \geq 0.17$ for CP and fat, respectively) on HCW, dressing, fat thickness, LM area, and yield grade of progeny carcasses. Moreover, plasma NEFA of steers at the beginning and end of the feedlot period were not affected by the increasing inclusion of CP ($P \geq 0.36$) or fat ($P \geq 0.23$) in the maternal diet. In summary, increasing CP or fat inclusion in the diets of cows during late gestation through mid lactation had no long-term effects on performance, carcass characteristics, and plasma NEFA concentrations of their male progeny.

Key Words: developmental, feedlot, progeny
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632 Effect of spring and fall calving on the subsequent impact of monensin supplementation in 1st and 2nd parity cows.

J. J. Ball*[1], E. B. Kegley[1], P. A. Beck[2], E. A. Backes[1], R. W. Rorie[1], T. D. Lester[1], D. S. Hubbell III[3], J. D. Tucker[3], K. M. Loeschner[3], and J. G. Powell[1], *[1]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, [2]SWREC, Division of Agriculture, University of Arkansas, Hope, [3]Division of Agriculture Livestock and Forestry Research Station, University of Arkansas, Batesville.*

A study was conducted to determine the effects of monensin, an ionophore that improves energy efficiency through alteration of VFA production in the rumen, in first or second parity lactating beef cows in a spring- and fall-calving herd. One hundred thirty-five (BW = 455 ± 20.2 kg) Angus crossbred cows and heifers (n = 88 fall calving; n = 47 spring calving) were blocked by calving season, stratified by parity, calving date, and sire, then randomly assigned to pastures within herd in a randomized complete block design. Pastures (n = 4/herd) were assigned randomly to 1 of 2 treatments: 1) CON (no supplemental monensin), 2) MON (200 mg/d monensin). All cattle received 2.3 kg/d of grain based supplement which served as the treatment carrier. Supplementation began 35 d prior to breeding in both herds and continued through weaning in the spring herd and through breeding in the fall herd. Body weights and BCS were collected at the initiation, 3 interim d, and end of study in both herds while hair coat scores (HCS; 1 = slick, short summer coat, 5 = full winter coat) were recorded for all cattle on the final d. Quantitative variables were analyzed using PROC MIXED, and categorical variables were analyzed using PROC GLIMMIX with an alpha of 0.05 for all dependent variables. Final cow BW were similar between treatments and calving season ($P \geq 0.42$). In the spring-calving herd, MON increased cow pre-breeding ADG compared to CON and both treatments in the fall-calving herd (treatment × calving season interaction, $P = 0.03$). Calf BW and ADG were not affected by MON supplementation or by calving season ($P \geq 0.54$). Cow BCS were not affected by treatment ($P \geq 0.18$); however, pre- and post-breeding BCS were greater in the spring-calving herd compared to the fall-calving herd ($P < 0.01$). Cow HCS was not affected by MON supplementation ($P \geq 0.23$), but as expected, the fall-calving herd had a greater HCS than the spring-calving herd ($P < 0.01$). The total percentage of cows bred regardless of conception method was similar between treatments ($P = 0.80$); however, there was a tendency for a greater percentage of pregnant cows in the spring-calving herd compared to the fall-calving herd ($P = 0.06$). Monensin supplementation did not affect gains of fall-calving cows consuming low quality forage but may affect spring-calving cows consuming a greater plane of nutrition.

Key Words: beef cows, ionophore, monensin
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633 Effects of low-moisture molasses block supplements on tissue concentrations of trace elements and growth performance of forage-fed beef cattle.

S. L. Katulski*, C. L. Van Bibber-Krueger, C. A. Blevins, N. F. D. Schrag, L. M. Horton, T. J. Ellerman, H. C. Muller, and J. S. Drouillard, *Kansas State University, Manhattan.*

Feed manufacturing processes, particularly those involving extremes of heat or pH, can alter bioavailability of nutrients. Similarly, the form of supplements (pellets, loose minerals, liquids, or blocks) can influence supplement consumption patterns, which may in turn impact nutrient utilization. This study was conducted to evaluate changes in tissue concentrations of Cu, P, and Zn in forage-fed heifers in response to supplementation with plain salt (S), a free-choice mineral supplement (M), or a low-moisture process block supplement (B). Heifers (n = 360, 253.9 ± 6.7 kg) were weighed, blocked by initial BW, and randomly allocated to treatments consisting of ad libitum access to salt (S), loose mineral (M), or low-moisture molasses block plus salt (B). The M and B treatments were manufactured using the identical mineral mixture, adding salt as a diluent to make M or incorporating the mineral mixture into a hot, pliable evaporated molasses/oil mixture to make B. Heifers were housed in 24 dirt-surfaced pens (15 animals/pen, 8 pens/treatment) and fed a basal diet consisting (DM basis) of 70% ground brome hay and 30% corn silage for 100 d. Blood and liver biopsy samples were collected on d 0 and 70 from 4 randomly selected heifers per pen to determine changes in concentrations of Cu in liver and Zn and P in plasma. No treatment differences were detected for DMI or G:F, but ADG was greater for M than for C or B. No differences were detected for changes in plasma P or Zn ($P > 0.10$). Liver copper concentration was different across treatments (114, 428, and 266 mg/kg tissue DM for S, M, and B, respectively; $P < 0.05$). The percent of heifers identified as having sufficient tissue Cu (i.e., >87.5 mg/kg tissue DM) was less for S than for M and B (59.4, 100, and 100%, respectively; $P < 0.05$). In conclusion, tissue mineral content was proportionate to mineral intake, but differences in mineral availability between loose mineral and block supplements were not evident.

Key Words: copper, phosphorus, zinc
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Table 633.

Item	Salt	Loose Mineral	Block	SEM	*P*-value
ADG, kg/day	0.55^a	0.58^b	0.55^a	0.013	0.03
DMI, kg/day	6.94	7.06	6.92	0.216	0.54
G:F	0.079	0.082	0.079	0.0018	0.11
Cu intake, mg/d	61^a	601^b	496^c	27.3	<0.01
P intake, g/d	55^a	73^b	65^c	1.6	<0.01
Zn intake, mg/d	112^a	2021^b	1296^c	89.9	<0.01

$^{a, b, c}$ Means without a common superscript letter are different, $P < 0.05$.

634 Analysis strategies for calculating intake for cattle with plant waxes.

E. J. Hilburger*[1], H. C. Wilson[1], H. C. Freetly[2], and R. M. Lewis[1], [1]*University of Nebraska–Lincoln, Lincoln,* [2]*USDA, ARS, U. S. Meat Animal Research Center, Clay Center, NE.*

Within grazing systems determining differences in efficiencies is difficult due to the complexity of measuring forage intakes. Plant waxes, particularly *n*-alkanes, have shown potential for estimating intakes. However, extracting and analyzing these compounds is costly. Minimizing the number of samples needed to reliably estimate intakes is key. We compared 3 strategies for using plant-wax contents of feces to estimate intakes: (i) from a single sample formed by pooling collections from 5 d, estimating intakes from the pool; (ii) from separate samples collected each of 5 d, averaging intake estimates; and (iii) from a mathematical average of the 5 samples, estimating intakes from the average. Twenty-six heifers were fed a total mix ration (**TMR**; 69.8% corn silage, 30% alfalfa hay, and 0.2% salt DM) with a Calan-gate system for 45 d. Heifers were dosed via supplement with C_{32} alkane at 1.3 mg/kg BW/d the final 14 d. Fecal grab samples were collected the final 5 d. The C_{31} and C_{33} alkane contents of the TMR and of its components were obtained using gas chromatography, with the values of the components proportionally weighted (0.7 corn silage; 0.3 alfalfa hay) to emulate TMR. The C_{31} and C_{33} contents of the fecal samples also were obtained. Intakes were estimated from ratios of C_{31} and C_{33} to C_{32} in the fecal samples and diets. Estimated intakes were more precise when based on pooled (R^2 0.60 to 0.62) as compared to averaging (R^2 0.47 to 0.51) strategies. This result reflected variability in daily intakes over 5 d. When regressing predicted on measured intakes, regardless of strategy or definition of diet, the intercept did not differ from zero ($P > 0.35$), and the slope did not differ from one ($P > 0.08$). When emulating TMR as a 2-component mixture the slopes were higher (1.4 to 1.5 vs. 1.1 to 1.2) and estimated less precisely (SE 0.17 to 0.24 vs. 0.23 to 0.31) than with TMR. This reflected the low C_{31} and C_{33} contents of corn compared to alfalfa, confounding their delineation in the mixture. With increasing complexity, such as rangelands, delineating individual plants becomes even more challenging. Intake estimates were adequate regardless of the approach adopted. However, using a pooled fecal sample decreased the number of samples evaluated and increased precision, both advantages. Furthermore, with simple diets, intakes could be reliably estimated using plant waxes. USDA is an equal opportunity provider and employer.

Key Words: alkanes, intake, plant-wax markers
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635 Effects of solvent- or mechanically extracted *Brassica carinata* meal on performance of cows.

E. J. Rosenthal*, J. A. Clapper, G. A. Perry, and D. W. Brake, *South Dakota State University, Brookings.*

Brassica carinata is an oilseed that requires a relatively short growing season and allows for good yields of aviation-based fuels. Further, *B. carinata* contains large amounts of glucosinolates that preclude use of *B. carinata* as food to humans. Synthesis of aviation-based fuels from *B. carinata* results in residues (carinata meal) not destroyed by fuel manufacture. We placed 56 cows (beginning BW = 482.4 ± 9.5 kg) blocked by BW into 8 pens and allowed ad libitum access to either long-stem or ground cornstalks for 56 d. Subsequently, 2 cows within each pen were provided canola meal or solvent- or mechanically extracted carinata meal daily in amounts designed to meet DIP requirements; 1 cow in each pen served as a negative control (no supplement). Intake of the daily protein supplement was complete among cows provided either solvent-extracted carinata meal or canola meal, but intake of cold-pressed carinata meal was small (14.3 ± 1.0% of daily supplement). Overall, ΔBCS was -0.6 ± 0.06 with no interaction between forage processing and supplemental protein ($P >$ 0.37). Differences among ΔBCS in response to supplemental protein were apparent after 14 d, and overall ΔBCS was less ($P < 0.01$) among cows fed canola meal and solvent-extracted carinata meal compared to negative control cows; however, ΔBCS among cows fed mechanically extracted carinata meal was similar to the negative control. Forage processing had no effect ($P > 0.13$) on ΔBCS. Changes in BW were apparent after 42 d. Overall ΔBW was greatest ($P < 0.01$) among cows fed canola meal and least among cows fed mechanically extracted carinata meal or no protein, and solvent-extracted carinata meal was intermediate. Additionally, cows fed ground cornstalks had less ΔBW compared to cows fed long-stem cornstalks. Because glucosinolates can effect thyroid function, we measured circulating T3 and T4 at the beginning, middle (d 28), and end (d 56) of our study. As expected, neither T3 or T4 differed at the beginning of the experiment; however, at d 56 T3 was greater ($P = 0.05$) among cows fed canola meal compared to negative control, and cows fed solvent- or mechanically extracted carinata meal were intermediate. Protein supplementation had no effect on T4, but T3 and T4 were less ($P < 0.04$) at d 28 and d 56 among cows fed ground cornstalks compared to cows fed long-stem cornstalks. Apparently, solvent- but not mechanically extracted carinata meal may be useful as a source of supplemental protein to cows.

Key Words: carinata meal, cattle, performance
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636 The effect of dietary grain inclusion and Zn concentration on rumen epithelial structure and Zn transporter expression in sheep.

O. N. Genther-Schroeder*, and S. L. Hansen, *Iowa State University, Ames.*

The objective of this study was to evaluate the effect of dietary grain inclusion and supplemental Zn on rumen epithelial structure and Zn transporter expression in ruminants. Twenty crossbred wethers (34 ± 5.3 kg) were individually fed in a 2×2 factorial with two diet types, 50% forage, 50% concentrate (HF) or 10% forage, 90% concentrate (HG), and two supplemental Zn concentrations, 0 (CON) or 120 mg Zn/kg DM from $ZnSO_4$ (ZINC). After 60 d, sheep were euthanized and blood, liver and rumen sections from the ventral sac were collected and preserved for trace mineral analysis, histology, tight junction protein expression, and in-situ RNA hybridization of Zn transporters. Data were analyzed as a 2×2 factorial, with the fixed effects of diet type and Zn concentration, and wether was the experimental unit. Plasma Fe and Zn concentrations were greater in HG ($P \leq 0.005$), and plasma Zn was greater ($P = 0.004$) and Cu tended to be greater ($P = 0.08$) in ZINC. There was a tendency for an interaction for liver Cu ($P = 0.08$), where within ZINC, HG was greater than HF ($P = 0.01$). The HF had greater liver Fe ($P = 0.01$) and liver Zn was not affected by either diet or Zn concentration ($P \geq 0.17$). There was an interaction within rumen epithelial Zn concentration ($P = 0.05$) where HG+ZINC were greatest followed by HF+ZINC while CON were not different ($P = 0.63$). The HG had greater rumen tissue Cu and lesser Fe concentrations ($P = 0.004$). Rumen papillae width, epithelial, non-keratinized, and keratinized layers were not affected by treatments ($P \geq 0.13$). There was an interaction within papillae length ($P = 0.05$) where HG+CON were greater ($P = 0.008$) than HG+ZINC, both of which were greater than HF ($P < 0.01$). Claudin-1, Claudin-4, and Occludin protein expression was not affected by treatments ($P \geq 0.32$). Claudin-7 protein expression was greater in HG ($P = 0.002$) and tended to be greater in CON ($P = 0.09$). In situ RNA expression of *zip4* and *zip5* were not affected by treatments ($P \geq 0.24$) but there was an interaction in RNA expression of *znt1*, a Zn exporter ($P = 0.04$), where HG+CON was greater than other treatments. These data suggest dietary Zn has minimal effect on rumen histology, but may influence tight junction protein and *znt1* expression in ruminants fed a high grain diet.

Key Words: zinc, diet type, rumen epithelium
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637 Effect of repeated trace mineral injections on beef heifer development and reproductive performance.

R. S. Stokes[*1], M. J. Volk[1], F. A. Ireland[1], P. J. Gunn[2], and D. W. Shike[3], [1]*University of Illinois, Urbana,* [2]*Department of Animal Science, Iowa State University, Ames,* [3]*Department of Animal Sciences, University of Illinois, Urbana.*

To determine the effects of repeated trace mineral injections on heifer development and reproductive performance, commercial Angus heifers (*n* = 290; 199 ± 34.3 kg) were utilized in a completely randomized design. Heifers were stratified by BW into 6 groups and assigned to injectable trace mineral (MM; Multimin90) or saline injection (CON) given post-weaning at 221, 319, and 401 ± 22 d of age. Throughout development, heifers grazed endophyte-infected fescue-red clover pastures and were supplemented with modified corn distillers grains (2.7 kg$\cdot$heifer$^{-1}\cdot$d^{-1}) and given access to free choice inorganic minerals formulated to meet or exceed NRC recommendations. Heifer BW and BCS were collected at trial initiation and 4-7 week intervals thereafter. Hair coat scores (HCS) and respiration rates (n = 30 heifers/treatment) were collected at 269, 310, and 361 ± 22 d of age. Additionally, blood and liver samples were collected at trial initiation and estrous synchronization from 30 heifers/treatment to determine trace mineral status. At 319, 372, and 421±22 d of age, antral follicle count and ovarian size were determined via ultrasonography. Two blood samples from all heifers were collected 10 d apart, concurrent with ultrasound dates, for puberty determination. Estrous synchronization was initiated and reproductive tract scores (RTS) were collected at 421±22 d of age. Heifers had AI at 430 ± 22 d of age. Heifer BW, BCS, and HCS did not differ ($P \geq 0.12$) throughout development, except at 268 ± 22 d of age when BCS was greater ($P = 0.03$) for MM than CON. Respiratory rates were greater ($P = 0.05$) for MM than CON at 269±22 d of age, but did not differ ($P \geq 0.66$) at 310 and 361 ± 22 d of age. Plasma Mn and Zn concentrations did not differ between treatments ($P \geq 0.54$). However, MM had greater ($P \leq 0.01$) plasma and liver concentrations of Cu and Se compared to CON. Interestingly, MM decreased ($P = 0.02$) liver Zn concentrations compared to CON and there was no difference ($P = 0.60$) in liver Mn concentrations. Antral follicle count and ovarian size did not differ ($P \geq 0.43$) between treatments. Throughout development, the number of pubertal heifers was less ($P < 0.01$) for MM than CON. However, there was no difference ($P \geq 0.26$) in RTS or AI pregnancy rates (36 and 37% for MM and CON, respectively). Supplementing an injectable trace mineral increased heifer Cu and Se status; however, no effect was noted on ovarian development or reproductive performance.

Key Words: selenium , antral follicle count, copper
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638 The influence of supplemental zinc and ractopamine hydrochloride on mineral and nitrogen retention of beef steers.

R. Carmichael[*], O. N. Genther-Schroeder, C. P. Blank, E. L. Deters, S. J. Hartman, E. K. Niedermayer, and S. L. Hansen, *Iowa State University, Ames.*

The study objective was to determine if N retention was improved with supplemental Zn above NRC concentrations with or without ractopamine hydrochloride (RH) inclusion. Angus crossbred steers (n = 32, 485 ± 57 kg) with Genemax gain scores of 4 or 5 were utilized in a 2x2 factorial arrangement (8 steers/treatment). Steers were blocked by BW to one of two finishing diets with no supplemental Zn (analyzed 32 mg Zn/kg DM; CON) or supranutritional Zn (analyzed 145 mg Zn/kg DM; SUPZN), fed for 56 days and then assigned to RH (Actogain, Zoetis) supplementation strategies of 0 (NORAC) or 300 mg$\cdot^{-1}$steer$\cdot^{-1}$d (RAC) fed the last 30 d before harvest. On d 57 (d 1 of RH supplementation), steers (4 groups; 8 steers/group; 2 steers/treatment) were moved to metabolism crates and adapted for 10 d, followed by 5 d of total fecal and urine collection. Total retention of Zn, Mn, Fe, Cu, and N were calculated. Data were analyzed as a 2x2 factorial in Proc Mixed of SAS with group as random and steer as the experimental unit. Initial 56 d ADG was not affected by treatment ($P = 0.67$) but DMI was lesser in SUPZN vs CON ($P < 0.01$). No interactions between dietary Zn and RH strategies were noted during collection ($P \geq 0.19$). Collection DMI did not differ by treatment ($P \geq 0.23$); however, SUPZN intake of Mn and Zn was greatest ($P < 0.01$). Fecal and urinary excretion of Zn and retention of Mn and Zn were increased in SUPZN vs CON ($P < 0.01$); however, Zn retention was not different between RAC and NORAC ($P = 0.11$). Retention of Cu and Fe were unaffected by treatment ($P \geq 0.85$). Urine output and urine N excretion were decreased by RAC ($P \leq 0.05$). Nitrogen retention as a percent of total ingested N tended ($P = 0.10$) to be greater in SUPZN (44.4%) vs CON (40.0%) and tended ($P = 0.06$) to be greater in RAC (44.8%) vs NORAC (39.7%). Using Proc Corr, Zn and N retention were found to be positively correlated (r = 0.48, $P < 0.01$). Average daily gain and G:F across the 86 d trial were increased in RAC vs NORAC ($P < 0.01$). Overall, SUPZN appears to improve N retention, suggesting that increasing dietary Zn may be important for cattle growth beyond that induced by RH.

Key Words: zinc, nitrogen retention, ractopamine hydrochloride
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639 Effect of trace mineral supplementation with or without hormone implants on growth and carcass characteristics of steers.

E. K. Niedermayer*[1], E. M. McDonald[1], O. N. Genther-Schroeder[1], D. D. Loy[2], and S. L. Hansen[1], [1]*Iowa State University, Ames,* [2]*Department of Animal Science, Iowa State University, Ames.*

To determine the effects of trace mineral (TM) supplementation and hormone implant strategy on growth and carcass characteristics of cattle, 72 Angus-cross steers (388 ± 17 kg) were blocked by BW (6 steers per pen) to a 2 x 3 factorial. Steers were either implanted (d 0 with Component TE-IS, reimplanted d 56 with Component TE-200; IMP) or not (NoIMP). Within implant treatments cattle received no supplemental TM (CON), TM supplemented at 2016 NRC recommendations of 10 Cu, 30 Zn, 20 Mn, 0.10 Se, 0.15 Co, and 0.50 I (mg/kg; NRC), or TM supplemented at feedlot consultant recommendations of 20 Cu, 100 Zn, 50 Mn, 0.30 Se, 0.20 Co, and 0.50 I (mg/kg; IND). Blood samples were collected on d -7, 70 and 124. Steers received a finishing diet for 124 d in GrowSafe bunks and were harvested on d 125. Data were analyzed in SAS as a 2 × 3 factorial with the fixed effect of block, and steer as experimental unit (n = 12 per combination). Day -7 glucose concentrations were used as a covariate in analysis. There was a tendency ($P = 0.06$) for an IMP × TM for d 124 plasma glucose with NoIMP/NRC being greater than NoIMP/IND and all other treatments intermediate. There were no IMP × TM for final BW, overall ADG, DMI, G:F, dressing percent, backfat, marbling score, or KPH ($P \geq 0.17$). Overall ADG tended ($P = 0.07$) to be and HCW was ($P = 0.03$) affected by TM, where IND was greater than CON (HCW: 373, 378, and 388 kg for CON, NRC, and IND, respectively). Overall DMI was increased by TM ($P < 0.0001$) with NRC and IND being greater than CON. Steers receiving implants had greater ($P < 0.0001$) final BW (559 and 617 kg for NoIMP and IMP, respectively), overall ADG (1.35 and 1.83 kg for NoIMP and IMP, respectively), DMI, G:F, and HCW (359 and 400 kg for NoIMP and IMP, respectively) than NoIMP. There was an IMP × TM ($P = 0.02$) for ribeye area (REA) with IMP/CON having greater REA than IMP/IND, with IMP/NRC being intermediate; NoIMP had smaller REA, regardless of TM supplementation. There was an IMP × TM ($P = 0.02$) for YG where NoIMP/IND was greater than IMP/CON with all other treatments intermediate. These data indicate NRC TM recommendations might not be adequate for finishing beef steers, irrespective of hormone implant administration.

Key Words: trace mineral, beef, implant
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640 Effect of dietary zinc amino-acid complex supplementation on cattle performance, biomarkers of inflammation and metabolism, and liver abscess formation in steers receiving a mild acidosis challenge.

E. L. Lundy*[1], O. N. Genther-Schroeder[1], M. E. Branine[2], and S. L. Hansen[1], [1]*Iowa State University, Ames,* [2]*Zinpro Corporation, Eden Prairie, MN.*

The study objective was to evaluate the effect of dietary Zn supplementation on steer performance, biomarkers of inflammation and metabolism, and liver abscess formation in response to a mild acidosis challenge. Forty-two steers (417 ± 1.5 kg; $n = 6$/pen) were housed in pens with bunks designed to measure individual DMI and fed one of two diets containing either 0 (CON; $n = 18$) or 90 mg Zn/kg from a Zn-amino acid complex (Zn-AA; $n = 18$; AvailaZn) for 109 days. Six additional steers were fed the CON diet and did not undergo the acidosis challenge (NON; $n = 6$). The acidosis challenge included restricting steers to 50% of the previous 7 d daily DMI on d 47, and on d 48, steers were individually provided 10% of DMI as cracked corn (as-fed) at 0800 h followed by ad libitum feed access 2 h post-grain consumption. Steer was the experimental unit, and two contrasts were constructed: NON vs CON and CON vs Zn-AA. Blood samples were collected on d 40, 49, 53, 69, 80, and 108 and analyzed as repeated measures. Final BW and overall ADG (2.29, 2.30, and 2.31 ± 0.920 kg/d for CON, Zn-AA, and NON, respectively) were not different ($P \geq 0.74$) between treatments. By design, DMI was greater ($P < 0.01$) for NON compared to CON on d 47 but was not different ($P \geq 0.41$) for the remainder of the experiment. While HCW (423, 428, and 424 ± 7.9 kg for CON, Zn-AA, and NON, respectively) and ribeye area were not different ($P \geq 0.53$) due to treatment, marbling score tended ($P = 0.06$) to be greater in CON compared to Zn-AA. The 12th rib backfat thickness was greater ($P = 0.05$) in NON vs CON steers. Liver abscess incidence was not different ($P = 0.12$) across CON (24% abscesses) and Zn-AA (6% abscesses). However, NON had a greater incidence ($P \leq 0.05$; 50% abscesses) compared to CON. Overall blood fibrinogen and leukocyte counts were not different between treatments ($P \geq 0.67$), but neutrophil-to-lymphocyte ratio tended to be greater in NON vs CON ($P = 0.08$). Serum aspartate aminotransferase and gamma-glutamyl transferase concentrations were greater in NON vs CON ($P \leq 0.02$), and serum alkaline phosphatase concentration was lesser in CON vs Zn-AA ($P < 0.01$). Overall, dietary Zn supplementation did not affect cattle performance in response to a mild acidosis challenge.

Key Words: acidosis, liver abscess, zinc
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641 Effect of supplemental sodium butyrate on gastrointestinal tract measurements in sheep.

P. Górka*[1], B. Śliwiński[2], J. Flaga[1], J. Barć[1], J. Olszewski[3], M. M. Godlewski[3], R. Zabielski[3], and Z. M. Kowalski[1], [1]*University of Agriculture in Krakow, Kraków, Poland,* [2]*National Research Institute of Animal Production, Balice, Poland,* [3]*Warsaw University of Life Sciences, Warszawa, Poland.*

The aim of the study was to determine the effect of sodium butyrate supplementation in the diet on reticulo-ruminal, omasal and abomasal digesta and tissue mass and small intestinal tissue mass and length. Eighteen rams (30.8 ± 2.1 kg; 12 to 15 months of age) were allocated to the study and fed diet without (CTRL) or with sodium butyrate (BUT; 3.6 g/kg of offered dry matter). The rams were allocated to the study in four blocks of 6, 4, 4 and 4 rams, within block paired by body weight (BW), and within pair randomly allocated to treatments (9 rams/treatment). Diet consisted of 65% of chopped meadow hay, 19.5% of concentrates and 15.5% of ensiled ground high moisture corn grain (on dry matter basis). Dry matter intake was limited to 2.75% of initial BW. Feed was offered in two equal meals at 0700 and 1500. Sodium butyrate was mixed with concentrates and high moisture corn grain prior to feed allocation. Experimental diets were fed for 2 weeks and rams were killed 3 h after morning feeding. The statistical model included the fixed effect of treatment and the random effect of block and animal within pair. Dry matter intake was not different between treatments (862 and 864 g/d for CTRL and BUT, respectively; $P = 0.82$). Initial BW did not differ between treatments (30.8 and 31.1 kg for CTRL and BUT, respectively; $P = 0.61$) but final BW was greater for BUT compared to CTRL (33.4 vs 32.2 kg; $P = 0.03$). Sodium butyrate supplementation increased butyrate concentration in the digesta of reticulo-rumen (20.7 vs 11.7 mmol/L; $P < 0.01$), abomasum (2.0 vs 1.3 mmol/L; $P = 0.01$) and proximal small intestine (0.68 vs 0.22 mmol/L; $P = 0.05$). Reticulo-ruminal tissue mass tended to be greater for BUT compared to CTRL (21.4 vs 20.4 g/kg of BW; $P = 0.09$). Omasal digesta mass was lower for BUT compared to CTRL (2.2 vs 2.8 g/kg of BW; $P = 0.02$). Reticulo-ruminal digesta mass, abomasal tissue and digesta mass, omasal tissue mass and small intestinal tissue mass and length were not affected by BUT ($P > 0.05$). Supplemental sodium butyrate tended to increase reticulo-ruminal tissue mass and decreased omasal digesta mass but did not affect omasal and abomasal tissue mass, and small intestinal tissue mass and length in sheep (The study was supported by the National Science Centre (Poland) based on decision No. DEC-2013/11/B/NZ9/01938).

Key Words: ruminant, butyrate, lower gastrointestinal tract
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642 Effect of supplemental sodium butyrate on the activity of carbohydrate-digesting enzymes in the reticulo-ruminal digesta and brush border enzymes in sheep.

P. Górka*[1], B. Śliwiński[2], R. Miltko[3], J. Flaga[1], J. Barć[1], M. M. Godlewski[4], R. Zabielski[4], and Z. M. Kowalski[1], [1]*University of Agriculture in Krakow, Kraków, Poland,* [2]*National Research Institute of Animal Production, Balice, Poland,* [3]*The Kielanowski Institute of Animal Physiology and Nutrition Polish Academy of Sciences, Jabłonna, Poland,* [4]*Warsaw University of Life Sciences, Warszawa, Poland.*

The aim of the study was to determine the effects of sodium butyrate supplementation in the diet on activities of carbohydrate-digesting enzymes in the reticulo-ruminal digesta and brush border enzymes in sheep. Eighteen rams (30.8 ± 2.1 kg; 12 to 15 months of age) were allocated to the study and fed a diet without (CTRL) or with sodium butyrate (BUT; 3.6 g/kg of offered dry matter). The rams were allocated to the study in four blocks of 6, 4, 4 and 4 rams, respectivrely, within block paired by body weight (BW), and ram within pair randomly allocated to treatments (9 rams/treatment). Diet consisted of 65% of chopped meadow hay, 19.5% of concentrates and 15.5% of ensiled ground high moisture corn grain (on dry matter basis). Dry matter intake was limited to 2.75% of initial BW. Feed was offered in two equal meals at 0700 and 1500. Sodium butyrate was mixed with the concentrates and high moisture corn grain prior to feed allocation. Experimental diets were fed for 2 weeks and rams were killed 3 h after morning feeding. Reticulo-ruminal digesta was collected and analyzed for amylase, cellulase, xylanase, inulinase and pectinase activities, whereas in the epithelia of the duodenum, proximal, middle and distal jejunum and ileum activity of maltase, aminopeptidase A, aminopeptidase N, and dipeptidylpeptidase IV were determined. The statistical model included the fixed effect of treatment and the random effects of block and animal within pair. Amylase activity in the reticulo-ruminal digesta was greater for BUT compared to CTRL (17.7 vs 14.9 U/g of digesta dry matter; $P = 0.04$) whereas cellulase and xylanase activities were lower for BUT compared to CTRL (8.4 vs 10.5 and 17.3 vs 26.1 U/g of digesta dry matter for cellulase and xylanase activity, respectively; $P \leq 0.02$). Aminopeptidase A and dipeptidylpeptidase IV activities in the distal jejunum were lower for BUT compared to CTRL (30.8 vs 44.6 and 14.5 vs 20.5 U/mg of protein for aminopeptidase A and dipeptidylpeptidase IV activity, respectively). Under the conditions of this study, dietary sodium butyrate increased amylase activity, but decreased cellulase and xylanase activity in the reticulo-ruminal digesta and decreased aminopeptidase A and dipeptidylpeptidase IV activities in the distal jejunum of sheep (The study was co-supported by the National Science Centre (Poland) based on decision No. DEC-2013/11/B/NZ9/01938 and Statutory Research

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Key Words: ruminant, butyrate, digestive enzymes
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643 Effects of feeding functional oils or monensin on rumen morphometrics of Nellore cattle.

A. L. J. Lelis*[1], A. C. Melo[1], M. C. Pereira[2], D. D. Estevam[2], A. F. Toledo[1], M. M. Ferreira[1], A. L. Rigueiro[2], M. M. Squizatti[1], and A. H. Assumpção[1], [1]*São Paulo State University (UNESP), Dracena campus, Dracena, Brazil,* [2]*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 on rumen morphometrics and rumenitis incidence of Nellore cattle fed high-concentrate diets. Eighty-eight 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 design with a 2×2 factorial arrangement of treatments, replicated 6 times. Factors were inclusion (DM basis) or not of functional oils or monensin, at a dose of 500 ppm 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. At harvest, rumenitis incidence was determined on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative rumenitis). Likewise, a 1-cm^2 fragment of each rumen was collect from the 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) functional oils or monensin main effects were observed for rumenitis (with functional oils = 1.41, without functional oils = 1.77; with monensin = 1.73, without monensin = 1.45). Also, no significant ($P > 0.10$) functional oils main effect was observed for MPA in cm^2 (with functional oils = 0.54, without functional oils = 0.55) and ASA in cm^2 (with functional oils = 33.60, without functional oils = 34.70). However, the addition of monensin led to larger ($P < 0.10$) MPA in cm^2 (with monensin = 0.60, without monensin = 0.48) and ASA in cm^2 (with monensin = 37.23, without monensin = 31.06). A significant ($P = 0.03$) interaction between functional oils and monensin was observed for NOP in cm^2 (control = 61.48^{ab}, monensin = 67.61^{a}, functional oils = 69.17^{a}, monensin + functional oils = 58.18^{b}), where the feeding of both additives reduced NOP when compared to the feeding of only monensin or functional oils. Thus, based on these results, the feeding of monensin promoted greater development of rumen epithelium, which could indicate greater short-chain fatty acids absorption.

Key Words: additive, ionophore, papillae
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644 Effect of pineapple cannery by-product on growth performance, blood parameters, carcass characteristics, and longissimus muscle fatty acid and free amino acid composition in growing-finishing Hanwoo steers.

Y. Na*, *Konkuk University, Seoul, Korea, Republic of (South).*

The objective of this experiment was to determine the effect of pineapple (*Ananas comosus L.*) cannery by-product (PCB) level on growth performance, blood parameters, carcass characteristics, and longissimus muscle fatty acid and free amino acid composition of growing-finishing Hanwoo (*Bos taurus coreanae*) steers. Feeding stage was divided into growing, early finishing, and late finishing stage. A total of 60 castrated Hanwoo steers (9.8 ± 0.8 months old, 301.6 ± 32.9 kg initial BW) were used for the experiment. In growing stage, steers were offered the experimental diets which contained 3 level of PCB (0, 6.6, or 13.1% level of PCB, as-fed basis). For the early finishing stage (13.9 ± 0.8 months old, 418.8 ± 36.5 kg initial BW) and the late finishing stage (22.8 ± 0.8 months old, 617.2 ± 49.7 kg initial BW), steers were blocked by initial BW and then randomly allotted into 12 pens (5 head/pen). The pens were randomly assigned to 1 of 3 experimental diets. Each diet contained 0, 10.6, or 21.2% of PCB. Pineapple cannery by-product level had no effects on body weight gain (BWG), average daily gain (ADG), dry matter intake (DMI), or feed conversion ratio (FCR) of growing and late finishing steers. On the other hand, for early finishing stage, BWG, ADG, and FCR of 0% and 10.6% of PCB feeding group were greater than 21.2% feeding group. There were linear and quadratic effects on BWG and ADG of early finishing stage with increasing dietary PCB level. There was linear decrease of FCR with increasing level of PCB. In growing stage, there was a quadratic effects on BUN concentration with increasing dietary PCB level. As PCB level increased, marbling score and quality grade were linearly decreased. For longissimus muscle free amino acid profile, histidine composition was linearly increased with increasing level of PCB.

Key Words: Pineapple by-product, beef steer, free amino acid
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645 Effects of *Saccharomyces boulardii*-based feed additive on performance, hormone level, diarrhea scoring and fecal microbial population in Holstein calves experiencing heat stress.

J. S. Lee*[1,2], N. Kacem[1], W. S. Kim[1,2], D. Q. Peng[1,2], Y. H. Jo[1,2], Y. G. Jung[3], Y. J. Kim[4], and H. G. Lee[1,2], [1]*Department of Animal Science and Technology, Konkuk University, Seoul, Korea, Republic of (South),* [2]*Team of An Educational Program for Specialists in Global Animal Science, Brain Korea 21 Plus Project, Konkuk University, Seoul, Korea, Republic of (South),* [3]*Eaglevet Co. Ltd.,, Seoul, Korea, Republic of (South),* [4]*Department of Food and Biotechnology, Korea University, Sejong, Korea, Republic of (South).*

As the climate changes, heat stress (HS) is becoming an increasing concern for heavily utilized agriculture assets like dairy calves. Dairy calves subjected to HS may benefit from supplementation with probiotics. The objective of this study was to investigate the impact of a *Saccharomyces cerevisiae boulardii* CNCM I-1079 (SB) based feed additive in Holstein calves fed diets with three concentrations of SB during HS. Sixteen Holstein calves (28 ± 2.1 d-old) grouped according to their body weights (46 ± 3.1 kg BW) were randomly divided into 4 groups: Control (milk replacer and starter diet), a low SB diet (1.4×10^9 cfu/L milk replacer), a middle SB diet (2.5×10^9 cfu/L milk replacer) and a high SB diet (5.0×10^9 cfu/L milk replacer) - and housed in a temperature-humidity controlled chamber (four dairy calves per chamber). Dairy calves were subjected to ambient temperature (21°C) for 21 days, after which chamber temperature was raised to 30°C (HS) for 7 days. Temperature-humidity index (THI) values during ambient condition never exceeded 71, whereas THI values during HS peaked at 83 and were above 80 for 10 h/d. Calves were fed twice (0700 h and 1900 h) per day for 28 days. Compared with the control diet during ambient temperature, SB diets reduced diarrhea score and heart rate ($P < 0.05$) but had no effect on growth performance. The low and middle SB diets decreased rectal temperature ($P < 0.05$). The *Enterobacteriace* population in feces was decreased by the low ($P < 0.05$) and high ($P < 0.05$) SB diets. Compared with the control diet during HS, SB diets reduced diarrhea score, rectal temperature and *Enterobacteriace* population in feces ($P < 0.05$), but had no effect on growth performance. In addition, both low and middle SB diets decreased heart rate ($P < 0.05$). The middle SB diet alone suppressed the level of serum cortisol ($P < 0.05$). In conclusion, the HS elicited the increased in rectal temperature, heart rate and diarrhea, but the supplementation of SB ameliorates the health responses of dairy calves experiencing HS.

Key Words: *Saccharomyces boulardii*, heat stress, Holstein dairy calf
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646 Inclusion of fennel herbaceous flavors in total mixed rations increased dry matter intake without affecting health, milk quality and fatty acid composition of lactation cow.

H. F. Wang[1,2], X. D. Wang[1], C. Wang[1], and M. L. He*[1,3], [1]*Zhejiang Agricultural and Forestry University, Hangzhou, China,* [2]*Zhejiang University, Hangzhou, China,* [3]*Lucta (Guangzhou) Flavours Co., Ltd., Guangzhou, China.*

Dietary flavor and taste may affect voluntary intake of lactation cows. The current study was designed to investigate effect of inclusion of flavor additive in total mixed rations (TMR) on dry matter (DM) intake, milk yield and quality, milk fatty acid composition and general health related blood biochemical parameters. Total 45 lactation Holstein cows were assigned to three groups (n = 15 per group) based on lactation yield and body condition. After a transition period the cows were fed with the following diets for 8 weeks: 1) a control TMR (1.45 McalNEl and 151 g CP/kg DM); 2) the control TMR plus 3 g/d/cow mixed Luctarom additives containing fennel herbaceous flavors and sweetener tastes (Luctarom A); 3) the control TMR plus 50 g/d/cow mixed Luctarom additives containing herbalmilk flavors and some other bioactive agents (Luctarom B). Data of milk yield and DM intake and samples of milk were collected weekly. The milk samples were used for milk quality and fatty acids composition analysis. Total lipids were extracted from milk and methylated for determination of fatty acids methyl esters by using a gas chromatography equipped with capillary column. At the end of feeding study blood samples were taken for analyzing general health related parameters. From the study it was found that inclusion of Luctarom A to the TMR increased ($P < 0.05$) average daily DM intake (18.53 kg) compared to the control (17.75 kg) and Luctarom B (17.94 kg) groups. The average daily milk yield was 22.6 kg, 22.0kg and 21.1kg for Luctarom A, Luctarom B and the control groups, respectively. The differences among the treatments were statistically not significant ($P > 0.05$). Inclusion of Luctarom additives did not affect ($P > 0.05$) milk quality and major fatty acid composition with an exception that Luctarom B group had less ($P < 0.05$) milk lactose compared to the control. The general health related blood serum parameters of all experimental groups were in normal ranges for healthy cows. Within the normal ranges both Luctarom additive groups had relatively larger ($P < 0.05$) blood serum triglycerides (TG) compared to the control, whereas Luctarom B group had larger ($P < 0.05$) blood total protein (TP) or albumin compared to the control or Luctarom A, respectively. In conclusion, inclusion of Luctarom containing fennel herbaceous flavors and sweetener tastes to TMR of lactation cows significantly increased DM intake and tended to increase milk

yield without negatively affecting animal health, milk quality and fatty acid composition.

Key Words: Flavor palatability enhancer, Dry matter intake, Lactation cow
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647 Comparison of ruminal protected versus non-protected live yeast on omasal flows, site and extent of digestion in the digestive tract of beef heifers fed high-grain diet.

P. Jiao[1,2], F. Liu[2], S. Ding[1], N. D. Walker[3], and W. 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]*AB Vista, Marlborough, United Kingdom.*

The objective of this study was to determine the effect of adding ruminal protected versus non-protected live yeast (LY) on DM intake, omasal flows, site and extent of feed digestion in the digestive tract of beef heifers. The LY was encapsulated using barley protein (mainly hordein and glutelin) extracted from barley grain. Five rumen cannulated beef heifers (BW = 650 ± 48.8 kg) were used in a 5 × 5 Latin square design. Heifers were fed ad libitum total mixed diet containing 10% barley silage and 90% barley-based concentrate (DM basis). Five treatments were: 1) control (no additives); 2) antibiotics (28 mg monensin + 11 mg tylosin/kg dietary DM); 3) 1.5 g LY/d; 4) 3.5 g encapsulated LY/d (ELY); and 5) combination of treatments #3 and 4 (MLY). The encapsulated LY consisted of 1.5 g LY and 2 g capsule. Number of yeast colonies was 1.71×10^{10} cfu/g. Digesta and rumen microbes were labeled with Yb and ^{15}N, respectively. Data were analysed using the MIXED procedure of SAS with model including fixed effect of treatment and random effects of heifer and period. Intake of DM (averaged 11.8 kg/d) was not affected by treatment. No treatment effects on flows (kg/d) of OM (5.4) and starch (0.75) to the omasum were observed, whereas flows of NDF were greater ($P < 0.02$) with antibiotics (1.9) than ELY (1.7). Ruminal digestibility of OM tended ($P < 0.09$) to be less with ELY (62.4%) or MLY (62.9) than control (66.4%) or antibiotics (68.1%), but no differences in ruminal digestibility of NDF (averaged 44.1%) and starch (averaged 83.0%) were observed among treatments. In contrast, greater ($P < 0.03$) postruminal digestibility (% of intake) of OM (30.9 vs 22.9%) and NDF (17.9 vs 7.9%) was observed with ELY and MLY than control and antibiotic groups. As a result, digestibility of OM (81.1 vs 77.0%) and NDF (64.1 vs 49.9%) in the total digestive tract was greater ($P < 0.01$) with ELY or MLY than control. No treatment effect was observed on the flows of N to omasum (averaged 292 g/d) and microbial protein synthesis (averaged 147 g/d). Digestibility of N in the total digestive tract was greater ($P < 0.02$) with ELY or MLY than control (79.2 vs 75.4%). These results indicate the potential postruminal activity of LY, and benefits to feeding protected LY on improving intestinal digestibility of nutrients in beef heifers fed high-grain diet.

Key Words: Beef heifer, digestibility, rumen protected live yeast
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648 Validation of micro-encapsulation method to protect probiotics and feed enzyme from rumen degradation.

Y. Shen*[1,2], P. Jiao[1,3], H. Wang[2], L. Chen[4], N. D. Walker[5], and W. Yang[1], [1]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*College of Animal Science and Technology, Yangzhou University, Yangzhou, China,* [3]*Northwest Agriculture and Forestry University, Yangling, China,* [4]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [5]*AB Vista, Marlborough, United Kingdom.*

We hypothesize that supplementation of live yeast or feed enzyme (FE) may improve intestinal digestion and gut health, but with ruminants, the challenge is to deliver additive with high activity post-ruminally due to the highly proteolytic environment of the rumen. The objective of this study was to develop a micro-encapsulation method by measuring ruminal stability of encapsulated yeast and FE, and its release in the intestine. Live yeast and liquid FE were encapsulated using barley protein hordein and glutelin as capsule material. The barley protein powders were hydrated at pH 11.0 to form a 15% (w/v) solution. The pH was then adjusted to 7.0 followed by an immediate mixing with yeast or FE to form a coarse emulsion using a homogenizer. Microcapsules were then formed by passing the premixed emulsion through a microfluidizer system. The mixtures were spray-dried using a laboratory scale spray dryer. The ratio of capsule to additive was 1:1. The stability of encapsulated products in the rumen was measured as DM disappearance (DMD) in batch culture. Briefly, the encapsulated products (100 mg) were weighed into Ankom bags and placed in 100-mL serum bottles. Rumen inoculant (15 mL) from beef heifer and buffer solution (45 mL) was added to each bottle and incubated at 39°C for 0, 3, 6, 12 or 24 h. The residues in bags were digested in 1% pancreatin solution for 1 h to remove the encapsulation protection. Number of yeast colonies (cfu/g) was enumerated by spread plate method. Enzyme activity (EC 3.2.1.1) was assayed and expressed as μmol glucose equivalents/min/g FE. The DMD of encapsulated yeast were 3.1, 7.8, 9.1, 12.0 or 16.0%, and the cfu were 9.5, 2.2, 1.3, 1.1 and 0.6 ($\times 10^9$), respectively, for residues after 0, 3, 6, 12, and 24 h of incubation. The DMD of encapsulated FE were 5.1, 31.4, 33.8, 40.6 or 43.6%, and the enzyme activity in residue were 41.9, 33.8, 19.7, 12.7 and 10.2 μmol/min/g, respectively, at 0, 3, 6, 12 and 24 h of incubation. The results showed that the encapsulated yeast products were stable in the rumen. Subsequently,

the encapsulated yeast was released by digesting in pancreatin solution and cfu counts demonstrated over 90% survival rates. It suggests that this encapsulation technique is applicable as a novel method for delivering active yeast to the intestine. However, this technique may be not efficacy to protect liquid enzyme from rumen degradation.

Key Words: live yeast, feed enzyme, encapsulation technique
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649 Nellore metabolism receiving exogenous amylase in high-concentrate diets.

C. F. Nascimento*[1,2], L. L. Oliveira[3], N. C. D. Silva[1], F. D. Santos[3], V. B. Holder[4], J. E. Pettigrew[5], G. R. Siqueira[1,6], and F. D. D. Resende[1,6], [1]*UNESP - Univ Estadual Paulista, Jaboticabal, Brazil,* [2]*FAPESP (grant #2015/07046-1 and grant #2016/08867-1), São Paulo, Brazil,* [3]*UNIFEB, Barretos, Brazil,* [4]*Alltech Inc, Nicholasville, KY,* [5]*University of Illinois at Urbana-Champaign, Urbana, IL,* [6]*APTA - Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil.*

The objective of this study was to evaluate the effects of supplementation with exogenous enzyme of *Aspergillus oryzae* (primarily alpha amylase) in high-concentrate feedlot diets on blood and ruminal parameters of Nellore cattle. Ten Nellore bulls with rumen fistulae, initial body weight between 350 to 400 kg and age of 24 months were housed in individual pens. The experimental design was *crossover*, in which the animals were randomized between treatments 1: Control - absence of amylase and 2: Amylase -*Aspergillus oryzae* extract containing alpha amylase activity (Amaize®, Alltech, Inc.), 5 g/animal daily. There was an initial adjustment period (25 days) and a data-collection period (25 days); after, there was rest period (25 days), then the treatments were reversed and the adjustment and collection periods repeated. The diet was composed of: sugar cane bagasse (12% DM), corn (62% DM), citrus pulp (17% DM), soybean meal (4.7% DM), Optigen®, a controlled-relaease urea (1.1% DM) and mineral salt (3.2% DM). The parameters evaluated were plasma concentrations of insulin, glucose, and beta-hydroxybutyrate plus molar proportions of volatile fatty acids (VFA), pH and ammonia concentration in rumen fluid. The data were analyzed using the MIXED procedure of SAS (9.0), considering the effects of treatment, time and random animals, with $P < 0.10$ declared significant. As shown in Table 649, plasma insulin concentrations were reduced in animals receiving Amylase (16.9 vs 27.8 μIU/mL; $P = 0.06$), as well as acetate and acetate:propionate to the same animals, while the propionate was higher in animals receiving Amylase (18.8 vs 20.4 molar proportion; $P = 0.03$). In conclusion, exogenous amylase can reduce insulin levels in the animals' blood and also cause effect on ruminal parameters. Acknowledgments: Alltech and FAPESP.

Table 649. Blood and ruminal parameters of Nellore cattle receiving exogenous amylase in high-concentrate feedlot diets.

	Treatments			
Item	Control	Amylase	SEM	*P*-value
Blood plasma				
Glucose, mg/dL	74.1	76.8	6.60	0.48
Insulin, μIU / mL	27.8	16.9	4.05	0.06
Beta-hydroxybutyrate, mmol/L	0.276	0.277	0.026	0.97
Ruminal fluids				
Total VFA , m*M***	115	115	4.87	0.99
Acetate, mM/100 mM	60.6	59.5	0.64	0.06
Propionate, mM/100 mM	18.8	20.5	1.43	0.03
Butyrate, mM/100 mM	9.32	8.65	0.36	0.12
Acetate:propionate	3.33	3.12	0.27	0.09
pH	6.53	6.57	0.07	0.45
Ammonia, mg/dL	14.8	15.8	1.30	0.48

* $P < 0.10$ declared significant.

**Isobutyrate, isovalerate, and valerate are not shown but were included in the calculation of total VFA.

Key Words: insulin, rumen fluid, Aspergillus oryzae
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650 High dosage of live yeast for transition dairy cows: Nutrition and health benefits.

C. Julien*[1], L. Desmaris[2], P. Dubois[2], M. Vagneur[3], J. P. Marden[1], and L. Alves de Oliveira[4], [1]*Phileo Lesaffre Animal Care, Marcq-en-Baroeul, France,* [2]*Service Promotion Elevage Laitier (Rhône Conseil Elevage) 18, avenue des Monts d'Or 69890, La Tour de Salvagny, France,* [3]*10 rue de Boyse 39300, Champagnole, France,* [4]*Vetagro-sup Campus Vétérinaire de Lyon 69280, Marcy-l'Etoile, France.*

Two groups of 23 cows from a French commercial dairy farm (Control and Yeast) were constituted. Yeast cows received 10 g/d of live yeast (Saccharomyces cerevisiae Sc47 CNCM I-4407, Phileo Lesaffre Animal Care, France) during close-up phase and 20 g/d/cow for 21 d postpartum. Individual milk yield was recorded daily whereas fat and protein contents were evaluated monthly. Blood BHB content was evaluated +8 and +22 d after calving (Free Style Optium, Abbott). Body condition score (BCS) was evaluated -22, +8 and +22 days. Ruminal filling (RFS) was also evaluated on the basis of a scoring scale (1 to 5). Means comparison was done by student or Chi² test with significant difference reported for $P \leq 0.05$ and trend discussed for $0.05 < P \leq 0.15$. Cows calved on 2016/01/21 with an averaged lactation rank of 2.11 ($P > 0.9$). Milk yield over the first 3 months of lactation was numerically higher for Yeast cows (34.6 ± 7.8 kg/d) than for Control (32.6 ± 10.2 kg/d). Milk fat and protein contents were not affected by treatment (Fat = 42.5 g/kg and Protein = 30.8 g/kg on average, $P > 0.9$). Blood BHB content at +22 days was significantly lower ($P = 0.024$) for Yeast cows: 0.79 mmol/L vs 1.41 mmol/L, showing clearly less subacute ketosis cases. RFS and BCS at +8d were significantly higher ($P < 0.01$) for Yeast cows than control: 2.81 vs 2.10 and 2.94 vs 2.42, respectively. A total of 18 cows per group was returned to breeding (the others were culled) with a success rate at first insemination of 27.8% and 50.0% ($P = 0.13$) at 120 days of lactation whatever is the group ($P > 0.8$). High dosage of Live Yeast in peri-parturient dairy cows goes beyond the nutritional impact. In addition to improve animal performance, less lipid mobilization and better BSC in the first week of lactation led to better health and reproductive performances.

Key Words: ketosis, transition cows, live yeast
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651 Effects of monensin or narasin on rumen metabolism of steers during the period of adaptation to high-concentrate diets.

D. M. Polizel[*1], M. F. Westphalen[2], A. A. Miszura[1], M. V. C. Ferraz Junior[1,2], A. V. Bertoloni[1], G. B. Oliveira[1], L. G. M. Gobato[1], J. P. R. Barroso[1], and A. V. Pires[1,2], [1]*FMVZ/University of São Paulo, Pirassununga, Brazil,* [2]*ESALQ/University of São Paulo, Piracicaba, Brazil.*

Narasin is a coccidiostatic and antibacterial agent and may change rumen fermentation. The objective in this trial was to determine the effects of monensin or narasin on rumen metabolism of steers during the period of adaptation after abrupt transition from high-forage to high-concentrate diet. Eight Nellore steers (BW 475.7 ± 3.7 kg), cannulated in the rumen, were used in a replicated 4x4 Latin Square design. The trial lasted 96 days, divided in 4 periods of 24 days each. Steers were fed daily with coastcross haylage during the first 8 d of each period. From day 9 to 24, steers were fed with the experimental diets, which were composed by 90% of concentrate. The experimental diets were: C (Control: no additives added), Mon (25 mg of monensin/kg of DM), N10 (10 mg of narasin/kg of DM) and N20 (20 mg of narasin/kg of DM). The rumen fluid was collected every four hours (starting prior feeding, 4, 8 and 12 hours after feeding), from days 8 to 14 of each period. Short chain fatty acid (SCFA) and rumen pH were analyzed as repeated measures over time using MIXED procedure. The effect of the experimental diets was evaluated using the Tukey test. There was no effect of experimental diets for acetate (59.86 ± 0.86 mM/100 mM, P = 0.20), propionate (22.15 ± 0.77 mM/100 mM, P = 0.14), butyrate (13.14 ± 0.67 mM/100 mM, P = 0.38), isovalerate (2.43 ± 0.16 mM/100 mM, P = 0.36) and acetate-to-propionate ratio (2.77 ± 0.12, P = 0.19). However, steers fed Mon had a greater molar proportion of isobutyrate (C: 1.03^{b}; Mon: 1.11^{a}; N10: 1.01^{b}; N20: 1.07^{ab} ± 0.05 mM/100 mM, P = 0.03) than C and N10. The Mon and N10 experimental diets decreased molar proportion of valerate (C: 1.18^{a}; Mon: 1.01^{b}; N10: 1.05^{b}; N20: 1.11^{ab} ± 0.06 mM/100 mM, P = 0.02). Diet containing monensin decreased total SCFA (C: 143.9^{a}; Mon: 132.6^{b}; N10: 145.8^{a}; N20: 140.4^{ab} ± 6.70 mM/L, P = 0.03) than C and N10. Steers submitted to Mon and N20 diets had a greater ruminal pH than steers fed C and N10 diets (C: 6.18^{b}; Mon 6.36^{a}; N10: 6.18^{b}; N20: 6.30^{a} ± 0.12, P = 0.01). The inclusion of 20 mg of narasin or 25 mg of monensin/kg of DM had a promising effect by increasing the ruminal pH during adaptation to high-concentrate diets.

Key Words: ruminal pH, short chain fatty acids, ionophore
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652 The supplementation with a flavonoid extract from *Citrus aurantium* reduces concentrate intake and improves rumen health parameters in Holstein bulls fed high-concentrate diets when fed in a single-space feeder.

M. Paniagua[*1], J. F. Crespo[2], A. Bach[3,4], and M. Devant[5], [1]*Quimidroga, Barcelona, Spain,* [2]*Interquim SA, Barcelona, Spain,* [3]*IRTA-Department of Ruminant Production, Caldes de Montbui; Balcelon, Spain,* [4]*ICREA, Barcelona, Spain,* [5]*IRTA - Department of Ruminant Production, Caldes De Montbui, Barcelona, Spain.*

This study evaluated the effects of a flavonoid extract from *Citrus aurantium* (Bioflavex® CA, 24% naringin) on eating pattern, performance, carcass quality, and rumen wall health of Holstein bulls fed with a single feeder. Ninety-nine bulls (195.2 ± 0.64 kg BW and 149 ± 0.22 d of age) were randomly allocated to one of 6 pens and assigned to control (C) or Bioflavex® CA (BF, 0.4 kg of Bioflavex® CA per ton of concentrate), study was repeated twice. Each pen had one drinker, one separate straw feeder, and one single-space feeder with lateral protections where concentrate (45% corn, 21% corn gluten feed, 11% barley, 11% wheat, 14% CP, 3.32 Mcal of ME/kg; DM basis) was offered. Concentrate intake was recorded daily and BW every 14 d. Animals were slaughtered after 168 d of study (12 periods of 14 d), HCW and carcass quality were recorded, and rumen wall was examined. Data were analyzed using a mixed-effects model with repeated measures and categorical data with a Chi-Square. Concentrate intake was greater ($P < 0.05$) in C (6.85 ± 0.065 kg/d) than in BF (6.65 ± 0.065 kg/d) bulls; however, ADG (1.64 ± 0.032 kg/d), and concentrate efficiency (0.24 ± 0.022 kg/kg) were not affected by treatments. Final BW tended to be greater ($P = 0.06$) in C (489.7 ± 3.98 kg) than in BF (479.3 ± 3.98 kg) bulls, but this tendency was not detected for carcass weight (256.1 ± 2.31 kg). No differences between treatments in mean eating pattern parameters were observed; this may be attributed to the great animal variability. During finishing phase (periods 9 to 12), the percentage of meal size data above 750 g was greater ($P < 0.05$) in C (57.3%) compared with BF bulls (49.3%). Thus, BF reduced large meal sizes and the number of feeder visits numerically increased (in BF meal size explained 74% of the feeder visit variation, $P < 0.01$). Color of rumen wall tended

($P = 0.06$) to be lighter for BF bulls (1.27% were "5", scale from "1" to "5", with "5" being the darkest) compared with C (9.76% were "5"). In the rumen, baldness areas were lesser ($P < 0.01$) in BF (48.1%) than in C (67.1%). In conclusion, bulls fed with a single-space feeder supplemented with Bioflavex® CA have a reduced feed intake and large meal sizes, these results may be related with an improvement in rumen health.

Key Words: eating pattern, beef, flavonoids
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653 Feeding red osier dogwood (*Cornus sericea*) affected feed intake and digestion in the digestive tract of beef heifers fed high-grain diet.

L. Wei[1,2], W. M. S. Gomaa[2,3], T. W. Alexander[2], R. Bazylo[4], R. Scales[5], and W. Yang[*2], [1]*Key Laboratory for Green Chemical Process of Ministry of Education, Wuhan Institute of Technology, WuHan, China,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*Department of Animal Nutrition and Clinical Nutrition, Faculty of Veterinary Medicine, Assiut University, Assiut, Egypt,* [4]*Manitoba Agriculture, Food and Rural Development, Winnipeg, MB, Canada,* [5]*Red Dog Enterprises Ltd, Winnipeg, MB, Canada.*

Red osier dogwood (ROD; *Cornus sericea*) is an abundant native shrub plant across Canada and it is rich in bioactive compounds with total phenolic concentration varying between 40 to 220 mg/g depending on the season. The phenolics include anthocyanins, gallic acid, ellagic acid, quercetin, and cyanin have both antioxidant and antimicrobial properties. Studies demonstrated that feeding ROD may reduce the use of antibiotics in livestock animals. It is hypothesized a greater feed value than barley silage in beef cattle diet. The objective was to determine the effect of increasing substitution of ROD for barley silage in high-grain diet on ruminal pH and fermentation, feed digestion in the total digestive tract in beef heifers. Five rumen cannulated Angus heifers (BW = 660 ± 40.8 kg) were used in a 5 × 5 Latin square design. Treatments were control diet containing 15% barley silage and 85% barley concentrate (DM basis), diet that substituted with 3%, 7% or 15% of ROD for equal barley silage, or diet supplemented with monensin (28 mg/kg diet DM). Ruminal pH was monitored continuously for 4 days using wireless pH probe of each period. Fermentation characteristics were measured for two consecutive days at 1, 3, 5, and 7 h of each day after the morning feeding. Apparent digestibility was determined using Cr_2O_3 as external marker by sampling feces from the rectum. Data were analysed using the MIXED procedure of SAS with model including fixed effect of diets and random effects of heifer and period. Intake of DM quadratically ($P < 0.02$) increased with increasing the replacement of silage by ROD from 0, 3, 7, to 10% (11.5, 12.1, 12.4, and 11.8 kg/d). Mean ruminal pH ranged from 5.95 to 6.14 and were not affected by diets, and no effects of diets on total VFA concentration (averaged 138 mM) were observed. However, ruminal NH_3-N concentration linearly ($P < 0.01$) decreased with increasing ROD (10.7, 9.0, 9.8, and 8.0 m*M*). Digestibility of DM quadratically ($P < 0.01$) increased with increasing ROD from 0, 3, 7 to 10% (72.9, 74.8, 77.2, and 75.0%). Furthermore, feeding ROD vs monensin increased DM intake (12.1 vs 11.2 kg/d; $P < 0.01$), DM digestibility (75.8 vs 72.1%; $P < 0.01$), and VFA concentration (141 vs 130 mM; $P < 0.05$). These results indicate greater feed value of ROD vs barley silage or monensin but it was dose-dependant. It suggests that ROD could be fed potentially as an alternative to silage or monensin in beef cattle.

Key Words: Beef heifer, red osier dogwood, digestibility
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654 Effect of fibrolytic enzyme and different supplementation strategies on performance and carcass characteristics of Nellore bulls in the finishing phase in pasture.

R. L. Miorin[*1], F. D. A. Nascimento[1], L. F. Gomes[2], L. F. Prados[3,4], F. D. D. Resende[1,5], G. R. Siqueira[1,5], V. B. Holder[6], and J. E. Pettigrew[7], [1]*UNESP - Univ Estadual Paulista, Jaboticabal, Brazil,* [2]*UNIFEB, Barretos, Brazil,* [3]*APTA, Colina, Brazil,* [4]*Federal University of Viçosa, Viçosa, Brazil,* [5]*APTA - Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil,* [6]*Alltech Inc, Nicholasville, KY,* [7]*University of Illinois, Urbana.*

The objective of this study was to measure performance and carcass characteristics of grazing Nellore bulls fed with fibrolytic enzyme (Fibrozyme®-Alltech) or not within two different supplementation strategies during the finishing phase in the dry season at low latitude. Twenty-eight Nellore bulls (24 mo; BW = 442 ± 16 kg) were used in a randomized complete block design with treatments in a 2 × 2 factorial arrangement of two supplementation strategies (constant or increasing levels) and presence (1.5g/100 kg BW) or absence of the fibrolytic enzyme product. The supplement was provided at the level of 10 g/kg BW supplement/d throughout the experiment (constant), or at 4, 8, 12 and 16 g supplement/kg BW during successive 35-d periods, with a total average of 10 g/kg BW. The increasing supplementation may compensate for the reduction in pasture quality and quantity as the dry season progressed. The pasture was composed of *Brachiaria brizantha* cv. Marandu (7 ha), divided into 7 paddocks (each one with 1 ha). Electronic individual feeding troughs (Intergado®) allowed all treatments to be represented in each paddock. The supplements were provided daily and the supplement intake (SI) was measured daily. Three reference animals were slaughtered initially to estimate the hot carcass weight (HCW). The remaining animals were slaughtered in a commercial abattoir after 140 d. The supplement efficiency (SE; g carcass gain/g supplement consumed) was calculated. All data were analyzed using the MIXED procedure of SAS (alpha = 0.10) with paddock considered random and animal as the experimental unit. There was no interaction ($P > 0.10$) between factors for BW, HCW, dressing percentage (DP), ADG, and SE. Final BW and ADG were not affected by supplementation strategy or fibrolytic enzyme. Feeding fibrolytic enzyme increased HCW (332 vs 324 kg, $P = 0.098$), and dressing percentage (58.4% vs 57.4%; $P = 0.078$) and SE (0.134 vs 0.123; $P = 0.066$). There was an interaction ($P < 0.10$) between supplementation strategy and enzyme for SI; the SI was lower with increasing supplement and enzyme (9.58 g/kg BW; $P = 0.045$) compared to the other treatments (mean = 9.92 g/kg BW). In conclusion, under the conditions of this study, providing the same amount of supplement with different strategies during the finishing phase in pasture does not alter animal performance. The inclusion of fibrolytic enzyme increased HCW, DP and SE.

Key Words: carcass weight, fibrolytic enzyme, supplementation
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655 Effect of carbohydrate additives on fermentation characteristics, chemical composition and ruminal degradability of Napier grass (*Pennisetum purpureum*) silage.

M. D. Rambau*, F. Fushai, and J. J. Baloyi, *University of Venda, Thohoyandou, South Africa.*

The objective of the study was to determine the effect of carbohydrate additives on the fermentation characteristics, chemical composition and ruminal degradability of Napier grass silage. Napier grass planted at the School of Agriculture Experimental Farm, University of Venda in 5 x 4 meter plots was irrigated once every week for a period of 12 weeks. After 12 weeks, the Napier freshly cut grass was ensiled with no additive, molasses, maize meal and brown sugar at 10% fresh weight in a completely randomized design replicated 6 times for 90 d in 1 liter glass jars. After 90 d, silages were determined for fermentation quality and nutritive composition using standard protocols. The DM and CP ruminal degradability was determined in sacco by incubating silage samples in nylon bags (external dimension: 6 × 12 cm, pore size of 46 µm) in the rumen in three Bonsmara steers fitted with rumen cannula for 0, 6, 12, 24, 48, 72, 96 and 120 hours. Parameters to describe the dynamics of ruminal degradability of DM and CP were obtained by fitting the data on the exponential equation $p = a + b (1 - e^{-ct})$ using NEWAY computer program, where "*a*" is the rapid degradable fraction, "*b*" is the slow degradable fraction, "*a + b*" is the potential degradability and "*c*" is the outflow rate. Collected data were subjected to analysis of variance using general linear model procedures of Minitab Statistical package version 17. Molasses treatment had higher ($P < 0.05$) residual water soluble carbohydrates, ash and DM content and lower ($P < 0.05$) ammonium nitrogen and neutral detergent fibre content of silage. In addition, maize meal silage had higher ($P < 0.05$) fat content and lower ($P < 0.01$) acid detergent fibre. However, additives increased ($P < 0.05$) DM disappearance for all incubation hours, and CP disappearance for 48 and 120 incubation hours. As a result, increased ($P < 0.01$) "*a*", "*b*" and "*a + b*" fractions, and effective degradability at 2, 5 and 8% outflow rate for DM and also "*a + b"* ($P < 0.05$) for CP were observed. Therefore, our results suggest that additives were effective in improving the quality of Napier grass silage leading to improved ruminal degradability, with molasses treatment yielding the best silage quality.

Key Words: Napier grass silage, Nutrient composition, Ruminal kinetics
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656 Effects of two sources of malate on milk performance and feed efficiency of dairy cows.

I. Guasch[1], G. Elcoso[1], M. Puyalto*[2], and A. Bach[3], [1]*Blanca, Lleida, Spain,* [2]*NOREL S.A., Madrid, Spain,* [3]*IRTA-Department of Ruminant Production, Caldes de Montbui; Balcelon, Spain.*

The aim of the study was to evaluate the efficacy of malic acid and sodium and calcium salts of malic acid (Rumalato®, Norel, Spain) on milk yield and feed efficiency of dairy cows. A total of 60 cows (176 ± 70.3 DIM, 32.3 ± 5.45 kg/d; 33 multiparous; 27 primiparous) were split in three groups ($n = 20$) and exposed for 63 d to 3 treatments following a randomized complete block design. Treatments consisted of no supplementation (CTRL), 40 g/d of Rumalato® (RUM), and 25 g/d of malic acid (MAL). The daily amount of malic acid provided by RUM and MAL was the same (25 g/d). Cows were fed a TMR (15.3% CP, 31.8% NDF, 1.63 Mcal of NEl/kg; DM basis). On a daily basis, feed intake, milk yield, and milk fat and protein contents were determined individually. Because treatments were applied at the animal level, the experimental unit will was the animal. Data were summarized by week of study and analyzed using a mixed-effects model for repeated measures. Overall, average feed intake (22.9, 24.1, and 22.7 ± 0.76 kg/d), milk yield (30.4, 32.5, and 31.1 ± 1.20 kg/d), milk fat content (5.04, 3.88, and 4.01 ± 0.08%), milk protein content (3.13, 3.10, 3.14 ± 0.02%), and feed efficiency (1.40, 1.42, and 1.46 ± 0.84 kg/kg) did not differ among CTR, RUM, and MAL cows, respectively. However, there was an interaction ($P < 0.05$) among treatment, week and parity on milk yield, with multiparous cows on RUM producing more milk than multiparous cows on CTRL and MAL after the 2 wk of study, and MAL multiparous cows producing more milk than CTRL multiparous cows between week 2 and 6 of study. But there were no differences among treatments in milk yield in primiparous cows. As a result, feed efficiency (kg of milk/kg of dry matter intake) was also affected by treatment, and multiparous cows on RUM had greater ($P < 0.05$) feed efficiency during the second and third week of the study than CTRL

multiparous cows. It is concluded that sodium and calcium salts of malic acid have the potential to improve milk yield and feed efficiency of multiparous cows in mid lactation.

Key Words: efficiency, fermentation, lactation
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657 Effects of adding live yeast or yeast derivative on dry matter disappearance of high-forage diet in batch culture.

P. Jiao[1,2], F. Liu[1], Z. He[2], S. Ding[2], N. D. Walker[3], and W. Yang*[2], [1]*Northwest Agriculture and Forestry University, Yangling, China,* [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [3]*AB Vista, 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), fermentation characteristics and microbial profiles in batch culture. The study was a 2 × 7 factorial arrangement including low (5.8) and high media pH (6.5); treatments were: control (no additives), three LY (LY1, LY2, LY3, 8×10^6 cfu/bottle for each LY), two YD (YD4, YD5, 30 mg/bottle for each YD), and monensin (positive control; 0.17 mg monensin/bottle). Substrate was a high-forage diet containing 60% barley silage and 40% concentrate (DM basis). Inoculum was obtained from two 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 three 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 level and their interactions, and the random effect of day. There was no interaction of yeast products with media pH on DMD. Increased media pH from 5.8 to 6.5 improved ($P < 0.01$) DMD (averaged 47 vs 54%). Supplementation of LY1 (48.2%) or YD5 (47.8%) had greater ($P < 0.05$) DMD than control (45.6%) or monensin (46.1%) at pH 5.8; and at pH 6.5, the DMD was greater ($P < 0.05$) with all 5 yeasts (averaged 54.8%) than control (52.8%) or monensin (52.7%). An interaction between pH and treatment was noticed ($P < 0.02$) for total VFA concentration (m*M*) which was greater ($P < 0.05$) with LY1, LY3, YD4 and YD5 (averaged 62.5) than control (57.0) and monensin (57.8) at pH 5.8. Ratio of acetate to propionate was less with monensin at either pH 5.8 (1.89) or pH 6.5 (2.22), whereas no differences were found between yeast and control. Overall, microbial profiles that were measured based on copy number of 16s rRNA gene ($\log_{10}$) were not affected by yeast supplementation except that the copy number of *Fibrobacter succinogenes* was less ($P < 0.01$) with monensin (7.16) than yeasts (7.95). These results suggest that in vitro DMD of high-forage diet varied with source of yeast and media pH. The improved DMD at pH 5.8 with LY1 and YD5 and at pH 6.5 with all five yeast products would be beneficial to high-forage fed cattle.

Key Words: batch culture, high-forage diet, yeast cultures
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658 Effect of feeding isoquinoline alkaloids on performance and carcass characteristics of finishing bulls fed a high-energy diet.

M. Neumann*[1], A. Michels[1], A. M. Reck[1], B. Beyer[2], H. Godoi Bertagnon[1], G. F. Mattos Leão[3], E. J. Askel[1], I. Goldoni[1], and L. da Costa[1], [1]*Universidade Estadual do Centro-Oeste - UNICENTRO, Guarapuava, Brazil,* [2]*Phytobiotics Futterzusatzstoffe GmbH, Eltville, Germany,* [3]*Universidade Federal do Paraná, Curitiba, Brazil.*

Feedlot diets have been associated with metabolic and digestive disorders. In-feed antibiotics, have been proposed to minimize the negative effects associated with feeding high grain diets to improve animal productivity. However, the need for reducing the use of antibiotics in food animal production systems has led to the development of alternative strategies aimed to improve animal health and performance. The objectives of this study were to assess the effects of an isoquinoline alkaloid (IQs) containing supplementation product on productive performance, apparent dry matter digestibility (ADMD), and carcass traits in feedlot yearling bulls fed a high-grain diet. Thirty-two Angus x Nelore bulls (11 ± 3 months, 365 ± 10 kg) were enrolled in the present study. Animals were randomly allocated to 2 treatment groups in 8 replicates: (1) no additive supplementation (CON, n = 16), and (2) supplementation with 4 g/head/d of an IQs containing product (Sangrovit® RS, Phytobiotics Futterzusatzstoffe GmbH, Eltville, Germany; SAN, n = 16) top-dressed at the time of feed delivery. During the study period, all animals were fed the same high concentrate diet containing a mixture of 85% whole corn grain and 15% protein-vitamin-mineral mix twice a day as a total mixed ration. Animals received the experimental diets for a period of 119 d with an initial adaptation period of 14 d. Dry matter intake (DMI) was estimated daily by subtracting the refusals to the amount of feed delivered. Performance parameters (body weight [BW], feed efficiency [FE], average daily gain [ADG] DMI, and ADMD) were evaluated during the adaptation period, and every 21 d intervals for 5 periods. Individual carcass measurements (e.g. weight, gain, yield) were recorded at slaughter. Results indicated that DMI, BW, FE, ADG and carcass weight were not affected ($P \geq 0.05$) by treatment. However, animals in the SAN group showed improved ($P < 0.05$) ADMD (SAN = 86.96%; CON = 81.49%), were more efficient in converting DM to carcass (SAN = 8.05 kg of DM/

kg carcass; CON = 8.68 kg of DM/kg carcass) and had higher ($P < 0.05$) carcass yields (SAN = 56.6%; CON = 55.4%) when compared to animals in the CON group. In conclusion, results from this study suggest that feeding IQs can be beneficial in favor of feed efficiency and carcass yield in finishing yearling bulls fed high grain diets.

Key Words: isoquinoline alkaloids, apparent dry matter digestibility, carcass yield
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659 The influence of microencapsulated secondary plant compounds on receiving beef cattle performance.

A. Budde*[1], S. Jalali[1], J. J. Wagner[1], O. Guimaraes[1], R. S. Goodall[2], and T. E. Engle[1], [1]*Colorado State University, Fort Collins,* [2]*EW Nutrition, Des Moines, IA.*

Six-hundred and fifty six newly weaned cross-bred steers (initial BW 254.4 ± 7.9 kg) were utilized to investigate the effects of microencapsulated secondary plant compounds (MSPC) on receiving performance of feedlot steers. We hypothesized that feeding MPSC would improve feedlot performance during the receiving phase of production as compared to monensin and tylosin. The experimental design was a randomized complete block design. Steers were blocked by weight within cattle source and randomly assigned within block by cattle source to one of 4 treatments (n = 8 pens/treatment; experimental unit = pen). Treatments consisted of: 1) Control (monensin: 32.8 g/metric ton DM + tylosin: 7.8 g/metric ton DM); 2) monensin only (32.8 g/metric ton DM); 3) MSPC only (148 g/metric ton DM); and 4) MSPC (148 g/metric ton DM) plus monensin (32.8 g/metric ton DM). Steers received a sorghum silage steam-flaked corn based growing diet (14.0% CP; 1.15 Mcal/kg NEg) over the 56 d receiving period. Steers were individually weighed on d -1, 0, 28, and 56 of the receiving phase. Initial and final body weights were similar across treatments. Day 0-28, 29-56, and d 0-56 ADG, DMI, and feed efficiency were similar across treatments. Morbidity and mortality rates were also similar across treatments. These data indicate, that under the conditions of this experiment, the addition of monensin and tylosin, monensin alone, MSPC alone, or MSPC plus monensin to beef cattle diets resulted in similar beef cattle performance over a 56 d receiving period.

Key Words: beef cattle, performance, receiving phase
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SMALL RUMINANT

661 Comparison of high-resolution aerial photography with manual field collection in assessing the control of red cedar using goats.

R. V. Lourencon*[1], S. P. Hart[1], T. A. Gipson[1], and M. White[2], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Department of Agriculture and Natural Resources, Langston University, Langston, OK.*

In a research study using goats to control red cedar (*Juniperus virgiana*), it was necessary to catalog trees in the study area by global positioning system (GPS) coordinates and basal diameter in order to monitor their control by goats. The purpose of this study was to compare the accuracy of high-resolution aerial photography with manual field GPS collection. A X8-M multicopter drone with a 12-megapixel Canon camera was used to take high-resolution aerial pictures (2 cm/pixel). The images were taken in the winter when red cedar is usually the only green plant in the field. An onboard GPS unit facilitated assembly of individual pictures into an orthomosaic using Pix4Dmapper software. The orthomosaic and the manual field GPS data were brought into ArcMap as layers, and tree diameter was calculated as shapefiles on the orthomosaic layer of the selected tree GPS data points. For field measurements, a Trimble GEO 7X was used to determine tree GPS coordinates and the radius was measured and doubled for diameter. The difference (DIFF) between the diameter measured by the GPS field data and that diameter calculated based on the orthomosaic, the distance (DIST) between the GPS coordinate in the field and the centroid of the shapefile, and the compass point position (BEAR) of the shapefile centroid relative to the GPS point were calculated. Regression analysis was used to determine linear relationships between DIFF, DIST, and BEAR using R (R Core Team, 2013). There was no significant relationship between DIFF and DIST or between DIFF and BEAR ($P > 0.10$). Therefore, no discernible bias exists between the 2 methods. The diameter measured by aerial photography showed a positive correlation ($R^2 = 0.59$, $P < 0.05$) with the diameter calculated from the manual field GPS collection. However, because some dispersion of the shapefiles on the orthomosaic was observed, aerial photography, at this time, cannot replace the manual field collection of the data.

Key Words: global positioning system coordinates, trees, vegetation measurement
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662 Effect of biosurfactant and oils over the morphometry of the rumen and duodenum of lambs.

S. B. Gallo*[1], I. Bueno[2], S. F. Costa[3], L. Brochine[2], T. Brochado[2], and I. Bohn[2], [1]*School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil,* [2]*Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, Brazil,* [3]*Universidade Federal de Lavras, Lavras, Brazil.*

Fat is an energy source to be taken into consideration in the diets of feedlot lambs, but an excess can cause metabolic disorders. Biosurfactant acts in the digestion and absorption of these lipids and thus increases energy utilization. The objective of the experiment was to evaluate the inclusion of biosurfactant with 2 different oil sources in a high-concentrate diet for feedlot lambs on the development of ruminal papillae and villi in the duodenum. A 2 × 2 factorial design was used (soybean or sunflower oil × inclusion or not of biosurfactant). The experiment was conducted at the Faculty of Zootechnics and Food Engineering of the University of São Paulo, Pirassununga, São Paulo, Brazil. Four diets were evaluated—2 oil sources (soybean or sunflower) with or without biosurfactant—with 10 animals per treatment. The diet contained 17% CO, 2,400 Mcal of ME, and 5% fat. The initial BW was 24 kg and the final weight was 42 kg, for a feedlotting period of 60 d. After slaughtering, an area of 5 cm^2 from the ventral ruminal sac and duodenum were fixed in formalin, embedded in paraffin, and sectioned. For morphometric analysis, slides were stained with hematoxylin–eosin. The measurements taken were the area and height of ruminal and intestinal villi and the depth of the intestinal glands. Data were analyzed using the GLM of SAS, comparing the means from the Student test with a 5% probability. In the rumen, the height of the papilla was not affected ($P > 0.05$), with a mean of 3.47 mm, but the area of the papilla ($P = 0.0017$) was influenced by the interaction of the oils with the inclusion of the biosurfactant, with greater areas for soy without biosurfactant, with a mean of 6.660 mm^2, and the other treatments having a mean of 5.315 mm^2. In the intestine, the depth of the crypt was not affected by the diet ($P > 0.05$), with a mean of 0.97 mm. There was an interaction for the height of the villus ($P = 0.0340$), with this being greater for the diet with sunflower oil and biosurfactant, with a mean value of 1.13 mm. The area of the intestinal crypt ($P = 0.0009$) was greater for the treatments without biosurfactant, with a mean of 293 mm^2. It is concluded that the different oil sources and the addition of biosurfactant have an effect on rumen papillae and duodenum villi.

Key Words: soybean, sunflower, surfactant
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663 Performance of lambs fed with different oil sources and biosurfactant.

S. B. Gallo*[1], C. G. Titto[2], L. F. Greco[3], L. Brochine[2], T. Brochado[2], B. Resende[2], and I. Bohn[2], [1]*School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil,* [2]*Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, Brazil,* [3]*Kemin South America, Indaiatuba, Brazil.*

Diets with a high energy and low fiber content are being used in lamb feedlotting to optimize performance, and the addition of biosurfactant may make the use of oil feasible as an energy source. Biosurfactant plays an emollient role when used in the diet of monogastric animals and presents possibilities for ruminants. The aim was to evaluate the inclusion or not of biosurfactant in diets with different oil sources (soybean or sunflower) in a high-concentrate diet for feedlot lambs and to evaluate animal performance. The experiment was carried out at the Faculty of Zootechnics and Food Engineering of the University of São Paulo, Pirassununga, São Paulo, Brazil. Four diets were evaluated—2 oil sources (soybean and sunflower) with the inclusion or not of biosurfactant—with 10 animals per treatment and without any defined racial pattern. The diet contained 17% CO, 78% NDT, 20% FDN, and 5% fat. The initial BW was 24 kg and the final weight was 42 kg, for a period of 60 d of feedlotting, with individual feeding and weighing every 14 d. A 2 × 2 factorial design was used (soybean or sunflower oil × inclusion or not of biosurfactant), with data analyses using the GLM of SAS, comparing the means using the Student test with a 5% probability. Dry material consumption was not affected by the diet ($P > 0.05$), with an average intake of 1.44 kg/d, nor was dry material consumption ($P > 0.05$) in relation to live weight, with an average of 4%. The ADG was greater for the animals that ingested biosurfactant ($P = 0.0263$), with an average of 0.356 kg/d, compared with the animals that did not ingest it, with a weight gain of 0.310 kg/d. The diets with biosurfactant ($P = 0.0439$) presented better dietary conversion, with an average of 4 kg dry material/GMP compared with 4,66 kg dry material/GMP for the diets without the additive, but there was no difference between the oil sources. The CMS values are as expected for live animal weight and as recommended by the NRC (2007). It is concluded that biosurfactant can be an ally when formulating diets with a high level of concentrate and the inclusion of oil, with the different sources studied not affecting performance.

Key Words: soybean, sunflower, surfactant
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664 Effect of antioxidants on the performance of lambs fed high-concentrate diets.

T. R. F. Lima*[1], T. Brochado[1], A. Stuart[1], I. Bohn[1], S. B. Gallo[2], and P. R. Leme[3], [1]*Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, Brazil,* [2]*School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil,* [3]*University of Sao Paulo / FZEA, Pirassununga, Brazil.*

This study aimed to evaluate the effects of the product Powerjet on the performance of lambs. This product is a patented combination of 3 plant extracts selected by their anti-inflammatory and antioxidant effects on the intestinal mucosa. The substances in these extracts, sanguinarine and honokiol and its isomer magnolol, also have an antioxidant effect inhibiting mitochondrial peroxidation in the liver and heart. Therefore, this study was carried out to evaluate these extracts compared with selenium (Se) plus E vitamin, known antioxidants, in the performance of lambs fed a high-concentrate diet. Forty-eight male lambs, just weaned, with a mean initial weight and age of 20 ± 1.5 kg and 60 d, respectively, were kept in individual pens with plastic bunks for feed and water and fed a diet composed exclusively of whole corn (80%) and a protein pellet (20%). The treatments differed only in the inclusion or not of the additives: a control diet without additives (CTL), a diet with the plant extracts (PX), a diet with Se and E vitamin (ES), and a diet with both additives (PXES). The PX inclusion in the diet was calculated to supply 4 mg/kg LW, and the Se and E vitamin inclusion was 1.0 mg/kg DM and 100 UI/kg DM, respectively. The CTL, PX, ES, and PXES diets had Se concentrations of 0.05, 0.05, 0.24, and 0.23 mg/kg DM, respectively. The Se requirement reported in the literature was between 0.10 and 0.20 mg/kg DM. The experimental design was random blocks in a 2 × 2 factorial (with or without PX and ES) arrangement, and the data were analyzed with the MIXED model of SAS 9.3 with a 5% level significance. The inclusion of ES and PX in the diets resulted in greater final weight ($P = 0.015$ and $P = 0.064$, respectively) and greater weight gains ($P = 0.045$ and $P = 0.060$, respectively), but there was no interaction between the studied factors ($P = 0.365$). The final weight means with ES and PX were 44.6 and 44.1 kg, respectively, and without ES and PX were 41.0 and 41.4 kg, respectively. The daily weight gains were, in the same order, 0.390, 0.389, 0.352, and 0.353. There was no effect ($P = 0.303$) of the inclusion of ES or PX in the DMI (mean 3.35%) nor interaction of the additives ($P = 0.296$). There was no difference ($P = 0.110$) in the feed efficiency, with a mean of 0.270 kg/kg DMI. Considering the results, the PX had a positive effect on performance.

Key Words: oxidative stress, performance, sheep
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665 Production, composition, and fatty acid profile of goat milk supplemented with buriti oil.

V. L. Lima Junior*[1], L. Rocha Bezerra[2], J. Santos de Morais[3], N. Eufrasino de Freitas[3], M. Jácome de Araújo[4], C. Batista de Oliveira Neto[5], A. M. de Azevedo Silva[6], J. M. Pereira Filho[3], J. F. Paulino de Moura[3], R. Loiola Edvan[4], R. L. Oliveira[7], and E. Sales Pereira[8], [1]*UFRN, NATAL, Brazil,* [2]*University Federal of Piauí, Bom Jesus, Brazil,* [3]*UFCG, PATOS, Brazil,* [4]*University Federal of Piauí, BOM JESUS, Brazil,* [5]*UFPI, BOM JESUS, Brazil,* [6]*University Campina Grande, PATOS, Brazil,* [7]*UFBA, SALVADOR, Brazil,* [8]*UFCE, FORTALEZA, Brazil.*

This study was conducted to test the hypothesis that buriti oil (*Mauritia flexuosa* L.) can replace ground corn in goats' diet, improving production, composition, and fatty acid profile of goat milk. This experiment was approved by the Ethics Committee for Experimentation with Animals. Four Anglo–Nubian multiparous goats with average 50 ± 4 d of lactation and weight of 38.4 ± 1.1 kg were treated for the control of internal and external parasites. The animals were randomly distributed in a double Latin square (4 × 4) comprising 4 periods and 4 buriti oil concentrations (0.00, 1.50, 3.00, and 4.50% of total DM) replacing ground corn. The animals were manually milked twice daily (at 6 and 16 h). The data were subjected to an ANOVA and regression analyses (linear and quadratic) using the GLM and REG procedures implemented in SAS statistical software (version 9.1.2; SAS Inst. Inc., Cary, NC). Goat milk production, corrected production$^{4\%fat}$, and chemical composition were not influenced by the concentration of buriti oil replacement; however, milk fat concentration ($P = 0.04$) and feed efficiency ($P < 0.01$) linearly increased with the amount of buriti oil in the diet. There was a linear reduction on hypercholesterolemic SFA, such as C12:0 ($P < 0.01$) and C14:0 ($P < 0.01$), as well as the atherogenic index ($P < 0.01$) with buriti oil inclusion in goat's diet. In contrast, the fatty acids C18:0 ($P < 0.01$) and C18:1 *cis*-9 ($P < 0.01$) linearly increased in the milk of goats that were fed with buriti oil. However, CLA ($P < 0.01$) quadratically varied; the maximum production of 0.62 g/100 g of fat was observed when using 1.50% buriti oil. The sensory characteristics of the milk were not changed ($P > 0.05$) by the replacement of corn with buriti oil in the goats' diet. It is recommended to replace corn with buriti oil in goat feed by up to 4.5% of total DM, resulting in improved milk fat without affecting production; this recommendation satisfies the minimum requirements of the industry and preserves the organoleptic characteristics of the milk and its acceptability for human consumption. In addition, buriti oil replacing ground corn by up to 4.5% DM in the diet of lactating goats decreased medium-chain SFA, which are hypercholesterolemic and increase the concentrations of

the C18:1 *cis*-9, CLA, and DFA in goat milk fat, helping to protect against cardiovascular disease.

Key Words: conjugated linoleic acid, *Mauritia flexuosa* L., vegetable oil
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666 Effect of oregano essential oil and black wattle tanniniferous extract in the diet of feedlot lambs on meat fatty acid composition.

K. C. Welter[*1], C. M. de Magalhães Rodrigues Martins[2], F. A. Melo[1], G. Benetel[1], C. M. D. Silva[1], A. M. Ferrinho[1], A. S. C. Pereira[1], S. B. Gallo[1], and I. C. D. S. Bueno[1], [1]*School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil,* [2]*School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil.*

The objective of the present study was to evaluate the effect of oregano essential oil and black wattle tanniniferous extract in the diet of feedlot lambs on meat fatty acid composition. At the beginning of the trial, 36 intact male lambs (Dorper × Santa Inês × Texel), at approximately 90 d of age and initial BW of 26 kg, were housed in individual stalls. The lambs were allocated into 3 treatments ($n = 12$) in a randomized block design, using initial BW as blocking criteria, and fed for 60 d. The experimental treatments evaluated were 1) a Control diet, 2) the Control diet with inclusion of oregano essential oil (1 mL/kg of concentrate), and 3) the Control diet with inclusion of black wattle tanniniferous extract (5% of diet; DM basis). Each diet had a dietary forage:concentrate ratio of 30:70. The samples were taken on deboned of animals, 96 h after slaughter. Meat samples were collected and ground for fatty acid profile; lipids were extracted as described by Folch et al. (1957), from 2 g of ground steak; and the fatty acids were quantified by gas chromatography. Data were analyzed using the MIXED procedure of SAS software (2001). The inclusion of oregano essential oil and black wattle tanniniferous extract in the diet of feedlot lambs increased the meat fat concentration of *n*-3 ($P = 0.01$). Additionally, lambs fed diets with supplements had a trend of increased meat concentration of vaccenic ($P = 0.07$) and *n*-6 ($P = 0.09$) fatty acids. However, the inclusion of oregano essential oil and black wattle tanniniferous extract reduced the oleic fatty acid concentration ($P = 0.01$) and had no effect on *n*-6:*n*-3 ratio ($P = 0.44$) and on *cis*-9 *trans*-11 CLA ($P = 0.55$). There was no difference between oregano essential oil and black wattle tanniniferous extract on meat fatty acid composition (Table 666). Therefore, we conclude that dietary inclusion of oregano essential oil and black wattle tanniniferous extract may change the meat fat composition, increasing the *n*-3 fatty acid content.

Key Words: meat quality, *n*-3, small ruminant
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Table 666. Lambs meat fatty acid composition

Item	Treatments Control	Oregano essential oil	Black wattle tanniniferous extract	SEM	*P*-value
n-3	0.70^b	0.85^a	0.90^a	0.03	0.01
n-6	9.74	10.53	11.15	0.30	0.09
n-6:*n*-3 ratio	13.26	12.23	12.30	0.36	0.44
CLA (*cis*-9 *trans*-11)	0.25	0.28	0.31	0.02	0.55
Vaccenic acid	0.471	0.492	0.604	0.03	0.07
Oleic acid	36.08^a	33.89^b	32.68^b	0.55	0.01

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667 Zilpaterol hydrochloride improved growth performance and some carcass characteristics in finishing ram lambs in feedlot.

J. Cayetano de Jesús[1], R. Rojo Rubio[*2], H. Lee-Rangel[1], L. Avendaño-Reyes[3], U. Macias-Cruz[4], J. F. Vázquez-Armijo[5], B. Albarran-Portillo[5], J. C. D. García-López[1], and M. A. Jaime[5], [1]*Universidad Autonoma de San Luis Potosí, San Luis Potosí, Mexico,* [2]*Centro Universitario UAEM Temascaltepec, Temascaltepec, Mexico,* [3]*Instituto de Ciencias Agricolas, Universidad Autonoma de Baja California, Ejido Nuevo Leon, Baja California, Mexico,* [4]*Universidad Autonoma de Baja California, Mexicali, Mexico,* [5]*Universidad Autónoma del Estado de México, Temascaltepec, Mexico.*

Twenty-four Dorper × Pelibuey ram lambs (32.19 ± 0.69 kg initial BW and 5 mo of age) were housed in individual pens during a 31-d feeding period and then slaughtered to determine the effects of zilpaterol hydrochloride (ZH) supplementation on productive performance, carcass characteristics, and wholesale cut yields. Lambs were assigned to 4 treatments ($n = 6$) under a randomized complete block design, where initial BW was used as the blocking factor. Treatments consisted of offering a basal diet and 3 different daily doses of ZH: 0 (control), 0.1, 0.2, and 0.3 mg/kg BW. All data collected were analyzed with ANOVA using the GLM procedure of SAS (SAS Inst. Inc., Cary, NC). Means were separated with a PDIFF STDERR statement. Significance was declared at $P < 0.05$ and tendency when $0.05 < P < 0.10$. Final BW ($P = 0.02$) and ADG ($P = 0.04$) were greater for lambs that received 0.2 mg/kg BW. Supplemental ZH tended to improve DMI ($P = 0.008$) and the ADG:DMI ratio ($P = 0.078$). Water intake was lower ($P < 0.01$) in lambs supplemented with ZH. Zilpaterol hydrochloride supplementation did not affect carcass characteristics such as hot and cold carcass weight, dressing, KPH, conformation, fat thickness, carcass and leg length, thorax depth, and pH of LM at 45 min; however, cooling loss ($P = 0.06$) and pH at 45 min ($P = 0.06$) showed a trend to increase as ZH supplementation increased. Wholesale cut yields were not affected by ZH supplementation. Percentage of head was greater ($P = 0.043$) in lambs treated with ZH. LD area increased ($P = 0.01$) with ZH addition. Percentage of blood presented a trend ($P =$

0.051) of decreasing with ZH supplementation. Also, the liver decreased in size ($P < 0.05$) for treatments in which ZH was included. In conclusion, using a daily ZH dosage of 0.2 mg/kg of BW produced the best productive performance and carcass characteristics in hair-breed rams.

Key Words: carcass characteristics, sheep performance, zilpaterol doses
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668 Daily ration intake and performance of semi-feedlot lambs in integrated crop–livestock system.

V. Zirondi Longhini*[1,2], C. Costa[3], P. R. L. Meirelles[3], C. M. Pariz[3], V. M. Protes[3], D. M. Souza[3], M. L. S. T. Piza[3], A. M. Castilhos[3], L. D. Fernandes[3], C. N. R. Braga[3], and A. P. O. Santos[3], *[1]Sao Paulo State University, Jaboticabal, Brazil, [2]FAPESP, São Paulo, Brazil, [3]Sao Paulo State University, Botucatu, Brazil.*

The objective of this study was to evaluate the effects of corn (*Zea mays* L.) silage intercropped with palisade grass [*Urochloa brizantha* (Hochst. ex A. Rich.) R. Webster cv. Marandu] and pigeonpea [*Cajanus cajan* (L.) Millsp.] in summer/fall and oversowing modalities of black oat (*Avena strigosa* Schreb.) in winter/spring on lambs' production in semi-feedlot. Crossbred male lambs (n = 48/yr; 27.2 ± 0.6 and 24.0 ± 0.7 kg initial BW in the first and second growing seasons, respectively) were used in a completely randomized design. Treatments were arranged in a 2 × 2 × 2 factorial arrangement of 2 silage production systems (SPS; corn + palisade grass + pigeonpea [C+PG+PP] and corn + palisade grass [C+PG], 2 black oat oversowing modalities (BO; drilled vs. broadcast), and 2 grazing cycles (GC). Animals spent the day grazing in the black oat (fixed stocking rate and rotational grazing), and during the night, they were herded into a barn and separated by treatments in collective pens, where they received concentrate and corn silage (C+PG+PP or C+PG) of their respective diets. Diets were formulated to be similar in energy and protein contents. Daily ration intake of concentrate + silage (DRI) was calculated as the difference between ration supplied and remaining. Every 18 d, lambs were individually weighed for ADG calculation. Data were analyzed using PROC MIXED, with SPS, BO, GC, and their interactions considered fixed effects. Animal (SPS × BO × GC) was considered a random effect. Treatments were considered different when $P \leq 0.05$. Daily ration intake (DRI) was lower for C+PG+PP compared with C+PG ($P = 0.05$; 0.754 vs. 0.800 kg/d) and in pastures with black oat oversowing drilled compared with broadcast ($P = 0.03$; 0.751 vs. 0.803 kg/d) in the first growing season. In first GC of the first and second growing seasons, the DRI was lower than in the second GC ([{$P < 0.001$} 0.547 vs. 1.007 kg/d and {$P < 0.001$} 1.76 vs. 2.51% BW] and [{$P < 0.001$} 0.559 vs. 1.283 kg/d and {$P < 0.001$} 1.98 vs. 3.45% BW], respectively). The ADG was lower in the first GC than in the second GC ($P = 0.005$; 0.222 vs. 0.264 kg/d) in the first growing season. This difference was due to the greater forage availability in the first GC reducing the DRI. Consequently, the greatest DRI resulted in increased ADG in the second GC. In conclusion, corn silage intercropped with palisade grass and pigeonpea did not affect performance of semi-feedlot lambs, being a strategy in integrated crop–livestock system.

Key Words: black oat, palisade grass, pigeonpea
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669 Effects of replacing corn with dried distiller's grains plus solubles and poultry fat on performance and meat quality of lambs consuming bermudagrass hay.

C. L. Greene*, B. Kouakou, P. Dangal, J. H. Lee, and J. N. Sheed, *Fort Valley State University, Fort Valley, GA.*

The Southeastern United States, with warm climate and relatively high humidity, is not suitable for wool production. For these reasons, hair-type sheep are being raised for meat. Grazing is the most economical way of raising livestock. Pasture quality is subjected to seasonal variations leading to nutrient deficiencies that limit animal performance. Supplements are often needed to improve animal performance. Grains are used for energy and soybean meal is used for protein supplementation. Corn and soybean are diverted for biofuel production, reducing their use for animal feed and thus increasing the cost of animal production. Dried distiller's grains plus solubles (DDGS), a byproduct of the grain biofuel industry, that is rich in protein and digestible fiber could be used to replace corn and soybean meal in livestock diets. A study was conducted to determine the effects of replacing corn with DDGS, poultry fat, or in combination on feed intake, growth, carcass characteristics, liver mass, and meat quality of lambs consuming Bermudagrass hay using 40 Katahdin × Dorper intact males (6 mo old). Treatments consisted of a Bermudagrass hay–based diet supplemented with corn (Control), DDGS, poultry fat (OIL), or DDGS plus poultry fat (DDGSOil). Diets were balanced for energy and protein and then fed once daily for 60 d to individually housed lambs. Lambs were processed at the end of the 60-d experiment after a 24-h fast. Data were analyzed as a completely randomized design using the mixed model of SAS. Results indicate that total protein intake %BW (0.4834 ± 0.0183), final weight (44.6 ± 1.24 kg), slaughter weight (42.5 ± 1.49 kg), hot (24.4 ± 0.74 kg) and chilled carcass weights (72.5 ± 0.74 kg), initial carcass pH (6.5 ± 0.06), cooking loss (16.6 ± 0.87%), and meat protein (21.2 ± 0.39%) were not affected ($P > 0.05$) by supplement type. Total DMI (1.66 vs. 2.07, 2.15, and 2.22 ± 0.07 kg for OIL, DDGS, DDGSOil, and Control, respectively) and liver weight (561 vs. 635, 674, and 678 ± 27.9 g) decreased ($P < 0.01$) with OIL supplement alone. Rumen pH was lowest ($P < 0.05$) with corn supplementation (7.23 ± 0.06) compared with DDGS (7.4 ± 0.06), OIL (7.5 ± 0.06), and DDGSOil (7.6 ± 0.06). Thiobarbituric acid reactive substances for DDGSOil (0.36 ± 0.0351

malondialdehyde [MDA]/kg) were higher ($P < 0.001$) compared with Control (0.118 ± 0.0351 MDA/kg), OIL (0.1712 ± 0.0351 MDA/kg), and DDGS (0.203 ± 0.0351 MDA/kg). The OIL supplement showed greater myoglobin quantities (31.3 ± 2.3 mg/mL) compared with Control (17.1 ± 2.3 mg/mL), DDGSOil (21.9 ± 2.3 mg/mL), and DDGS (24.3 ± 2.3 mg/mL. These results show that DDGS or OIL alone or in combination can be used in a growing lamb diet without negatively affecting animal performance and meat quality.

Key Words: dried distiller's grains plus solubles, lamb, poultry fat corn
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671 Longissimus muscle fatty acid profile of lambs fed diets containing babassu oil or buriti oil.

M. O. M. Parente[1], K. S. Rocha[1], H. N. Parente[1], S. P. Alves[2], J. M. S. Sousa[1], N. A. F. Machado[1], R. M. S. Gomes[1], G. S. de Oliveira[*1], A. M. Zanine[1], R. J. Bessa[3], and I. Susin[4], *[1]Universidade Federal do Maranhão, Chapadinha, Brazil, [2]Universidade de Lisboa, Lisboa, Portugal, [3]CIISA, FMV-Ulisboa, Lisboa, Portugal, [4]ESALQ/University of Sao Paulo, Piracicaba, Brazil.*

Brazil has a great potential for vegetable oil production. Babassu (*Orbignya phalerata* Mart.) and buriti (*Mauritia flexuosa*) are examples of important species found between Amazon rain forest and Cerrado biomes, whose oils have applications in the food and feed industries. Babassu is one of the most important palm trees in Brazil, especially in Maranhão state, and its oil represents 65% of the seed and is rich in medium-chain SFA. Buriti oil is extracted from the fruit of the Buriti palm tree and is rich in MUFA and natural antioxidants. Twenty-one lambs (18.9 ± 3.8 kg initial BW) were used in a complete randomized block design to determine the effects of adding babassu oil or buriti oil to the diet on LM fatty acid profile. Lambs were individually penned for 50 d and fed 1 of 3 diets: a control diet, containing 70% concentrate and 30% Tifton 85 hay (CON); the CON plus 40 g/kg of babassu oil (BA); and the CON plus 40 g/kg of buriti oil (BU). At the end of feeding trial, lambs were slaughtered and LM samples were collected for total lipid determination and fatty acid analysis by gas chromatography. Means were compared using Tukey's method ($P < 0.05$). The total fatty acid content of LM was higher ($P < 0.05$) for the BU than for the BA, which was similar to the control (98, 80, and 129 mg/g DM for CON, BA, and BU, respectively). The proportions of medium-chain fatty acid (i.e. 12:0 and 14:0), *trans*-MUFA, and total biohydrogenation intermediates were increased ($P < 0.05$) with BA when compared with CON and BU, whereas CON and BU did not differ. The sum of *trans*-MUFA was 1.1, 3.8, and 1.5% for CON, BA, and BU, respectively. The increase of *trans*-MUFA was mostly explained by the *t*10-18:1 (0.2, 2.6, and 0.4% of total fatty acids for CON, BA, and BU, respectively), and thus the *t*10- to *t*11-18:1 ratio was greatly increased with BA (0.6, 6.0, and 1.2 for CON, BA, and BU, respectively). On the other hand, BA reduced the *cis*-MUFA compared with CON and BU (48.5, 39.9, and 47.6% for CON, BA, and BU, respectively). The BA increased total PUFA compared with BU but not compared with CON. However, this increase in PUFA was mostly explained by the differences in total fatty acid content of muscle. In conclusion, the fatty acid profile of LM from lambs was greatly modified by BA in contrast to the mild effects of BU.

Key Words: fatty acid, lamb, meat
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672 How much does a ram lose during the breeding season? Assessment of pre- and postbreeding reproductive traits of rams in a range flock in the Pacific Northwest.

M. J. Stotts[*], M. R. Corpron, N. R. Moffitt, J. L. Mutch, S. M. Smith, J. R. Busboom, M. E. Benson and M. G. Maquivar, *Washington State University, Department of Animal Sciences, Pullman.*

The objective of the study was to assess reproductive soundness of rams during 2 consecutive prebreeding (PRE) and postbreeding (POST) seasons in a range flock management system in the Pacific Northwest. The present study includes data from 2 yr. Thirty-two animals were evaluated 15 d prior to the beginning of the breeding season (average 6 mo of age) and 7 d after the termination of a 120-d breeding season (average 10 mo of age). Animals were followed up during their second year as adult rams at 17 mo of age and again at the end of the breeding season (23 mo of age). Animals were group mated with a flock of ewes (1:35 male:female) and grazed federal lands during the breeding season. The variables assessed PRE and POST were BCS (using a 1–5 scale), scrotal circumference (SC), and percentage of spermatozoid motility (MOT). Data were analyzed using a mixed model with repeated measures assessing the main effect of season on the variables identified. During the first breeding season, no animals were culled; however, by the end of the second year, 34% (11/32) were culled. Over the first breeding season, ram lambs ($n = 32$) lost ($P < 0.01$), on average, 0.5 points of BCS, PRE (2.54 ± 0.03 units) to POST (2.04 ± 0.09 units), and by the second breeding season, the mature rams ($n = 23$) gained, on average, 0.03 points of BCS, PRE (1.85 ± 0.08 units) to POST (1.86 ± 0.08 units). Similarly, during the first year, the ram lambs had a reduced ($P < 0.01$) SC measurement from PRE (38.2 ± 0.3 cm) to POST (35.9 ± 0.5 cm). Values greater than 36 cm were considered exceptional for fertility; during the second year, rams decreased ($P < 0.01$) SC from PRE (38.8 ± 0.52 cm) to POST (31.1 ± 1.4 cm). Based on the MOT, no differences ($P > 0.05$) were observed between PRE and POST measures (66.2 ± 5.6% for PRE vs. 62.1 ± 5.7% for POST) during the first year. The MOT decreased ($P < 0.01$) during the second year (PRE 91.9 ± 3.8% vs. 55.8 ± 3.8% 7.8%). It is concluded that in range flock systems, the first year of life is critical to manage and maximize the reproductive potential of the rams. Additionally, year-round management is necessary to ensure the reproductive success of sheep flocks and to maximize the productive longevity of rams.

Key Words: ram fertility, ram management, range flocks
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673 Hematological and biochemical parameters of Saanen goats supplemented with selenium and vitamin E during the transition period.

A. Saran Netto*[1], B. Barcelos[2], J. A. Cunha[3], and M. A. Zanetti[4], [1]*University of São Paulo, Pirassununga, Brazil,* [2]*School of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, Brazil,* [3]*FZEA-USP, Pirassununga, Brazil,* [4]*University of São Paulo – USP/FZEA, Pirassununga, Brazil.*

The objective of this study was to evaluate serum and milk selenium (Se) and vitamin E (VitE), hematological, and biochemical parameters of Saanen goats that were supplemented with Se and VitE. Fifteen goats were supplemented starting on the fourth month of pregnancy until 28 d postpartum. The experimental design was a complete randomized design with repeated measures, with 5 replications. The animals were divided into 3 groups and received the following treatments: a control (base diet with 50% forage and 50% concentrate), Se (3.2 mg of Se/kg DM added to the diet), and Sev (3.2 mg of Se/kg DM and 1,145 IU/d of VitE per kilogram DM). The experiment took 12 wk. Blood samples were collected before the supplementation, during the partum, and 2, 7, 14, 21, and 28 d postpartum. Blood samples were analyzed for Se, VitE, erythrogram, leukogram, serum protein analysis, albumin, gamma-glutamyl transferase, total cholesterol, high-density lipoproteins (HDL), low-density lipoproteins (LDL), triglycerides, aspartate aminotransferase, creatine phosphokinase (CK), glucose, lactate, urea, creatinine, beta-hydroxybutyrate, NEFA, and total antioxidant status (TAS). Milk samples were analyzed for Se and VitE. Time was analyzed when the interaction was significant, except for VitE, which was analyzed by ANOVA, and the means were compared by Tukey's test ($P \leq 0.05$). There was a significant increase in Se concentration in serum and goats' milk ($P < 0.05$). For VitE in serum and milk, TAS, and hematological and biochemical parameters, there was no significant effect of treatment ($P > 0.05$); the Sev treatment tended to improve several parameters such as higher red blood cells and lower cholesterol, HDL, LDL, and CK, indicating a better oxidant activity in the group treated with Se and VitE.

Key Words: antioxidants, nutrition, partum
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674 Lying and standing behavior of a small herd of goats in a woodland pasture.

T. A. Gipson*[1] and C. A. Clifford-Rathert[2], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO.*

Lying and standing behavior is an excellent indicator of animal well-being. The objective of this study was to evaluate breed and temporal effects on lying and standing behavior in a small herd of goats. Nineteen goats (4 Boer, 5 Kiko, 5 Savannah, and 5 Spanish) were fitted with Icetags, which are 3-axis accelerometers that record percentage lying, standing, and active behavior every minute, and were released into one of three 0.5-ha wooded paddocks. Goats were assigned to the same paddocks each year. Icetags were deployed for 7 d during the late spring for 3 consecutive years (maximum of 29°C and minimum of 16°C for yr 1; maximum of 24°C and minimum of 13°C for yr 2; and maximum of 26°C and minimum of 14°C for yr 3). Overall, average percentages were 56% lying, 34% standing, and 10% active per minute. Individual 1-min intervals (483,840 observations) were aggregated into hours (8,064 observations). Hours between 0600 and 2000 h were coded as day and all other hours were coded as night. Mixed model methodology was used to evaluate the effects of breed (Boer, Kiko, Savannah, and Spanish), year (1, 2, and 3), day (2 to 8), daytime (day or night), and all 2-way interactions, with animal and paddock as random effects, on behavior. For lying, standing, or active, all 2-way interactions, except breed × day and except breed × daytime, for active were highly significant ($P < 0.01$). For lying, Spanish during night had the greater minutes per hour ($P < 0.05$) compared with Spanish during day, Kiko during day, Savannah during night, and Savannah during day (39.5 vs. 33.5, 29.3, 28.8, and 27.6 min/h, respectively [SEM 3.65]). Kiko during night, Boer during night, and Boer during day were intermediate and not different ($P > 0.10$) than the other breed × daytime means (35.9, 34.8, and 33.7 min/h, respectively). Conversely, for standing, Savannah during night had greater minutes per hour ($P < 0.05$) compared with Spanish during night (25.9 vs. 15.6 min/h [SEM 2.99]). Savannah during day, Kiko during day, Boer during night, Boer during day, Spanish during day, and Kiko during night were intermediate and not different ($P > 0.10$) than the other breed × daytime means (24.4, 23.1, 21.4, 20.4, 19.7, and 19.5 min/h, respectively). Goats were more active ($P < 0.01$) during the day than at night (7.1 vs. 4.4 min/h [SEM 0.55]). These results indicate that breed and time of day may affect the lying and standing behavior in goats, and these differences in behavior should be taken into account when ascertaining well-being criteria.

Key Words: dairy goats, lying, standing
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675 Effect of water restriction on hair sheep breeds from different regions of the United States.

A. Hussein*[1,2], R. Puchala[1], I. Portugal[1], T. A. Gipson[1], B. K. Wilson[2], and A. L. Goetsch[1], [1]*American Institute for Goat Research, Langston University, Langston, OK*, [2]*Department of Animal Science, Oklahoma State University, Stillwater.*

Twenty-four Dorper (DOR; 60 ± 2.8 kg initial BW), 23 Katahdin (KAT; 63 ± 2.6 kg BW), and 21 St. Croix (STC; 40 ± 2.7 kg BW) female sheep (0.9–8.9 yr) from 45 commercial farms in the Midwest, Northwest, Southeast, and central Texas were used to evaluate resilience to water restriction. Animals were housed and fed a 15% CP, 50% concentrate pelleted diet at 160% of the ME requirement for maintenance. In period 1, 2 wk in duration, ad libitum water intake was determined followed by 25 and 50% decreases in water availability in periods 2 and 3, which were 2 and 5 wk in duration, respectively. Water was offered at 0700 h and blood was sampled at 0800 and 1400 h on the last 2 d of each week. Data presented are means of values within periods, with breed and region means separated by LSD and linear and quadratic contrasts addressing period effects. There were no effects of or interactions involving region for the variables analyzed. During the baseline period, water intake was 3.59, 3.79, and 3.00 kg/d for DOR, KAT, and STC, respectively (SEM 0.140), and DMI averaged 58.6 ± 0.98 g/kg $BW^{0.75}$. There were linear decreases ($P < 0.01$) in DMI from period 1 to 3 of similar magnitude for DOR and KAT (134 and 153 g/d, respectively), whereas there was no change for STC ($P = 0.52$; 27 g/d [pooled SEM 41.5]). Plasma osmolality (mOsmol/kg) was 301, 307, and 303 for DOR; 302, 307, and 305 for KAT; and 306, 308, and 307 for STC in periods 1, 2, and 3, respectively (SEM 1.4), with a quadratic effect of advancing period for DOR ($P < 0.01$) and linear and quadratic effects ($P < 0.05$) for KAT. There were no effects on packed cell volume ($P > 0.05$). Serum protein concentration quadratically changed ($P < 0.001$) as period advanced for each breed (7.1, 6.0, and 7.2 g/dL in periods 1, 2, and 3, respectively [SEM 0.11]). In conclusion, there were no indications of influences of region on resilience to water restriction based on period means, and the lack of change in DMI by STC with limited water availability suggests relatively high resilience for this breed.

Key Words: feed intake, hair sheep, water
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676 Effects of grain source and starch concentration in dairy goat diet on ruminal fermentation, milk production, and inflammation.

Y. Shen*[1,2], W. Yang[2], L. Chen[1], J. Xu[1], and H. Wang[1], [1]*College of Animal Science and Technology, Yangzhou University, Yangzhou, P.R. China*, [2]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

The objective of this study was to evaluate the effects of grain (corn vs. wheat) and starch concentrations (low vs. high starch) on ruminal pH, milk production, and inflammatory response in dairy goats. Eight ruminally cannulated lactating goats (34 ± 3.1 kg of BW and 180 ± 8.2 d in milk) were used in a crossover design with a 2 × 2 factorial arrangement. Each period lasted for 27 d. During the first 10 d, goats were fed low-starch (LS) diets (d 8 to 10 for data collection); d 11 to 17, they were transitioned to high-starch (HS) diet; d 18 to 25, the goats were fed the HS diet; and data was collected d 25 to 27. Goats were fed a total mixed diet ad libitum twice daily. Diets were formulated as isonitrogenous (13.6%) and isoenergetic with forage-to-concentrate ratios of 60:40 and 35:65 for LS (24%) and HS (39% starch, DM basis) diets, respectively. Data were analyzed using PROC MIXED of SAS with model including diets as fixed effects and random effect of period and animal. Intake of DM (averaged 1.06 kg/d) was affected neither by grain source nor by starch concentration. However, goats fed the HS diet produced more ($P < 0.05$) milk (0.82 vs. 0.67 kg/d) and lactose (35.0 vs. 27.3 g/d) than goats fed the LS diet. Ruminal pH (averaged 6.15) did not differ but duration of pH < 5.6 was longer ($P < 0.05$) with wheat (232 min/d) than with corn (140 min/d). Ruminal pH was greater (6.16 vs. 5.87; $P < 0.05$) and duration of pH < 5.6 was shorter (33 vs. 339 min) for the HS diet than the LS diet. Concentration of ruminal lipopolysaccharide (LPS) was greater ($P < 0.05$) with wheat than with corn (35.5 vs. 22.1 $\times 10^3$ EU/mL). Goats fed the HS diet also had greater ($P < 0.05$) LPS concentration in ruminal fluid (40.3 vs. 17.3 × 10^3 EU/mL) than goats fed the LS diet. Blood concentration of serum amyloid A (SAA; 75.7 vs. 62.7 μg/mL), haptoglobin (Hp; 96.3 vs. 91.6 μg/mL), and LPS binding protein (LBP; 2.3 vs. 1.6 μg/mL) were not affected by grain source, but goats fed the HS diet had more ($P < 0.05$) SAA (89.3 vs. 49.1), Hp (116.7 vs. 71.2), and LBP (2.4 vs. 1.5 μg/mL) than goats fed the LS diet. These results indicated that replacing corn with wheat in a lactating goat diet had little impact on ruminal pH and milk production. However, increasing starch concentration in goat diets is beneficial to improve milk production and immune activity by stimulating inflammatory response.

Key Words: dairy goats, grain source and starch concentration, inflammation
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677 Prevalent weeds in a southern-pine silvopasture system managed with Kiko wethers.

U. Karki*, S. Poudel, Y. Karki, and A. Tillman, *Tuskegee University, Tuskegee, AL.*

Kiko goats are considered to use a wide variety of vegetation present in the grazing land. However, not much information is available about weeds that are present in grazing systems managed with goats. The objective of this study was to document the major weeds present in a Southern-pine silvopasture system grazed with Kiko wethers. Southern-pine silvopasture plots (3; 0.4-ha each) were planted with cool- and warm-season forages to develop year-round grazing for goats. Trees in the silvopasture consisted of longleaf (*Pinus palustris*) and loblolly pine (*Pinus taeda*) species (longleaf:loblolly ratio of 0.59) with 261 trees/ha; the trees were 11 yr old. Twenty Kiko wethers (21–23 m old) were rotationally stocked in the silvopasture plots to use the available forages from January to August 2016. Goats had free access to fresh water, mineral supplements, and shelters. Animals were taken off the plots when available forages were limited and were brought to other grazing sites. At the end of warm-season grazing in August, observations were taken on weeds present in the study plots, and the percentage of defoliation that occurred on those weeds was recorded on a preformatted sheet. Data were analyzed for prevalence and extent of defoliation in SAS 9.4 using the GLM procedure. Thirty-two weed species were detected in the study plots, among which 9 species were prevalent. Poorjoe (*Diodia teres* Walter) was the most dominant species covering the greatest plot area (14.8 ± 1.02%) and tropic croton (*Croton glandulosus* L.) was the least occurring species among the prevalent weeds. Horseweed (*Conyza* Less.) was the most defoliated species (21.5 ± 1.79%) followed by common ragweed (*Ambrosia* L.; 17.8 ± 1.79%) and poorjoe (11.5 ± 1.79%). Results suggest that goats may not readily eat several plant species present in the grazing system, and appropriate management strategies need to be considered to deal with these species.

Key Words: goats, horseweed, poorjoe
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678 Effect of solar radiation and increased salinity on Awassi ewe adaptation and production.

B. Al Masri[1], K. Houchaymi[2], and P. Y. Aad*[3], [1]*Universite Saint Joseph, Taanayel, Lebanon,* [2]*Lebanese Agricultural Research Institute, Terbol, Lebanon,* [3]*Notre Dame University, Zouk Mosbeh, Lebanon.*

With the recent changes in environmental patterns with climate change, higher maximum summer temperature, increased solar radiation, and lower water quality are anticipated; indicators for such changes are already being detected in Lebanon. With Awassi sheep managed in a transhumant system where animals walk for at least 4 to 5 h in the summer sun, and little research on the effect of heat/sun stress and water quality in transhumant animals, 30 lactating Awassi ewes were assigned from LARI from June to August, the hottest summer months, to 6 treatment groups in a 2 × 3 factorial treatment arrangement where water salinity (high salt vs. no salt) and solar/heat stress exposure were tested. Calcium carbonate was added to the feed and $MgSO_4$ was added to drinking water of the salt-treated ewes (SALT) and drinking water to the control, whereas for solar/heat stress, animals were kept in the sun (SUN) or provided partial (Control) or full shade (SHADE). Awassi ewes were allowed 2 wk of adaptation to the experimental plot under control conditions of partial shade and diet and exposed to experimental conditions for 1 mo, which was followed by 2 wk of recovery from heat and salt stress. Feed and water intake was measured twice a week on 2 consecutive days to estimate daily intake. Respiration (RR) and heart rate, body temperature, and panting scores (0 to 5) were recorded twice a week AM and PM and BCS, BW, and milk quantity were recorded. Body condition score and BW did not differ ($P < 0.05$) between all treatment groups. Results showed that animals consumed the entire ration, and SALT animals drank less water per hour ($P < 0.05$) than control animals irrespective of the sun exposure or time of measurement (noon vs. all day). Heart rate, RR, and panting scores did not differ ($P > 0.1$) between SHADE and Control ewes but was significantly higher ($P < 0.05$) in SUN ewes; however, panting scores did not exceeded 2.5 for the duration of the experiment, attesting to the adaptation of the Awassi breed to sun exposure and heat stress. Milk production slightly decreased ($P < 0.05$) in animals exposed to both sun and high salt with no difference between the Control and SHADE ewes. Therefore, Awassi sheep have the potential to withstand the anticipated changes in sun radiation and salt content.

Key Words: adaptation, Awassi ewes, solar/heat stress
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679 Effects of restricted periods of diet access on feed intake, behavior, and performance of Alpine goats in early lactation.

N. C. D. Silva[1,2], R. Puchala[1], T. A. Gipson[1], T. Sahlu[1], and A. L. Goetsch*[1], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Universidade Estadual Paulista Julio de Mesquita Filho, Jaboticabal, Brazil.*

Restricting periods of diet access to lactating dairy goats could influence level or efficiency of production and offer different management options. Therefore, 40 Alpine goats (12 and 28 of parity 1 and ≥2, respectively) with initial BW of 58.0 kg (SEM 1.50) and 14.2 d in milk (SEM 0.72) were offered a 40% forage diet (16.6% CP and 37.5% NDF; 20% alfalfa pellets, 10% cottonseed hulls, 10% coarsely ground grass hay, 12.9% wheat middlings, 12.9% rolled oats, 12.9% rolled corn, 11.0% soybean meal, 3.0% soybean oil, 5.0% molasses, and

2.3% other ingredients) free choice in Calan gate feeders for 12 wk. Feed access was continuous other than during morning and afternoon milking (Control), during the day for 8 h (Day) or night for 16 h (Night), or for 1 or 2 h after morning and afternoon milking (2Hour and 4Hour, respectively). Digestibilities were not influenced by treatment (e.g., OM: 73.1, 76.9, 77.1, 76.3, and 77.3% [SEM 1.81]), DMI was greater ($P < 0.05$) for Control than for most treatments (2.07, 2.23, 2.70, 2.33, and 2.01 kg/d [SEM 0.157]), and ADG was greater ($P = 0.019$) for Control than for the mean of restricted feeder access treatments (39, 11, 73, 24, and 21 g [SEM 17.7] for 2Hour, 4Hour, Control, Day, and Night, respectively). Milk yield was similar among treatments (2.60, 3.24, 3.05, 3.07, and 2.58 kg/d [SEM 0.375]), fat concentration tended ($P = 0.089$) to be lower for Control than for other treatments (3.88, 4.21, 3.41, 3.70, and 3.49% [SEM 0.208]), and milk energy yield was not affected by treatment (7.36, 9.53, 8.20, 8.56, and 6.91 MJ/d [SEM 1.071] for 2Hour, 4Hour, Control, Day, and Night, respectively). Intake of ME (22.69, 25.92, 31.25, 26.69, and 23.46 MJ/d [SEM 2.184]) and heat energy (13.34, 14.09, 17.51, 15.54, and 15.25 MJ/d [SEM 0.921]) were greater ($P \leq 0.011$) for Control than for other treatments, resulting in milk energy that was 31.9, 37.6, 26.0, 31.4, and 30.0% of ME intake for 2Hour, 4Hour, Control, Day, and Night, respectively (SEM 3.08). In conclusion, continuous diet access may affect partitioning of nutrients between milk synthesis and tissue accretion differently than some restricted feeder access treatments, particularly 4Hour.

Key Words: behavior, dairy goats, feed access
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680 Growth and FAMACHA scores in purebred and terminal sire crossbred lambs produced from landrace hair sheep under an accelerated mating system.

S. Wildeus* and D. O'Brien, *Virginia State University, Petersburg.*

Landrace hair sheep (Barbados Blackbelly and St. Croix) are well suited for low-input, pasture-based production, but lamb growth rates and weaning weights are smaller than in more traditional breeds. This project evaluated the use of Dorset rams as terminal sires for lamb production with landrace hair sheep breeds under pasture-based production. A flock of 110 purebred Barbados Blackbelly and St. Croix ewes were mated with like-breed sires or Dorset rams in an accelerated breeding system. Rams were mated at 8-mo intervals in 3 single-sire groups per sire breed to 10 to 28 ewes. Lambs were born on pasture in April, December, and August during two 2-yr production cycles. Birth weights and litter size (birth type) was recorded within 24 h of birth. Lambs were not creep fed but had access to a corn/soybean meal supplement (16% CP) provided to ewes at 1.5% BW during lactation. Lambs were weaned at 9 wk of age, and weaning weights and FAMACHA anemia eye scores were measured and recorded. Records of 956 lambs were analyzed by ANOVA with breed type, birth type, lambing season, and year as main effects. Birth weights were heavier in crossbred lambs than in purebred lambs (3.34 vs. 2.73 kg; $P < 0.001$) and in ram lambs than in ewe lambs (3.15 vs. 2.93 kg; $P < 0.001$) and heavier in single than in twin and in twin than in triplet lambs (3.73 vs. 3.18 vs. 2.78; $P < 0.001$). Crossbred lambs had heavier birth weights in August, whereas there were no differences between lambing seasons in birth weight of purebred lambs (breed type × season interaction, $P < 0.01$). Preweaning ADG and adjusted 60-d weaning weights were higher in crossbred lambs than in purebred lambs (144 vs. 121 g/d and 12.21 vs. 10.15 kg, respectively; $P < 0.001$) and higher following August lambing than April and September lambing (12.2 vs. 10.6 and 10.7 kg; $P < 0.001$). In contrast, FAMACHA scores were higher in crossbred lambs than in purebred lambs (1.41 vs. 1.24; $P < 0.001$) and higher following April lambing than August and September lambing (1.44 vs. 1.26 and 1.27, respectively; $P < 0.001$) regardless of breed type. FAMACHA scores were not affected ($P > 0.1$) by litter size or sex. Results indicate that crossbreeding increased weaning weight by 20% despite indications of higher susceptibility to gastrointestinal parasitism in crossbred lambs. This suggests terminal sire mating as a viable management option in landrace hair sheep ewes.

Key Words: accelerated mating, crossbreeding, hair sheep
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681 Quality of fresh lamb from pasture-raised purebred and crossbred hair sheep lambs gradually removed from soy hull supplementation before harvest.

D. Kafle*[1], J. H. Lee[1], S. Wildeus[2], A. Discua[1], and C. Tripp[1], [1]*Fort Valley State University, Fort Valley, GA,* [2]*Virginia State University, Petersburg.*

Soy hull supplementation (SH) in grazing lambs increased growth rate and altered carcass traits. Yet SH removal effect before harvest on the quality of fresh lamb has not been studied. This grazing trial with lambs grazing cool-season pastures evaluated the effect of SH removal before harvest on the quality characteristics of fresh lamb. Thirty-six 6-mo-old purebred hair (Barbados Blackbelly [BB; 20.0 ± 1.9 kg BW] and St. Croix [SC; 20.4 ± 3.1 kg BW]) and crossbred wool (Dorset) × hair (BB [24.8 ± 3.1 kg BW] or SC [24.5 ± 4.0 kg BW]) sheep lambs rotationally grazed predominantly stockpiled tall fescue (13.3 to 19.4% CP) and ryegrass (16.5% CP) pastures. Lambs were allocated to 4 supplementation treatments (no supplementation and supplementation until 42, 21, and 0 d before harvest), and SH was provided at 2% BW daily at individual feeding stations. After 63 d of grazing, lambs were harvested using standard procedures. After 24 h cooler storage (2°C), each carcass was fabricated to obtain 2.5-cm thick loin chops (LM) for meat quality analyses. Data were analyzed as a completely randomized design with a 2 × 4 factorial treatment arrangement (breed type and supplement duration). The CIE L* (lightness), a* (redness), and b* (yellowness) values of lamb chops were significantly influenced by supplement duration. Chops from lambs removed from SH 42 d before harvest had lower ($P < 0.001$) CIE a* values than those from lambs removed from supplementation 21 or 0 d before harvest. The amount of protein in LM was higher ($P < 0.05$) in crossbred lambs than in purebred lambs. Longissimus muscle from nonsupplemented lambs (22.0 and 2.49%, respectively) had lower ($P < 0.05$) protein and fat contents than that from supplemented lambs. Furthermore, LM from lambs removed from SH 0 d before harvest had the highest ($P < 0.05$) fat content (4.23%). The percent metmyoglobin and thiobarbituric acid reactive substances of LM from lambs were significantly affected ($P < 0.05$) by breed type and supplement duration. Chops from lambs removed from SH 0 d before harvest had higher ($P < 0.01$) shear force values (3.74 vs. 2.91 kg) than those from lambs removed from SH 42 d before harvest. Discontinuing supplementation before lamb harvest changed the meat quality of fresh lamb, but changes in meat quality were not consistently related to the time lambs were removed from supplementation.

Key Words: lamb, meat quality, soy hull
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682 Fatty acid composition of different fat depots from purebred and crossbred hair sheep lambs gradually removed from soy hull supplementation before harvest.

D. Kafle[1], J. H. Lee[*1], S. Wildeus[2], C. Tripp[1], and A. Discua[1], [1]*Fort Valley State University, Fort Valley, GA,* [2]*Virginia State University, Petersburg.*

Soy hull has been recognized as an economical source of feed and can provide a highly digestible fiber supplemental for pasture-raised ruminants. Soy hull supplementation in grazing lambs has increased growth rate and altered meat composition. Yet its timed removal before harvest on the fatty acid profile of different fat depots in lambs has not been reported. Thirty-six 6-mo-old purebred hair (Barbados Blackbelly [BB; 20.0 ± 1.9 kg BW] and St. Croix [SC; 20.4 ± 3.1 kg BW) and crossbred wool (Dorset) × hair (BB [24.8 ± 3.1 kg BW] or SC [24.5 ± 4.0 kg BW]) sheep lambs rotationally grazed predominantly stockpiled tall fescue (13.3 to 19.4% CP) and ryegrass (16.5% CP) pastures. Lambs were allocated to 4 supplementation treatments (no supplementation and supplementation until 42, 21, and 0 d before harvest). Lambs grazed as a single group, and supplement was provided at 2% BW daily at individual feeding stations. After 63 d of grazing, lambs were harvested and 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 and then analyzed using a gas chromatograph. All data were analyzed as a completely randomized design with breed type (pure breed or crossbreed) and supplement duration as main effects. The fatty acid profiles of different fat depots from experimental lambs were significantly influenced by breed type and supplement duration. Compared with nonsupplemented lambs, lambs removed from supplementation 0 d before harvest had higher ($P < 0.05$) concentrations of palmitic (C16:0; 17.4 vs. 15.0%) and *trans*-hexadecenoic acids (C16:1*n*-9*t*; 0.99 vs. 0.73%) but a lower ($P < 0.05$) concentration of elaidic acid (C18:1*n*-9*t*; 0.23 vs. 0.28%) in intramuscular fat, a lower ($P < 0.05$) concentration of α-linolenic acid (C18:3*n*-3; 0.76 vs. 1.24%) in subcutaneous fat, and a lower ($P < 0.05$) concentration of C18:1*n*-9*t* (0.28 vs. 0.36%) in kidney fat. Furthermore, lambs removed from supplementation 42 or 21 d before harvest had less ($P < 0.05$) C18:1*n*-9*t* (0.23 vs. 0.28%) in intramuscular fat, but lambs removed from supplementation 42 d before harvest had more ($P < 0.05$) linoleic acid (C18:2*n*-6; 4.44 vs. 2.87%) in intramuscular fat compared with nonsupplemented lambs. The results indicate that discontinuing supplementation before lamb harvest differentially affects fatty acids in fat depots from grazing lambs.

Key Words: fatty acid composition, lamb, soy hull
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683 Effects of dried distiller's grains with solubles and poultry fat as supplements for bermudagrass hay–based diet on blood metabolites, growth, meat and carcass characteristic of Spanish goats.

P. Dangal[*], B. Kouakou, C. L. Greene, J. H. Lee, and J. N. Sheed, *Fort Valley State University, Fort Valley, GA.*

Increased consumption of goat meat in the United States is primarily a consequence of influx of immigrants and health-conscious consumers about high fat and cholesterol intake with other red meats. Deficit in national production is partially compensated by frozen imports from New Zealand and Australia. Goats are raised mostly on pasture with seasonal variations in nutrient availability. On the other hand, the high cost of feed supplements (grains and soybean meal) limits profitability of goat production. On a unit weight basis, fats have more energy than grains or grain supplements. Dried distiller's grains with solubles (DDGS), a byproduct of the biofuel industry and rich in protein and soluble fiber, may be an alternative for corn and soybean, which are being diverted to biofuel production. Hence, the objective of this study was to evaluate the effects of replacing corn with DDGS, poultry fat, or DDGS plus poultry fat on growth and carcass parameters of growing goats (6 mo old) consuming Bermudagrass hay–based diets. Treatments consisted of Bermudagrass hay–based diet supplemented with corn (Control), DDGS, poultry fat (PF), or DDGS plus poultry fat (DDGSPF). Animals were individually housed and fed 1 of 4 isonitrogenous and isocaloric diets once daily for 60 d. At the end of the 60-d feeding period, animals were processed after a 24-h fast. Collected data were analyzed as a completely randomized design using the mixed model procedure of SAS. When significant at $P < 0.05$, treatment means were separated using LSD. Results indicate that final weight and hot and chilled carcass weights were decreased ($P < 0.05$) when poultry fat alone was used to replace corn. Goats supplemented with corn had lower ruminal pH (6.97) compared with DDGSPF (7.30), DDGS (7.32), and PF (7.40 ± 0.036) but DMI (1.210 ± 0.042 kg) was greater compared with PF-supplemented animals (1.020 ± 0.042 kg). Total protein intake was not affected ($P > 0.05$) by supplement type (162 ± 0.11 g). Meat protein content was not significantly different (21.02 ± 0.22%). Blood glucose levels were not significantly different ($P > 0.05$) among treatments (70.70 ± 3.13 mg/dL). Ruminal ammonia nitrogen was higher in control (11.24 mg/dL) compared with DDGS (6.45 mg/dL), PF (3.30 mg/dL), and DDGSPF (2.59 ± 1.36 mg/dL) animals. These results indicate that DDGS and poultry fat can be excellent substitutes for corn in growing goats consuming Bermudagrass hay–based diets.

Key Words: dried distiller's grains with solubles, meat goat, poultry fat corn
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684 Growing in silvopastoral system does not affect the performance or carcass and meat characteristics of lambs finished in feedlot.

F. de Oliveira Scarpino van Cleef*[1,2], V. Zirondi Longhini[1], L. Freitas de Oliveira Melo[1], T. Silva do Nascimento[1,2], P. Costa Borges[1], E. H. C. B. Van Cleef[1], J. M. Bertocco Ezequiel[1], and A. C. Ruggieri[1,2], *[1]São Paulo State University, Jaboticabal, Brazil, [2]CNPq, Brasília, Brazil.*

The aim of this study was to evaluate performance, feed efficiency, and carcass and meat characteristics of sheep in a feedlot coming from silvopastoral system during the dry season in Jaboticabal, state of São Paulo, in Brazil. For the growth phase, 24 lambs (23 ± 2.4 kg BW) were distributed into 3 treatments—unshaded, which is unshaded Massai grass (*Panicum maximum* × *Panicum infestum*) pasture; moderate shading, which is Massai grass pasture with eucalyptus trees spaced 12 by 2 m; and intense shading, which is Massai grass pasture with eucalyptus trees spaced 6 by 2 m—where they stayed for 60 d. Subsequently, lambs were individually housed in feedlot pens for 30 d. Animals were fed 1 diet (18.2% CP and 2.8 Mcal ME/kg of DM), containing 40% corn silage and 60% concentrate (corn grain, distiller's dried grains with solubles, soybean meal, urea, and vitamin–mineral premix). When lambs reached approximately 30 kg BW, animals were slaughtered. After evisceration, the HCW was obtained, hot carcass yield was calculated, and temperature (T0h) and pH (pH0h) were measured. Also, a cut between 12th and 13th rib was performed to expose myoglobin of LM to oxygen, and 30 min later, the meat color (luminosity [L*0h] and intensity of red [a*0h] and yellow [b*0h]) was read. Measurements were also taken 24 h after slaughter (chill period at 4°C): cold carcass weight (CCW), used to estimate the cold carcass yield; meat color (luminosity [L*24h] and intensity of red [a*24h] and yellow [b*24h]); temperature (T24h); and pH (pH24h). Data were analyzed using the MIXED procedure of SAS, and the treatment means were compared using Tukey's test at 5% significance. The DM intake was similar among treatments (1.14 kg; $P > 0.005$) as well as the ADG (0.30 kg; $P > 0.005$), and consequently, no differences in feed efficiency were observed (0.272; $P > 0.05$). No differences were observed in the HCW (14.1 kg) or CCW (13.9 kg) or for the yields (45.5 and 44.8%, respectively). Therefore, color (L*0h = 29.6, L*24h = 33.2, a*0h = 12.6, a*24h = 13.2, b*0h = 2.3, and b*24h = 3.9), pH (pH0h = 6.4 and pH24h = 5.7), and temperature (T0h = 34.2 and T24h = 4.8°C) did not differ among treatments ($P > 0.05$), and the averages observed in the present study were considered adequate for all variables. The silvopastoral system used during the growth phase did not affect the performance, feed efficiency, or carcass and meat characteristics of lambs finished in feedlot.

Key Words: dried distiller's grains with solubles, eucalyptus, sheep
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685 Effects of replacing corn and soybean meal with dried distiller's grains with solubles on blood metabolites and milk yield and composition of dairy goats during late lactation.

T. L. Williams, B. Kouakou*, and J. H. Lee, *Fort Valley State University, Fort Valley, GA.*

In the southern United States, warm-season grasses make up the bulk of the roughage consumed by livestock, including small ruminants. Digestibility of grasses generally declines with maturity, such that these forages may not always provide the necessary nutrients to support optimal animal performance or maintain product quality. Supplementation with protein and a moderate level of grain generally increases forage intake and digestibility. The diversion of corn away from human and animal feed for biofuel production has created a need for alternative energy supplements. Dried distiller's grains with solubles (DDGS), high in bypass protein and digestible fiber, is a good alternative to replace corn and soybean meal (SBM) in small ruminant diets. The objective of this study was to determine intake, blood metabolites, and milk yield and composition of Alpine and Saanen dairy goats, in late lactation, consuming ground eastern gamagrass (EGG; *Tripsacum dactyloides* L.) or Bermudagrass hay (BG; *Cynodon dactylon*) supplemented with DDGS or corn and SBM. The does were stratified based on milk yield and allotted to 4 groups. The groups were randomly assigned to 1 of 4 treatments (9 does/treatment). The does were group fed daily to allow ad libitum intake. The supplement and hay was mixed together and consumed by the does. The trial lasted 19 d. Blood plasma samples from each animal were analyzed for plasma urea nitrogen (PUN), glucose, and NEFA concentrations. Combined morning and evening milk samples were analyzed for protein, fat, lactose, and total solids. Data were analyzed as a mixed model for a completely randomized design using SAS. Replacing corn and SBM with DDGS did not affect ($P > 0.05$) milk yield (0.93 ± 0.155 kg), plasma glucose, milk protein, or lactose. However, PUN and milk fat were significantly different ($P < 0.05$). Bermudagrass hay increased PUN (37.02 and 35.04 ± 1.71 mg/dL) relative to EGG treatments (29 and 32.6 ± 1.71 mg/dL). Supplementing EGG with DDGS increased the NEFA concentration (209.3 ± 22.02 μEq/L) compared with BG and EGG with corn supplementation (120.6, 114.3, and 126.8 ± 22.02 μEq/L). Replacing corn with DDGS over a short feeding period does not affect milk yield and its basic components.

Key Words: blood metabolites, dairy goats and late lactation, dried distiller's grains with solubles
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686 Effect of licking molasses–urea block on weight gain, rumen fermentation, and the main microbe populations of grazing sheep during grass withering period.

C. Li*, A. X. S. Xue, and Q. Zhao, *Inner Mongolia Academy of Agriculture and Animal Husbandry Sciences, Huhhot, P.R. China.*

Sheep were grazed on grassland for 6 to 7 mo during withering period in north China. Crude protein of grass dramatically decreased, crude fiber significantly increased, and pasture digestibility decreased by 50% in this period. Sheep grazing these pastures as the sole diet may not be able to consume sufficient energy to meet the requirements for a preferred level of performance (Moore and Kunkle, 1995).The pasture can also be low in soluble nutrients and have an unbalance of energy and nitrogen (Johnson et al., 2001), causing producers to rely on grain or protein products to make up for the nutritional shortfalls. This experiment studied the effect of molasses–urea on rumen fermentation and microbial populations in grazing sheep during the grass withering period. Seventy sheep, with similar BW, were divided into 2 groups: 40 served as the experimental group and 30 served as the control group. The experimental group was fed molasses–urea after grazing. The experiment last for 60 d. At the beginning and finishing period, the BW of each animal was measured. Six sheep from each group were selected, and rumen fluid was collected through the mouth in the morning in the first 3 d and last 3 d of experimental period. Rumen fermentation parameters, including pH, MCP, and NH_3–N, were measured. In addition, the population of the *Selenomonas ruminantium*, *Anaerovibrio lipolytica*, *Fibrobacter succinogenes*, *Ruminococcus flaveciens*, and *Ruminococcus albus* were investigated by real-time PCR. The average daily molasses–urea consumption was 43.18 g/sheep, the ADG was 64.83 g for the experimental group whereas it was 30.92 g for the control group, and the difference was significant between the 2 groups ($P < 0.05$). There was no significant difference in pH value between the 2 groups, although MCP concentration tended to be increased in the experiment group compared with the control group. Ammonia-nitrogen significantly increased in the experiment group (18.2 ± 0.36 mg/100 mL) compared with the control group (16.2 ± 0.53 mg/100 mL; $P < 0.05$). At the end of experiment, the population of *S. ruminantium*, *A. lipolytica*, *F. succinogenes*, *R. flaveciens*, and *R. albus* in the experimental group was significant higher than in the control group ($P < 0.05$). These changes can affect fiber digestion, possibly by decreasing the rumen pH and inhibiting cellulolysis (Piwonka and Firkins, 1996). These data corroborate that population of rumen bacteria can be improved by the addition of molasses–urea to a diet (Kostenbauder et al., 2007). The molasses–urea block provides NPN and sugar for rumen microorganism and promoted growth and reproduction of microorganism and then improved the nutrient digestibility.

Key Words: grass withering period, molasses–urea block, rumen
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687 Performance of goat kids suckling does fed supplement at different times.

O. J. Gekara*[1], J. Onyilagha[2], and G. Wangila[3], [1]*Cal Poly Pomona, Pomona, CA,* [2]*University of Arkansas at Pine Bluff, Pine Bluff.*

Demand for goat meat in the United States continues to exceed local supply. Consumer perception that goat meat is healthier than other meats (beef, pork, and lamb) is driving this demand. Furthermore, year-round production of goat meat is inconsistent in the United States due to lack of organized markets and low productivity of existing local herds. Low animal productivity can be remedied through good feeding and health management. Well-fed does necessarily translates into faster growth in goat kids and their ability to overcome disease/parasite challenges. We hypothesized that timing of supplement feeding time (AM or PM) could be more important to doe/kid performance than quantity of supplement offered. Consequently, the objective of this study was to determine the performance of kids suckling does fed different levels of supplement at 0900 or 1500 h. Variables measured included ADG (kids), BCS (does), grazing behavior (does), and fecal egg count (kids). Eighteen does (48.3 ± 3.7 kg BW) of Savannah breeding aged 3 to 5 yr and their 27 kids (8.5 ± 0.9 kg BW) were randomly assigned to 3 treatments, replicated 3 times. Treatments were 1) high AM supplement (HAM; 0.91 kg DM $goat^{-1}\cdot d^{-1}$), which served as the control; 2) low AM supplement (LAM; 0.68 kg DM $goat^{-1}\cdot d^{-1}$); and 3) low PM supplement (LPM; 0.68 kg DM $goat^{-1}\cdot d^{-1}$). The control diet (goat pellets) was sourced from the local feed store; the experimental diet was mixed on farm. The study lasted for 28 d. Goats were weighed, scored for body condition, and sampled for feces to determine parasite eggs per gram of feces (EPG) on d 1 and 28. Data were subjected to ANOVA of SAS, and plot with 2 does and kids was the experimental unit. Kids suckling LPM does grew the fastest ($P < 0.05$; 0.147 kg/d) followed by HAM (0.124 kg/d) and LAM kids (0.080 kg/d). The LPM does tended ($P = 0.10$) to regain body condition faster (3.13) compared with HAM (3.08) and LAM does (2.71). Conversely, kids suckling LAM does had the greatest parasite load ($P < 0.05$; 6,686 EPG) followed by kids suckling HAM (2,381 EPG) and LPM does (1,419 EPG). Control (HAM) does tended ($P = 0.10$) to graze more intensely and most likely allocated more energy to support this activity, which may explain the poor kid performance in this group. Further work should establish if timing of supplementation should follow diurnal and seasonal changes in forage quality.

Key Words: average daily gain, does, goat kids
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688 Abstract withdrawn.

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689 Effect of increasing levels of babassu mesocarp flour on feed intake, nutrient digestibility, and rumen fermentation in sheep.

M. O. M. Parente[1], H. N. Parente[1], O. A. Gerude Neto[1], P. A. Carvalho[1], R. M. S. Gomes[1], M. A. Moreira Filho[1], V. L. F. Santos[2], A. M. Zanine[1], D. J. Ferreira[1], G. S. de Oliveira*[1], and J. S. Araújo[1], [1]*Universidade Federal do Maranhão, Chapadinha, Brazil,* [2]*Universidade Federal do Piauí, Bom Jesus, Brazil.*

In Northeastern Brazil, an important alternative food source is the babassu palm (*Orbignya* spp.). The babassu coconut is composed of 11% exocarp, 23% mesocarp, 59% endocarp, and 7% kernels. A low-cost flour can be extracted from the mesocarp. An important feature of babassu byproducts is their availability during the off-seasons of conventional grains, thus making it an important alternative for regional producers. Twenty crossbred lambs were used in a randomized complete block design (29.17 ± 2.23 kg BW) to evaluate the effect of increasing levels of babassu mesocarp flour (BMF; 0, 10, 20 and 30% [DM basis], corresponding to experimental diets 0BMF, 10BMF, 20BMF, and 30BMF, respectively) on feed intake, digestibility of nutrients, and ruminal fermentation. Lambs were individually confined and fed an isonitrogenous diet (16.5 ± 0.2 CP, DM basis) containing 70% of concentrate and 30% of Tifton 85 hay (DM basis) for 21 d, with 15 d for diet adaptation, 5 d for data collection of orts and feces, and 1 d for ruminal content collection (0, 2.5, 5.0 and 7.5 h after feeding). A representative sample of ruminal content from each animal was collected via esophageal tube. The first portion of rumen fluid was discarded, and the second portion, after being squeezed through 2 layers of cheesecloth, was used for determining pH, ammonia nitrogen, and short-chain fatty acids (SCFA). Orthogonal polynomials for diet responses were determined by linear and quadratic effects ($P < 0.05$). There was a quadratic effect ($P < 0.05$) on DMI (1,157.6, 1,397.6, 1,171.2, and 815.6 g/d for BMF0, BMF10, BMF20, and BMF30, respectively), nutrients intake, CP digestibility, and nonfiber carbohydrate digestibility. The digestibility of DM, OM, total carbohydrates, and NDF linearly decreased ($P < 0.05$) whereas ether extract digestibility linearly increased ($P < 0.05$) with increasing levels of BMF. There was no effect ($P > 0.05$) of increasing levels of BMF on pH, butyric acid, and total SCFA concentrations. There was a quadratic effect for propionic acid concentration (20.8, 21.5, 19.1, and 19.6 mol/100 mol for BMF0, BMF10, BMF20, and BMF30, respectively). The increasing levels of BMF linearly increased the acetic acid proportion (63.7, 63.8, 67.8, and 68.0 mol/100 mol for BMF0, BMF10, BMF20, and BMF30, respectively) and linearly decreased the A:P ratio, NH_3–N, isobutyrate, and valerate concentrations. The BMF is an alternative for energy source in sheep feed and can be added at levels up to 10%.

Key Words: neutral detergent fiber, ruminal pH, short-chain fatty acids
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690 Effects of supplementation of lambs' diets with babassu oil or buriti oil on nutrient digestibility and growth performance.

J. M. S. Sousa[1], H. N. Parente[1], R. M. S. Gomes[1], K. S. Rocha[1], R. J. Bessa[2], G. S. de Oliveira*[1], L. M. Freitas[1], L. F. dos ANjos[1], D. J. Ferreira[1], N. A. F. Machado[1], and M. O. M. Parente[1], [1]*Universidade Federal do Maranhão, Chapadinha, Brazil,* [2]*CIISA, FMV-Ulisboa, Lisboa, Portugal.*

Babassu (*Orbignya phalerata* Mart.) and Buriti (*Mauritia flexuosa* Mart.) are palm trees abundant in the northeast and north of Brazil, in the transition between Amazon rain forest and Cerrado biomes. The oil extracted from their fruits is locally available and therefore can be an alternative lipid source to increase energy density of growing lambs' diets. Twenty-one lambs (18.9 ± 3.8 kg initial BW and 120 d old) were used in a complete randomized block design to determine the effects of adding babassu oil or buriti oil on apparent digestibility and growth performance. Lambs were individually penned during 50 d and fed 1 of 3 diets: a control diet containing 70% concentrate and 30% Tifton 85 hay (CONT), the CONT plus 40 g/kg of babassu oil (BAO), and the CONT plus 40 g/kg of buriti oil (BUO). At the end of performance monitoring period, the intake was recorded and total feces collected for 4 d. Data were analyzed by 1-way ANOVA and when a significant diet effect ($P < 0.05$) was found, means were compared using Tukey's method. No significant differences were detected for DM (840 ± 176 g/d), CP (155 ± 38 g/d), NDF (290 ± 74 g/d), and ME (2.3 ± 0.5 Mcal/d) intake. Also, no significant differences were observed for DM (74.74 ± 5.0%), CP (75.9 ±

6.3%), and NDF (60.2 ± 7.8%) digestibility. The ether extract (EE) intake was higher ($P < 0.05$) with BUO (60.5 g/d) than with BAO (47.8 g/d) and both BUO and BAO were higher ($P < 0.05$) than CONT (23.3 g/d). However, the apparent digestibility of EE was higher ($P < 0.05$) with BAO (79.5%) than with BUO (68.7%) and both BAO and BUO were higher ($P < 0.05$) than CONT (55.4%).The ADG did not differ ($P > 0.05$) and averaged 187 ± 51 g/d across treatments. Moreover, the G:F did not differ ($P > 0.05$) and averaged 0.22 ± 0.09 across treatments. In conclusion, the addition of babassu oil or buriti oil did not affect the growth performance or nutrient apparent digestibility, except for EE.

Key Words: feed efficiency, intake, lipid supplementation
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691 Effects of selecting growing male hair sheep of different flocks for internal parasite resistance on performance.

Y. Tsukahara*[1], T. A. Gipson[1], S. P. Hart[1], L. J. Dawson[1,2], Z. Wang[1], R. Puchala[1], and A. L. Goetsch[1], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Center of Veterinary Health Sciences, Oklahoma State University, Stillwater.*

Katahdin, Dorper, and St. Croix male lambs from farms (2 Katahdin, farms A and B; 1 Dorper; and 1 St. Croix) in the south-central United States were categorized as resistant (RS), moderately resistant (MR), and susceptible (SS) to *Haemonchus contortus* based on artificial larvae challenge in a central performance test at Langston University over 3 consecutive years. Animal groups consisted of 17, 15, and 15 Katahdin-A (initial age 3.9 mo and 38.8 kg); 18, 7, and 8 Katahdin-B (3.7 mo and 18.9 kg); 20, 15, and 16 Dorper (5.5 mo and 34.2 kg); and 13, 14, and 19 St. Croix (4.2 mo and 19.2 kg) in yr 1, 2, and 3, respectively. Males were randomly selected in yr 1, whereas progeny of RS and MR sires were evaluated in yr 2 and 3. The test entailed 2 wk of adjustment and 8 wk of data collection, with free access to a 15% CP and 50% concentrate diet in automated feeders. During adaptation, anthelmintic treatment resulted in low fecal egg count (FEC; <600 eggs/g), after which 10,000 infective larvae were orally administered. Body weight and packed cell volume (PCV) were measured weekly, and FEC was determined 4 to 5 times in wk 6 to 8. The cubic clustering criterion of SAS was used for resistance categorization, which resulted in 49, 35, and 37 RS; 38, 33, and 39 MR; and 28, 17, and 36 SS in yr 1, 2, and 3, respectively. The statistical model included animal group, resistance classification, year, interactions, and covariates; GENMOD of SAS was used for mean FEC. There were interactions ($P < 0.05$) in mean FEC between animal group and resistance classification (473, 928, 1,089, and 297 eggs/g for RS; 1,793, 3,058, 2,199, and 1,084 eggs/g for MR; and 4,198, 5,073, 3,164, and 2,176 eggs/g for SS [SEM 144.7]) and between animal group and year (1,573, 2,261, 3,196, and 1,388 eggs/g in yr 1; 2,417, 4,793, 1,932, and 1,006 eggs/g in yr 2; and 2,475, 2,005, 1,325, and 1,163 eggs/g in yr 3 for Katahdin-A, Katahdin-B, Dorper, and St. Croix, respectively [SEM 146.0]). The PCV ranked ($P < 0.01$) RS > MR > SS (29.9, 28.0, and 26.9% [SEM 0.25]). Intake of DM, ADG, and the ADG:DMI ratio were similar among resistance classifications ($P > 0.05$) and were not correlated with FEC or PCV ($P > 0.05$). In conclusion, hair sheep can be selected for resistance to internal parasites without adversely affecting growth performance, and selection progress appeared greatest for the Dorper flock, although FEC were relatively low for the St. Croix farm.

Key Words: hair sheep, internal parasitism, resistance
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692 Effects of high heat load conditions on rectal temperature, panting score, and respiration rate of hair sheep breeds from different regions of the United States.

D. Tadesse*[1], R. Puchala[1], T. A. Gipson[1], I. Portugal[1], T. Sahlu[1], L. J. Dawson[1,2], and A. L. Goetsch[1], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Center of Veterinary Health Sciences, Oklahoma State University, Stillwater.*

Thirty-seven Dorper (DOR), 35 Katahdin (KAT), and 31 St. Croix (STC) ewes (57, 58, and 44 kg [SEM 2.2]) from 45 commercial farms in the Midwest (MW), Northwest (NW), Southeast (SE), and central Texas (TX), between 2.2 and 3.4 yr of age, were used to evaluate responses to high heat load index (HLI) conditions. There were 4 sequential 2-wk periods (8 wk total) with target HLI during day/nighttime of 70/70, 85/70, 90/77, and 95/81, with weekly measures at 0700 (before increased daytime HLI), 1300, and 1700 h (preceding lower nighttime HLI). Rectal temperature (RT; °C) was affected ($P = 0.003$) by breed × time (38.58, 38.92, and 39.07 for DOR, 38.67, 38.92, and 39.05 for KAT, and 38.45, 38.69, and 38.85 for STC at 0700, 1300, and 1700 h, respectively [SEM 0.034]). There were interactions between week and time ($P < 0.001$) in respiration rate (RR; breaths/min; 52, 72, 66, and 85 at 0700 h; 120, 130, 151, and 144 at 1300 h; and 116, 123, 141, and 142 at 1700 h [SEM 3.1]) and panting score (0–4; 0.05, 0.03, 0.11, and 0.28 at 0700 h; 0.48, 0.86, 1.61, and 1.47 at 1300 h; and 0.76, 0.91, 1.54, and 1.51 at 1700 h in wk 5, 6, 7, and 8, respectively [SEM 0.042]). Breed × time RR ($P = 0.008$) means were 57, 107, and 103 for DOR, 55, 101, and 96 for KAT, and 47, 88, and 90 for STC at 0700, 1300, and 1700 h, respectively (SEM 3.1); however, there was an interaction ($P = 0.007$) among breed, region, and time (57, 110, and 101 for MW DOR; 59, 110, and 108 for MW KAT; 43, 89, and 88 for MW STC; 65, 113, and 111 for NW DOR; 54, 104, and 96 for NW KAT; 56, 92, and 94 for NW STC; 49, 93, and 96 for SE DOR; 52, 105, and 96 for SE KAT; 45, 79, and 87 for SE STC; 57, 110, and 104 for TX DOR; 54, 83, and 84 for TX

KAT; and 46, 91, and 89 for TX STC at 0700, 1300, and 1700 h, respectively [SEM 6.1]). In conclusion, RT of STC was low at all times compared with DOR and KAT, even with lower RR. There appeared to be considerable adaptation from wk 1 to 2 during the 2 highest HLI periods via evening respiration. Region effects varied with breed, such as relatively high RR by STC from the NW to maintain low RT, lower RR of DOR from the SE than other regions, and a smaller difference among times in RR of KAT from TX.

Key Words: adaptation, hair sheep, heat
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693 Feeding behavior of grazing lambs in a silvopastoral system during dry season in Brazil.

F. de Oliveira Scarpino van Cleef*[1,2], T. Silva do Nascimento[1], D. J. A. Santos[1], E. H. C. B. Van Cleef[1], and A. C. Ruggieri[1,2], *[13]São Paulo State University, Jaboticabal, Brazil, [2]CNPq, Brasilia, Brazil.*

The aim of this study was to evaluate the presence of shade on the behavior of grazing lambs during dry season in Jaboticabal, State of São Paulo, Brazil. The climate in Jaboticabal is classified as tropical-Aw, and the dry season starts in June, when this study occurred. Massai grass (*Panicum maximum* × *Panicum infestum*) was used as the forage and eucalyptus (*Eucalyptus urophylla* × *Eucalyptus grandis*) was used as the trees. Twenty-four crossbred lambs (23 ± 3.3 kg BW and approximately 90 d old) were blocked by initial BW and assigned into 3 experimental treatments: unshaded (UN), which is unshaded Massai grass pasture; moderate shading (MS), which is Massai grass pasture with eucalyptus trees spaced 12 by 2 m; and intense shading (IS), which is Massai grass pasture with eucalyptus trees spaced 6 by 2 m. Light interception was the criteria for starting grazing period, and the residual pasture height was fixed at 20 cm. Animals were observed over 8 consecutive days in order 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 (OA). Previously trained observers recorded the behavioral activities, every 10 min, from 0800 to 1700 h. Data were submitted to ANOVA, using the MIXED procedure of SAS, and the treatments' means were compared using Tukey's test at 5% significance. Animals in UN spent more time on FE (64% for UN, 54% for MS, and 51% for IS; $P < 0.0001$), with no differences observed between treatments with trees. Time of LR was greater for IS (23% for UN, 25% for MS, 32% for IS; $P < 0.0001$). On the other hand, animals in MS spent more time SS (0.8% for UN, 4% for MS, 1% for IS; $P < 0.0001$) and SR (0.5% for UN, 0.9% for MS, and 0.3% for IS; $P = 0.0001$), but both activities were similar between UN and IS. The activities LY, SF, and OA did not differ among treatments ($P = 0.28$, $P = 0.61$, and $P = 0.09$, respectively). The silvopastoral system improved the state of welfare of the lambs, as shown by the greatest time spent lying ruminating.

Key Words: eucalyptus, heat stress, shade
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694 In vitro methane production of diets containing high concentrations of crude glycerin for feedlot sheep.

E. H. C. B. van Cleef*[1,2,3], M. T. C. Almeida[1,2], F. O. S. van Cleef[1,4], A. L. Abdalla Filho[3,5], P. P. Santos[5], A. L. Abdalla[5], and J. M. B. Ezequiel[1], *[1]São Paulo State University, Jaboticabal, Brazil, [2]FAPEMIG, Belo Horizonte, Brazil, [3]FAPESP, São Paulo, Brazil, , [4]CNPq, Brasilia, Brazil, [5]Centre for Nuclear Energy in Agriculture, University of São Paulo, Piracicaba, Brazil.*

Crude glycerin is the major byproduct of the biodiesel industry. Previous studies have indicated this byproduct as an enteric methane (CH_4) mitigating agent. An in vitro rumen batch culture study was conducted to compare the effects of high inclusions of crude glycerin in diets for feedlot sheep on CH_4 production. The technique used in this trial involved the measurement of gaseous species produced during fermentation by a pressure transducer. Isonitrogenous (18.4% CP) and isoenergetic (2.7 Mcal ME/kg DM) diets were composed of corn silage, soybean hulls, soybean meal, mineral premix, cracked corn grain, and crude glycerin included at 0 (G0), 10, 20, or 30% (G30) of the total diet (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. Three adult male rumen-cannulated sheep were used as rumen fluid donors. To carry out this study, 160-mL serum bottles ($n = 30$) containing 0.5 g test feed (placed into F57 Ankom filter bags), 50 mL buffer solution, and 25 mL ruminal fluid were used. The bottles were sealed and placed into a forced-air oven (39°C). Each mixture was incubated in triplicate. The pressure was measured and gas samples were collected at 0, 4, 8, 12 and 24 h after incubation, and the cumulative gas production was evaluated. After the 24-h incubation period, terminal pH was measured. Filter bags containing feed residues were washed, dried, and incinerated to determine OM disappearance. Gas samples were evaluated for CH_4 concentration by gas chromatography. Data were analyzed using the MIXED procedure of SAS, and whenever the F-test was significant, contrast analyses (linear, quadratic, and 0 × glycerin) were performed. No interaction of treatment × inoculum was observed in this trial ($P > 0.10$). Total gas production (mL/g OM disappeared) was not altered ($P = 0.44$) by crude glycerin inclusion (average 54.5 mL). However, CH_4 concentration was linearly increased ($P = 0.004$) with values from 4.6 (G0) to 7.4 mL/g OM disappeared (G30). Terminal pH was also affected by treatments, with values linearly decreasing from 6.7 (G0) to 6.6 (G30; $P = 0.003$). The inclusion of high concentrations of crude glycerin in feedlot diets for lambs does not alter in vitro gas production but linearly increases methane concentrations and linearly decreases terminal pH.

Key Words: crude glycerin, methane, sheep
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695 Effects of high concentrations of crude glycerin on rumen microbial populations in sheep.

E. H. C. B. van Cleef*[1,2,3], M. T. C. Almeida[1,3], F. O. S. van Cleef[1,4], A. L. Abdalla Filho[3,5], P. S. Correa[5], A. L. Abdalla[5], and J. M. B. Ezequiel[1], [1]*São Paulo State University, Jaboticabal, Brazil,* [2]*FAPEMIG, Belo Horizonte, Brazil,* [3]*FAPESP, São Paulo, Brazil,* [4]*CNPq, Brasilia, Brazil,* [5]*Centre for Nuclear Energy in Agriculture, University of São Paulo, Piracicaba, Brazil.*

Crude glycerin, the major byproduct of biodiesel industry, can alter ruminal kinetic parameters. The objective of this trial was to evaluate the effects of high concentrations of crude glycerin on rumen microbial groups. Isonitrogenous (18.4% CP) and isoenergetic (2.7 Mcal ME/kg DM) diets, composed of corn silage, soybean hulls, soybean meal, mineral premix, cracked corn grain, and crude glycerin (83% glycerol, 95% DM, 6% salt, and less than 0.01% methanol) included at 0 (G0), 10 (G10), 20 (G20), or 30% (G30) of the total diet (DM basis), in a roughage:concentrate ratio of 40:60, were used as substrates in an in vitro rumen batch culture trial. Three adult male rumen-cannulated sheep were used as rumen fluid donors. The incubation was carried out in 160-mL serum bottles ($n = 30$) containing 0.5 g test feed (placed into F57 Ankom filter bags), 50 mL buffer solution, and 25 mL ruminal fluid. The bottles were sealed and placed into a forced-air oven (39°C). After 24 h of fermentation, bottles were placed into an ice bucket to halt microbial activity. Deoxyribonucleic acid extraction was performed using commercial kits and used for the quantitative PCR assay, using primers for bacteria (BACT), rumen fungi (FUNG), *Ruminococcus flavefaciens*, *Fibrobacter succinogenes*, and rumen methanogens (METH). The relative population sizes of microbial groups were expressed as proportion of BACT 16S rDNA. The ΔCt values were calculated by subtracting the Ct (threshold cycle) value of target gene from the Ct value of reference gene. The relative expression of target groups was calculated from the ΔCt values as $2^{-\Delta Ct}$ and the relative quantification as $100 \times (2^{\Delta Ct})^{-1}$ (%). Data were analyzed using the MIXED procedure of SAS, and whenever the *F*-test was significant, contrast analyses (linear, quadratic, and 0 × glycerin) were performed. No interaction of treatment × inoculum was observed in this trial ($P > 0.10$). The Ct of reference gene was not different ($P > 0.10$) among treatments (average 14.9). Experimental substrates also did not alter ($P > 0.10$) relative proportions of FUNG (0.003%), *R. flavefaciens* (0.003%), and *F. succinogenes* (0.05%) but tended to linearly ($P = 0.07$) decrease METH (13.9, 10.2, 10.8, and 9.2% for G0, G10, G20, and G30, respectively). In conclusion, crude glycerin, even in high concentrations (up to 30% DM), has minimal impact in the amount of rumen BACT and proportions of FUNG, *R. flavefaciens*, and *F. succinogenes* but tends to linearly decrease METH.

Key Words: crude glycerin, microorganism, sheep
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696 Whole-genome single nucleotide polymorphism study of Romanov sheep.

T. Deniskova*[1], A. V. Dotsev[1], M. Selionova[2], K. Wimmers[3], H. Reyer[3], V. R. Kharzinova[1], G. Brem[1,4], and N. A. Zinovieva[1], [1]*L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation,* [2]*All-Russian Research Institute of Sheep and Goat, Stavropol, Russian Federation,* [3]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany,* [4]*Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.*

The Romanov breed stands out from the global variety of sheep breeds. Romanovs originated from local sheep at the end of 17th century in the Volga Valley. Since the 1970s, the breed has become popular in France, Canada, and the United States. Some unique traits are of permanent interest to this Russian breed. Primarily, Romanovs have outstanding reproduction qualities: early sexual maturity, out-of-season breeding ability, and extraordinary prolificacy. Using Romanov ewes in crossbreeding programs is a profitable, practical method to increase the number of highly viable hybrids. In addition, the Romanov breed has unique wool properties, which are very suitable for manufacturing felt products, rugs, and mats. However, detailed genetic information on the breed is lacking. Therefore, we performed the whole-genome SNP analysis of the original Romanov sheep to study its genetic diversity and genetic relationships with other Russian breeds. We genotyped 42 samples of Romanovs using the OvineSNP50K BeadChip and pooled the data with the set from 24 Russian breeds. Quality filtering was performed in PLINK version 1.07. Calculations were done in PLINK version 1.07, GENETIX version 4.05, and HP-Rare 1.1. We found a lower level of genetic diversity in Romanovs (Ho = 0.350 and Ar = 1.862) in comparison with other coarse wool breeds (Ho = 0.377 and Ar = 1.899). At the same time, Romanovs, compared with the 24 breeds, were characterized by the most insignificant deviation from Hardy–Weinberg equilibrium (Fis = −0.005). In other breeds, Fis values varied from −0.028 to −0.082. Pairwise Fst values ranged from 0.084 to 0.124 between Romanovs and Kuibyshev and Kuchugur, respectively. The MDS analysis revealed the genetic uniqueness of Romanov sheep. Principal component (PC) 1 divided all breeds into 2 groups according the wool type (fine wool + semifine wool and coarse wool) with 4.7% of total genetic variance. By PC1 the Romanov formed an incorporated bunch

and logically clustered with coarse-wool breeds. However, the Romanov was clearly separated from the others by PC2, which explained 3.8% of additional genetic variability. Most likely, a high level of consolidation and genetic differentiation of the Romanov breed from other Russian sheep are explained by its "pure gene" origin and was not improved by any breed. Our study is the first attempt to reveal the outstanding genetic nature of original Romanov sheep on whole-genome level. We will extend our study by genotyping more samples with medium-density DNA chip and using NGS technology. The research was performed under financial support of Russian Scientific Foundation (number 14-36-00039).

Key Words: MDS analysis, sheep breeds, whole-genome studies
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697 Effects of high heat load conditions on body weight, dry matter intake, and blood constituent levels of Dorper, Katahdin, and St. Croix sheep from different regions of the United States.

D. Tadesse[1], R. Puchala[*1], T. A. Gipson[1], I. Portugal[1], L. J. Dawson[1,2], T. Sahlu[1], and A. L. Goetsch[1], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Center of Veterinary Health Sciences, Oklahoma State University, Stillwater.*

Thirty-seven Dorper, 35 Katahdin, and 31 St. Croix ewes (57, 58, and 44 kg [SEM 2.2]) from 45 commercial farms in the Midwest (MW), Northwest (NW), Southeast (SE), and central Texas (TX), between 2.2 and 3.4 yr of age, were used to evaluate responses to high heat load index (HLI) conditions. There were 4 sequential 2-wk periods with target HLI during day/nighttime of 70/70, 85/70, 90/77, and 95/81. A 15% CP and 50% concentrate pelleted diet was fed at 120% of the ME requirement for maintenance, and water was offered free choice. Body weight was measured 3 times each week, and blood was sampled at 1300 h on the last day of each period. There was an interaction ($P < 0.001$) between period and week within period in BW, with slightly greater values in wk 2 vs. 1 of periods 3 and 4 and a greater difference between period 1 and 4 values in wk 2 than 1 (53.1, 54.1, 54.9, and 55.4 kg in wk 1, and 53.0, 54.2, 55.4, and 56.1 kg in wk 2 in periods 1, 2, 3, and 4, respectively [SEM 0.85]). There was an interaction ($P = 0.037$) in DMI (g/kg $BW^{0.75}$) among region, period, and week, with values generally similar between weeks in periods 1 and 2 relative to those in periods 3 and 4 (51.0, 52.4, 51.0, and 51.2 in period 3 and wk 1; 49.5, 52.1, 50.8, and 51.6 in period 3 and wk 2; 49.6, 52.1, 50.6, and 49.4 in period 4 and wk 1; and 48.9, 52.0, 49.7, and 46.3 in period 4 and wk 2 for MW, NW, SE, and TX, respectively [SEM 1.09]). Neither blood glucose nor lactate concentration was affected by breed ($P > 0.05$), but there were breed differences ($P < 0.02$) in serum concentrations of creatinine (0.91, 0.81, and 0.77 mg/dL [SEM 0.023]), total protein (6.13, 6.42, and 6.81 g/dL [SEM 0.156]), and urea N (17.4, 18.0, and 20.0 mg/dL [SEM 0.54] for Dorper, Katahdin, and St. Croix, respectively). In conclusion, some blood constituent levels suggest breed differences in resilience to high HLI. Differences among periods and weeks in BW presumably relate to increased water consumption with high HLI. The interaction in DMI may reflect differences among regions in rate of adaptation to high HLI and the contribution of decreased feed intake to coping with high HLI.

Key Words: adaptation, hair sheep, heat
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698 Effects of level of intake of a fifty-percent concentrate pelleted diet on digestion and energy utilization by Katahdin wethers.

D. Tadesse[*1], R. Puchala[1], I. Portugal[1], A. Hussein[1,2], and A. L. Goetsch[1], [1]*American Institute for Goat Research, Langston University, Langston, OK,* [2]*Department of Animal Science, Oklahoma State University, Stillwater.*

Nine mature Katahdin wethers (70 ± 1.5 kg initial BW) were used in a crossover experiment to evaluate effects on digestion and energy utilization of levels of feed intake being used in studies addressing the maintenance energy requirement with limited nutrient intake. A 50% concentrate pelleted diet composed of 20.0% ground alfalfa, 29.1% cottonseed hulls, 9.0% cottonseed meal, 20.0% ground corn, 13.0% wheat middlings, 5.0% pelleting agent, and 3.9% other ingredients was fed near the ME requirement for maintenance (Control; 44.4 g/kg $BW^{0.75}$ DMI) and at 55% of this level (Restricted; 24.4 g/kg $BW^{0.75}$ DMI). Periods were 4 wk in length, with 3 wk for adaptation, measures in the final week when situated in metabolism cages, and 2 d for gas exchange measurement via a head-box respiration calorimetry system. Apparent total tract digestibilities of DM (65.8 and 73.9% [SEM 1.92]), OM (76.3 and 81.7% [SEM 1.48]), CP (72.1 and 78.5% [SEM 1.70]), NDF (32.3 and 49.0% [SEM 3.34]), and GE (64.7 and 73.0% [SEM 1.97]) were greater ($P < 0.05$) for Restricted intake than for Control intake. Expressed in megajoules per day, quantities of energy in urine (0.94 and 0.72 [SEM 0.320]) and ruminally emitted methane (1.02 and 0.76 [SEM 0.085]) were greater for Control vs. Restricted intake ($P < 0.05$), but as a percentage of DE, they tended to be greater for Restricted intake (8.1 and 10.8% [SEM 3.52; $P = 0.056$] in urine and 9.0 and 11.1% [SEM 0.75; $P = 0.096$] in methane for Control and Restricted intake, respectively). As a consequence, ME intake as a percentage of GE intake did not differ ($P = 0.301$) between treatments (53.5 and 57.3% [SEM 2.88] for Control and Restricted intake, respectively). The difference in heat energy (447 and 379 [SEM 15.1]) was less than that in ME intake (395 and 225 kJ/kg $BW^{0.75}$ [SEM 21.4] for Control and Restricted intake, respectively). In conclusion, restricted feed intake had marked influences on digestibility, although effect on metabolizability

was tempered by changes in urinary and methane energy, the former presumably impacted by lean tissue mobilization. Based on the magnitude of difference between ME intake and heat energy with restricted intake, lower heat energy and less tissue mobilization would be expected with longer periods.

Key Words: digestion, feed intake, sheep
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699 Effect of dietary sulfur on in vitro true digestibility of various feedstuffs.

V. Garza[*1], K. C. McCuistion[1], G. Faz[1], C. L. Lara[2], J. J. Martinez[1], L. P. Sastre[1], and N. L. Bell[1], [1]*Texas A&M University – Kingsville, Kingsville,* [3]*Texas A&M University – Kingsville, Rio Grande City, TX.*

The effect of dietary sulfur on digestibility of feedstuffs is not well defined. The primary objective of this study was to evaluate the effect of dietary sulfur on in vitro true digestibility (IVTD) of various feedstuffs. A secondary objective was to determine the effect of sulfur-treated rumen fluid on IVTD of various feedstuffs. Treatments consisted of 0 (CON) or 0.3% (SUL) sulfur mixed into the ration of 8 Dorper wethers (29.87 ± 0.52 kg BW) consuming a commercial growing ration (Purina Honor Show Chow Show lamb Grower 15% DX Medicated feed) with chopped coastal hay mixed at 90:10%. Wethers were individually housed for the duration of the 56-d trial. Feedstuffs were selected to represent a variety in nutrient quality and included 4 roughages (wheat straw, bluestem hay, coastal hay, and alfalfa hay) and 3 commercial feedlot rations (starter, intermediate, and finisher diets). Ground feedstuff samples containing CON or SUL treatments were weighed into F57 nylon filter bags in quadruplicate. Sheep were slaughtered 56 d after commencing sulfur inclusion. Gastrointestinal tracts were collected during slaughter to allow for rumen fluid collection. Rumen fluid was processed and IVTD protocol was performed in accordance with ANKOM (2005) using an ANKOM Daisy^{II} Incubator. Data were analyzed using the MIXED procedure of SAS 9.3 (SAS Inst. Inc., Cary, NC). An interaction between treatment and feedstuff was not observed ($P \geq 0.64$). A main effect of treatment was not observed ($P \geq 0.22$). A main effect of feedstuff was observed ($P < 0.01$) with starter feedlot ration having the greatest IVTD and wheat straw having the lowest. Results suggest that dietary sulfur does not impact IVTD of feedstuffs, but great diversity exists amongst different types of diets.

Key Words: digestibility, Dorper, sulfur
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SWINE SPECIES

700 Utilization of high-quality cassava peel mash as an alternative source of energy in weaned pigs' diet.

A. O. Adesehinwa[*1], A. A. Fatufe[2], A. Samireddypalle[3], E. Ajayi[2,4], T. A. Adetunji[2], and I. Okike[3], [1]*Institute of Agricultural Research & Training, Ibadan, Nigeria,* [2]*Obafemi Awolowo University, Ile Ife, Nigeria,* [3]*Internatinal Livestock Research Institute, Ibadan, Nigeria,* [4]*Nigeria Institute of Animal Science, Ibadan, Nigeria.*

A growth trial was carried out with weaned crossbred (Large White × Landrace) pigs to determine the replacement value of high-quality cassava peel (HQCP) fine mash for maize and its optimal dietary inclusion levels in weaned pig's diet. One hundred five weaned pigs with an average initial weight of 7.45 kg (SEM 0.17) were allotted to 5 dietary treatment groups comprising 7 pigs per replicate and 3 replicates per treatment in a completely randomized design. Dietary treatments consisted of a control diet with 40% maize without HQCP, and HQCP replaced maize at 7.5, 15, 22.5, and 30% to constitute 4 more diets. The daily feed intake and weekly BW were recorded throughout the 70-d study period. Pigs on the control diet had significantly ($P < 0.05$) higher daily gains and feed intake compared with the other treatment groups (Table 700). Daily gain and feed intake tended to linearly decrease with increasing levels of HQCP. However, feed efficiency was comparable in the 0 (control), 7.5, and 15% HQCP groups. Pigs on 22.5 and 30% HQCP levels had significantly ($P < 0.05$) lower feed efficiency compared with pigs on replacement levels up to 15%. It could be concluded that HQCP was inferior to maize grains for optimum performance of the weaned pigs and, hence, the possible need for energy and protein fortification to match the nutrient profile of the maize grains; however, in terms of the feed efficiency, HQCP demonstrated potential for replacement of up to 15% of the 40% maize inclusion.

Key Words: alternative feedstuff, high-quality cassava peel, weaned pigs
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Table 700. Performance of weaned pigs fed diets containing graded levels of high-quality cassava peel (HQCP)

Parameters	0% HQCP	7.5% HQCP	15% HQCP	22.5% HQCP	30% HQCP	SEM
Initial weight, kg	7.59	7.81	7.36	7.36	7.12	0.17
Final weight, kg	24.62^{a}	22.00^{ab}	19.49^{bc}	17.84^{cd}	15.57^{d}	0.60
BW gain, kg	17.05^{a}	14.19^{b}	12.12^{bc}	10.52^{c}	8.45^{d}	0.47
Daily weight gain, g	243.5^{a}	202.72^{b}	173.13^{bc}	150.26^{cd}	120.75^{d}	6.77
ADFI, g	661.65^{a}	579.25^{ab}	502.14^{b}	511.52^{b}	398.53^{c}	17.03
Feed efficiency	0.37^{a}	0.34^{a}	0.35^{a}	0.29^{b}	0.30^{b}	0.01

701 Decreased ileal permeability in piglets at weaning following exposure to irradiated topsoil.

M. A. Sales*[1], T. C. Tsai[1], C. V. Maxwell[1], and D. A. Koltes[2], *[1]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, [2]Department of Poultry Science, Division of Agriculture, University of Arkansas, Fayetteville.*

Weaning is a difficult transition for piglets that can result in significant loss of performance. Increased isolation of piglets early in life may prevent early exposure to pathogenic bacteria but may also reduce exposure to beneficial bacteria, which may prevent or delay intestinal development. In combination with the shift from a liquid-based diet to a solid corn–soy–based diet, these factors may be contributing to increased intestinal permeability following weaning. Therefore, we wanted to determine if exposure of piglets to topsoil or irradiated topsoil could decrease ileal permeability prior to weaning and potentially reduce the loss of performance experienced during weaning. Piglets were farrowed under normal commercial protocols and allowed 2 to 4 d prior to the topsoil exposure. At the commencement of the study, a pan containing nothing, topsoil, or irradiated topsoil was added to each pen. Pans were refreshed every 24 h. Prior to weaning on d 17 to 20, a pig of average weight of each pen was selected to measure ileal permeability from the control ($n = 5$), irradiated topsoil ($n = 6$), and topsoil ($n = 5$) treatments. Pigs were euthanized using captive bolt immediately followed by exsanguination. A 10-cm section of the distal ileum was excised, flushed, transported under aeration, and then mounted in an Ussing chamber. Transepithelial electrical resistance (TEER) was collected for 10 min prior to measuring the flux of fluorescein isothiocyanate labeled dextran from the mucosal to serosal side over the course of 1 h (permeability). Data were analyzed using PROC GLIMMIX in SAS where treatment was fit as a fixed effect and pig as a random effect. Body weight, age, and TEER were similar across the control, topsoil, and irradiated topsoil treatments ($P = 0.60$, $P = 0.88$, and $P = 0.42$, respectively). Ileal permeability was altered with exposure to the topsoil treatment ($P = 0.01$). Ileum samples collected from piglets exposed to irradiated topsoil were less permeable compared with ileum samples collected from control piglets ($P = 0.01$). Ileum samples collected from piglets exposed to topsoil were intermediate in permeability compared with ileum samples from control ($P = 0.25$) and irradiated topsoil ($P = 0.07$) piglets. Although we did not see an improvement in the BW prior to weaning, littermates exposed to topsoil and irradiated topsoil, on average, had 1 kg heavier BW at the end of the nursery phase, suggesting that the decreased permeability may help mitigate performance loss during weaning.

Key Words: integrity, topsoil, weaning
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702 Differential gene expression in peripheral mononuclear cells of pigs exposed to topsoil in early life.

T. C. Tsai*[1], D. A. Koltes[2], M. A. Sales[1], C. V. Maxwell[1], and J. E. Koltes[3], *[1]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, [2]Department of Poultry Science, Division of Agriculture, University of Arkansas, Fayetteville, [3]Department of Animal Science, University of Arkansas, Fayetteville.*

The objective of this study was to evaluate the effect of exposure to topsoil in early life on gene expression in peripheral mononuclear cells in an attempt to explain improved post-weaning performance as observed in previous studies. Litters ($n = 12$; PIC 29 × 380) delivered within 24 h were selected and blocked by sows' farrowing BW and parity and then randomly assigned to 1) control/no topsoil and 2) free access to topsoil from d 4 to 21 of lactation. Upon weaning, piglets (5/litter) were transferred to a nursery facility and housed in the same pen throughout the nursery period. Nursery diets were devoid of antibiotics and formulated to meet or exceed nutrient requirements recommended by PIC. Blood was collected through venipuncture via jugular vena cava into EDTA tubes from piglets with median BW at d 11 in each litter when they were 11, 20 (weaning), and 56 d old (the end of nursery). Peripheral blood mononuclear cells were isolated using Histopaque-1077 gradient centrifugation and total RNA was extracted using TRIzol. Total RNA that passed quantity and quality criteria (RQI = 5.1–9.8) were sequenced using Illumina chemistry with samples blocked by treatment and age within each sequencing lane. Sequencing reads were quality checked with FASTQC/0.11.1 and aligned with the *Sscrofa* 10.2.84 reference genome using Tophat/Bowtie 2. HTseq analysis was performed to assess the number of unique read per gene. Read counts were analyzed using PROC GLIMMIX of SAS with treatment, lane, RQI, parity of sows, age, sex, and treatment × age interaction fit as fixed effects and pig fit as a random effect. The q-values were calculated in R using the q-value package to control the false discovery rate (FDR) at 0.10. A total of 420 transcripts were differentially expressed for the treatment × age interaction ($P < 0.01$, $q < 0.10$) with 320 genes annotated by DAVID (version 6.8). Significantly overrepresented pathways and biological processes (FDR < 0.10) included acetylation, ubiquitin-like conjugation, serine/threonine protein kinase, phosphoprotein, carbohydrate metabolism, platelet activation, aminoacyl-tRNA biosynthesis, PI3K-AKt, insulin, and HIF-1 signaling pathway. Changes in gene expression in these biological processes may be related to previously observed differences in growth and immune system maturation in pigs exposed to topsoil.

Key Words: gene expression, pigs, topsoil
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703 Evaluation of National Research Council method of estimating body protein-to-lipid ratio in growing pigs.

S. Ghimire* and C. Pomar, *Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

A study was conducted to evaluate the accuracy of the equation estimating body lipid–to–body protein ratio (BLBP) of growing pigs proposed in the NRC (2012) model. In this model, BLBP is set as initial condition for growing finishing pigs to predict body composition from BW and is described by the equation $\text{BLBP} = (0.305 - 0.000875 \times \text{PD}_{\text{Max}}) \times \text{BW}^{0.45}$, in which PD_{Max} (g/d) is the maximum protein deposition potential of the animal. The assessment was done using body composition data of 57 growing barrows (28 ± 2 kg BW) of a terminal cross line. The body protein and lipid content was measured using dual energy absorptiometry. The mean protein deposition of barrows from 25 to 55 kg BW ($n = 19$) and from 70 to 100 kg BW ($n = 20$) from the same batch was used to extrapolate the representative PD curve of the barrows as described by the NRC (2012). The maximum value from the curve was used as PD_{Max} (190 g) in the BLBP equation. All the animals were fed at or above recommended nutrient requirements. The residual error analysis for BLBP prediction by the NRC equation revealed a root mean squared prediction errors (RMSPE; as a percentage of observed mean) of 35%. The average BLBP predicted value was 0.62, whereas the average observed value was 0.94. Most of the errors (89%) were due to mean bias and some were due to slope bias (9%). These errors indicate that the NRC-proposed BLBP equation underestimates BLBP. When the default PD_{Max} (145 g/d) for growing barrows was used for BLBP prediction, the RMSPE was reduced to 19%, with 60% of errors partitioned to mean bias and 33% to slope bias. It was therefore concluded that the BLBP equation used in the NRC 2012 model underestimates body lipid–to–body protein ratio in pigs with high genetic potential for protein deposition.

Key Words: body lipid-to-protein ratio, model, pigs
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704 Effects of plant extracts on amino acid metabolism in pig small-intestinal bacteria in vitro.

L. Zhang[1], Z. Dai[*1], W. Zhu[2], Z. Wu[1], and G. Wu[1,3], [1]*State Key Laboratory of Animal Nutrition, China Agricultural University, Beijing, P.R. China,* [2]*College of Animal Science and Technology, Nanjing Agricultural University, Nanjing, P.R. China,* [3]*Texas A&M University, College Station.*

As alternatives to feed antibiotics, plant extracts have been used in animal husbandry for many years to improve animal health and growth. However, the underlying mechanisms remain largely unknown. Recent studies showed the important role of bacteria in AA metabolism in the pig small intestine. We hypothesized that the beneficial effect of plant extracts may result, in part, from their regulatory role in AA catabolism by small-intestinal bacteria. Three plant extracts, cinnamaldehyde, thymol, and anethol, were incubated with pig small-intestinal bacteria. Ileal digesta collected from the ileal cannula of four 20 ± 5 kg Duroc × Landrace × Large White pigs were mixed, processed, and inoculated into the chemically defined media (including mixtures of AA). Concentrations of the plant extracts in the media were 0 (control), 25 , 50 or 100 μmol/L. Incubation was carried out for 24 h at 37°C, and samples were taken at different time points for the determination of ammonia nitrogen (NH_3–N), AA, and polyamines. At the end of the 24-h culture, the addition of thymol, cinnamaldehyde or anethol at concentration of 100 μmol/L reduced ($P \leq 0.05$) ammonia production by 16, 22, and 42%, respectively. Compared with the control, 50 and 100 μmol/L thymol, cinnamaldehyde or anethol reduced ($P \leq 0.05$) the bacterial utilization of aspartate, glutamine, histidine, tyrosine, and tryptophan over a 12-h period of incubation. In addition, 50 and 100 μmol/L thymol or cinnamaldehyde reduced the 12-h bacterial utilization of glycine, and similar observations were observed with anethol after a 24-h period of incubation. Putrescine concentration increased ($P \leq 0.05$) in the media with 50 and 100 μmol/L thymol after a 12-h period of incubation. Likewise, cadaverine concentration increased ($P \leq 0.05$) in the media with 50 and 100 μmol/L thymol or cinnamaldehyde. Collectively, these observations indicate that thymol, cinnamaldehyde, or anethol can inhibit AA degradation in pig small-intestinal bacteria and that the essential oils serve as good alternatives to antibiotics for improving AA nutrition, growth, and health in pigs. Works in the laboratory were supported by the National Key Basic Research Program of China (2013CB127303) and the Natural Science Foundation of China (31301979). The authors also thank Ms. Yan Lei (Dadhank Biotech Corp) for support.

Key Words: amino acid metabolism, plant extracts, small-intestinal bacteria
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705 Evaluation of the compositional and nutritional values of *mCry1Ac* corn and *maroACC* corn in growing pigs.

R. Zhong[*1,2], L. Chen[1], L. Gao[2], L. Zhang[2], and H. Zhang[2], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P.R. China,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

The aim of this study was to evaluate the nutrient digestibility in growing pigs of 2 transgenic corn lines containing the *mCry1Ac* gene from a *Bacillus thuringiensis* strain (BT) and the *maroACC* gene from *Agrobacterium tumefaciens* strain (CC), respectively. Expression of the *mCry1Ac* gene confers resistance to *Pyrausta nubilalis* and the *maroACC* gene confers tolerance to herbicides. Eight pigs (60.5 ± 3.6 kg initial

BW) were surgically fitted with T-cannula in the distal ileum and allotted to a duplicated 4 × 4 Latin square design with 4 diets and 4 periods. The pigs were provided 4 corn-based diets formulated with the nontransgenic near-isoline control corn (CT), BT corn, CC corn, and commercially available nontransgenic reference corn (RF), respectively. The proximate components of the 4 corn ingredients and 4 diets were measured. The apparent ileal digestibility (AID), apparent total tract digestibility (ATTD), and hindgut fermentation of nutrients and energy were determined. The contents of proximate components, NDF, ADF, and AA in BT corn and CC corn were comparable to those in CT and RF corn. The AID, ATTD, and hindgut fermentation of DM, CP, ether extract, ash, NDF, ADF, and GE for pigs fed the 2 transgenic corn-based diets (BT and CC) were not different with those for pigs fed the CT corn–based diet. No difference was observed in DE among the 4 dietary treatments. The AID of AA, exception of isoleucine, was not affected by the dietary treatment. The AID of isoleucine for pigs fed the BT corn–based diet and the CC corn–based diet were less ($P < 0.05$) than for those fed the CT corn–based diet, but there was no difference in the AID of isoleucine among the 2 transgenic corn-based diets and the RF corn–based diet. In conclusion, the *mCry1Ac* corn and *maroACC* corn have compositional and the nutritional values similar to those of nontransgenic corn.

Key Words: nutritional values, pig, transgenic corn
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706 Lycopene affects hepatic gene expression of the main antioxidant enzymes in gilts.

M. R. Fachinello[1], A. V. S. Partyka[2], A. D. S. Khatlab[3], E. Gasparino[2], R. V. Nunes[4], and P. C. Pozza*[2], [1]*Universidade Estadual de Maringá/CAPES, Maringá, Brazil,* [2]*Universidade Estadual de Maringá/CNPq, Maringá, Brazil,* [3]*Universidade Estadual de Maringá/CNPq, Maringá, PR, Brazil,* [4]*Universidade Estadual do Oeste do Paraná/CNPq, Marechal Cândido Rondon, Brazil.*

The objective of this work was to evaluate the effects of lycopene 10% extract levels in the diet of pigs, barrows, and gilts on the gene expression of antioxidant enzymes in the liver. Fifteen barrows and 15 gilts (Piétrain × Landrace × Large White) with an initial weight of 75.23 ± 1.13 kg were used. Animals were distributed in a randomized block design with 3 replicates, using a 2 × 5 factorial scheme consisting of 2 sexes (male and female) and 5 levels of lycopene (0, 125, 250, 375, 500 mg/kg feed). Gene expression of the enzymes glutathione peroxidase, superoxide dismutase (SOD), and catalase were measured in the liver by quantitative PCR in real time. The F test was applied to the means obtained for the sex. The degrees of freedom related to the lycopene levels were unfolded in orthogonal polynomials to obtain the regression equations. There was a significant interaction between lycopene levels and sex for SOD ($P = 0.018$) and catalase ($P = 0.001$). A linear reduction in the gene expression of SOD and catalase in the gilts' liver was observed as the lycopene levels increased in the diet, adjusting the equations $y = -0.00125x + 0.9155$ ($R^2 = 0.50$) and $y = -0.00024x + 0.2418$ ($R^2 = 0.64$), respectively. Gene expression of SOD was lower ($P = 0.001$) in gilts with a supplementation of 500 mg of lycopene/kg of feed. Likewise, catalase was less expressed in gilts at levels of 0, 125 and 500 mg of lycopene, in relation to barrows. Lycopene levels did not influence ($P > 0.050$) the GLPx gene expression in the liver of the pigs, but the gilts presented a lower gene expression ($P = 0.001$) in relation to the barrows. These results indicate that lycopene may reduce the expression of antioxidant enzymes as a result of an adjustment of the cellular redox state due to the consumption of an exogenous antioxidant. It was concluded that lycopene reduced the gene expression of SOD and catalase enzymes in gilts' liver.

Key Words: catalase, glutathione peroxidase, superoxide dismutase
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707 Effect of fermented liquid potato hash diet with or without exogenous enzyme on growth performance of Growing Large White × Landrace crossbred pigs.

R. R. Thomas*[1], A. A. Kanengoni[2], and M. C. Chimonyo[3], [1]*Agricultural Research Council-Animal Production Institute, Irene, South Africa,* [2]*College of Agriculture and Environmental Sciences, University of South Africa, Florida, South Africa,* [3]*Animal and Poultry Science, School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal,, Pietermaritzburg, South Africa.*

The study aimed to evaluate growth performance of pigs fed fermented liquid potato hash with or without exogenous enzymes. A back-slopping fermentation approach was followed to prepare fermented diets. Potato hash was mixed with water at 1:2 ration and fermented for 8 hours before being fed to pigs. Diets were stored in a closed 100 L drum at 25°C room temperature. Diets containing either 200 g/kg fermented liquid potato hash (LFPH) (either enzyme treated or not) or no fermented potato hash (control) were formulated to to provide 14 MJ/kg digestible energy (DE), 180 g crude protein (CP)/kg and 11.6 g lysine /kg. Dietary treatments were control (no LFPH), enzyme treated LFPH (LFPHE), and untreated LFPH (ULFPH). The exogenous xylanase enzyme (Natugrain TS L®) was added in LFPH diet to provide a minimum of 560-840 TXU/TDU xylanase per kg feed, at an inclusion rate of 100 g/tonne.The diets were fed ad-lib to 36 Large White x Landrace crossbred grower pigs (25 ± 2.3 kg BW) that were individually housed. Pigs were allocated in a complete randomized design with six boars and six sows per diet. The control had higher ($P < 0.001$) final weight, average daily gain (ADG) and lower ($P < 0.001$) average daily feed intake (ADFI) and feed conversion ratio (FCR) compared to pigs fed diets containing LFPH. However, the LFPHE diet had higher ($P < 0.001$) final weight, ADG and lower ($P < 0.001$) ADFI and FCR compared to diet containing ULFPH. It was concluded that diet containing LFPHE may be an alternative feed source for growing pigs as indicated by higher intake compared to ULFPH.

Key Words: exogenous enzymes, fermented potato hash , grower pigs
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708 Influence of conjugated linoleic acid supplementation on body composition of growing pigs.

K. J. Stutts*[1], C. E. Lindsey[1], M. J. Anderson[1], J. L. Leatherwood[2], S. F. Kelley[1], and M. M. Beverly[1], *[1]Sam Houston State University, Huntsville, TX, [2]Department of Animal Science, Texas A&M University, College Station.*

Thirty-two crossbred gilts (8 wk and 15.9 kg) of similar breeding were used in a randomized complete block design to evaluate the effects of dietary supplementation of CLA on body composition of young, growing pigs. Pigs were blocked by BW and randomly assigned and evenly distributed among 3 treatment groups or a control group for an 84-d feeding trial. Diets consisted of a commercially available concentrate (Nutrena, Minneapolis, MN) with CLA supplemented at the rate of 0.33, 0.66, or 1.0% of the diet. The CLA source (BASF Corp., Florham Park, NJ) contained 55% CLA (mixture of *cis*-9, *trans*-11; *trans*-10, *cis*-12; and *trans*-9, *trans*-11 isomers). The control group received the same pelleted concentrate in addition to soybean oil supplemented at 0.33% of the total diet. Oil was administered as a drench to the control group and all treatment groups at 0600 h daily to ensure consumption. Body weight was obtained every 7 d with the intake of concentrate and supplement was adjusted accordingly. Fat thickness (cm) was measured at 14-d intervals via ultrasonography at the 10th rib, and LM area (LMA) was collected via ultrasonography at d 0, 42, and 84. Data were analyzed using the MIXED procedure of SAS. Overall effects were analyzed using repeated measures, and data from individual days were analyzed using fat thickness from d 0 as a covariate. Overall, there was no difference between treatments in BW ($P = 0.74$), 10th-rib fat thickness ($P = 0.36$), or LMA ($P = 0.70$). There was a significant treatment × time interaction for fat thickness. Tenth-rib fat thickness was lower at d 70 ($P < 0.03$) and 84 ($P < 0.04$) for pigs consuming 0.66 and 1.0% CLA compared with the control group. These data indicate that CLA supplemented at 0.66 or 1.0% of the diet fed to young, growing pigs has no effect on BW or LMA but did result in a decrease in back fat thickness after d 70 of treatment. It is likely that this trend would continue if the feeding period had been extended; however, further studies are needed to fully elucidate dietary CLA supplementation to alter body composition when fed to young, growing pigs.

Key Words: conjugated linoleic acid, fat thickness, swine
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709 Betaine affects muscle lipid metabolism via regulating the fatty acid intake and oxidation in finishing pig.

H. Wang*, S. Li, X. Wang, Y. Wang, and J. Feng, *College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China.*

This experiment was conducted to investigate how betaine affect muscle lipid metabolism. A total of 120 crossbred gilts (Landrace × Yorkshire × Duroc) with an initial BW of 70.07 kg (SD 0.70 kg) were randomly allocated into 3 treatments. Pigs were fed a corn–soybean meal basal diet supplemented with betaine at 0, 1,250, or 2,500 mg/kg, respectively. The feeding experiment lasted 42 d after a 7-d adaptation period. At the end of the trial, 18 pigs (6 from each dietary treatment) were euthanized and individual blood samples were collected and samples of LM between the 6th and 7th rib were obtained on the left side of the carcass. All data were analyzed using 1-way ANOVA of SAS 9.1. The results showed that betaine significantly increased the concentration of free fatty acid (FFA) in muscle ($P < 0.05$) and numerically decreased serum FFA ($P > 0.05$). Furthermore, the levels of serum cholesterol and high-density lipoprotein cholesterol were decreased ($P < 0.05$) whereas total cholesterol content was increased in muscle ($P < 0.05$) with dietary betaine supplementation. Experiments about key factors involved in fatty acid transportation showed that the gene expression of lipoprotein lipase, fatty acid translocase/cluster of differentiation (FAT/CD36), fatty acid binding protein (FABP3), and fatty acid transport protein (FATP1) were significantly increased with betaine supplementation ($P < 0.05$). Besides, the protein expressions of FATP1 and FABP3 were enhanced as well ($P < 0.05$). As for the key factors involved in fatty acid oxidation, although the level of carnitine and malony-CoA in muscle were not affected, both gene expression and protein expression of carnitine palmitransferase-1 (CPT1) were significantly increased with betaine supplementation ($P < 0.05$). Additionally, the gene expression of AMPKα2 and PPARα as well as the protein expression of p-AMPK was increased ($P < 0.05$). The results suggest that betaine supplementation could promote fatty acid uptake in the muscle and enhance fatty acid oxidation, leading to an increase of fatty acids in muscle.

Key Words: betaine, lipid metabolism, pig
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710 Effect of oregano essential oil supplementation to a reduced-protein diet on meat quality, fatty acid composition, and oxidative stability of longissimus thoracis muscle in growing-finishing pigs.

C. Chuan-Shang[1], H. Wei[2], and J. Peng*[2,3], [1]*Huazhong Agricultural University, WUHAN, China,* [2]*Department of Animal Nutrition and Feed Science, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China,* [3]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China.*

We investigated the effects of reduced-protein diet supplemented with oregano essential oil (OEO) on the meat quality, fatty acid composition and oxidative stability in longissimus thoracis (LT) muscle of growing-finishing pigs. A total of 36 growing barrows (Large White × Landrace) with an initial body weight (BW) of 29.0 ± 1.00 kg were obtained from a commercial farm in the Hubei province of China. Pigs were randomly allotted to 1 of 3 treatments based on BW in a randomized complete block design with 12 replicates of one pig per replicate. Pigs were penned individually. Three experimental treatments were formulated to consist of: 1) normal protein diet (NPD), 2) reduced-protein diet (RPD), and 3) identical reduced-protein diet supplemented with 250 mg/kg OEO (OEO). The three diets were based on corn-soybean meal-dried distillers grains with soluble (DDGS). The pigs in the NPD group were offered diets which contained 17% and 15.6% crude protein during the growing (days 0–49) and finishing (days 51–98) periods, respectively. The pigs in the RPD group were offered diets which contained 15% and 13.6% crude protein during their growing and finishing periods, respectively. Experimental diets were balanced with four amino acids (L-lysine, L-methionine, L-threonine, and L-tryptophan) to meet the requirements of growing-finishing pigs (NRC, 2012). RPD and OEO increased ($P < 0.05$) the b^*_{45min}, tenderness, overall acceptance and intramuscular fat (IMF) content of pork compared with NPD. The percentage of n-3 polyunsaturated fatty acid (n-3 PUFA) and the percentage of monounsaturated fatty acid (MUFA) in muscle of pigs fed with OEO supplemented diet were higher ($P < 0.05$) and lower ($P < 0.05$) than those in RPD, respectively. OEO improved ($P < 0.01$) oxidative stability, total antioxidative capacity and catalase but decreased ($P < 0.01$) drip loss in LT muscle compared with dietary NPD and RPD. In our study, reduced-protein diet supplementation with oregano essential oil enhanced the sensory attributes and anti-oxidative status of pork meat by improving IMF and n-3 PUFA percentage and antioxidative capacity.

Key Words: pigs, oregano essential oil, meat quality
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711 Occurrence of noninfectious lameness during rearing of gilts and its relationship with body weight and growth rate.

L. Fabà*[1], D. Solà-Oriol[1], E. Varella[2], and J. Gasa[1], [1]*Animal Nutrition and Welfare Service, Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra, Spain,* [2]*Tecnología & Vitaminas, S.L., Alforja, Spain.*

Within a herd, higher growth rate could be related with increased probabilities of showing leg problems. The aim of this study was to evaluate the current growth of rearing gilts and their relationship with occurrence of noninfectious lameness. A total of 600 gilts (Landrace × Yorkshire) between 57 and 106 d of age and 25.6 ± 8.6 kg of BW were monitored for a 137-d study. Gilts were blocked by BW (4 categories) and randomly distributed into 15 pens (10/pen) within the blocks of BW. Feed was offered ad libitum and fed in 3 phases (12.5, 11.9, and 11.5 MJ ME/kg; 180, 167, and 142 g CP/kg; and 12.5, 10.2, and 8.0 g Lys/kg CP in phases 0–14, 15–90, and 90–137, respectively) of corn, wheat, barley, and soya meal diet. Individual BW and observations of gait were performed on d 0, 22, 42, 69, 94, 116, and 137 by free walk on a 10-m corridor. Lameness was defined as any degree of gait difficulty without visual infection and swelling. Variables BW, ADG between measurements, and ADG calculated from BW intervals before lame detection (29–111 kg and 50–111 kg) were analyzed through ANOVA. Lameness and BW were analyzed through repeated measures over time including sow as random effect. Logistic regression was used to analyze BW at lameness detection with age or time. Occurrence of lameness was 8.34%, which eventually showed a recovery of 46.15%. The first lameness detection was at BW [114.6, 130.5] kg as confidence interval (CI) and age of [170.9, 187.8] d CI. From 115 d onwards, lame gilts showed lower BW and ADG than those not lame ($P < 0.029$). Besides, differentiation of lame gilts through BW or ADG was not possible 3 wk before lameness detection (last observation). In fact, for ADG calculated from the 29-to-111-kg and 50-to-111-kg BW, no differences were observed. Nevertheless, when the interval of BW for the calculation of ADG was broadened to 29 to 130 kg, the lame gilts showed a lower growth rate than those not lame [0.942, 0.963] vs. [0.882, 0.949] kg/d ADG CI ($P < 0.039$). Therefore, it was observed that lameness increased with BW and time ($P < 0.001$). In conclusion, noninfectious lameness is directly related to BW and independent of previous growth rate. Lameness generally appeared in gilts above 115 kg. Performance was compromised after lameness was detected Apparently, prediagnosis of lameness in replacement gilts cannot be related to a higher growth rate or BW when regime is ad libitum and the diet formulated for gilts.

Key Words: growth performance, leg weakness, osteochondrosis
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712 Carcass traits and meat quality of Berkshire crossbreds sired by heritage breeds.

H. S. Park*[1], T. Tennant[2], K. Spann[1], Y. Robbins[1], D. Hanson[2], N. C. Whitley[3], and S. H. OH[1], [1]*North Carolina A&T State University, Greensboro,* [2]*North Carolina State University, Raleigh,* [3]*Fort Valley State University, Fort Valley, GA.*

The objective of this study was to investigate the carcass traits and meat quality of Berkshire crossbreds sired by heritage breeds. The experiments were conducted at the North Carolina A&T State University farm located in Greensboro, North Carolina, where the climate features subtropical summer temperatures and mild winters with an average annual precipitation of approximately 110 cm. Berkshire sows were artificially inseminated with semen from Berkshire (BB), Hereford (HB) and Tamworth (TB) boars in each of three trials after feeding Matrix® for estrus synchronization. The sows used for breeding are raised in an outdoor hoop structure, free of antibiotics, until the last month of pregnancy. During the last month of pregnancy, the sows are moved to a pasture-based unit of 0.8 hectares and then moved to individual lots (14 x 24 m^2) with access to a farrowing hut, shade, and water ad libitum for farrowing. Piglets were farrowed outdoors and were housed in a deep-bedded hoop structure after weaning at 4 weeks of age. The boars were not castrated. Piglets were given standard NRC feed and water ad libitum. Total of 112 randomly selected animals were harvested at an USDA inspected abattoir at approximately 200 d of age. For the first two trials, the sows farrowed in the fall and the pigs were harvested in the spring, whereas for the third trials, the sows farrowed in the spring and the pigs were harvested in the fall. Live weights before harvest were recorded at the university farm. At harvest, hot carcass weight was collected prior to refrigeration. After 24-h refrigeration, carcass traits were collected following the NPPC guidelines. Boneless loins were packed in ice and transported to the NCSU Processed Meat Laboratory for further analyses, including marbling score, and objective and subjective color scores. All analyses were analyzed with PROC GLM in SAS 9.3. Breed and sex were included as fixed effects, and day of age was included as a covariate in the statistical model. Interaction between breed and sex was not included because it wasn't statistically significant. Overall, the males consistently had lower backfat at last lumbar throughout all trials ($P < 0.05$). In the first trial, BB had a significantly higher marbling score and a lower a* score than HB, and in the second trial, TB had a significantly larger longissimus muscle area than HB ($P < 0.05$); however, when three breeds were compared in the third trial, no significant difference was found.

Key Words: Berkshire, Outdoor, Meat quality
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713 Sensory characteristics of Berkshire crossbreds sired by heritage breeds.

H. S. Park*[1], T. Tennant[2], K. Spann[1], Y. Robbins[1], D. Hanson[2], N. C. Whitley[3], and S. H. OH[1], [1]*North Carolina A&T State University, Greensboro,* [2]*North Carolina State University, Raleigh,* [3]*Fort Valley State University, Fort Valley, GA.*

The objective of this study was to evaluate the sensory characteristics of Berkshire crossbreds sired by heritage breeds. The experiments were conducted at the North Carolina Agricultural and Technical State University farm located in Greensboro, North Carolina. Berkshire sows were artificially inseminated with semen from Berkshire (BB) and Hereford (HB) boars. Piglets were farrowed outdoors and were housed in a deep-bedded hoop structure after weaning at 4 weeks of age. The boars were not castrated, and the piglets were given standard NRC feed and water ad libitum. Animals were randomly selected and harvested at an USDA inspected abattoir at approximately 200 days of age. Loins were removed from one side of 14 BB and 10 HB pigs after harvest, and were packed in ice and transported to the NCSU Food Science for sensory panel testing. Samples of loin chops from BB and HB female and male pigs were presented to 101 panelists. The panelists evaluated the overall liking, as well as the overall flavor, freshness, texture and meaty flavor likings for each of the four samples on a 9-point hedonic scale where 1 = dislike extremely and 9 = like extremely. They also evaluated the texture, moisture and meaty flavor of the samples on a 5-point JAR scale where 1 or 2 = too little, 3 = just about right, and 4 or 5 = too much. The responses were analyzed with PROC GLM in SAS 9.3. Breed and sex were included as fixed effects. Interaction between breed and sex was not included because it wasn't statistically significant ($P > 0.05$). The difference between the breeds, as well as the sexes, were not significant for the overall, overall flavor, freshness, and meaty flavor likings ($P > 0.05$). There was a significant difference between both breeds and sexes for the texture liking ($P < 0.05$). Berkshire sired pigs and females scored higher than HB and males, respectively. However, when the panelists were asked to evaluate the texture of the loin chops on a 5-point JAR scale, they could not tell the difference between the samples. Boar taint did not affect the sensory characteristics of pork from pigs reared outdoors. Even though there was a statistical difference in the texture liking of the samples from different sexes, the difference was not observed when the range of the evaluation scale was reduced. However, BB and females received higher scores for purchase intent than HB and males, respectively ($P < 0.05$).

Key Words: Berkshire, Outdoor, Sensory Characteristics
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714 The association of DMD gene with productive traits of Russian Landrace pigs.

T. V. Karpushkina, M. S. Fornara, O. V. Kostyunina, V. R. Kharzinova*, and N. A. Zinovieva, *L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation.*

Stress syndrome is a significant problem for pig producers. One of the genetic factors responsible for porcine stress-sensitivity is a mutation C→T resulted in R1958W amino acid substitution in the dystrophin (*DMD*) gene, which is localized on the X chromosome. Recent studies have shown the association of T allele with the appearance of stress syndrome in Landrace pigs. The aim of this work was study the effect of *DMD* gene polymorphism on the variability of growing capacity and carcass traits in Russian Landrace pigs. Polymorphism C→T in *DMD* gene was determined by pyrosequencing. Among 507 pigs, 76 (14.99%) were detected as heterozygous carriers of the mutant allele T, and 431 (85.01%) were homozygous for C allele. Productive traits of 9329 offspring of 66 boars (15 boars were the carriers of mutant T allele and 51 boars were the non-carriers) were analyzed using two-way cross-classification model with interaction. Variance analysis showed a statistically significant effect of the factor «*DMD* genotype of boar» on the traits variability in their offspring: body weight at the end of growing period ($P < 0.05$), the average daily gain from birth to the statement on the growing ($P < 0.01$), the average daily gain during growing period, the average daily gain for the entire period, the carcass meat content, the back fat thickness and muscle deeps ($P < 0.001$). The interaction between «DMD genotype of boar × offspring sex» had a significant effect on the variability of two traits: the back fat thickness and the carcass meat content ($P < 0.05$). Offspring of boars, which are the carriers of the mutant T allele, were characterized by lower back fat and higher carcass meat content comparing to non-carriers. Thus, pig breeding for productive traits can lead to the increase of the frequency of T allele of *DMD* gene, due to its positive associations with some productive traits. To avoid the T allele of *DMD* gene from breeding herds, the DNA diagnostics is necessary This work is carried out in the framework of the fundamental research (14:0600-2016-0005)

Key Words: DMD gene , Landrace, productive traits
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715 Effect of leucine supplementation to a reduced crude protein diet on nitrogen utilization in lactating sows.

S. Zhang*, N. Regmi, M. Qiao, and N. L. Trottier, *Michigan State University, East Lansing.*

The objective of the study was to test the hypothesis that partial substitution of dietary CP with crystalline amino acids (CAA) increases nitrogen (N) utilization and milk production, and with CAA in combination with Leu decreases N utilization and milk production. Lactating multiparous Yorkshire sows (36) were used in the experiment and were assigned to 1 of 3 diets: 19.60% CP (CON); 14.22% CP (OPT); 14.56% CP (OPT+LEU). Sow body weight (BW) and backfat were measured on d 1 and 21 of lactation while piglet BW was measured on d 1, 4, 7, 14, 17 and 21 of lactation. Nitrogen balance was measured on sows between d 4 and 7 (early) and d 14 and 17 (peak) of lactation. Overall mean of sow BW change (– 4.5 ± 4.47 kg), backfat change (– 2.2 ± 0.79 mm), average daily intake (5.36 ± 0.19 kg), and litter growth rate (2.5 ± 0.13 kg/d) did not differ across diets over the 21-d lactation period. Nitrogen intake decreased as dietary CP concentration decreased (149.5, 112.0, and 104.9 ± 3.29 g/d; 206.3, 156.6, and 152.9 ± 5.29 g/d for CON, OPT and OPT+LEU, in early and peak lactation, respectively; $P < 0.01$). In early lactation, maternal N retention (NRm) (N intake – fecal and urinary N) did not differ between diets (overall mean: 84.5 ± 4.04 g/d) and total N retention (NRt) (N intake – fecal and urinary N – milk N) differed ($P < 0.05$) across diets (32.9, 20.7, and 17.0 ± 3.57 g/d). In early lactation, as dietary CP decreased, NRt as percentage of N intake (61.0%, 74.6%, and 73.0% ± 0.02%) or percentage of N absorbed (N intake – fecal N) (69.3%, 84.8%, and 82.7%) increased ($P < 0.01$). In peak lactation, NRt (65.0, 14.4, and 29.3 g/d) and NRm (147.0, 116.7, and 125.2 ± 5.27 g/d) differed across diets ($P < 0.01$). As percentage of N intake, NRm (71.0%, 74.5%, and 82.0% ± 0.02%) or of N absorbed (80.7%, 84.6%, and 93.2% ± 0.03%) differed across diets ($P < 0.05$). Feeding lactating diets reduced in CP from 19.6 to 14.2% with CAA inclusion as partial replacement for limiting AA, with or without Leu, improved N utilization efficiency.

Key Words: amino acid intake, lactating sows, nitrogen retention
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716 Maternal supplementation of DL-Met or OH-Met above the requirement in total sulfur amino acids benefits to neonatal growth of piglets.

B. Y. Xu[1], D. I. Batonon-Alavo*[2], Y. Mercier[2], F. Rouffineau[2], L. B. Ma[1], N. Y. Zhang[1], and L. Sun[3], [1]*Department of Animal nutrition and Feed Science, Huazhong Agricultural University, Wuhan, Hubei, China,* [2]*Adisseo France SAS, Commentry, France,* [3]*Department of Animal Nutrition and Feed Science, Huazhong Agricultural University, Wuhan, Hubei, China.*

The objective of this study was to compare the effect of methionine supplementation above the requirements, as DL-Met (DLM) or OH-Met (HMTBA), during gestation and lactation periods on sows and neonatal piglets' performance. Thirty cross-bred (Landrace x Yorkshire) primiparous sows were fed with a control (CON), DLM or HMTBA diet from 30 days before farrowing to 21 d post-partum. Diets were formulated to meet NRC (2012) recommendations in amino acids except for total sulfur amino acids (TSAA) which were supplied 25% above the level present in the CON, respectively for DLM and

HMTBA diets. Dietary Met content in the CON during the gestation period was 0.29% and 0.32% in the lactation period. Dietary Met+Cys content of the CON was 0.52% and 0.60%, respectively for the gestation and lactation periods. Within 12 h of farrowing, all litters were standardized to have 10 piglets per sow. Body weight and backfat thickness (body score) of sows at day 85 and 110 of gestation and 21 d postpartum were measured. Feed intake was also recorded. The reproductive performance of sows, i.e. litter size, total born alive, birth weight and weight gain of progeny was also measured at lactation d7, 14 and 21. Results showed no significant difference of feed intake, body weight and backfat thickness between sows during the gestation and lactation periods. However, when expressed as bodyweight and backfat thickness changes between d21 and d1, significant differences were observed for these two parameters during the lactation period. Sows in the HMTBA treatment showed the lowest changes in body weight as well as backfat thickness in comparison to the CON and DLM groups ($P < 0.05$). No significant difference was observed on the litters at birth. At postnatal d 14, piglets in the HMTBA (3.81 ± 0.17 kg) and the DLM (3.64 ± 0.20 kg) groups had higher body weights than those in the CON group (3.06 ± 0.19 kg). Similar results were obtained at d 21 with the highest body weight observed with the HMTBA group (+14% in comparison to the CON). Altogether, these results indicated that maternal supplementation of DL-Met and HMTBA, 25% above the recommended level leads to significant improvement of piglets' body weight at weaning age.

Key Words: Swine, Growth, Methionine
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717 Combination of multi-strain *Bacillus* spp. direct-fed microbial and a protease enzyme improved wean-to-finish pig performance - a commercial scale evaluation.

W. Li*, L. Payling, and M. C. Walsh, *Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, United Kingdom.*

A trial was carried out to evaluate the effect of a multi-strain *Bacillus* spp. direct-feed microbial (DFM) in combination with a protease on growth performance and death loss of wean-finish pigs fed corn/soybean meal type diets under commercial conditions. Two treatments were tested (18 replicates per treatment and 31 pigs per replicate): 1) negative control (NC), and 2) NC + *Bacillus*-based DFM (Danisco Animal Nutrition, Marlborough, UK) and a *Bacillus subtilis* protease (Danisco Animal Nutrition, Marlborough, UK). A corn/SBM/DDGs based NC diet was formulated to meet the nutrient requirements (NRC, 2012) with the exception of net energy which was reduced by 80, 25 and 15 kcal/kg in nursery (d 0-48), grower (d 48-104) and finisher (d 104-132), respectively. The DFM supplied three strains of *Bacillus* in equal proportions to provide 1.5 x 10^5 cfu/g. The protease preparation supplied 5000 U/kg. All pigs in the trial were fed the mash diet with ad lib. access from weaning (d 0 post-weaning, BW=6.00±0.33 kg) to finish (d 132). Both diets were supplemented with 750 FTU/kg *Buttiauxella* sp. phytase. Performance, including body weight and feed intake by pen, was measured on d 0 and every subsequent 28 days until the end of the trial. Over the entire growth period, liveability was 87.5% in pigs fed NC and 89.9% in pigs fed NC+DFM+protease. Overall FCR (d 0-132) of pigs fed DFM+protease diet was 6 percentage points lower (2.38 vs 2.43 g/g, $P < 0.01$), with numerically greater ADG (794 vs 777 g/d, $P > 0.05$) and ADFI (1909 vs 1891 g/d, $P > 0.05$) than those fed NC treatment. Responses of pigs to DFM+protease inclusion differed depending on growth phase. The ADG and ADFI were similar between pigs fed NC and NC+DFM+protease diets during nursery (average, 528 g/d) and grower (average, 979 g/d) phases ($P > 0.05$). As a result, FCR was not affected by diet treatments, with an average of 1.54 and 2.39 g/g for nursery and grower, respectively ($P > 0.05$). During finisher phase, even though there were only numerical improvements in ADG (874 vs 821 g/d; $P = 0.07$) and ADFI (2,926 vs 2,793 g/d; $P = 0.07$) due to DFM+protease inclusion, the resulting FCR was 15 percentage points lower as compared to those fed NC only diet (3.26 vs 3.41 g/g, $P < 0.01$). In conclusion, the combination of a multi-strain *Bacillus* spp. DFM and a protease improved FCR of pigs fed reduced energy diet, which was most effective during the finisher phase.

Key Words: wean to finish pig, direct-fed microbial and protease combination, performance
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718 Factors affecting the color of dried distillers grains with solubles.

B. J. Breitling*[1], and K. J. Herrick[2], *[1]POET Research Inc., Sioux Falls, SD, [2]POET Nutrition Inc., Sioux Falls, SD.*

A very common and easily measured metric to characterize dried distillers grains with solubles (DDGS) is color. Drying practices and equipment used by ethanol biorefineries during the early stages of the industry often resulted in dark and burnt DDGS with poor digestibility. These early experiences led to the perception that heating was the only factor contributing to DDGS color. It was our objective to review ethanol production variables to identify additional factors which affect the color of DDGS. Data was collected from 27 POET (Sioux Falls, SD) biorefineries during the period from January 1, 2016 to December 31, 2016. Hunter L color values of DDGS were matched with production variables collected during the ethanol process for each batch of DDGS. Preliminary evaluation of the data identified an obvious difference of dryer type on DDGS color and therefore only data from biorefineries with dual ring dryer technology were selected. This resulted in a data set of 7,575 Hunter L color observations from 16 biorefineries. Data from 57 variables on a batch basis that where shown to be correlated to DDGS Hunter L color were analyzed using the multiple linear regression platform of JMP (JMP Pro, version 12.2.0). All variables had a variance inflation factor less than 2 so multicollinearity was not an issue. The Hunter L Color of DDGS ranged from 41 to 63 for these batches and averaged 54.26 ± 3.49 (SD). Nineteen variables were identified as being related to DDGS color and included in the model. The R^2 for the actual color by predicted color for the model was 0.51 and the root mean square error was 2.45. The LogWorth statistic is a logarithmic transformation of the *p*-value and used to determine contribution of each variable to the model. Greatest LogWorth values were for residual glucose (403.0), syrup dryer temperature (148.6), syrup dryer exit temperature (146.9), normalized syrup addition to the wetcake dryer (88.7), oil separation process temperature (85.7), and syrup percent solids (82.5). In conclusion, this evaluation identified several factors that affect color of DDGS at biorefineries using a similar ethanol process. The data would suggest there are factors that are not routinely collected at biorefineries which may also have an effect on DDGS color. Additional research needs to be conducted to not only better understand factors associated with DDGS color, but also further identify how these factors affect DDGS digestibility and quality.

Key Words: Quality, Dried distillers grains with solubles, Color
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719 Identifcation of risk factors associated with slow growth rate of swine in commercial conditions.

S. López-Vergé*[1], M. Farré[2], D. Solà-Oriol[1], J. Bonet[3], J. Coma[3], and J. Gasa[1], [1]*Animal Nutrition and Welfare Service, Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra (08193), Spain,* [2]*Department of Mathematics, area of Statistics and Operations Research, Universitat Autònoma de Barcelona, Bellaterra, Spain,* [3]*Vall Companys Group, Polígono Industrial El Segre, Lleida, Spain.*

Body weight (BW) variability in swine production hinders farm efficiency and occupies time, especially in growing-finishing facilities. Pigs with a slower growth rate perform worse than their faster counterparts, increasing the period until reaching the market BW and, hence, reducing the farmer's income. The aim of this observational study was to identify risk factors associated with a reduced growth rate of swine regarding the whole production cycle. The study was conducted in a commercial farm, in which pigs were slaughtered in three times, at d 163 (n = 423), d 188 (n = 402) and d 205 (n = 203). A total of 1028 male and female crossbreed pigs [*Pietrain x (Landrace x Large White)*] from 110 dams were included in the trial. Piglets were weighed weekly from birth to weaning and then every three weeks until slaughter. Piglets that did not survive until the finishing period were excluded from the trial. Variables including length of gestation, length of lactation, parity, litter size, sex, birth BW and ADG (0-7, 21-64, and 65-83 d) were considered. Pigs leaving the farm in the third group were defined as slow growing pigs (20% of pigs). Statistical analyses were performed with the R software (R Core Team, 2015). A multiple logistic regression, taking the growth rate as a binary response (1 = slow; 0 = fast), was calculated to identify and rank all the variables that were significant ($P < 0.05$). None of the variables included presented collinearity (VIF < 5). The Risk Ratio (RR), Odds ratio (OR) and the Population Attributable Risk (PAR) were calculated for all the significant variables, after transforming all them into binary factors using 25th percentile as the cutting point. The results showed that lactation length <19 d (RR:1.53, OR:1.73), birth BW <1.2 kg (RR: 2.01, OR: 2.49), ADG from 7 to 14 d <140 g/d (RR:2.74, OR: 3.79), ADG from 21 to 64 d <200 g/d (RR:4.52, OR: 7.70) and ADG from 65 to 83 d <550 g/d (RR:5.70, OR: 11.21) were associated with a slow growth rate. If animals with these five risk factors were eliminated, the percentage of slow growth pigs would be a 5.1% instead of a 20%. In fact, the differential PAR associated to lactation, transition and the beginning of the fattening period were 4.5%, 3.9% and 2.6% respectively. These results suggest that the most critical risk factors associated with retardation of growth rate in swine are lactation and transition.

Key Words: growth rate, risk factors, pigs
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720 Gene expression profile of porcine tissues in response to short-term feeding of dietary fiber followed by a high-fat diet.

K. M. Ajuwon*, and V. V. Almeida, *Department of Animal Sciences, Purdue University, West Lafayette, IN.*

Sixty-three mixed-sex Ossabaw pigs (28 d of age, 5.62 ± 0.20 kg BW) were used to investigate the effects of early feeding of dietary fiber on later gene expression of markers of lipid metabolism, inflammation, and tight junction proteins. Pigs were blocked by BW and allotted by sex and litter to 1 of 4 treatments (8 pens/treatment; 2 pigs/pen). Treatments were arranged in 2 x 2 factorial design, with 2 fiber types (inulin or cellulose) and 2 fat levels (5 or 15%, as-fed basis; LF and HF, low- and high-fat diets, respectively). Pigs received diets containing either inulin or cellulose for the first 56 d and thereafter were fed LF and HF containing no added fiber type from d 56 to 140. On d 140, samples of omental and mesenteric fat, liver, LM, jejunum, and ileum were collected to measure mRNA abundance of ACO (acyl-CoA oxidase), CPT1a (carnitine palmitoyltransferase 1a), FAS (fatty acid synthase), SREBP-1c (sterol regulatory element-binding protein-1c), PGC1a (PPAR-γ coactivator 1a), PPARa, IL-6 (interleukin-6), and TNFa (tumor necrosis factor a) by quantitative real-time PCR. Claudin (CL)-3 and CL-4 mRNA abundances were also quantified in the jejunum and ileum samples. Relative gene expression was calculated by the $\Delta\Delta$Ct method after normalization to 18S rRNA or GAPDH. Data were log-transformed and analyzed using the MIXED procedure of SAS. No fiber x fat interactions were observed for the mRNA abundance of any of the genes studied in the omental fat, liver, LM, and jejunum. There was a fiber x fat interaction for PGC1α expression ($P = 0.03$) in the ileum and for TNFα expression ($P < 0.01$) in the mesenteric fat, as PGC1α mRNA abundance was decreased ($P = 0.03$) and TNFα mRNA abundance was increased ($P < 0.01$) when the HF was fed only for pigs that received dietary inulin during early life. Regardless of fat level, adding dietary inulin increased ($P \leq 0.02$) jejunal expression of SREBP-1c and CL-4, but reduced ($P = 0.02$) TNFα expression in the ileum. Pigs fed HF had greater ($P = 0.03$) TNFα expression in the LM than pigs fed LF, regardless of fiber type. Feeding either cellulose or HF to pigs led to greater ($P \leq 0.02$) ileal IL-6 expression than inulin and LF, respectively. In summary, HF following dietary inulin inclusion during early life of pigs may contribute to future obesity and gastrointestinal inflammation.

Key Words: High Fat diet, pigs, Fiber
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721 Effects of the standardized ileal digestible methionine to lysine ratio on milk performance, litter growth and plasma indices of lactating sows.

H. Wei*[1], X. Zhao[2], M. Xia[3], J. Gao[4], J. K. Htoo[5], and J. Peng[1,6], [1]*Department of Animal Nutrition and Feed Science, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China,* [2]*Huazhong Agricultural University, Wuhan, China,* [3]*Huazhong Agricultural University, WUHAN, China,* [4]*Evonik Degussa (China) Co., Ltd, Beijing, China,* [5]*Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany,* [6]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China.*

The objective of the study was to determine the effects of the dietary methionine (Met) to lysine ratio (Met:Lys) for lactating sows suckling more than 11 piglets on milk production, litter growth and plasma indices. 120 Large White sows (parity 1 to 4) were randomly allotted to 4 dietary treatments with 30 sows per treatment based on parity, back fat thickness and body weight from farrowing day. Litters were standardized to 12 piglets. The sows were fed corn-soybean meal based diets containing 0.27, 0.37, 0.47 or 0.57 SID Met:Lys from day of farrowing until day 21 of lactation. On all 120 sows, BW and back fat thickness (BF) were registered at day 110 of gestation and day 7 and 21 (weaning) postpartum. Piglets weight, ADG and litter weight were determined weekly during a 21 days experimental period. Blood samples were taken from sows at day of farrowing, day 7 and 21 for the measurement of the homocysteine (Hcy) and thiobarbituric acid reaction substances (TBARS) level and glutathione peroxidase (GSH-Px) activity. Milk yield, and the DM, lactose, protein and fat concentrations of milk, were similarly not affected by dietary treatments. The ADG increased quadratically during first week and third week ($P < 0.001$) with increasing SID Met:Lys level. The TBARS level was increased as SID Met: Lys elevated from 0.27 to 0.57 at day 7 of lactation ($P < 0.05$) and weaning day ($P = 0.06$). Moreover, at day 7 of lactation, GSH-Px showed the higher activity in SID Met: Lys 0.37 and 0.47 group compared to other groups ($P < 0.01$). Methionine metabolites Hcy and taurine both increased linearly ($P < 0.01$) as SID Met: Lys increased. These results showed that lactation diet with 0.37-0.47 SID Met: Lys is optimal to achieve the better litter growth. However, along with the increased level of dietary methionine during lactation, gradually increased plasma Hcy and TBARS indicated that the high SID met to lys ratio greater than 0.47 might increase the risk of oxidative stress, regardless of the increased GSH-Px activity.

Key Words: methionine, sow, lactation
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722 Increased consumption of methionine by piglets fed with DL-Met or OH-Met strengthens piglets' ability to cope with LPS-induced inflammatory stress during post-weaning period.

B. Y. Xu[1], L. Zhao[2], D. I. Batonon-Alavo*[3], Y. Mercier[3], D. Qi[1], and L. Sun[2], [1]*Department of Animal nutrition and Feed Science, Huazhong Agricultural University, Wuhan, Hubei, China,* [2]*Department of Animal Nutrition and Feed Science, Huazhong Agricultural University, Wuhan, Hubei, China,* [3]*Adisseo France SAS, Commentry, France.*

The objective of this study was to determine whether an LPS-induced inflammatory stress might be attenuated by increased consumption of methionine either as DL-Met (DLM) or OH-Met (HMTBA) in both lactating sows and weaned piglets. Sows received during the last month of gestation and lactating period, three treatments: a control diet at the requirement in TSAA (0.52% and 0.60% of Met+Cys, respectively for gestation and lactation periods) and two treatments supplemented with DLM or HMTBA at 25% above the requirement. Results on sows and piglets during the lactation were presented in a separate paper (See Abstract no. 21279). Piglets were weaned at 21d and received three weaned diets according to the sows' treatments: a control diet at the requirement in TSAA (CON-P) and two treatments supplemented with either DLM (DLM-P) or HMTBA (HMTBA-P) at 25% above the requirement. Dietary content of Met+Cys in the CON-P diet was 0.88%. After 2 weeks of feeding, 20 male piglets from each treatment were selected according to their body weight for a 2 x 3 factorial design that included dietary treatments (CON-P, DLM-P and HMTBA-P) and immunological challenge (saline and LPS) at d 35. Growth performance of piglets were measured at d 35, 49 and 63 respectively. At d 35, piglets' body weights were significantly higher in the HMTBA-P group (8.47 ± 0.38 kg) than in the CON-P (7.66

± 0.24 kg). Body weight of the DLM-P group (8.25 ± 0.27 kg) was intermediate and was not significantly different than both the CON-P and the HMTBA-P. Feed intake and feed to gain ratio during the 21-35 d period was not significantly different between treatments. The LPS significantly affected piglet's performance in all groups. However, HMTBA-P and DLM-P fed piglets showed the highest body weights following the LPS challenge at d 49 and d 63, in comparison to the CON-P. Body weight gain and feed to gain ratio were the best in piglets fed the HMTBA-P treatment during and after LPS stress ($P < 0.05$). HMTBA is known to be better transsulfurated than DLM, thus leading to more glutathione in comparison to DLM. Therefore, it can be hypothesized that the better growth performance observed with HMTBA under LPS stress might be related to the better antioxidant status. Consequently, these results pointed out the better ability of piglets fed with HMTBA through maternal supplementation and during the post-weaning period to cope with an inflammatory stress.

Key Words: Piglets, Methionine, LPS challenge
doi:10.2527/asasann.2017.722

TEACHING/UNDERGRADUATE AND GRADUATE EDUCATION

723 Comparing student learning outcomes in a flipped classroom to a traditional lecture pedagogy in applied animal physiology.

L. M. Judd*, E. F. Orlando, and S. A. Balcom, *University of Maryland, College Park.*

Applied Animal Physiology is a 200-level course requirement for animal science majors. In recent years, student performance has been satisfactory for the animal reproduction questions on the final exam. However, students have struggled with the intricacies of hormonal changes during the estrous cycle, and making comparisons between the estrous and menstrual cycles. We hypothesized that across all demographics, performance on the mammalian reproduction section of the final exam would be higher for students who received instruction on reproduction using a flipped method (2016 cohort, n = 62) compared to students who had been taught this information using traditional lecturing (2015 cohort, n = 73). The reproduction section was taught in the last three lectures of the semester for both cohorts. The 2016 cohort received three, fifty-minute flipped course classes during the course's normal meeting time, all of which emphasized areas of common confusion. The intervention consisted of in-class hands on activities. Subsequently, there was no effect of intervention ($P = 0.49$) on the percentage of reproduction related questions answered correctly on the final exam for the 2016 group (74.1%) vs the 2015 group (75.8%), SE±1.78; however, when the 2016 cohort was separated into four treatment groups: A. full attendance (three days), B. two days, C. one day, D. did not attend, compared to the E. 2015 cohort-traditional lecture, performance was different ($P < 0.05$). Student average exam performance was highest on the reproduction questions for the full participants (84% average correct) compared to treatments B-E 70%, 69%, 63%, and 75% respectively; SE ± 3.2. To gauge student attitudes about the flipped teaching experience, all 2016 cohort students were asked to complete a pre- and post-intervention survey. Twenty-one students completed both surveys (34% response rate). Confidence in knowledge and understanding of reproduction for treatment A increased from 2.4/5.0 (before intervention) to 3.1/5.0 SE ± 0.37 (after intervention). When reviewing mammalian reproduction material before class, student confidence was lower than when reviewing the same material after class for treatment A (2.5/5.0 vs 3.2/5.0) and treatment B (2.2/5.0 vs 2.8/5.0) SE ± 0.24. There was no effect on confidence in treatment C or D. Student engagement and participation in a flipped module is essential in order to have a successful classroom intervention.

Key Words: flipped module, animal science, undergraduate teaching
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724 Methods of daily student engagement in an introductory level animal science course.

P. L. Harrelson*, *Morehead State University, Morehead, KY.*

Within an introductory animal science course, information can be overwhelming depending upon the background and preparation of the student. This is especially true during the transition period between graduating high school and completing the freshman year of college. Students often struggle with the change in study habits, comprehension of more difficult material, and communication with instructor(s). After three semesters of teaching a freshman level Anatomy and Physiology of Livestock (AGR 143) course, two new methods were implemented to create more class engagement, increase student communication, and improve student success. Daily attendance cards ($n = 28$) and weekly Kahoot! quizzes ($n = 14$) were added in the Fall 2016 semester to the AGR 143 course. Kahoot! is an interactive quiz that the student takes during class and gets immediate feedback. Kahoot! was used to identify information that needed clarification from the previous week's material. Students utilized their smartphones to log on and answer five multiple choice or true/false questions. Students within the top 5 total points for that day were awarded bonus points. Students became more competitive as each week passed. One student commented via a post-course survey that "The Kahoot! quizzes every week were extremely helpful and made me remember more of the material." Another student added, "the instructor encourages her students to do well though healthy competitive competitions with quizzes using the Kahoot! program." When comparing previously taught semesters average grade ($n = 44$ students, 67.4%; $n =$

37 students, 80.1%; n = 81 students, 78.9%), students in the Fall of 2016 course performed slightly better (n = 37 students, 80.8%). In addition to the Kahoot!, students were also given daily response cards to answer questions and to include additional questions and/or comments. Students had the opportunity to ask questions they did not feel comfortable asking about during class along with constructive feedback. Students asked a wide variety of questions over previously covered material, application of new material, and methods to help improve their study habits. A quick review of cards, allowed for valuable insight into the student progress within the course. Overall, student engagement in the course and average student grade was positively impacted.

Key Words: Teaching, Engagement, Quiz
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725 Difference in opinion of sustainable agriculture concepts between master of science and master of agriculture cohorts.

P. Urso[1], M. M. Beverly*[1], S. F. Kelley[1], E. F. Miller[2], M. J. Anderson[2], and K. J. Stutts[1], [1]*Sam Houston State University, Huntsville, TX,* [2]*Sam Houston State University, Huntsville, TX.*

Sustainable agriculture concepts and its practices are becoming increasingly prevalent in today's society and agriculture settings. Classes teaching sustainable agriculture practices are also becoming more common in agriculture programs at institutions of higher education. Sam Houston State University has implemented coursework and degree plans that focus on these practices and ideals, allowing students to develop conceptual philosophies and knowledge in both traditional and sustainable agriculture practices. Students (n = 39), from two separate sections, enrolled in a sustainable agriculture and food environment (SAFE) course in the fall of 2015 and fall of 2016, completed a free response pre/post-survey polling their beliefs on sustainable topics and concepts discussed in class. Students were divided into two cohorts, consisting of students pursuing a Master of Science degree in Agriculture (MS), and those obtaining a Master of Agriculture degree in SAFE (MA). Student responses comparing the two cohorts were analyzed using the GLM and FREQ procedures in SAS. A significant difference (P < 0.01) existed between the two cohorts in their definitions of sustainable agriculture and defining the causes of the sustainable agriculture movement. MS students identified the sustainable movement to be driven by economic shifts in their pre-responses, MA students, on the other hand, stated that environmental concern has driven the industry to implement and establish more sustainable practices. Likewise, the MA students noted a difference between sustainable agriculture and organic practices (P < 0.01) in their pre-course responses. MA students were also more likely to label sustainable agriculture as a global movement (P < 0.01); whereas, MS students were more likely to consider these concepts to be more regional (P < 0.01) in their pre-course responses. All other questions that were different in the pre-course survey had no significant difference in the post-course survey across cohorts other than the MA students believed that sustainable practices should be mandated by the government (P < 0.01). These results suggest that MS or traditional agriculture students exposed to sustainable content and curriculum are likely to displace their preconceived notions of sustainable agriculture and its practices for more favorable and accurate definitions and ideals of the concepts and practices. This considered, further research examining the opinions of students exposed to these courses with sustainable agriculture topics could help further explain the need for future course development in this area of study.

Key Words: Sustainable, Graduate, Opinions
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726 Are there only 2Rs in agricultural animal research and production?

W. R. Stricklin*, *University of Maryland, College Park.*

Care of agricultural animals is a topic increasingly addressed through a lens and language identified as animal welfare. Welfare inherently is about how animals should be treated. Thus, animal care oversight is unavoidably normative; meaning the topic is undeniably one of ethics. Oversight of USA animal care arose first in publically funded laboratory animal use with the adoption of principles, codes and standards of practices. More recently, oversight has expanded to include agricultural animal research. While the goal of ensuring appropriate animal treatment is common to both lab and agricultural research, there are differences. Consequentially, principles initially implemented for lab animals with specific purpose and positive outcome can be shown to have a counter intuitive outcome when broadly applied. As an example, the 3Rs (Replacement, Reduction, Refinement) were initially specific to lab animal research but are mandated for all animal research today. Lab animals serve only one purpose. They are solely research subjects. Agricultural research animals have utility beyond serving as data points. Specifically, when not contrary to health food standards, they are marketed as food. Thus, an IACUC that attempts to Reduce the herd size may be acting in a manner contrary to both better research numbers and also the maintenance of brood cow numbers necessary for a viable operation. Attempts to expand the application of the 3Rs beyond public institutions and to private animal agriculture raise even more questions. Production of beef or pork and not poultry would considerably Reduce the number of animals used in food production. But a question that remains unanswerable is how to compare the value of an animal life of one species to another. Thus, a measure of total harm using animal numbers alone becomes problematic for both science and ethics. Futurists suggest it may become possible to Replace the food animal altogether. But is a steak without the steer a higher moral position? Is the Replacement of animal discomfort and death through their non-existence more ethically defensible? Yes, Refinement in care animals regardless of purpose should be employed to attain appropriate animal quality of life. Additionally, Reduction of animal numbers would be consistent with better welfare, e.g., sexing offspring in dairy breeding. In summary, the 3Rs proposed by Russell and Burch in 1959 have continued application to lab animal oversight, but a simplistic application of these principles to animal agriculture can be shown to not always be the most defensible position.

Key Words: Bioethics, Animal Agriculture, Three R's
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727 What we deserve: A survey of student entitlement.

M. J. Anderson*, S. F. Kelley, M. M. Beverly, and K. J. Stutts, *Sam Houston State University, Huntsville, TX.*

In order to excel at teaching, one must first understand the thought process of the person being taught. Today, our students have a number of inherent expectations that are rarely voiced, yet clearly anticipated. The objective of this survey was to determine student expectations of their instructors and how their expectations change as they progress through their academic career. To accomplish this, students ($n = 406$) enrolled in animal science courses completed a survey that contained questions regarding their expectations of course instructors and what privileges they were entitled to as a student enrolled in that course. Distributions of responses were compared using a chi-squared analysis with pairwise comparisons to determine differences between student academic classifications. However, because multiple pairwise comparisons can lead to errors in analysis, comparisons were limited to the change during an undergraduate degree (freshmen to senior) and entering graduate school (senior to graduate). Of the seven questions pertaining to what students expect from their instructors, four questions displayed changes in student expectations among academic classifications. When asked if an instructor should be required to give a review before an exam, there was a significant change ($P < 0.01$) in the distribution of responses from freshmen to senior classification, going from overwhelmingly in favor of a required review for freshmen to a roughly even split for seniors. A change was also noted ($P < 0.01$) in students as they progressed from senior classification to entering graduate school where the majority thought a review should not be required. A similar pattern emerged for the remaining questions when comparing freshmen to seniors. When asked the following questions: "Should an instructor allow an alternative assignment for those students who fail an exam?", "Should an instructor provide you with his/her slides and notes if requested?", and "Should an instructor respond to student emails/texts/phone calls after 5pm and on weekends?", there was a significant change in distribution ($P < 0.05$) of the responses of freshmen to seniors, while no change was detected ($P > 0.10$) between seniors and graduate students. In all cases, the responses shifted more towards the response of "No" as students advanced through their academic classifications. These data illustrate that there is a distinct change in the mindset of students as they progress through their academic career and the expectations of students in a freshmen level class are very different than those of students in a senior or graduate level course.

Key Words: Entitlement, Students, Perceptions
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728 Workshop on teaching bioethics in animal agriculture: Outcomes for faculty in animal science and veterinary medicine.

C. C. Croney[1], R. Anthony[2], A. Bauer[1], C. Elbert[3], J. M. Siegford[4], W. R. Stricklin*[5], J. C. Swanson[4], and G. Varner[3], *[1]Purdue University, W. Lafayette, IN, [2]University of Alaska Anchorage, Anchorage, [3]Texas A&M University, College Station, [4]Michigan State University, East Lansing, [5]University of Maryland, College Park.*

A USDA funded Challenge Grant workshop entitled, "Teaching Bioethics in Animal Science and Veterinary Medicine Curricula" was held in January 2017 in Baltimore, MD. The workshop, led by Purdue University in collaboration with four other land grant institutions aimed to facilitate knowledge and confidence of instructors in animal sciences and veterinary medicine tasked with delivering agricultural animal bioethics course content. A standardized curriculum for teaching agricultural animal bioethics, supplementary materials, active learning exercises, and a project website were developed by the multidisciplinary team of principal investigators. These resources were shared with workshop participants. Two philosophers with expertise in bioethics served as discussion facilitators. The 2-day workshop was attended by 20 participants from universities across the US. Participants' teaching duties ranged from covering overviews of animal bioethics topics in introductory courses to delivering specific upper-level courses focused on animal welfare and bioethics. Prior to the workshop, participants were asked to identify their teaching challenges and workshop goals. The most commonly noted challenges were facilitating/promoting classroom discussion, personal knowledge of or experience with teaching the subject matter, "going deeper" and incorporating multiple ethical frameworks into discussions, and stimulating student interest in bioethics. Common goals included course improvements, improving personal knowledge or skills related to bioethics instruction, and networking. The basic curriculum and content delivery strategies were explored using multiple concurrent breakout group sessions, among which participants were able to choose. Participants were asked to rate the applicability of these workshop sessions to their teaching roles and their levels of usefulness. For the session on Understanding Basics of Moral Philosophy and Translating to Bioscience Students, 14 participants attended and responded. Of these, 35% (n = 5) strongly agreed and 57% (n = 8) agreed that the material was relevant; 85% (n = 12) said they would incorporate the material into their courses. For the session on Reviewing and Delivering Basic Concepts Related to Sustainability, 5 participants responded. All strongly agreed that the material was applicable to their roles in academia, and all five said they would incorporate the material into their courses. Each of the other workshop sessions was similarly perceived to be both applicable and useful. The overall responses indicated that participants' goals were met and that the workshop helped to enhance the quality of their instruction on bioethics and stimulate further interest in related pedagogy.

Key Words: Animal Agriculture, Bioethics, Teaching
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729 Effect of an active learning classroom on critical thinking dispositions, motivation to go to class, social community, and learning skills in an animal Sciences course.

M. G. Maquivar*[1], and N. Sundararajan[2], [1]*Department of Animal Sciences, Washington State University, Pullman,* [2]*Washington State University. College of Education, Pullman.*

In this parallel mixed method study, we investigate the role of classroom setting in the relationship between student perception of critical thinking dispositions and skills, social community, and their learning in an Animal Sciences course (Animal rights and animal welfare). Classroom A (n = 40 students) was a general university classroom with individual arm chairs. Classroom B (n = 42 students) was an active learning classroom with collaborative table set up seating five students per table. A total of 77 (n = 40 classroom A and n = 37 classroom B) students voluntarily answered the survey. For the quantitative observational study, data was collected on student perception of social community, critical thinking skills, and dispositions through a survey with 152 five point Likert scale questions at the end of the semester. Student grades were tracked in the course. For the qualitative case study, observational field notes and instructor interviews were collected through the course of the semester. No statistically significant differences were observed through *t*-tests in student grades at the end of the semester (Classroom A = 89.3 ± 4.5, Classroom B = 86.8 ± 11.3). No statistically significant difference was observed between Classroom A and Classroom B in student perceptions of social community (Classroom A = 107.88 ± 18.57, Classroom B = 109.91 ± 17.81; maximum 133), their motivation to attend class (Classroom A = 3.56 ± 0.92, Classroom B = 4.00 ± 0.79, maximum 5), their perception of their critical thinking dispositions (Classroom A = 43.28 ± 3.87, Classroom B = 43.74 ± 4.46, maximum 55), and their perception of their critical thinking abilities (Classroom A = 140.60 ± 14.24, Classroom B = 142.78 ± 16.88; maximum 170) ($P > 0.05$). Nevertheless, students in each class improved significantly in their self-perception of their critical thinking disposition (Classroom A by 2.56 ± 2.98, Classroom B by 2.69 ± 2.38) and overall skills (Classroom A by 10.52 ± 9.92, Classroom B by 9.00 ± 9.53) over the course of the semester. Further, we found that social community was a significant predictor of motivation to attend class, with the strength of relationship stronger in the active learning classroom than in the general university classroom. The findings of this study are of interest to researchers and practitioners interested in active learning strategies.

Key Words: learning, active learning classroom, critical thinking
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730 Development and implementation of a peer evaluation teaching protocol in a large animal science program.

E. J. Huff-Lonergan, J. E. Cunnick, A. K. Johnson, and J. A. Sterle*, *Department of Animal Science, Iowa State University, Ames.*

Over time and with enough semesters and students, student course evaluations can provide valuable information about instructor effectiveness and course organization. However, student evaluations are anonymous, and responses often lack accountability and constructive comments for improvement. The student point of view, while important, may lack perspective that faculty assessment is able to provide. Additionally, as promotion documents increasingly require more documentation of teaching effectiveness, a consistent, fair, summative peer evaluation of teaching can add breadth and depth to the assessment while strengthening the departmental curriculum. Therefore, a protocol was developed to provide guidance and continuity in the peer evaluation of teaching process. Peer evaluation of teaching includes all materials and assessments from the course as well as classroom presentation and delivery. The undergraduate teaching coordinator accepts requests from faculty who wish to have their course reviewed at the beginning of each semester and then assigns two peer reviewers. The three faculty then meet to discuss course objectives and learning outcomes. The instructor also shares their teaching philosophy for the course, and the syllabus, handouts, assignments, quizzes and exams. Some instructors also choose to add the reviewers to the learning management platform for the class. The reviewers plan to attend the class (and/or laboratory) at least two different times (not necessarily together) throughout the semester and record their observations. If at all possible, it is advised that the instructor and reviewer meet immediately after class to discuss initial thoughts, reactions and questions. Both evaluators then meet together with the instructor to visit about their evaluation and then draft a letter with their assessment. The peer evaluation document is then shared with the instructor. Informal feedback from instructors includes the fact that many faculty enjoy talking about teaching, but that these conversations are preempted by daily activities and duties unless given a specific reason. The evaluation

process gives a platform to visit about pedagogy, course content and teaching techniques. Outcomes and impacts of implementation of this protocol have not only yielded improvement of classroom teaching practices (via student course evaluation improvement) and exchange of ideas, but also increased faculty relationships and collaboration. Additionally, anecdotal improvement of overall course content, especially amongst related courses or courses within a series or sequence was mentioned. A coordinated, transparent protocol that assesses not only classroom performance but course content can be an effective tool for both class delivery and instruction as well as curricular improvements.

Key Words: Teaching, Peer evaluation, Undergraduate
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731 How to increase student participation and engagement using Padlet: A case study of collaborative discussion in an animal sciences course.

N. Sundararajan[1], and M. G. Maquivar[*2], [1]*Washington State University. College of Education, Pullman,* [2]*Department of Animal Sciences, Washington State University, Pullman.*

In this paper, we present a case study of using an online collaborative tool – Padlet® (www.padlet.com) in two sessions of a course on Animal Rights and Welfare. The animal rights and animal welfare course is divided in two sections: section A (n = 40 students) and section B (n = 42 students). Padlets act as a giant online post-it board allowing participants to post text, audio, image, GIF, video, or URL. Padlet® was used during one class in the semester in which students in both sections were asked to brainstorm on the question "What factor(s) would you consider to be able to use animals for entertainment?" with the learning objective of identifying if students recognized and were able to discuss the use of animals for entertainment. Students had five minutes to post their response to the question. Section A was in a general university classroom and students were not required to write their names on their padlet post. Section B was in a technology enabled active learning classroom and students were asked to write their names on their post. The padlets were analyzed using social-cognitive theory, with an emphasis on content and multimedia use. Observations were recorded in field notes, and student feedback and their perception of social community was collected through surveys. Additionally, the instructor's reflection was recorded on the experience of using Padlet in class. In section A, 6 of a total of 53 posts, and in section B, 17 of a total of 51 posts had multimedia such as image, video, or web URL. Further, all multimedia posts in section B were relevant to the discussion while only half the multimedia posts in section A contributed to the discussion. The use of this free media technology (Padlet®) allowed students to prime their responses simultaneously and thus encouraged discussion with more participants, some of whom do not usually respond in class. Lastly, while no statistical difference was found in student perceptions of social community (Section A = 107.88 ± 18.57, Section B = 109.91 ± 17.81; maximum 133), student feedback provides insight into differences in the overall success of the activity based on the nature of students' engagement in regular discussion, comfort with using technology in class, and availability of convenient device.

Key Words: Student engagement, Collaborative Discussion, Padlet
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732 Animal science students' perception of learning and the link to student learning outcomes in an introductory course.

B. D. Whitaker[*], *University of Findlay, Findlay, OH.*

Introductory Animal Science courses often contain purposefully constructed student learning outcomes based on the material that is presented during the semester. Traditional assessment methods in the form of assignments and exams provide feedback to the student and instructor as to whether those student learning outcomes are being met. Anecdotally, students fail to acknowledge the link between assessment tools and the learning outcomes of the course. Students often ignore learning outcomes of a course and focus solely on content and assessment success. Other than assessment scores, instructors lack the means to determine whether or not the student learning outcomes are being met. To begin evaluating the efficacy of animal science students' perception of achieving the learning outcomes of a course, students (n = 683) enrolled in an introduction to animal science course were given the option to complete a survey. Students were evaluated through pre- and post-course assessments to determine what their perceived level of achievement of student learning outcomes was, based on a scale where 1 = not at all and 10 = expert level. Each of the 9 statements were linked to one of three student learning outcomes, based on acquisition of knowledge, comprehension and application. Each learning outcome was linked to each of the three themes of the course: industry, products, and animal biology. Results indicate that students significantly increased ($P < 0.05$) their perceived ability to meet all student learning outcomes from the beginning of the course (3.46 ± 0.18) compared to the end of the course (8.83 ± 1.34). The animal science students' perception of learning should be considered when designing the content of a course and can provide a means to assess whether or not student learning outcomes have been met.

Key Words: student learning outcomes, students, introduction to animal science
doi:10.2527/asasann.2017.732

INVITED ABSTRACTS

733 Genetically engineered feed: Impact on animal performance, health and products.

A. E. Young*, and A. L. Van Eenennaam, *University of California, Davis.*

Genetically engineered (GE) feed crops became widely adopted following their introduction in 1996 and today more than 90% of sugar beet, soy, cotton and corn acreages in the U.S. are planted with GE varieties. It is estimated that 70-90% of GE crop biomass has been consumed by multiple generations of food-producing animals for the past 20 years. Numerous studies have shown compositional equivalence between GE and non-GE crops, and hundreds of peer-reviewed studies have shown no deleterious health effects associated with feeding GE crops to livestock. Additionally, the available USDA productivity trends and health metrics for the different livestock industries over the past 20 years do not show unexpected perturbations following the introduction of GE crops into the US feed supply. However, a few controversial and highly-publicized studies have claimed that consumption of GE feed resulted in deleterious health effects in a small number of animals. Despite being widely criticized for experimental design and other flaws, these outlier studies have been used to support views that there is a need to label meat, milk and eggs from animals that consume GE crops. Neither recombinant DNA (rDNA) nor protein from GE feed crops are reliably detected in the milk, meat and eggs from livestock that have been fed GE feed. Studies have shown that DNA from GE crops is chemically equivalent to DNA from non-GE crops and both are broken down the same way during digestion. The total amount of plant DNA remaining in animal feed is dependent upon many factors including how the feed is processed, and in feed from GE varieties rDNA makes up only a fraction of the total genomic DNA. As part of the natural digestive process, dietary DNA has been shown to move across the intestinal wall, but there is no evidence suggesting DNA or rDNA transfer from plants to animals. Since dietary DNA and protein cannot be reliably detected in animal products, and considering the wide trade and usage of GE feeds globally, managing separate supply chains to satisfy mandatory labeling requirements for products from animals that consumed GE feed would be complicated and expensive. There would be no food safety benefit from the substantial costs associated with segregating milk, meat and eggs from animals fed GE feed due to the fact that such products are both compositionally and analytically indistinguishable from those derived from animals fed non-GE crops.

Key Words: GE feed, recombinant DNA, GMO
doi:10.2527/asasann.2017.733

734 Engaging the public about science - it is not about science.

K. Folta*, *University of Florida, Gainesville.*

New technologies in genetic engineering and precision agriculture are poised to revolutionize food and farming. However, will we choose to regulate new technologies with expensive, arbitrary, or over-reaching barriers that will slow their translation to the field? We live in a time of rapid innovation, but application is slow. A significant driver is public sentiment, which skews demand and influences policy. Consumers are influenced by an internet replete with false or misleading information. Scientists and farmers are slow to enter the conversation, and when they do they are not typically effective with allaying the concerns of a public seeking answers and wondering who to trust. The goal of this seminar is to provide a new strategy for public interaction, based on the premise that facts hold no weight until you establish trust. We will discuss how to build trust, based on findings from social psychology. Finally, we'll discuss how to apply these principles to biotechnology, and present tips for content generation and network building using social media, with the goal of amplifying trusted messages.

Key Words: science communication, public outreach, education
doi:10.2527/asasann.2017.734

735 Can cover crops pull double duty: Conservation and profitable forage production?

E. Drewnoski*, J. Parsons, D. Redfearn, H. Blanco-Canqui, and J. C. MacDonald, *University of Nebraska, Lincoln.*

Data from a recent survey suggests that the major reasons Nebraska crop producers plant cover crops are to improve soil organic matter, reduce erosion, improve soil water holding capacity, produce forage, and improve soil microbial biomass. Fortunately, many of these benefits appear to be positively correlated with production of above-ground biomass. Thus, selecting species that will produce the greatest biomass should be beneficial for both conservation and forage production. Furthermore, the limited data available suggests grazing of cover crops does not have large negative crop production, soil, or environmental impacts. In the north central US the production window following wheat harvest, male row destruction in hybrid seed corn, and to a lesser extent following corn silage harvest is long enough to produce 2,500 to 4,500 kg DM/ha of high-quality, fall forage. In the past 4 years, we have conducted 8 trials using predominantly oats and brassicas planted in mid- to late-August. Forage nutritive value of oats and brassicas is extremely high (70 to 80% IVDMD; 14 to 23% CP in early November) and remains high through December with only a 4 to 7% unit decrease in IVDMD and no change in CP. Thus, it appears that delayed grazing could be an option to maximize potential forage yield. Fall-weaned calves (200 to 290 kg BW) grazing oats with or without brassicas in November and December (48- to 64-days) at stocking rates of 2.5 to 4.0 calves/ha have gained between 0.60 to 1.10 kg/d. The cost of gain has ranged from \$0.46 to \$2.20/kg when accounting for seed costs plus establishment (\$52 to 106/ha), nitrogen plus application (\$0 to 72/ha), fencing (\$12/ha) and labor (\$0.10/calf/d). While soybeans and corn harvested for grain do not provide a large enough growing window to accomplish fall grazing, similar dual purpose cover crop practices are often accomplished by planting winter hardy small cereal grass, such as cereal rye or winter triticale in the fall and grazing in the spring. However, traditional planting dates for corn and soybean result in a 30- to 45-day grazing period prior to corn and a 45- to 60-day period prior to soybean planting. Planting cover crops to provide late fall or early spring grazing has potential. However, incorporating forage production into current cropping systems greatly increases the need for timeliness of management since the window of opportunity for forage production is quite narrow.

Key Words: Forage, Cattle, Cover Crop
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736 Annual forages: Influence on animal performance and water/nutrient management.

S. L. Dillard*[1], D. W. Hancock[2], D. D. Harmon[2], M. K. Mullenix[3], P. A. Beck[4], and K. J. Soder[1], [1]*USDA-Agricultural Research Service, University Park, PA,* [2]*Department of Crop and Soil Sciences, University of Georgia, Athens,* [3]*Dept. of Animal Science, Auburn University, Auburn, AL,* [4]*Department of Animal Science, University of Arkansas, Hope.*

Annuals can provide short-term grazing between crop rotations or can be interseeded into perennial pastures to increase forage quality and productivity. They provide an opportunity to increase the economic and environmental sustainability of traditional grazing systems. However, to be profitable, annuals must produce a significant amount of highly nutritious forage within a short time (3 – 6 months). In a 2-yr plot study, 70 d after planting, rapeseed (*Brassica napus* L.) and turnip (*B. rapa* L.) produced 1,484 and 1,023 kg DM/ha, respectively. The CP, NDF, and ADF were similar for both forages (average of 26.2, 17.9, and 13.8%, respectively). Daily production of CH_4 and CH_4 per gram of NDF fed were 84 and 80% lower, respectively, in turnip and rapeseed compared with annual ryegrass (ARG; *Lolium multiforum* Lam.) when fed in continuous culture. Wheat (*Triticum aestivum* L.)/ARG, triticale (× *Triticosecale*)/ARG, and wheat/triticale/ARG pastures provided similar grazing days per hectare, ADG, and cost of gain (375 d/ha, 1.44 kg/d, and \$1.46/kg BW, respectively) in a grazing study in the Gulf Coast region. No-till (NT) establishment was shown to be as effective as conventional tillage for establishing small grain pastures in the Ozark Plateaus. Furthermore, stocker performance during the fall was not affected by tillage treatment, but during the spring grazeout, BW gain per hectare was 8% greater in NT pastures. Research in Southern Piedmont has shown that brown mid-rib sorghum-sudangrass (BMR SSG; *Sorghum bicolor var. bicolor × bicolor var. sudanense*) and pearl millet [PM; *Pennisteum glaucum* (L.) R.Br.] with crabgrass [*Digitaria sanguinalis* (L.) Scop.] tended to have greater ADG (0.98 kg/d) than sorghum-sudangrass or PM alone (0.85 kg/d). Feeding of BMR SSG reduced daily production of CH_4 and CH_4 per gram of NDF fed by 66 and 50%, respectively, compared with a perennial cool-season forage in continuous culture. Additional research in the Southern Piedmont has shown that interseeding of cool- and warm-season annuals into a perennial pasture reduced the concentration of NO_3-N and PO_4-P in runoff by 50 and 36%, respectively. Annuals not only provide economic incentives to producers, but also potentially reduce nutrient runoff, increase soil cover, increase soil carbon sequestration, and decrease enteric CH_4 emissions. However, establishment method, grazing management, and weather conditions all play important roles in the productivity and environmental impact of these systems. Further research is needed to better characterize how management and climatic conditions impact the long-term economic and environmental sustainability of grazing annuals.

Key Words: Annuals, Grazing, Nutrient Management
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737 Perinatal programming of pancreatic islets during intrauterine growth restriction.

S. W. Limesand*, *University of Arizona, Tucson.*

Placental insufficiency and intrauterine growth restriction (IUGR) of the fetus is associated with short- and long-term disturbances in metabolism. In pregnant sheep, exposure to elevated ambient temperatures results in a small, defective placenta that restricts delivery of nutrients and oxygen to the fetus, resulting in IUGR. Fetal hypoxemia caused by placental insufficiency increases plasma catecholamine concentrations. We propose that the chronic elevation of catecholamines observed in the IUGR fetus produces developmental adaptations in pancreatic β-cells that impair β-cell proliferation and insulin secretion. Experimental evidence supporting this hypothesis shows that sustained high catecholamines in IUGR fetuses persistently inhibit insulin concentrations. However, a compensatory enhancement in insulin secretion responsiveness occurs following inhibition or cessation of adrenergic stimulation in IUGR fetuses. This finding has been replicated in normally grown sheep fetuses following a seven-day norepinephrine infusion. Together, these developmental adaptations will result in an imbalance between insulin secretion and insulin action in the lamb which suggests additional insults that impact the maturation of β-cell function.

Key Words: Fetus, Pancreas, Insulin
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738 Use of new technologies to evaluate the environmental footprint of feedlot systems.

N. A. Cole*[1], D. B. Parker[2], R. W. Todd[2], A. B. Leytem[3], R. Dungan[3], and S. L. Ivey[4], *[1]USDA-ARS Conservation and Production Research Laboratory (retired), Bushland, TX, [2]USDA Agricultural Research Service, Bushland, TX, [3]USDA-ARS, Kimberly, ID, [4]New Mexico State University, Las Cruces.*

Livestock production systems can have appreciable effects on the environment; especially concentrated animal feeding operations (CAFO) where large numbers of animals and the nutrients they consume and excrete are concentrated. The major environmental issues of feedlots are gaseous emissions of ammonia, odors, and greenhouse gases, nutrient losses in manure, and nutrient losses in runoff, if runoff control systems are improperly managed. Gas concentrations can be measured using techniques ranging from simple adsorbents to gas chromatography to open-path-lasers and FTIR. Use of absorbents is less expensive, but more labor intensive. In addition laser technologies can provide concentrations in real time. Gaseous emissions can be measured using several micrometeorological techniques. The backward Lagrangian stochastic (bLS) model is the most commonly used because of its simplicity; however, the equipment can be expensive. Micro-met methods are generally limited to use in large areas (> 1 square km), and are not appropriate for small research feedlots. Small (< 1 square m) static, or flow-through chambers maybe used to measure gaseous emissions from pen surfaces. These are adequate for comparing treatments, but chambers with air exchange rates of less than 15/min usually underestimate true flux rates; especially for gases such as ammonia. Newer "static-type" chambers that measure gas concentrations continuously may accurately measure emissions because of their short sampling time. The SF6 method and the GreenFeed system (C-Lock, Inc., Rapid City, SD) are frequently used to measure enteric methane emissions from individual animals. The GreenFeed requires less labor, but has a higher initial cost. Large "respiration type" chambers that house groups of animals, are used to measure emissions from simulated pens. These have the advantage of measuring both animal and manure emissions; however, they may have limitations in measuring some emissions because of their low air exchange rates. Capture of bioaerosols, and use of molecular techniques are also gaining in acceptance. Sampling systems commonly used to capture bioaerosols include impaction, impingement, and high-volume. Culture-independent techniques are also gaining in acceptance for the identification and quantification of microorganisms in the gut, manure, and air. Losses of nutrients from entire research pens and commercial feedyards have been estimated using natural internal digestion markers and the change in the N/P or N/ash ratio between diets and pen manure. Unfortunately, many air quality studies that use new technologies frequently forget to use long-established technologies, such as adequate nutrient analysis of animal diets and measurements of nutrient intake.

Key Words: Beef cattle, environment, techniques
doi:10.2527/asasann.2017.738

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739 Measuring the respiratory gas exchange of grazing cattle using the GreenFeed emissions monitoring system.

S. A. Gunter*[1], S. E. Duke[2], and M. R. Beck[3], *[1]USDA-ARS, Woodward, OK, [2]USDA-ARS, College Station, TX, [3]Oklahoma State University, Stillwater.*

Ruminants are a source of enteric methane, which has been identified as a greenhouse gas that contributes to climate change. With interest in technologies to decrease enteric methane emission, novel systems are currently being developed to measure the methane emission by cattle. An issue with grazing cattle is the ability to measure emissions in open-air environments. A scientific instrument for this task is the GreenFeed emission monitoring system (GEM; C-Lock, Inc.; Rapid City, SD). The GEM is a head-chamber that grazing cattle occasionally visit and while the animal consumes a small portion of bait (3 to 8 min), the GEM captures the animal's breath cloud by exhausting air through the system. The breath cloud is then analyzed for methane and carbon dioxide. Data are hourly uploaded to a server where it is processed using algorithms to determine total daily emissions. Several factors affect the emission estimates generated by the GEM including the animal's visitation rate, length of sampling period, and airflow through the GEM. The location of the GEM is an important factor in determining the cattle's willingness to visit it. Further, cattle need to be trained to use the GEM, which normally requires 4 to 8 wk. Several researchers have shown that 30 or more visits are required to obtained high-quality estimates of emissions. Once cattle are trained to use the GEM, the bait delivery rate has little effect, as long as visitation length is greater than 3 min. Airflow through the GEM is an important factor, but as long as airflow is maintained above 26 L/s breath-cloud capture seems complete. There is great concern regarding diurnal variation in the instantaneous production rates of methane because the GEM only spot-samples 3 to 4 times/d. Preliminary analysis have shown that the variation in the instantaneous production rates of methane do not vary as greatly with grazing cattle compared to meal-fed cattle; hence, the variation can be managed. It seems that increasing the visitation length decreases variation in emission estimated, but there is a diminishing return to increasing visitation length. Post-processing of emissions data is a critical part of the quantification process. Post-processing data from situations where correction is needed has been shown to be successful and to improve the quality of estimates. The GEM is a useful tool for researching the nutrition and emissions of grazing cattle, but great care must be taken to obtain the best quality data possible.

Key Words: Carbon Dioxide, Cattle, Enteric Methane
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740 Use of GPS tracking collars and accelerometers for rangeland livestock production research.

D. W. Bailey*[1], M. G. Trotter[2], C. W. Knight[3], and M. G. Thomas[4], [1]*Department of Animal and Range Sciences, New Mexico State University, Las Cruces,* [2]*Central Queensland University, Rockhampton, Australia,* [3]*University of Maine, Orono,* [4]*Department of Animal Sciences, Colorado State University, Fort Collins.*

Global positioning system (GPS) collars have been used to track livestock in research studies for over 20 years. Accelerometers are commonly combined with GPS on commercial tracking collars. Today, accelerometers are sensitive and can record movements at fine temporal scales for periods of weeks to months. Tracking collars have become easier to develop and construct, making them significantly less expensive than commercially available collars. The primary use of GPS tracking has been to document livestock spatial movements and to evaluate management practices designed to manipulate grazing distribution patterns. For example, cattle use of feed supplement placed in areas far from water and on steep slopes can be measured with GPS tracking and corresponding impacts on distribution patterns estimated. Ongoing research has identified genetic markers that are associated with cattle spatial movement patterns. If the results can be validated, genetic selection for grazing distribution may become feasible. Some research questions can be designed so that dependent variables are measured by spatial movements of livestock, and in such cases, GPS tracking is a practical tool for conducting studies on extensive and rugged rangeland pastures. The combination of GPS tracking and accelerometers appear to be useful tools for identifying changes in livestock behavior that are associated with livestock diseases and other welfare concerns. Recent technological advancements may make real time or near-real time tracking on rangelands feasible. This would allow development of applications that could remotely monitor livestock well-being on extensive rangeland and notify ranchers when animals require treatment or other management.

Key Words: Global Positioning System, Behavior, Cattle
doi:10.2527/asasann.2017.740

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741 The use of a rumination monitoring device for finishing beef steers receiving different particle size and inclusion rate of dietary roughage.

J. S. Jennings*[1], W. W. Gentry[1], C. P. Weiss[1], C. M. Meredith[1], N. A. Cole[2], and F. T. McCollum[1], [1]*Texas A & M AgriLife Research and Extension Center, Amarillo,* [2]*USDA-ARS Conservation and Production Research Laboratory (retired), Bushland, TX.*

New technologies have immerged to aide in establishing the appropriate recommendations for roughage inclusion in finishing diets. Two experiments were completed using a collar (HR Tag; SCR Dairy, Netanya, Israel) which measured rumination minutes continuously via a sensory microphone. Different grind sizes of corn stalks were fed at 5 or 10% inclusion (DM basis; DMB) to determine their effects on feedlot performance, rumination behavior, and ruminal fermentation characteristics of beef steers. Differences in particle size were obtained by grinding corn stalks once (LG) or twice (SG) using a tub grinder equipped with a 7.62 cm screen and quantified using the Penn State Particle Separator to estimate physically effective NDF (peNDF). Experiment 1 was a feeding study using steam-flaked corn-based finishing diets fed with 10% SG (10SG), 5% SG (5SG), and 5% LG (5LG; DMB). Steers were fed once daily using Calan head gates for an average of 155 d. Experiment 2 was a metabolism study using diets from Exp.1 with an additional treatment diet containing 10% LG (10LG; DMB). Four ruminally cannulated steers were used in a 4 × 4 Latin square experiment. Treatments were arranged as a 2 × 2 factorial. Each period included 14 d for adaptation and 4 d for diet, fecal, ruminal fluid collections, and rumination activity. Overall, long grind corn stalks contained more ($P < 0.01$) peNDF than SG, and the 10LG had the greatest ($P < 0.01$) percentage of estimated peNDF than the other treatments. In Exp. 1, carcass-adjusted ADG, G:F, and dressing percent were greatest ($P \leq 0.03$) for steers consuming 5LG and 5SG than 10SG. A significant interaction ($P < 0.01$) occurred for rumination min x day. Rumination (min/day) were greatest ($P = 0.01$) for steers consuming 10SG, followed by 5LG, and lowest for 5SG. In Exp. 2, cattle consuming LG had greater ($P < 0.01$) rumination time, and greater ($P < 0.01$) ruminal pH than cattle consuming diets containing SG. Cattle receiving the 5% inclusion rate of roughage tended to have greater ($P = 0.09$) time (hr/d) under a ruminal pH of 5.6 and a larger ($P = 0.03$) area under the threshold compared to 10% roughage treatments. Feeding a lower inclusion of roughage with a larger particle size may aid in ruminal buffering similar to that of a higher inclusion of roughage with a smaller particle size, without negatively impacting fermentation and feedlot performance.

Key Words: beef cattle, finishing diet, rumination
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742 Continuous ruminal pH measurement: Validation, opportunities, and limitations.

G. B. Penner*, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

Microbial fermentation of feed in the rumen drives net energy and metabolizable protein supply for ruminants emphasizing the importance for a comprehensive understanding of fermentation characteristics. However, ruminal fermentation does not occur in steady-state and, hence, data collection must occur frequently to adequately characterize the response to diet, management, and host-factors. In addition, substantial regional stratification occurs in the rumen; thus, further requiring clear information for the region of pH measurement. Given the importance of fermentation, indwelling systems have been designed to evaluate ruminal pH in real-time. These systems have been validated and have remarkable accuracy and precision relative to samples measured using spot sampling approaches. Initial continuous pH measurement systems required cattle to be tethered to support hard-wire connections between the pH electrode, pH meter, and data-logger. While these systems provided novel information, application was. More recently, indwelling pH systems have been developed that enable measurement in group-housed cattle. This advancement has allowed for application of pH measurement under loose-housed dairy, feedlot, and grazing conditions. Surprisingly, ruminal pH measurement in feedlot cattle has revealed much lower risk for low ruminal pH than would have been previously thought. However, as these systems are smaller and lighter than the previous indwelling systems, differences in their inherent design and method of application (oral dosing vs via a ruminal cannula) affect interpretation of the results. In particular, the ability to orally dose pH systems and the subsequent measurement of reticular pH has drawn questions regarding the relationship between reticular and ruminal pH. Most studies conducted have demonstrated that reticular pH is greater and less responsive than ruminal pH; however, this relationship may not hold true for cattle fed high-concentrate diets. While there is a greater opportunity to measure ruminal pH with indwelling devices, challenges to the relevance of pH as a sole predictor of fermentation conditions is warranted. Advancements in ability to measure reticular and ruminal pH have improved our understanding of how management, diet, and host-factors affect ruminal pH, but, conclusions based on pH data alone should be regarded with caution.

Key Words: beef cattle, dairy cattle, ruminal pH
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743 Using advanced technologies to quantify cattle behavior.

J. T. Richeson*, *West Texas A&M University, Canyon.*

For many decades, we have relied upon visual observation of animal behavior to define clinical disease, assist in breeding selection and predict growth performance. Limitations of visual monitoring of cattle behavior include training of personnel, subjectivity, and brevity; however, extensive time and labor is required to monitor behavior in a large number of animals. Furthermore, the prey instinct of cattle to disguise abnormal behaviors in the presence of a human evaluator is problematic. More recently, cattle behavior has been quantified objectively and continuously using advanced technologies to assess animal welfare, indicate lameness or disease, and detect estrus in both production and research settings. Some of these technologies include 3-axis accelerometers that quantify physical activity, systems that document feeding and watering behavior via radio frequency, and triangulation or global positioning systems to determine location and movement of cattle within a pen or pasture. Advances in Wi-Fi and radio frequency technology have allowed many of these systems to operate in real-time and efforts are underway to develop commercial applications that may allow early detection of respiratory or other cattle diseases in the production environment. Current challenges with commercial application of technology for early disease detection include establishment of an appropriate algorithm to ensure maximum sensitivity and specificity, cost benefit, and infringement of traditional methodology for clinical diagnosis. Advanced technologies have also allowed researchers to determine temporal variance in behavior or variability between experimental treatments. Specifically, we have used 3-axis accelerometers to continuously record standing and lying duration, step count, lying bouts and motion index generated in 15 min intervals. Our research efforts include effects of castration method and timing, weaning method, transportation, beta-adrenergic agonist feeding, and bovine respiratory disease on physical behavior in cattle. Benchmark activity data will also be discussed for cattle fed in confinement and during transport and lairage at a commercial beef processor.

Key Words: Accelerometer, Behavior, Disease
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744 Automated collection of heat stress data in livestock: New technologies and opportunities.

J. E. Koltes*, *Department of Animal Science, University of Arkansas, Fayetteville.*

Heat stress is a major source of economic losses in the US livestock industry. Estimated annual losses top $369 million in the beef cattle industry alone. A variety of technologies have been developed to monitor body temperature in an attempt to manage its detrimental effects on production. Ear tags that measure body temperature, intra-vaginal thermosensors and additional technologies have been used to automate the process of detecting heat stress. These automated technologies allow researchers to generate data on an unprecedented scale over time. These data can be integrated with omics data to identify biomarkers, used to generate genetic predictions

of heat tolerance, or to develop nutritional or management strategies to reduce the burden of heat stress. It may also be interesting to consider how these technologies might be used in sentinel animals to monitor and manage heat stress in commercial production systems. Strategies to use these technologies and examples of research that utilize these heat stress monitoring technologies will be presented.

Key Words: Beef cattle, Heat stress, Thermosensors
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745 How nutritional requirements differ among various working canines.

R. L. Kelley*, *Royal Canin, Lewisburg, OH.*

The exact origin of man's best friend remains somewhat unclear (Vila et al., 1997; doi:10.1126/science.276.5319.1687), however it is accepted that they have co-existed alongside us for more than 14,000 years (Giemsch et al., 2015; Hugo Obermaier Society for Quaternary Research and Archaeology of the Stone Age: 57th Annual Meeting in Heidenheim, 7th – 11th April 2015, 36-37). Human intervention, through selection, has slowly transformed canines to the array of breeds that we know today. Accompanying the development of these breeds and their phenotypic traits are the behavioral traits that contributes to their uniqueness. We currently employ canines to assist with various tasks including detection, guide or service, law enforcement, a plethora of sporting activities, as well as a growing number of additional activities. It is almost a certainty that in the future there will be new activities where we will utilize canine assistance. Working canines, like their species, are extremely diverse in their make as well as their nutritional requirements. Competitive canines are most commonly in the 15-40 kg range, however there are representatives that are greatly different from this range. Just considering the number of breeds and the range in size among working canines, it should not be surprising that the nutritional requirements for this segment would also vary greatly. However, the more intriguing considerations are those nutritional changes dictated by activity level rather than body size. In general terms, most dogs in the working segment possess a neutral environment resting energy requirement of approximately 1300-1400 kcal/day (Hill, 1998. J. Nutri 128(12): 2686S-2690S, Bermingham et al., 2014. PLOS 9(10) e109681). However when we consider the impact of activity, the energy requirements can dramatically change. Consider the racing segment, where the work load on the dog can range from a few hundred meters / day (Sprints) to race distances approaching 200 km /day for endurance sled dogs. Hill (1998) reported on slight increases above resting maintenance energy requirements for racing Greyhounds. In contrast, the energy requirements for endurance sled dogs has been reported to be greater than 11,000 calories per day (Hinchcliff et al., 1997. AM J Vet Res, 58: 1457-62; Loftus et al, 2014. J Nutri Sci, 3: 1-5; DOI:10.1017/jns.2014.31). This review will further examine the impact of activity type and work load on the nutritional requirements of canine athletes as well as the effect specific nutrient class has on performance across multiple segments of working canines.

Key Words: Nutrition, Canine, Performance
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746 Be the impact: A graduate student's role in mentoring undergraduates in animal science.

S. A. Reed*, *Department of Animal Science, University of Connecticut, Storrs.*

In many research laboratories, there is a hierarchy of individuals and relationships; principal investigators, postdoctoral associates, research technicians, graduate students, and undergraduate students often work together to advance the research. These relationships provide unique opportunities for mentorship, in particular, mentorship of undergraduate students in animal science research. Undergraduate students involved in mentored research report increased curiosity, confidence, and independent learning. In addition, undergraduate research experiences increase retention in science and matriculation to graduate programs. This is often the undergraduate student's first exposure to research, and may be a formative experience in their career. Graduate students are ideally positioned to provide direct mentorship to undergraduate students because of the degree of supervision required and teaching opportunities provided when conducting research projects. Importantly, this interaction may be the first opportunity for a graduate student to mentor a junior person, and therefore it is important that graduate students actively seek resources to curate and improve mentorship skills. This presentation will focus on ways graduate students can actively mentor undergraduate students in animal science research. In addition to teaching scientific skills, graduate students can develop relationships with, provide guidance to, model appropriate behaviors for, and provide encouragement and motivation to undergraduate researchers. For graduate student mentors, the mentoring experience develops leadership skills crucial for professional development and often provides personal satisfaction. Successful mentoring relationships provide positive experiences and lasting benefits for both undergraduate and graduate students, preparing both populations to better serve the animal science community.

Key Words: graduate student, undergraduate student, mentoring
doi:10.2527/asasann.2017.746

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747 Navigating pre-tenure: Strategies to establish a successful early career in animal science.

J. M. Gonzalez*, *Department of Animal Sciences and Industry, Kansas State University, Manhattan.*

Beginning a university career as tenure track Assistant Professor can be both exciting and stressful. In the end, an Assistant Professor has only a fixed amount of time, typically 7 years,

in which he or she must demonstrate enough productivity to be granted a promotion and more importantly, tenure. While that may seem like a long time, the rigors associated with the university system, establishing a laboratory, and general everyday life compresses this time period into what seems like months. As a tenure track faculty member who recently received a promotion and tenure, this interactive session will cover several approaches to my career that helped me achieve this outcome. Topics that will be covered include managing your appointment split, establishing a research team, forming collaborations, securing funding, publication strategies, and allocating personal time. Understanding how your university determines success in each of these areas and allocating your time to meet these expectations, is the key to success. As with any career, there will be "ups" and "downs"; however, learning to weather the "downs" and not becoming complacent during the "ups" will ensure one has a long and impactful career. The major aim of this session is to inspire students to pursue tenure track positions in the Animal Sciences and help them understand this process is not as intimidating as it seems.

Key Words: Career, Promotion, Tenure
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748 Mining farm- and animal-level data to optimize beef cattle production.

J. R. R. Dorea*, and G. J. M. Rosa, *University of Wisconsin-Madison, Madison.*

Data mining is defined as the practice of examining large databases in order to generate useful information from discovered patterns. Although the term "large databases" is relative and context dependent, the concept of analyzing datasets to generate predictive models is a key part of data mining. Data mining in livestock systems include both the animal- and farm-level components. At the animal level, measurements such as feed intake, gain, diet and milk composition, health recordings, behavior, etc., can be collected. In recent years, sensor systems have been developed to aid in cattle management. For instance, sensors are able to measure rumination time, activity, lameness, health indices, and grazing time among other variables. In addition, image analysis has become an important tool to measure body characteristics such as carcass composition in beef cattle and backfat thickness in dairy cows. Farm-level data reflect a larger picture of livestock systems where management and economic factors play an important role. Those factors can include cattle sales price, feed price, transportation costs, medication, herd size, nutritional strategy, weather condition, etc. To illustrate farm-level data analytics, we will present two different datasets. The first one refers to data on Brazilian beef cattle from two sources: *JBS S.A.* (81,053 farms) and *DSM Produtos Nutricionais* (22,223 farms). The combined dataset comprised 7,248 farms and 1,571,023 carcasses slaughtered in the past three years (2014-2016). In this first example, we investigated the effect of different nutritional supplements, adoption of frequent technical consulting, season, animal category, and other variables on carcass quality, body weight and age at slaughter. The second dataset is from CMA, a cattle feeding company in Brazil, consisting of 777 pens and 62,992 cattle slaughtered in the past 3 years (2014, 2015, and 2016). Seventeen economic and management variables such as breed, days on feed, diet cost, transportation, medication, season and others were used to predict profitability. The models were developed to create a decision-making tool for earlier prediction of negative profits in feedlot systems. Interest on data mining in livestock systems has markedly increased and reflects the necessity to uncover hidden patterns present in large datasets and transform them into useful information.

Key Words: beef cattle, data mining, feedlot
doi:10.2527/asasann.2017.748

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749 Effects of postruminal flows of protein and amino acids on small intestinal starch digestion in cattle.

D. W. Brake*, *South Dakota State University, Brookings.*

A large amount of cattle in the United States are fed starch-based diets because limitations to efficient production of meat and milk by cattle are frequently associated with limits in NE. Many nutritionists adopt feeding strategies designed to increase ruminal starch fermentation because ruminal capacity for starch degradation often exceeds amounts of starch able to be digested in the small intestine of cattle. However, increases in fermentable energy supply are positively correlated with increased instances of metabolic disorders and reductions in DMI, and energy derived by cattle subsequent to fermentation is less than that derived when glucose is intestinally absorbed. Apparently, small intestinal starch digestion (SISD) is limited by α-glycohydrolase secretions and a precise understanding of digestion of carbohydrates in the small intestine remains equivocal. Interestingly, small intestinal α-glycohydrolase secretions are responsive to luminal appearance of high-quality protein (i.e., casein) in the small intestine of cattle, and SISD is increased by greater postruminal flows of individual AA (i.e., Glu). Indeed, greater flows of casein and Glu appear to augment SISD but by apparently different mechanisms. Greater small intestinal absorption of glucose has been associated with increased omental fat accretion even though SISD can increase NE from starch by more than 42% compared to ruminal starch degradation. Nonetheless, in vitro data suggest that greater glucogenicity of diets can allow for greater intramuscular fat accretion, and if greater small intestinal absorption of glucose does not mitigate hepatic gluconeogenesis then increases in SISD may provide opportunity to increase synthesis of intramuscular fat. If duodenal metabolizable AA flow can be altered to allow for improved SISD in cattle, then diet modification may allow for large improvements in feed efficiency and beef quality. Few data are available on direct effects of increases in

SISD in response to greater casein or metabolizable Glu flow. An improved understanding of effects of increased SISD in response to greater postruminal flow of Glu and casein on improvements in NE and fates of luminally assimilated glucose could allow for increased efficiency of energy use from corn and improvements in conversion of corn grain to beef. New knowledge related to effects of greater postruminal flow of Glu and casein on starch utilization by cattle will allow nutritionists to more correctly match dietary nutrients to cattle to allow large improvements in nutrient utilization and efficiency of gain among cattle fed starch-based diets.

Key Words: cattle, small intestinal starch digestion, Amino acid
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750 Animal models to study germ line stem cells and spermatogenesis.

I. Dobrinski*, *University of Calgary, Calgary, AB, Canada.*

Mammalian spermatogenesis is a stem cell-driven system. Germ line stem cells (spermatogonial stem cells) form the basis of male fertility and are the only cells in an adult body that divide and can contribute genes to subsequent generations, making them immediate targets for genetic manipulation. Stem cells have to maintain a delicate balance between self-renewal to maintain a functional stem cell pool and differentiation to sustain efficient, life-long production of sperm. However, relatively little is known about the mechanisms that govern this fate-decision. Similar to stem cells in other organs, germ line stem cells reside in a specialized microenvironment, the stem cell niche. Interactions between stem cells and their niche are essential for tissue homeostasis. Our work utilizes various mammalian animal models and transplantation technology to elucidate aspects of stem cell function, formation of the stem cell niche, and applications of stem cell-based technology to preservation of fertility and genetic modification of non-rodent animal models.

Key Words: stem cells, animal models, testis
doi:10.2527/asasann.2017.750

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751 Divergent vascular endothelial growth factor a (VEGFA) signaling determines spermatogonial stem cell fate.

A. S. Cupp*, J. R. Essink, M. L. Bremer, W. E. Pohlmeier, M. M. Laughlin, and K. M. Sargent, *University of Nebraska-Lincoln, Lincoln.*

The vascular endothelial growth factor A (*Vegfa)* gene can be spliced into divergent isoform family types- angiogenic and antiangiogenic. Our laboratory has been investigating the role of these sister isoform families in male fertility and the mechanisms by which they contribute to maintenance of spermatogonial stem cells (SCC). Our hypothesis is that there must be a balance of VEGFA angiogenic to antiangiogenic isoforms to maintain the spermatogonial stem cell niche. Specifically, angiogenic isoforms stimulate SSC renewal and proliferation while antiangiogenic VEGFA isoforms induce differentiation or apoptosis of male germ cells. Initial experiments involved postnatal mice (day 5-7) treated with either VEGFA165 angiogenic or VEGFA165b antiangiogenic isoforms whose germ cells were harvested at day 8 and then transplanted into recipient mice. Reduced colonization of SSCs was observed after 6 weeks in recipient males that received germ cells from donor mice testes that were treated with VEGFA165b. These data suggest that the antiangiogenic VEGFA isoforms may arrest SSC proliferation or renewal by causing apoptosis or by differentiating them into later-stage spermatogonia. Using conditional knockout mice we eliminated both VEGFA isoform types in Sertoli and germ cells (using Dmrt1-Cre) which resulted in reduced sperm counts despite compensatory increases in genes known to promote SSC maintenance (*Ret*, *Sin3a*, and *Neurog3*). Elimination of NRP1, a co-receptor that binds angiogenic VEGFA isoforms but not antiangiogenic isoforms, from Sertoli and Leydig cells (using Amhr2-Cre) reduced fertility, reduced angiogenic VEGFA signaling and downregulated genes important in SSC maintenance (*Gdnf*, *Ret*, *Sin3a*, *Neurog3*, *Foxo1*, and *Kitl*). Additionally, NRP1 loss reduced phosphorylation of RET, which is a receptor of GDNF a major initiator of SSC self-renewal. Interestingly, NRP1 also appeared to be co-localized with cells that were positive for ID4, a putative SSC marker, and there were reductions in ID4/NRP1 double positive cells following NRP1 elimination. Thus, elimination of NRP1 also appeared to accelerate putative SSC cell loss, possibly due to apoptosis or reduction of VEGFA angiogenic isoform survival functions. To compare the effects of all VEGFA isoforms to inhibiting just angiogenic isoform signaling, we used Sertoli cell-specific knockouts of both NRP1 and VEGFA (*Sry-Cre*). Males had reduced fertility in both cases. Preliminary findings from spermatogonial stem cell transplantation experiments indicated reduced SSC colonization in donor mice testes. Taken together, these findings further implicate the importance of regulating VEGFA signaling to ensure SSC maintenance and male fertility and suggest that VEGFA isoforms are regulators of the SSC niche.

Key Words: VEGFA, testis, Spermatogonial stem cells
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752 Historical perspectives of lactation biology in the late 20th and early 21st centuries.

R. J. Collier*[1], and D. E. Bauman[2], [1]*University of Arizona, Tucson,* [2]*Cornell University, Ithaca, NY.*

The latter half of the 20th century and the first half of the 21st century will be recognized as the “Golden Age” of Lactation Biology. This period corresponded with the rise of systemic , metabolomic, molecular and genomic biology. It opens with the discovery of the structure of DNA and ends with the sequencing of the complete genomes of humans and all major domestic animal species including the dairy cow. This included the ability to identify polymorphisms in the nucleic acid sequence which can be tied to specific differences in cellular, tissue and animal performance. Prior to this period classic work using endocrine ablation and replacement studies identified the mammary gland as an endocrine dependent organ. In the early 1960s the development of radio-immuno and radio-receptor assays permitted the study of the relationship between endocrine patterns and mammary function. The ability to measure nucleic acid content of tissues opened the door to study of factors regulating mammary growth. The development of high speed centrifugation in the 1960s allowed separation of specific cell organelles and their membranes. The development of transmission and scanning electron microscopy permitted the study of the relationship between structure and function in the mammary secretory cell. The availability of radioactive isotopes opened the doors to the study of metabolic pathways and end products of metabolism. The development of concepts regarding the coordination of metabolism to support lactation integrated our understanding of nutrient partitioning and homeostasis. The ability to produce recombinant molecules and organisms permitted enhancement of lactation in farm animal species and the production of milk containing proteins of value to human medicine. These discoveries and others contributed to a vastly increased dairy farm productivity in the U.S. and world-wide. This review will include the discussion of the thought leaders and laboratories who labored in these fields to produce the harvest of knowledge we enjoy today.

Key Words: lactation biology, endocrinology, nutrient partitioning
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753 Dietary regulation of allometric ductal growth in the mammary glands.

R. C. Hovey*[1], G. E. Berryhill[2], S. Miszewski[2], A. Derpinghaus[1], C. Donovan[2], and J. F. Trott[1], [1]*University of California, Davis, Davis,* [2]*University of California Davis, Davis.*

Development of the mammary glands is a continual process spanning from prenatal establishment of the epithelial primordium through to the full establishment of the secretory gland during lactation and its subsequent regression during involution. While the accretion of parenchymal tissue is greatest during phases such as gestation, it is the growth and establishment of the mammary ductal network prior to and during puberty that sets the stage for all subsequent periods of development and function. Depending on the species, ductal elongation can involve large amounts of epithelial proliferation and apoptosis in terminal end bud structures that interface with the surrounding stromal microenvironment. Ultimately all these processes are considered to be driven by a changing endocrine environment – but is it that simple? Of course, postnatal development also occurs against a changing nutritional background. Our findings from various models emphasize that dietary nutrients and plane of nutrition can dramatically impact mammary growth – either positively or negatively. We will review some of these key findings and summarize the potential for alternate mechanisms of ductal growth regulation in the mammary glands across species.

Key Words: duct, estrogen, mammary gland
doi:10.2527/asasann.2017.753

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754 The role of milk fat in modern human nutrition: What is the current state of knowledge?

X. Zhao*[1], and L. B. Agellon[2], [1]*McGill University, Department of Animal Science, Ste-Anne-de-Bellevue, QC, Canada,* [2]*School of Dietetics and Human Nutrition, McGill University, Ste. Anne de Bellevue, QC, Canada.*

Milk is a good source of fats and proteins as well as essential nutrients such as calcium and phosphorus. Milk has been an important part of the human diet since the domestication of animals. Milk consumption, particularly cow's milk, is at an all-time high in western societies, and steadily increasing in societies undergoing nutrition transition. Milk is regarded as an important component of a healthy diet especially during childhood and adolescence. In recent times, controversy abounds regarding the role of dairy products, especially dairy fat, in cardiovascular health as many recent studies have reported inconsistent findings. Here, we present a review of the current state of knowledge focusing on effects of milk fat and fatty acid compositions, biomarkers for fatty acid intake and microRNA in milk exosomes, on human health. We suggest that interdisciplinary approaches and trans-sectorial collaboration are needed to clarify the role of milk fat in human health. The quality and composition of milk fat can vary widely, even between individual animals in the same breed. Constraints and potential for modulation of milk fatty acid composition by nutritional and genetic strategies will be discussed. Finally, we propose that dairy foods, including regular-fat milk and other dairy products, can remain as an important component of an overall healthy dietary pattern for a majority of individuals across the lifespan.

Key Words: Milk fat, Human nutrition, Fatty acids
doi:10.2527/asasann.2017.754

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755 Beef: From a good source of nutrients to a functional food.

P. Vahmani*[1], S. D. Proctor[2], F. Kolahdooz[2], S. Sharma[2], J. L. Aalhus[1], M. E. R. Dugan[1] [1]*Agriculture and Agri-Food Canada, Lacombe, AB, Canada,* [2]*University of Alberta, Edmonton, AB, Canada.*

Invited speaker- CSAS symposium: Healthy animals producing healthy foods. Let food be thy medicine" is a quote attributed to Hippocrates. Moving a link down the food it might be more appropriate to say "Let feed be medicine for thy food and thy food be medicine for you". We live in times when links between diet and health are being recognized more and more as the first line of support to promote longevity and quality of life in later years. The content and composition of nutrients in feeds can play a role in animal health and productivity, and in turn the content and composition of animal derived foods can influence human health and wellness. The objectives of the current presentation will be to outline the effects of diet on the nutrient content and composition of animal derived foods, and to review how animal derived foods can functionally contribute to human health and wellness. Emphasis will be on the content and balance of omega-3 and -6 fatty acids in beef, the potential for accumulation of polyunsaturated fatty acid biohydrogenation products in beef, and our current understanding of how these may influence consumer health and wellness.

Key Words: beef, functional foods, fatty acids
doi:10.2527/asasann.2017.755

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756 Reconstruction of metabolic and physiologic adaptations to lactation using systems biology.

J. J. Loor*, *Mammalian NutriPhysioGenomics, Department of Animal Sciences, University of Illinois, Urbana, IL; University of Illinois, Urbana, IL; Department of Animal Sciences, University of Illinois, Urbana, IL; Division of Nutritional Sciences, Illinois Informatics Institute, University of Illinois, Urbana, IL*

Along with functional bioinformatics, high-throughput 'omics' are the foundation of modern systems biology, a field of study widely used in model organisms (e.g., rodents, yeast, humans) to enhance understanding of the complex biological interactions within cells and tissues at the gene, protein, and metabolite level. The "systems approach" is particularly well-suited for the study of the interactions between nutrition and physiological state with tissue metabolism and function during key life stages of organisms such as the transition from pregnancy into lactation. This physiological state is often referred as the "periparturient" or "transition" period. In modern dairy cows with an unprecedented genetic potential for milk synthesis, the nature of the physiologic and metabolic adaptations during the periparturient period is multifaceted and involves the rumen and its microorganisms along with key tissues such as liver, adipose, mammary gland, and cells of the immune system. Application of the systems approach in periparturient cows already has allowed a better understanding of the degree of these multifaceted adaptations. Modern bioinformatics tools capable of discerning functional outcomes and biologically-meaningful networks complement the ever-increasing ability to generate large molecular, microbial, and metabolite data sets. The ultimate goal is to visualize the complexity of the systems under study and uncover key players involved in the cow's adaptation to physiological state and nutrition.

Key Words: Nutrition, Gene networks, Bioinformatics
doi:10.2527/asasann.2017.756

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757 Associations between gut, mammary and vaginal microbiomes in dairy cows: Role in health and disease.

E. Khafipour*, H. Derakhshani, K. B. Fehr, H. Khalouei, Z. Zhang, and J. C. Plaizier, *Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada.*

The crucial role of rumen and hindgut microbiomes in intestinal and extra-intestinal diseases is emerging. Both rumen and hindgut microbiomes have been shown to impact host physiology, metabolism, and immune function and to confer direct and indirect (immune-mediated) resistance against enteric pathogens. Disruption of rumen and hindgut microbiomes or dysbiosis – which is referred to as an abnormal balance of beneficial and protective versus opportunistic members of microbiota – have been linked to a number of metabolic disorders that occur around early to mid-lactation periods, such as acute and subacute ruminal acidosis, milk fat depression, and bloat. Dysbiosis of the gut microbiome impacts the profile of microbially-driven metabolites and compounds produced by the microbiota. These molecules influence the metabolic and immunological capacities of the host both within and outside of the gut, e.g. through the enterohepatic pathway or the gut-brain axis, which retroactively impacts the diversity and behaviour of the microbiome in the digestive tract, and also potentially influences the microbiomes of other body sites, such as vaginal tract or mammary gland resulting in initiation or progression of infectious or inflammatory diseases in those systems, e.g. mastitis. The research by our group and others shows that interactions among commensal members inhabiting different ecological niches of the udder (i.e. teat apex, teat canal, and milk) are crucial for shaping the composition and functional properties of the mammary gland microbiome, and potentially govern the susceptibility of dairy cows to infectious mastitis. Similarly, a healthy vaginal microbiome has a key role in improving ruminants' reproductive performance and preventing infectious diseases. It is thus speculated that nutritional and physiological stressors at early lactation, which are one of the significant underpinnings of the microbiome-gut-brain axis, not only impact the diversity and behavior of the gastrointestinal tract microbiome but also the vaginal and mammary gland microbiomes and thus susceptibility to infectious diseases. In this presentation, I will review the role of rumen and hindgut microbiomes in the context of their association with vaginal tract and mammary microbiomes in dairy cows subjected to subacute ruminal acidosis during early lactation. I will also highlight the pressing need for development of synthetic microbial communities to improve gut, mammary and vaginal health and production efficiency of ruminant animals.

Key Words: Mammary gland microbiome, Vaginal tract microbiome, Rumen and hindgut microbiomes
doi:10.2527/asasann.2017.757

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758 Understanding the nature of complex phenotypes in beef cattle using systems biology.

A. Canovas*[1], M. G. Thomas[2], J. Casellas[3], and J. F. Medrano[4], [1]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*Department of Animal Sciences, Colorado State University, Fort Collins,* [3]*Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain,* [4]*Department of Animal Science, University of California, Davis.*

In recent years, breeders have combined the use of phenotypic appraisal and the estimation of breeding values (EPD) to make genetic selection decisions in beef and dairy cattle that have resulted in a steady genetic gain of 2% per year. However, the most extensive application of genomics has occurred in the dairy industry with the estimation of molecular breeding values that has improved selection efficiency to a much higher order of magnitude. Despite a growing molecular and physiological understanding of complex traits, little is known about the genes determining the traits and their precise function, and a significant unexplained source of variation of phenotypes remains in livestock. Within this context, a more complete understanding of the genes and regulatory pathways and networks involved in economically important traits (i.e. fertility and reproduction, feed efficiency, meat quality and carcass traits) in beef cattle will provide knowledge to help improve genetic selection and reproductive management. Currently, with all the new available technologies in livestock combined with statistical methodologies, the integration of structural and functional genomics information with other –OMICS into a systems biology approach has allowed development of a better biological understanding of phenotypes complementing the traditional genetic tools and further advance identification of functional genes. As part of the genomics tool box and the HD-genotyping SNP chips, whole genome sequencing technologies are now available in cattle and extensively utilized in genetic improvement. As a part of high throughput tools available for genomic analysis, RNA-Sequencing allows measuring not only gene expression, but also examining genome structure identifying SNP and other structural variation such as insertions, deletions and splice variants. The expectation is that the integration of all these types of genomic data will accelerate the genetic improvement by improving accuracy of selection and reducing the generation interval. Combining the information from the –OMICS technologies (i.e., transcriptomics, metagenomics, metabolomics, amongst several others) together with metabolic pathways and functional/biological analysis into a systems biology approach allows the identification of functional SNP increasing the accuracy of selection. The particular benefits of new integrated high-throughput genomics technologies within a systems biology approach will most likely be used to accelerate the genetic improvement of those traits that are difficult to measure such as health, feed efficiency, methane emission and fertility and reproduction traits in beef cattle.

Key words: OMICS technologies, Genetical Genomics, Systems biology
doi:10.2527/asasann.2017.758

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810 Glyphosate residues in feed.

D. A. Goldstein*, *Monsanto, St. Louis, MO.*

There is widespread confusion on pesticide residue tolerances in feed and food. Assumptions that tolerances are safety-based limits and that exceedances will result in a risk of illness in animals or humans are generally incorrect. Tolerances are set based on actual residue values following proper application in accordance with label instructions and are designed primarily to enforce proper application. Although tolerances in feed must ultimately protect both animals and animal product consumers (through meat, milk, and eggs), the large majority of tolerances fall far below any level of safety concern. Glyphosate residues occur in animal feed because of the use for in-crop weed control in glyphosate-tolerant cropping systems and some use as a preharvest desiccating agent. Based on extensive data, allowable glyphosate tolerances in feed are set far below levels of health concern. Animal feed efficiency and other data demonstrate no adverse effects of glyphosate residues (or genetically modified crops) on animal performance measures. Actual measurements of glyphosate in meat, milk, and eggs are generally undetectable, and overall human intake is far below levels of regulatory concern as reflected in human biomonitoring data.

Key Words: glyphosate, pesticide, residue
doi:10.2527/asasann.2017.810

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829 Controlling meat quality through product functionality enhancement.

H. L. Bruce*, *University of Alberta, Department of Agricultural, Food and Nutritional Science, Edmonton, AB, Canada.*

Meat can be considered a functional food because it is an excellent source of protein; minerals such as iron, zinc, and selenium; and B vitamins, but recent associations of red meat with diseases such as cancer and cardiovascular disease provide an impetus to look at increasing the healthfulness of meat. Modification of the eating quality of meat is currently accomplished through management of animal breed and/or growth-enhancing pharmaceuticals, with gene marker selection for meat tenderness commercially available in cattle and under investigation in pigs. Other antemortem meat quality enhancements include alteration of fat content and fatty acid composition through animal diet; supplementation of animals with vitamins D and E to improve meat tenderness and shelf life, respectively; and provision of glucose and electrolytes prior to slaughter to decrease the likelihood of dark cutting and improve meat color. Given that ground, seasoned, cured, and injected/tenderized products are readily accepted in the

North American market, the use and development of additional postmortem strategies and technologies to enhance meat quality and healthfulness warrant reconsideration. Improvement of the healthfulness of meat through prevention of the growth of pathogenic bacteria is easily substantiated, and bacteriocins from lactic acid bacteria have been shown to be effective. Recent research has focused on increasing the proportions of muscle protein and omega-3 fatty acids and reducing sodium chloride and sodium nitrite concentrations in processed meat products. Also, incorporation of "functional" plant products to enhance meat healthfulness and quality through the addition of natural antioxidants has been investigated with some success at reducing heterocyclic aromatic amines. Fermented meats are gaining credibility as functional foods because of the potential proteolytic release of bioactive peptides that exhibit either inhibitory activity on the angiotensin I-converting enzyme (ACE) or opiod properties or have a prebiotic function. Meat from ruminants may have potential anticancer, antioxidative, and antiageing effects due to its conjugated linoleic acid content, but most potential healthfulness claims for meat have not been substantiated in humans. There is also the opportunity to improve flavor and eating quality through the introduction of reactive 5-carbon sugars such as ribose and xylose to pork products. Future research improving both meat healthfulness and eating quality while maintaining affordability may return health-conscious consumers to processed and unprocessed meat products.

Key Words: eating quality, functional food, meat
doi:10.2527/asasann.2017.829

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830 Milk fatty acids: Emerging perspectives.

R. Gervais*, E. Baumann, M. Leduc, and P. Y. Chouinard, *Université Laval, Department of Animal Science, Quebec, QC, Canada.*

Nutritional quality is an important determinant of consumer food choices due to the growing awareness of the association between diet and health. Milk fatty acid composition is a major component of the nutritive value of dairy products, in addition of being associated with both their physical and organoleptic properties. The fatty acid profile of milk can be significantly altered through feeding of cows, offering the flexibility to respond to consumer demands and public health recommendations. Strong evidence suggests that specific intermediates of ruminal biohydrogenation of PUFA inhibit the growth of different human cancer cell lines, slow the development of tumors, affect lipoprotein metabolism and immune function, and enhance lean body mass in animal models. Consequently, several studies have investigated the potential to alter distribution and concentration in milk fat of different isomers of ruminal biohydrogenation, such as conjugated dienes and *trans* octadecenoic acids. Also, because milk fat is a common component of the human diet, its enrichment with *n*-3 PUFA provides the opportunity to increase intake of these essential fatty acids by the general population. However, dietary PUFA are extensively metabolized in the rumen. Protecting fatty acids represents a major challenge in formulating feed supplements that will enhance the postruminal supply of *n*-3 PUFA. Feeding fatty acids as Ca salts has been proposed as a way to provide such protection. Recent work in our laboratory has demonstrated that *n*-3 PUFA included in large particles of Ca salts are physically protected against ruminal biohydrogenation, which increases the efficiency of their transfer from diet to milk fat. Furthermore, dairy products are the main source of branched-chain fatty acids (BCFA) in the human diet. These fatty acids are synthesized by ruminal microorganisms and are essential components of their lipid membranes. For humans, health benefits such as prevention of necrotizing enterocolitis, symptom attenuation of some neurological diseases, or anticarcinogenic properties have been associated with these bioactive molecules. A series of experiments carried out in our laboratory provided more insight into the effect of different physiological and nutritional factors on milk BCFA composition in dairy cows. These trials showed that milk fat concentrations of BCFA are affected by lactation stage as well as forage type, level of concentrate, and dietary lipid supplementation. In conclusion, milk fat contributes to human health in many important ways. Nutrition and management of dairy cows offers the possibility to adjust milk fatty acid composition as our knowledge of individual and combined health effects of numerous milk fatty acids develop.

Key Words: branched-chain fatty acids, dairy cow, omega-3 fatty acids
doi:10.2527/asasann.2017.830

LATE-BREAKING ABSTRACTS

862 The use of ultrasonography to examine mammary gland development in ewe lambs with different live weight–gain profiles between 12 and 20 weeks of age.

A. J. Molenaar*[1], B. Thompson[2], A. Wall[2], S. McCoard[3], S. R. Leath[4] , C. McKenzie[1], J. Koolaard[1], and D. Stevens[2], [1]*AgResearch, Palmerston North, New Zealand,* [2]*AgResearch, Mosgiel, New Zealand,* [3]*AgResearch Limited, Palmerston North, New Zealand,* [4]*AgResearch Ltd, Ruakura Research Centre, Hamilton, New Zealand.*

This study aimed to noninvasively examine the mammary composition of lambs on differing feeding levels, between weaning and puberty (70–260 d of age). Feeding during critical periods between birth and puberty appears to affect mammary growth. Current knowledge suggests that high growth rates and, in particular, fat deposition in the udder before puberty can have a negative influence on mammary growth and future milk production. It has been hypothesized that this

negative effect on milk production is due to the reduction in age at puberty and first pregnancy achieved through faster growth and the associated immaturity of the mammary tissue. However, the size of the fat pad also dictates the maximal area into which the mammary parenchyma can grow and hence may determine the gland's ultimate production potential. Therefore, early simple measurement of mammary tissue using ultrasound may provide a means to select animals with higher milking potential prior to 1) puberty and/or 2) insemination and first milking. East Friesian–cross ewe lambs at 70 d of age were randomly allocated to 2 levels of pasture feeding (a high nutrition plane, consuming, on average, 1.34 kg DM/lamb per day, and a 70% nutrition plane, consuming, on average, 0.85 kg DM/lamb per day) until 140 d ($n = 60$/group). At d 140, lambs were reallocated to nutrition treatment using a crossover design resulting in 4 treatment groups ($n = 30$/group). After the end of the treatment period (d 260), mammary gland size was imaged using ultrasonography. Total depth of the mammary gland, putative fat pad, and parenchyma, at the widest point for each subcompartment (estimated from 4 images/animal), was used as a proxy for tissue volume. The ratios of the different tissue depths were calculated. Data were analyzed using a linear mixed model with Image, with the 70 to 140 d treatment and 140 to 260 d treatment as fixed effects, animal as a random effect, and live weight as a covariate. Lamb live weights at d 260 were 36.2, 37.5, 40.0, and 41.3 kg ($P < 0.001$, SE 0.37) for the 70%–70%, High–70%, 70%–High, and High–High groups, respectively. The ratio of parenchyma to total mammary depth was reduced ($P = 0.043$) in response to only the nutrition treatments imposed during the second period. This decrease was by 5.4% in the lambs fed the high nutrition level compared with the 70% nutrition plane–fed lambs, indicating the proportion of fat tissue in the gland increased in the high group. This nondestructive measurement method was able to determine changes in the composition of the young sheep mammary gland related to prepubertal nutrition.

Key Words: mammary development, sheep, ultrasonography
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863 Effects of engineered antimicrobial peptide KR-32 on intestinal inflammation in weaned piglets.

W. Hu*, *Zhejiange University, College of Animal Science, Hanghzou, China.*

Diarrhea is a serious issue in raising livestock, especially in weaned piglets. Overuse of antibiotics leads to severe environment pollution. Therefore, our objective was to determine whether engineered antimicrobial peptide KR-32, a 32-residue peptide, displays high antimicrobial activity with minimal hemolytic activity and cytotoxicity. Results of minimum inhibitory concentration (MIC), transmission electron microscopy (TEM), indicated that antimicrobial peptide KR-32 exerts antimicrobial activity by destroying cell membrane integrity. Piglets with clinical diarrhea were divided into 3 groups (8 piglets each group) and treated with saline (control), KR-32, or ciprofloxacin lactate for 3 d. The diarrheal index was scored according to a fecal consistency scoring system (0 = normal, 1 = soft feces, 2 = mild diarrhea, and 3 = severe diarrhea) as previously described (Bhandari et al., 2008; Yi et al., 2016). The diarrheal index showed that all piglets had diarrhea. Comparisons were made by 1-way ANOVA or Student's *t*-test with SPSS 16.0 software (SPSS Inc., Chicago, IL). Effects were considered significant at $P < 0.05$. We found that the treatments of both antimicrobial peptide KR-32 and ciprofloxacin lactate effectively attenuated the diarrheal rate ($P < 0.05$) and diarrhea index ($P < 0.05$) compared with the control group. Proinflammatory cytokines such as IL-6 and TNF-α were the important indicators for intestinal inflammation during weaning. It has been demonstrated that low levels of IL-6 and TNF-α are beneficial for controlling diarrhea of piglets (Yi et al., 2017). Here, we found that KR-32 treatment significantly reduced levels of IL-6 ($P < 0.05$) and TNF-α ($P < 0.05$) in serum, indicating that KR-32 regulates inflammation and diarrhea. In conclusion, we defined a novel role of antimicrobial peptide KR-32 in regulating infectious disease and gut health in livestock.

Key Words: antibacterial activity, antimicrobial peptide, diarrhea, weaned piglets
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864 Identification of differentially expressed microRNAs in peripheral blood mononuclear cells of topsoil-exposed piglets.

M. A. Sales*, T. Tsai, C. V. Maxwell, D. A. Koltes, and J. E. Koltes, *University of Arkansas, Division of Agriculture, Department of Animal Science, Fayetteville.*

Exposure of immature immune systems to nonhygienic conditions has been shown to improve future immune function in humans and growth performance in swine. Long-term effects of exposure to a "dirty" environment indicate modulation in physiological programming or epigenetic regulation related to life-long immunity as opposed to short-term transcriptional effects. MicroRNAs (miRNA) are post-transcriptional regulators of gene expression that modulate whole pathways in response to the environment that may permanently alter transcription. In our previous studies, exposure to topsoil prior to weaning improved postweaning growth performance. Therefore, we wanted to determine if exposure to topsoil would alter miRNA abundance. Piglets were selected from litters (PIC 29 × 380) that farrowed within 24 h of each other and randomly assigned to rearing environments without ($n = 8$) or with ($n = 5$) topsoil from d 4 to 21 of lactation. Piglets were weaned and transferred to a nursery facility at d 21. Peripheral blood mononuclear cells (PBMC) were collected from piglets at 11, 20, and 56 d of age. Small RNA (18–30 nucleotides) libraries generated from high-quality PBMC-derived total RNA (RQI

= 7.4–9.9) for 39 samples were sequenced using Illumina technology. Sequenced reads were quality checked using FastQC and then used for novel miRNA identification or differential expression analysis. Reads were aligned by TopHat/Bowtie2 to the Sscrofa 10.2 reference genome (Ensembl v84) and binned by gene annotation with HTSeq. A total of 583 miRNA were identified using mirDeep2, among which 413 constituted novel miRNA (false discovery rate [FDR] < 0.15). Annotated miRNA ($n = 170$; Ensembl v84) were analyzed for differential expression following 75th quantile normalization. The miRNA expression was modeled in PROC GLIMMIX of SAS (SAS Inst. Inc., Cary, NC) where treatment, piglet age, and interaction of treatment and age were fit as fixed effects; piglet was fit as a random effect; and piglet gender, sow parity, litter size, and RQI were fit as covariates. To control the FDR, q-values were calculated for all miRNA in R. Twenty-three known miRNA were identified as differentially expressed across the topsoil treatment × piglet age interaction ($q < 0.1$). These miRNA include miR-29, which regulates innate and adaptive immune responses to intracellular bacterial infection; miR-31, which regulates gut development and homeostasis; and other miRNA involved in tumor suppression, apoptosis, T-cell function, lipid metabolism, and growth and lipid deposition. Additional research is needed to investigate the potential that these miRNA have to reprogram the epigenome of young piglets to enhance growth performance beyond the period of environmental exposure.

Key Words: epigenetics, microRNA, swine
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865 Audio and time-lapse imagery analysis of lamb grazing behavior in silvopasture systems.

G. J. Pent*[1] and J. H. Fike[2], [1]*Virginia Polytechnic Institute and State University, Blackstone* [2]*Virginia Polytechnic Institute and State University, Blacksburg.*

Silvopastures—systems where trees are intentionally managed in conjunction with forages—provide distributed shade for grazing livestock. The objective of this study was to determine the grazing behavior and productivity of lambs in silvopasture systems. The growth of lambs in black walnut (*Juglans nigra*) silvopastures and lambs in honey locust (*Gleditsia triacanthos*) silvopastures was compared with the growth of lambs in open pastures during 3 summers. Intravaginal temperature sensors were constructed from blank controlled internal drug release (CIDR) devices and small temperature loggers. Body temperatures of ewe lambs ($n = 9$) were recorded every 10 min for 3 d within a replicate within a week. For 1 d of each week in the second and third summers, a wideband audio recording device was also secured on the ewes to detect prehension events. Time-lapse cameras documented sheep behavior every 60 s. In the silvopastures, the lambs spent over 90% of daylight hours within shade boundaries. During the hottest part of the day (1300–1700 h), ewes in the open pasture had 0.4°C hotter vaginal temperatures than ewes in the black walnut silvopastures ($P \leq 0.0202$). Ewes in the open pasture experienced more fluctuation in day to nighttime core temperature change ($P < 0.0001$). Lambs in silvopastures spent more time lying down than animals in the open pastures ($P \leq 0.01$), whereas lambs in the open pastures spent more than 2 h longer each day standing ($P < 0.0001$). Lambs in the black walnut silvopastures spent more time grazing (488 ± 14 min/d) than lambs in the honey locust silvopastures (438 ± 14 min/d; $P = 0.0493$) and lambs in the open pastures (417 ± 14 min/d; $P = 0.0026$). There was no difference in grazing time for lambs in the latter 2 systems ($P = 0.5597$). Spectral analysis revealed that the lambs in the black walnut silvopastures grazed more frequently than the lambs in the other systems. The acoustic analysis, although limited by recorder durability to 47 complete recordings, revealed no difference in total bites taken per day ($P \geq 0.7222$) or in the morning ($P \geq 0.2069$), afternoon ($P \geq 0.5816$), and evening periods ($P \geq 0.9337$).

Key Words: behavior, lamb, silvopasture
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866 Dietary supplementation with *Yucca schidigera* extract alleviates heat stress–induced growth restriction in chickens.

R. Rezaei, J. Lei, and G. Wu*, *Texas A&M University, College Station.*

Global warming threatens to adversely impact livestock and poultry productivity. Animals raised in hot climates exhibit elevated concentrations of glucocorticoids, which reduce their growth. Few nutritional means are available to effectively mitigate production problems brought about by heat stress. We used growing chickens to test the hypothesis that *Yucca schidigera* extract (containing steroidal saponins, which are natural structural analogues of corticosterone and cortisol) may ameliorate negative effects of heat stress on animal growth. Beginning at 35 d of age, male broilers had free access to a basal diet supplemented with 0, 120, or 180 ppm *Yucca schidigera* extract. Chickens were randomly assigned to their treatment groups (24/group; 6/pen). The maximum ambient temperature of the chicken housing facility was naturally gradually elevated during 1 wk and was 27, 29, 32, 35, 36, 37, and 37°C on d 1, 2, 3, 4, 5, 6, and 7, respectively, of the trial; the corresponding average ambient temperatures were 18, 21, 23, 27, 29, 31, and 31°C, respectively. The composition of the basal diet (as-fed basis) was 64.79% corn grain, 25.91% soybean meal, 0.50% glycine, 0.21% DL-methionine (98%), 0.08% L-lysine HCl, 4.98% blended fat, 1.57% limestone, 1.28% BIOFOS-16, 0.38% salt, 0.05% trace mineral premix, and 0.25% vitamin premix. Body weights of individual chickens and the amounts of feed/pen at the beginning and end of the study were measured. Data were analyzed using 1-way ANOVA and the Student–Newman–Keuls test. Results are expressed as means ± SEM. During the 1-wk experimental period, birds in the control group exhibited a weight gain of

264 ± 14 g/wk per animal ($n = 24$), an average feed intake of 912 ± 20 g/wk per animal ($n = 4$), and a G:F of 0.284 ± 0.013 ($n = 4$). *Yucca schidigera* extract supplementation did not affect ($P > 0.05$) feed intake by birds but enhanced ($P < 0.05$) their weight gain by 38 to 43% and feed efficiency by 46 to 52% compared with controls. In a separate experiment, *Yucca schidigera* extract supplementation matched the previously described treatments, but the chickens were housed at an average ambient temperature of 24°C (maximum = 27°C); birds in the control group exhibited a weight gain of 756 ± 28 g/wk per animal ($n = 24$), an average feed intake of 1,124 ± 27 g/wk per animal ($n = 4$), and a G:F of 0.675 ± 0.022 ($n = 4$); *Yucca schidigera* extract supplementation had no effect on their feed intake or growth under the experimental conditions without heat stress. We suggest that by antagonizing glucocorticoids, *Yucca schidigera* extract ameliorates the adverse effects of heat stress on chicken growth and feed efficiency. (Supported by AGROIN Baja Agro International, Mexico.)

Key Words: chickens, heat stress, yucca extract
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867 Porcine intestinal epithelial cells initiate an early stage protection against *Escherichia coli* K88.

Z. Li*[1] and Y. Wang[2], [1]*Zhejiang University, College of Animal Science, Institute of Feed Science, Hangzhou, China,* [2]*Zhejiang University, College of Animal Sciences, Hangzhou, China.*

Enterotoxigenic *Escherichia coli* (ETEC) is a major intestinal pathogen, resulting in serious diarrhea or even death in animal husbandry. Recent studies mainly focus on exogenous treatment, whereas the internal protective reaction is not fully clarified. In this study, we discovered a defensive response in porcine intestinal epithelial cell line IPEC-J2 against ETEC infection. After a 15-min challenge with *E. coli* K88 (multiplicity of infection was 10:1), the transepithelial electrical resistance (TEER) was decreased ($P < 0.01$), expression of tight junction (TJ) proteins occludin and claudin-1 was reduced ($P < 0.05$), and immunofluorescence (IF) showed disassembly of TJ occludin, claudin-1, and zonula occluden 1 (ZO-1). Meanwhile, the TJ restoration was already initiated through increased transcription of occludin ($P < 0.05$), claudin-1 ($P < 0.001$), ZO-1 ($P < 0.05$), and myosin cytoskeleton F-actin ($P < 0.001$). Fifteen minutes later, we detected an elevation in TEER (1.29 fold; $P < 0.05$), upregulation of occludin and claudin-1 (both $P < 0.05$), and relocalization of occludin, claudin-1, and ZO-1 compared with the noninfected control. The repaired barrier would gradually diminish in 90 min according to observations on TEER, TJ expression, and IF. Interestingly, when we eliminated *E. coli* K88 after 15 min of infection, the rapid response was replaced by a long-term recovery within 120 min. In order to elucidate the molecular mechanism, we compared gene expression patterns of the noninfected control 15 and 60 min after infection using a PCR array. Factors in 4 signaling pathways, including interferon-gamma (IFN-γ), fibroblast growth factors, epidermal growth factors, and GnRH, were enhanced ($P < 0.05$) at 15 min. At 60 min, however, the majority of those enhanced factors were not differentially expressed compared with the noninfected control, suggesting the signaling pathways may be suppressed. Altogether, the intestinal epithelial cells will initiate an immediate protective system to restore the damaged intestinal integrity caused by ETEC. The defensive mechanism works effectively at the early stage and will be blocked as the infection progresses.

Key Words: enterotoxigenic *Escherichia coli* K88, intestinal barrier, IPEC-J2 cell line
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868 Impact of essential oils on the growth performance of newborn Holstein calves.

T. Liu*[1], H. Chen[1], D. P. Casper[2], and J. Wu[3], [1]*Gansu Agricultural University, Lanzhou, China,* [2]*Furst-McNess Company, Freeport, IL,* [3]*Gansu Academy of Agricultural Sciences, Lanzhou, China.*

Plant-extracted essential oils (EO) can exhibit antimicrobial properties that make them potential alternatives to antibiotics. The objective was to evaluate the use of plant EO (oregano blend) on the growth, development, health status, and rumen development of newborn calves. Forty (40) Holstein heifer calves were blocked by birth date and alternately assigned to 1 of 2 calf starters (CS). Twenty calves receive a control (CN) CS without EO and 20 calves received the EO CS (40 g/t). Calves were fed the CS for ad libitum consumption starting the 3rd day after birth through 70 d, with weaning occurring at 42 d of age. Calves fed EO CS demonstrated significantly ($P < 0.05$) greater DMI than calves fed CN for the time periods of 8 to 14 d (0.14 and 0.16 kg/d for CN and EO, respectively) and 64 to70 d of age (2.95 and 3.11 kg/d). The ADG were significantly ($P < 0.05$) greater for calves fed EO (0.78 and 0.87 kg/d) compared with calves fed CN throughout the study. At 70 d of age, calves fed EO demonstrated significantly ($P < 0.01$) greater body frame growth measurements (96.2 and 101.9 cm hip height, 98.0 and 104.6 cm body length, 96.6 and 103.4 cm abdominal girth, 97.5 and 101.8 cm chest girth, and 12.8 and 14.1 cm pastern) than calves fed CN. Scour incidences were lower for calves fed EO compared with calves fed CN ($P < 0.01$). The blood total serum protein (54.2 and 57.2 mg/dL), IgG (110.8 and 117.2 mg/dL), IgA (5.8 and 9.0 mg/dL), and IgM 19.8 and 22.4 mg/dL) concentrations were significantly ($P < 0.01$) higher for calves fed EO compared with calves fed CN at 14 d. The blood VFA concentrations were significantly ($P < 0.01$) higher for calves fed EO compared with calves fed CN. The calves fed EO demonstrated significantly ($P < 0.01$) greater nutrient digestibilities of DM (88.61 and 92.2%), CP (86.7 and 91.9%), ADF (48.1 and 66.0%), NDF (49.2 and 66.8%), and starch (98.5 and 99.4%) compared with calves fed

CN. This study demonstrated that incorporating an EO in a CS resulted in positive benefits, similar to antibiotics, including increased calf growth, ruminal development, intestinal health, and nutrient digestibility, compared with a CN CS without EO.

Key Words: calf, essential oils, oregano
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869 Adaptation period during changing diet of dairy cows changes rumen fermentation characteristics and microbial qualities and communities.

L. L. Mamuad*[1,2], S. H. Kim[2,3], S. S. Lee[2], and C. Dae[2], [1]*The Ohio State University, Columbus,* [2]*Sunchon National University, Suncheon, Republic of Korea (South),* [3]*The Ohio State University, Wooster.*

The adaptation period is important during evaluation of in vivo nutritional studies. Populational and metabolic changes occur in the rumen microbiota during this period. Therefore, we determined the changes in the rumen fermentation characteristics and microbial quantities and communities. Three Holstein Friesian cows were used in this study and assigned as replicates. They were initially fed with Italian ryegrass ad libitum and 2 kg concentrate diet/d for 30 d. Then, the concentrate diet was increased to 8 kg/d for 14 d and decreased to 2 kg/d for another 14 d. Rumen fluids were collected 2 h after the morning feeding through stomach tubing at the start of the experiment on d 7 and 14 of the diets. pH, VFA, and microbial quantities and communities were determined using a pH meter, HPLC, qPCR, and Illumina MiSeq, respectively. All analyses were carried out using SAS (SAS Inst. Inc., Cary, NC). The highest pH (7.02) was observed at the start of the experiment. Concentrations of acetate, propionate, and butyrate also peaked at d 14 of consuming the 8 kg concentrate at 56.76 ($P < 0.001$), 13.28 ($P < 0.008$), and 6.60 mM ($P < 0.011$), respectively. The total bacteria quantity was comparable throughout the feeding trials. *Ruminococcus flavefaciens* (4.64 and 5.08) and protozoa (1.94 and 2.00) log copies were highest at d 7 of feeding the 8 kg and 2 kg concentrate diets whereas the lowest methanogen quantity was observed at the start of the experiment (2.96 log copies) with increasing copies until the end of the feeding trial. Bacteroidetes predominated the bacterial communities in this study and were found to be the highest with lower feed concentrate (2 kg/d) whereas the opposite was observed with higher feed concentrate (8 kg/d) given to the animals. Relative abundances of Spirochaetes and Chloroflexi increased with increased feed concentrate (8 kg/d) given to animals. *Prevotella ruminicola* had the predominate the species level, which was found to be highest at the start of the experiment. Notably, *Olsenella profusa* and *Syntrophococcus sucromutans* increased their relative abundances with increased concentrate (8 kg/d) given to the animals. The rumen fermentation characteristics, microbial quantities, and bacterial communities changed with changing diet during adaptation period.

Key Words: adaptation, rumen quantities and communities, volatile fatty acids
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870 In vitro and in situ digestion characteristics and feedlot performance of cattle fed steam-flaked Enogen (high-amylase) feed corn.

L. M. Horton*, C. L. Van Bibber-Krueger, H. C. Muller, S. L. Katulski,
T. J. Ellerman, and J. S. Drouillard, *Kansas State University, Manhattan.*

Enogen feed corn (EFC; Syngenta Seeds, LLC) is genetically modified to express high amylase content in grain. In vitro and in situ studies evaluated the impact of moisture addition before steam conditioning (0, 3, and 6%), steam conditioning time (15, 30, and 45 min), and percentage of EFC (0, 25, 50, 75, or 100) mixed with mill-run corn using a 3 × 3 × 5 factorial arrangement in a randomized complete block. Particle size distribution, in situ DM disappearance, starch availability, and in vitro fermentation (gas production and VFA) were measured. Grain mixtures were tempered with water for 1 h, steam conditioned, and flaked to 360 g/L. Data were analyzed as mixed models (SAS, version 9.4; SAS Inst. Inc., Cary, NC), with moisture, conditioning time, percent EFC, and 2- and 3-way interactions as fixed effects and block as a random effect. Gas production analyses included time as a repeated measure. Linear and quadratic contrasts were examined. No 2- or 3-way interactions were observed ($P > 0.10$). Mean geometric particle size of flaked grains linearly decreased in response to EFC content ($P < 0.01$). Particle size was unaffected by moisture addition ($P > 0.10$) but quadratically responded to conditioning time ($P < 0.01$), with 30 min yielding the smallest particle size. Starch availability increased with greater levels of EFC and added moisture ($P < 0.01$) and was optimal for 30 min of steam conditioning (quadratic effect, $P < 0.01$). In situ DM disappearance and in vitro production of gas, acetate, propionate, valerate, and total VFA increased with increasing proportion of EFC ($P < 0.01$). Volatile fatty acid was greatest with 30 min of steaming ($P < 0.05$), but moisture addition had no impact ($P > 0.10$). In a follow-up study with feedlot heifers (n = 700; 314 ± 8.5 kg initial BW), cattle were blocked by origin and initial BW, allocated to 28 pens, and fed diets containing mill-run corn or EFC. Grains were flaked to achieve

Table 870.

Item	Mill-run corn	Enogen	SEM	P-value
ADG, kg	1.60	1.69	0.028	<0.01
G:F	0.1602	0.1681	0.0022	<0.01
Liver abscess, %	34.4	26.6	2.47	0.03
HCW, kg	366.2	372.1	6.41	<0.01

similar starch availabilities, targeting densities of 360 and 390 g/h and mill throughputs of approximately 5,445 and 8,165 kg/h for mill-run corn and EFC, respectively. Cattle were transitioned to finishing diets (7% alfalfa and 93% concentrate; 300 mg/d monensin and 0.4 mg/d melengestrol acetate; no tylosin) over 21 d and harvested after 136 d on feed. Compared with mill-run corn, Enogen feed corn improved feedlot performance and decreased energy inputs for grain processing.

Key Words: amylase, Enogen, feedlot
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871 Lipid metabolism and mitochondrial energy production are key pathways involved in adipose tissue of cows transitioning from feed restriction to ad libitum diets.

H. C. Cunningham[1], K. M. Cammack[1], K. Hales[2], H. C. Freetly[3], and A. K. Lindholm-Perry*[3], [1]*University of Wyoming, Department of Animal Science, Laramie,* [2]*USDA-ARS, Clay Center, NE,* [3]*USDA- ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Feed costs account for over 70% of the annual expenditures in cow/calf production. The majority of the nutrients are used to support the cow's maintenance requirements, and substrate cycling has been identified as one of the major contributors toward this type of energy expenditure. The objective of this study was to determine if cows that differ in the efficiency of weight gain differ in the relative abundance of transcripts for enzymes associated with lipid turnover of subcutaneous adipose tissue. Mature cows were subjected to feed restriction followed by ad libitum feed. Adipose tissue from 12 cows with high (n = 6; ADG = 2 kg/d) and low gain (n = 6; ADG = 1 kg/d), based on performance during the ad libitum feeding period, was collected during restriction and during ad libitum studies and evaluated for transcriptome expression differences using the Affymetrix GeneChip Bovine 1.1 ST Array. Differentially expressed genes were identified using an unpaired 1-way ANOVA for each pair of condition groups. None of the differentially expressed genes from high- versus low-gain animals by diet (feed restriction or realimentation) passed correction for multiple testing. However, 496 genes were differentially expressed (corrected $P < 0.05$) for the high-gain animals compared over the 2 studies and 491 genes were differentially expressed among low-gain animals between studies. Of these gene lists, 144 genes were common for both groups of animals. Enriched pathways based on differentially expressed genes includes oxidative phosphorylation, mitochondrial dysfunction, and cholesterol biosynthesis pathways that were commonly associated with the high-gain animals between feed restriction and realimentation as well as with the low-gaining animals between the 2 time points. Specific to cows with greater gain were valine degradation and lipopolysaccharide/IL-1 mediated inhibition of retinoid X receptor function pathways. Genes involved in lipid metabolism, mitochondrial respiration, and oxidative phosphorylation pathways appear to be critical to mature cows during times of abundant feed after feed restriction. The USDA is an equal opportunity provider and employer.

Key Words: beef cattle, feed efficiency, growth
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872 Effects of including ruminally inert fat in the diet of heat-stressed lambs on dry matter and water intake and physiological parameters.

V. Morales, E. Benabe, L. C. Solorzano, and A. A. Rodriguez*, *University of Puerto Rico, Mayaguez, PR.*

The effect of 3 ruminally inert fat supplements in the diet of crossbred lambs on DMI, water intake (WI), and physiological parameters associated with heat stress under tropical conditions (28–30°C and 75% relative humidity) was determined. Twelve lambs (25.83 kg average initial weight) were fed to meet or exceed current NRC recommendations with a basal diet providing 17% CP and consisting of 50% alfalfa hay, 36.24 cracked corn, and 12.01% soybean meal and supplemented or not with 1.75% of ruminally inert fat provided as free fatty acids (FFA) or 2 experimental fat products from palm oil (E1 and E2). The lambs were assigned to 1 of 3 Latin squares. Treatments were no additive or diets containing FFA, E1, and E2. Feed was offered daily at 4% of lamb BW (DM basis). Experimental periods were 21 d, consisting of 14 d of adaptation to the diet followed by 7 d of data collection. Data collected included DMI (g/d), WI (L/d), and percentage WI in relation to animal BW, and the DMI:WI ratio was determined. Physiological parameters associated with heat stress included respiration rate (RR), heart rate, (HR), and rectal temperature (RT). Data were analyzed according to a 4 × 4 Latin square experimental design replicated 3 times. The Tukey test was used for mean comparison. There were no differences ($P > 0.05$) in DMI or WI among experimental treatments, averaging 1,190 g/d and 4.48 L/d. Percentage WI in relation to animal BW and the DMI:WI ratio were also similar for all experimental treatments (averaging 21.93% and 3.76, respectively). Inclusion of ruminally inert fat did not affect HR, RR, and RT and resulted in an average of 109 breaths/min, 73.24 beats/min, and 102.9°C. In summary, the inclusion of 1.75% ruminally inert fat in the diet of crossbred lambs did not affect DMI, WI, and physiological parameters associated with heat stress under tropical conditions.

Key Words: intake, physiological parameters, ruminally inert fat
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873 fam134b, a novel Golgi protein, influences adipogenesis by regulating Golgi vesicular transport in porcine adipocytes.

M. Cai*, *Zhejiang University, Hanghzou, China.*

The global epidemic of obesity is associated with high risks of metabolic diseases. The domestic pig is considered an important laboratory animal model for human diseases including obesity. Of particular interests, the Chinese Jinhua pigs are known for their rich subcutaneous and intramuscular fat content, making them an ideal model to study fat deposition. We recently reported that compared with the Landrace pigs, Jinhua pigs expressed higher levels of the gene *family with sequence similarity 134, member B* (*FAM134B*) in their subcutaneous fat, indicating that FAM134B might play a crucial role in regulating fat deposition and lipid metabolism in animals. In this study, we found that the expression of FAM134B increases during porcine adipocytes differentiation. Transfection of preadipocytes with FAM134B resulted in accelerated differentiation and increased triglyceride accumulation after hormonal stimulation. The mRNA expression of adipogenesis-related genes *C/EBPα*, *C/EBPβ*, and *FAS* were upregulated ($P < 0.05$) whereas the key lipolysis gene *ATGL* was downregulated ($P < 0.05$) by FAM134B overexpression. Immunofluorescence staining demonstrates that FAM134B is directly targeted to the *cis*-Golgi membrane, potentially functioning to affect transport of vesicle and lipid-related proteins in adipocytes. In addition, overexpression of FAM134B upregulated Golgi protein ARFRP1, and knockdown of ARFRP1 abolished the effect of FAM135B overexpression on lipid accumulation. The ARF-like GTPases and the family of PAT genes. The expression of ARF1, ARF6, ARFRP1, PLIN, and ADRP were upregulated ($P < 0.05$) by FAM134B overexpression (Fig. 2M) and were downregulated ($P < 0.05$) by FAM134B knockdown in porcine adipocytes (Fig. 2O). Guanosine triphosphatase's enzyme activity, the key factor of vesicle transport in porcine adipocytes, was also increased ($P < 0.05$). These results indicate that FAM134B positively regulates the lipid accumulation and adipogenic differentiation by targeting vesicle transport in the Golgi apparatus.

Key Words: adipogenesis, fam134b,
vesicular transport
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874 Effect of dietary fish oil and vitamin E on DNA damage in dogs undergoing training.

A. L. Risso*[1], F. Pellegrino[1], Y. Corrada[1], N. Nicolof[1], A. Seoane[2], and A. Relling[3], [1]*The National Scientific and Technical Research Council (CONICET), College of Veterinary Science, Buenos Aires, Argentina,* [2]*The National Scientific and Technical Research Council (CONICET), College of Veterinary Science, La Plata, Argentina,* [4]*The Ohio State University, Department of Animal Sciences, Wooster.*

The aim of the present study was to evaluate the effect of dietary supplementation with fish oil (FO) alone or FO and vitamin E (VE) on DNA damage and serum VE concentration in dogs undergoing training. Using a replicate 3 × 3 Latin square design, 6 male dogs (2–6 yr and 21–35 kg) were assigned to 3 groups: 1) a control diet (CG), 2) the same diet supplemented with 54 mg FO/kg $BW^{0.75}$ (FG), and 3) a similar diet plus FO (54 mg/kg $BW^{0.75}$) and 400 mg VE (FEG) per day for 60 d. Blood samples were collected on d 0, 30, and 60. Deoxyribonucleic acid damage was measured using a single-cell gel electrophoresis assay in peripheral whole blood leukocytes. Deoxyribonucleic acid damage was classified in 4 classes (I = undamaged, II = minimum damage, III = medium damage, and IV = maximum damage). Furthermore, a DNA damage index (DI) was calculated using the formula DI = [(I) + 2(II) + 3(III) + 4(IV)]/N(0–IV), in which 0–IV represents the nucleoid type and N0–NIV represents the total number of nucleoids scored. Dogs were trained on a treadmill at 8 km/h and a 7.5% slope twice a week for 60 d. Each session lasted 30 min. Data were analyzed using PROC MIXED of SAS (9.4; SAS Inst. Inc., Cary, NC). Treatment, time, and their interaction were considered fixed variables and dog and period were considered random. The SLICE option of SAS was used for mean separation when there was a treatment × time interaction. On d 30, there was a significant increase in DI in FG compared with CG and FEG ($P < 0.01$). Deoxyribonucleic acid damage index values were 0.002, 0.105, 0.109, 0.053, 0.743, 0.467, 0.175, 0.127, and 0.193, for CG, FG, and FEG on d 0, 30, and 60, respectively. There was a time × treatment interaction for the serum VE concentration ($P < 0.01$). On d 0 and on d 30, there were no differences in serum VE concentrations of the 3 groups ($P > 0.1$). However, on d 60, serum VE concentrations were higher in FEG compared with those in CG and FG (6,200 vs. 2,300 vs. 2,000 μg/d, respectively; $P < 0.01$). In conclusion, FO supplementation produces DNA damage after 30 d but not at 60 d. The supplementation of FO with VE could prevent the damage at 30 d. Supplementation with VE increases serum VE concentration.

Key Words: DNA damage, fish oil, vitamin E
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875 Effects of a twelve-hour sequential feeding cycle with diets varying in amino acid content on performance and body composition of growing–finishing pigs.

W. C. D. Silva[1], L. Hauschild*[1], L. S. D. Santos[1], P. H. R. F. Campos[2], A. M. Veira[1], and A. Z. Fraga[1], [1]*São Paulo State University (UNESP) Jaboticabal, Brazil,* [2]*Federal University of Vales do Jequitinhonha e Mucuri (UFVJM), Diamantina, Brazil.*

Recent studies have shown that nutrient metabolism, utilization, and excretion may vary during the 24-h circadian period. For instance, greater absorption and utilization of AA in the morning than in the evening has been reported in pigs. In this regard, this study aimed at evaluating the effects of different AA feeding programs over the day on the performance and body composition of growing–finishing pigs. Forty-five 30-kg (±2.8) BW barrows were assigned to 1 of 3 feeding programs (15 animals per treatment): 1) conventional feeding (CONV), in which pigs received 100% of standardized ileal digestible (SID) AA recommendations for the entire day;, 2) sequential feeding (SEQ110-70), providing 110% SID AA recommendations from 2400 to 1200 h and 70% from 1201 to 2359 h; and 3) sequential feeding (SEQ70-110) providing 70% SID AA recommendations from 2400 to 1200 h and 110% from 1201 to 2359 h. The experimental period lasted 84 d and was subdivided into phase 1 (from d 0 to 35), phase 2 (from d 36 to 63), and phase 3 (from d 64 to 84). Body lean and fat mass were assessed by dual-energy X-ray absorptiometry at the beginning and at the end of each phase. An individual pig was considered the experimental unit, and data were analyzed using the MIXED procedure in SAS (SAS Inst. Inc., Cary, NC) including the fixed effects of treatments. Initial BW was included as a covariate. Average daily feed intake, ADG and G:F did not differ between feeding programs ($P > 0.05$). Lysine intake was lower in SEQ-fed pigs than in CONV-fed pigs (16.60 vs 17.82 g/d, respectively, on average; $P < 0.05$). Feeding program did not affect body lean (61.24 kg for CONV vs 60.71 kg for SEQ, on average; $P > 0.05$) or fat content (14.46 kg for CONV vs 14.67 kg for SEQ, on average; $P > 0.05$). Fat gain was greater in individuals fed the SEQ110-70 diet than in those fed the SEQ70-110 diet (240 vs 222 g/d, respectively; $P < 0.05$); however, there was no difference between individuals in either SEQ group and those in the CONV group (230 g/d; $P > 0.05$). According to our results, SEQ feeding reduced consumption of AA (lysine) without impairing the performance or body composition of growing–finishing pigs. This feeding strategy may be considered as a potential tool to reduce feed costs and nutrient excretion in pig production.

Key Words: dual-energy X-ray absorptiometry, feeding programs, lysine
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876 Effects of sporoderm-broken spores of *Ganoderma lucidum* on growth performance, antioxidant function, and immune response of broiler chickens.

T. Liu*[1], L. Zhao[1], Y. Fan[1], L. Xi[2], J. Zhang[1], C. Ji[1], Q. Ma[1], and X. Rong[1], [1]*China Agricultural University, Beijing, China,* [2]*North Carolina State University, Raleigh.*

This study was conducted to evaluate the effects of sporoderm-broken spores of *Ganoderma lucidum* (SSGL), a traditional Chinese medicinal herb, on growth performance, oxidative stress, and immunity of broiler chickens. A total of three hundred 1-d-old male Arbor Acre broiler chickens with similar BW (40 ± 1.0 g) were assigned randomly to 4 dietary treatments. Each treatment contained 5 replicate pens of 15 birds per pen. The treatment diets were prepared by supplementing SSGL to a basal corn–soybean meal diet with the concentrations of 0 (control), 100, 200, and 500 mg/kg diet. The BW and feed intake were recorded based on pen on d 21 and 44 after a 12-h feed withdrawal. On 44 d of the experiment, 1 bird from each pen with BW close to the average was selected and slaughtered. Blood was drawn from the wing vein with a heparinized syringe and collected into tubes and then centrifuged at 1,000 × g for 10 min to obtain serum. The serum was immediately stored at −20°C. A portion of liver and spleen tissues were harvested, coded snap-frozen in liquid nitrogen, and then maintained at −80°C for analyses. Pen was used as the experimental unit, and 1-way ANOVA was performed using the GLM procedure in SAS software (version 9; SAS Inst. Inc., Cary, NC). Duncan's multiple range test was used for multiple comparisons when a significant difference was detected. The results showed that diets with SSGL significantly increased ($P < 0.05$) ADFI and ADG and decreased the feed:gain ratio ($P < 0.05$) of the birds during the finisher period (22–44 d). Dietary SSGL also increased hydroxyl radical scavenging activity and decreased the concentrations of malondialdehyde and lipid peroxidation in the liver and spleen of the broilers ($P < 0.05$). Furthermore, the capability of total antioxidant, the activities of glutathione reductase and catalase, and the concentration of reduced glutathione in the liver and spleen were significantly higher in broilers fed diets with SSGL than in broilers that received the control diet ($P < 0.05$). In addition, the levels of serum IL-2, IgA, and IgG in the broilers fed SSGL were significantly increased compared with those from the broilers fed the control diet ($P < 0.05$). These results suggest that dietary supplementation of SSGL has ameliorative effects on growth performance, free radical scavenging activity, antioxidant capability, and immune function of broilers.

Key Words: antioxidant capability, oxidative stress, spore of *Ganoderma lucidum*
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Table 877.

	Haptoglobin, mg/mL			Rectal temperature, °C	Treatment × day		*P*-value	
Day	VAC	CON	SE	VAC	CON	SE	Hp	RT
0	0.285	0.330	0.24	38.75	38.80	0.12	0.86	0.67
1	1.250	0.514	0.23	39.22	38.78	0.11	< 0.01	< 0.01
2	1.762	0.665	0.24	38.68	38.69	0.11	< 0.01	0.96
3	1.639	0.821	0.24	38.63	38.54	0.12	< 0.01	0.44
5	1.560	0.836	0.24	38.28	38.41	0.11	< 0.01	0.25
7	1.539	0.981	0.23	38.57	38.60	0.11	0.02	0.76
10	1.113	0.717	0.24	38.39	38.35	0.12	0.10	0.76
14	0.423	0.381	0.24	38.78	38.66	0.12	0.86	0.32

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877 Serum haptoglobin concentrations in water buffalo heifers: Impacts of the vaccination and animal handling.

C. L. Francisco*[1,2], A. M. Castilhos[1], D. C. M. Silva[1], F. M. Silva[1], H. L. Correa[1], A. S. Aranha[1], and A. M. Jorge[1], *[1]São Paulo State University (UNESP), School of Veterinary Medicine and Animal Science (FMVZ), Botucatu, Brazil, [2]São Paulo State Foundation (FAPESP), São Paulo, Brazil.*

Effects of animal handling procedures on animal physiology should be considered. Haptoglobin (Hp) is known as an acute phase protein, and its level may increase during stressful and acute conditions (e.g., disease, infection, injury, stress). The objective was to evaluate the serum Hp concentrations at determined time points of 18 water buffaloes heifers (*Bubalus bubalis*; 19 ± 1.53 mo of age and 403 ± 36 kg BW). Heifers were randomly assigned by BW and divided into 2 treatments: vaccinated (VAC; $n = 9$) or not (CON; $n = 9$). Animals were maintained on pasture (*Urochloa brizantha* cv. Xaraés; 3.36 ha) provided with natural shade, water trough, and mineral feeder. Heifers from the VAC treatment received a vaccination against infectious bovine rhinotracheitis virus, bovine viral diarrhea, bovine respiratory syncytial virus, parainfluenza 3 virus, and *Leptospira* spp. (5 mL, subcutaneous; CattleMaster Gold FP 5/L5; Zoetis) on d 0. Rectal temperatures (RT) and blood samples were collected at 0, 1, 2, 3, 5, 7, 10, and 14 d from heifers of both treatments. Serum Hp concentrations were determined using commercial kit ("PHASE" Haptoglobin Assay, Tridelta Development Limited). Data were analyzed with the MIXED procedure (SAS; SAS Inst. Inc., Cary, NC) with the term day used for repeated measures. A treatment × day interaction was detected for serum Hp ($P < 0.01$). Vaccinated heifers had greater ($P \leq 0.02$) Hp concentrations from d 1 to 7 and tended ($P = 0.10$) to have greater Hp concentration on d 10 compared with CON heifers. The Hp concentration of CON heifers also increased during the study, probably caused by the handling used. A treatment × day interaction was also detected for RT ($P = 0.02$). Vaccinated heifers had greater ($P \leq 0.02$) RT on d 1 than CON heifers. In conclusion, the handling procedures impacted serum haptoglobin concentrations, suggesting that the animal management should be carried out with the aim of reducing stress and possible undesirable effects it may cause on production of water buffaloes heifers (Table 877).

Key Words: acute phase protein, animal handling and water buffaloes
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878 Effect of monensin and protein on digestion and ruminal fermentation parameters in cattle consuming low-quality forage.

J. J. Martinez*[1], K. C. McCuistion[1], C. A. Loest[2], L. P. Sastre[1], J. I. Solis[1], M. A. Fonseca[3], and N. L. Bell[1], *[1]Texas A&M University, Kingsville, [2]New Mexico State University, Las Cruces, [3]University of Nevada, Reno.*

The effect of monensin and protein on digestion and ruminal fermentation parameters in cows consuming low-quality forage (LQF; 4.1% CP chopped bluestem hay) was evaluated. Four ruminally cannulated cows (637 ± 24 kg BW) were used in a 4 × 4 Latin square design (20 d periods). Treatments were arranged as a 2 × 2 factorial: the first factor was monensin (0 or 200 $\text{mg·cow}^{-1}\text{·d}^{-1}$) and the second factor was protein (0 or 0.64 $\text{kg·cow}^{-1}\text{·d}^{-1}$ CP provided as cottonseed meal). A carrier supplement (0.23 $\text{kg·cow}^{-1}\text{·d}^{-1}$) consisting of ground hay, cracked corn, molasses, salt, dicalcium phosphate, and a commercial mineral premix was provided to all animals and allowed for inclusion of monensin. Animals were housed and individually fed at 0600 h daily. To prevent carryover effects from previous monensin feeding, 14 d were required before sampling. However, to obtain the optimal response from monensin, only 10 d were needed for treatment adaptation. Therefore, during d 1 through 4 of each period, animals were fed LQF with no treatment. Day 5 through 14 allowed for treatment adaptation and d 15 to 20 was used for sample collection. Digestion measurements were taken d 15 through 19. Rumen fluid was collected h 0, 2, 4, 8, 12, 16, and 20 on d 20 for VFA analyses. Data were analyzed using the MIXED procedure in SAS 9.3 (SAS Inst. Inc., Cary, NC) with terms in the model including protein, monensin, and their interaction, with animal and period included as random effects. There was no protein × monensin interaction ($P \geq 0.30$) or effect of monensin ($P \geq 0.37$) on any digestion parameter measured. Protein increased OM digestibility ($P = 0.01$), total digestible OM intake ($P < 0.01$), and total digestible NDF intake ($P < 0.01$) by 10.7, 112, and 71.2%, respectively. Protein had no effect on NDF digestibility ($P = 0.13$). A protein × monensin interaction ($P = 0.17$) or effect of monensin ($P = 0.15$) was not observed for total VFA concentration. Protein increased ($P < 0.01$) total VFA concentration by 20.0%. A protein × monensin interaction was observed for the acetate:propionate ratio ($P = 0.05$), with protein reducing the ratio when no monensin was present and increasing the ratio when monensin was present. No protein × monensin interaction ($P = 0.51$) was observed for acetate or propionate concentration. Protein had no effect on acetate ($P = 0.11$) or propionate ($P = 0.67$). Monensin increased ($P = 0.03$) propionate concentration by 8.6% but had no effect ($P = 0.41$) on acetate. Results suggest that protein increases digestibility when feeding a LQF but that no added benefit is observed with monensin inclusion.

Key Words: digestion, monensin, protein
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879 Reduction of *Campylobacter* on chicken livers using a low-acid processing aid.

M. A. Landrum*[1], N. A. Cox[2], D. E. Cosby[2], M. E. Berrang[2], S. C. Mize[2], and J. S. Jackson[1], [1]*University of Georgia, Athens,* [2]*The U.S. National Poultry Research Center, Athens, GA.*

The objective of this study was to evaluate the reduction of *Campylobacter* in livers treated with a low-pH processing aid, CMS PoultrypHresh, with and without a surfactant (PoultrypHresh Plus). Chicken livers ($n = 36$) were obtained from a local grocery; 13 livers were used in each of the 2 experimental treatment groups and 10 livers were used as untreated controls. Each liver was individually surface inoculated with a cell suspension of approximately 10^8 cells of a gentamicin-resistant *Campylobacter coli* marker strain in 0.1 mL of PBS. Cells were allowed 5 min to attach prior to treatment. Thirteen inoculated livers were individually placed into separate sterile specimen cups containing 100 mL of PoultrypHresh or PoultrypHresh Plus. Livers were subjected to a 15-s nonagitated dip before being removed and allowed 5 s to drain. Each liver was placed into an individual sterile specimen cup with 50 mL of buffered peptone water and hand shaken for 60 s. Untreated controls were treated as experimental samples, without undergoing any type of treatment dip. Rinsates were collected from each liver, serially diluted, and plated onto Campy Cefex agar with 200 ppm gentamicin. Plates were microaerobically incubated for 48 h at 42°C (5% O_2, 10% CO_2, and 85% N_2); colonies were counted and the colony-forming units per milliliter was log transformed. On untreated livers, mean recovery was 5.51 $\log_{10}$ cfu/mL; using PoultrypHresh, a 1.66 log reduction (97.8%) was observed compared with untreated livers. With PoultrypHresh Plus there was a 2.16 log reduction (99.3%). This study demonstrated that the use of PoultrypHresh and PoultrypHresh Plus reduced numbers of *C. coli* on the surface of chicken livers by greater than 97.0%. No change in appearance was noted.

Key Words: broiler livers, *Campylobacter*, sanitizer
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880 The effect of partial replacement of corn with a high-lipid, high-fiber byproduct pellet on hepatic indicators of metabolic efficiency and insulin sensitivity in beef steers throughout the finishing period.

J. J. M. Kim*[1], G. B. Penner[2], J. P. Cant[1], and K. M. Wood[1], [1]*University of Guelph, Department of Animal Biosciences, Guelph, ON, Canada,* [2]*University of Saskatchewan, Department of Animal and Poultry Science, Saskatoon, SK, Canada.*

The objective of this study was to evaluate the effects of dietary energy source (starch vs. lipid and fiber) in finishing diets for steers and time on feed on indicators of hepatic metabolic efficiency.

Key Words: beef steers, insulin sensitivity, metabolic efficiency
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881 Assessment of current musher practices across the sled dog industry.

J. R. Templeman*, S. Mai, and A. K. Shoveller, *University of Guelph, Guelph, ON, Canada.*

A great deal of variation exists within the sled dog industry as a result of differences in training regimes, nutritional programs, and environmental management of these high-demand canine athletes. It is likely that these differences result in variable health and well-being. This study aimed to assess the current habits and practices in the sled dog industry using an online questionnaire circulated throughout the mushing community and anonymously accessed by 72 respondents. The questionnaire was developed based on guidelines set forth by mushing organizations established to facilitate communication and education among recreationalists, professional racers, and sled dog breeders. The questionnaire covered topics pertaining to the management of sled dogs, including nutritional programs, housing and training practices, the dogs' health and well-being, and the owners' overall knowledge of mushing practices. Nutritional programs for sled dogs remain a controversial area, with differences arising between mushers and researchers in terms of adequate dietary requirements. Although we have collected all the survey data, this report focuses on evaluating nutrition programs used among mushers and dietary management differences between the racing and off-seasons. The food type provided differed among mushers ($P = 0.01$) with combination diets (commercial food brand combined with homemade diet or raw meat) accounting for

62% of responses. The number of mushers feeding a combination diet was 27% greater during the racing season versus the off-season. The source of these homemade diet recipes differed ($P < 0.0001$), with 50% of mushers sourcing their diet recipes from experienced mushers rather than data-based scientific consultants (e.g., animal nutritionists, 16%; veterinarians, 6%; peer-reviewed journals, 3%). When ranking dietary nutrients based on importance, 85 and 95% of respondents considered fat and protein, respectively, to be the most important nutrients. A majority of mushers provided the same amount of feed (1–2 cups) and water (1–5 L) during the racing and off-seasons, even though dogs' nutrient demands and hydration requirements increase when racing. These results suggest that alterations in food and nutrient supply aimed at maximizing the health, well-being, and performance of sporting dogs should be examined. The data indicates that nutrition programs are largely tailored towards high-protein and -fat diet formulations, with too little attention paid towards nutritional balance of macro- and micronutrients and adequate hydration. This survey successfully identified a number of areas that require further controlled research to demonstrate potential benefits of individualized nutrition as well as environmental and athletic management.

Key Words: mushing, nutrition, sled dog
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AUTHOR INDEX

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