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ABSTRACTS

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O01-GS **The potential of 3-nitrooxipropanol to lower enteric methane emissions from beef cattle.** A. Romero Perez[1,2,*], K. Beauchemin[1], S. McGinn[1], E. Okine[2], L. Guan[2], M. Oba[2], S. Duval[3], [1]*Agriculture and Agri-Food Canada, Research Centre, Lethbridge, Alberta*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [3]*DSM Nutritional Products France, Research Centre for Animal Nutrition and Health, Saint Louis Cedex, France*

This study evaluated a new compound (3-nitrooxypropanol, NOP) designed to reduce enteric CH_4 emissions. Inhibition of enteric CH_4 production is of great importance because CH_4 is a potent greenhouse gas that contributes to global warming and because it represents a loss of energy for ruminants. The objective was to determine whether enteric CH_4 emissions from beef cattle could be reduced by supplementing the diet with NOP. Eight ruminally cannulated heifers receiving a ration consisting of 60% barley silage, 35% barley grain and 5% vitamin-mineral supplement (dry matter [DM] basis) were used in a duplicated 4×4 Latin square with 28-d periods. Dietary treatments were NOP fed at 0, 0.75, 2.25 and 4.5 mg/kg of body weight. The NOP was top dressed onto the ration once daily at the time of feeding. Data were analysed using a mixed model that included the fixed effect of treatment, sampling time and their interaction, with period and animal as random effects. Sampling time was considered a repeated measure. Dry matter intake (DMI) was reduced compared with the control when 2.25 mg/kg of NOP was supplemented, yet DMI was not affected by higher or lower inclusion levels of NOP. No effect of NOP on digestibility was observed. Methane production (g/kg DMI) was reduced linearly with dose of NOP, with a 33% reduction compared with the control at the highest dose of NOP. Average ruminal pH (measured continuously for 7 days) was not affected, but minimum pH increased linearly with dose of NOP. Acetate (A) concentration was reduced and propionate (P) concentration increased with increasing dose of NOP, which in turn led to a reduction in the A:P ratio. Total bacteria and methanogens were not affected by NOP supplementation and protozoa populations were inconsistently affected. Results show the potential of NOP to reduce CH_4 production in ruminants, but further research is needed to confirm whether such reductions are maintained over longer feeding periods. The NOP compound warrants further investigation as a CH_4 reduction strategy; however, the small reduction in DMI could potentially negatively affect animal performance if confirmed.

Keywords: 3-nitrooxipropanol, Cattle, Methane

O02-GS **Relationship of severity of sub-acute ruminal acidosis with rumen fermentation, chewing activities and milk fat concentration in lactating dairy cows when fed a common high grain diet.** X. Gao[*], M. Oba, *AFNS, University of Alberta, Edmonton, Canada*

The objectives of this study were to evaluate the variation in severity of sub-acute ruminal acidosis (**SARA**) among lactating dairy cows fed a common high-grain diet, and to determine factors characterizing animals that are tolerant to high-grain diets. Sixteen ruminally cannulated late lactating dairy cows (DIM = 282 ± 33.8; BW = 601 ± 75.9 kg) were fed a common high-grain diet consisting of 35% forage. After 18 d of diet adaptation, ruminal pH was measured every 30 s for 72 h, and chewing activities were monitored for a 24 h period. Acidosis index, defined as the severity of SARA (pH < 5.8; duration of SARA multiplied by the extent of SARA) divided by dry matter intake (DMI), was determined for individual animals to assess the severity of SARA normalized for a feed intake level. Although all cows were fed a common diet, minimum pH values ranged from 5.16 to 6.04, and the acidosis index ranged from 0.0 to 10.9 pH·min/kg DMI. Six cows with the lowest acidosis index (0.04 ± 0.61 pH·min/kg) and four with the highest acidosis index (7.67 ± 0.75 pH·min/kg) were classified as animals that were tolerant and susceptible to the high-grain diet, respectively. Total VFA concentration and VFA profile were not different between the groups. However, the tolerant cows had shorter total chewing time (35.8 vs. 45.1 min/kg DMI). In addition, although DMI, milk yield, and milk component yields did not differ between the groups, milk urea nitrogen (MUN) concentration was higher for tolerant cows compared with susceptible cows (12.8 vs. 8.6 mg/dl; $P < 0.05$). These results suggest that a substantial variation exists in the severity of SARA among lactating dairy cows fed a common high-grain diet, and that cows tolerant to the high-grain diet might not necessarily have longer chewing time than susceptible cows.

Keywords: Chewing, Milk fat, Rumen acidosis

O03-GS **Effect of Harvest Maturity of Whole-Crop Oat (Avena spp.) on Forage Intake, Rumen Fermentation and Total Tract Digestibility.** C. L. Rosser[1,*], A. D. Beattie[2], H. C. Block[3], J. J. McKinnon[1], H. A. Lardner[1,4], G. B. Penner[1], *[1]Department of Animal and Poultry Science, [2]Department of Plant Science, University of Saskatchewan, Saskatoon, [3]Brandon Research Center, Agriculture and Agri-Food Canada, Brandon, [4]Western Beef Development Center, Humboldt, Canada*

The objective of this study was to determine whether stage of maturity at harvest for whole-crop oat affects forage intake, ruminal fermentation, and total tract digestibility. Oat (c.v. CDC Weaver) was seeded on May 17, 2012 and harvested at the late milk (LM), hard dough (HD) and mature (MAT) stages. The whole-crop oat forage was offered ad libitum daily to 3 ruminally cannulated heifers in a 3× 3 Latin square design with 24-d periods. Each diet was supplemented (DM basis) with 1 kg alfalfa pellet, 0.8 kg vitamin/mineral supplement, and 2.2 kg of a rolled barley:canola meal combination that was formulated to balance CP among treatments. Mean forage yield was 2.11, 4.72 and 4.17 MT/ha, respectively for LM, HD and MAT. Forage intake was greatest ($P = 0.007$) for MAT (4.80 kg/d), intermediate for LM (4.58 kg/d), and lowest for HD (4.24 kg/d). Mean ruminal pH was greater for LM (6.36; $P = 0.003$) compared to HD (6.30) and MAT (6.28). Total rumen short-chain fatty acid concentration was not affected by maturity and averaged 117 m*M*. Acetate concentration was greatest ($P < 0.001$) for LM (71.3%), intermediate for MAT (70.2%) and least for HD (69.6%; $P < 0.001$). The molar proportion of propionate decreased with advancing maturity from 16.7 to 14.7 % ($P < 0.001$) while the molar proportion of butyrate increased with advancing maturity ($P < 0.001$). Digestibility of DM and energy were not affected by harvest maturity ($P = 0.76$ and 0.77, respectively) both averaging 69%. The DE of the oat forage did not differ with advancing maturity, but total energy intake was greatest for MAT, intermediate for LM and least for HD ($P = 0.009$). This data suggests that harvesting whole-crop oat forage at advanced maturity affects forage intake and increases propionate and butyrate concentration at the expense of acetate, but does not affect total tract digestibility.

Keywords: Harvest maturity, oat, swath grazing, voluntary intake

O04-GS **Management system and marine oil supplementation affect the milk fatty acid profile.** P. Vahmani[1,*], K. E. Glover[2], L. MacLaren[3], J. Green-Johnson[4], A. Fredeen[3], *[1]Department of Biology, Dalhousie University, Halifax, [2]Azar Agriculture, [3]Department of Plant and Animal Sciences, Dalhousie University, Truro, [4]Department of Biology, University of Ontario Institute of Technology, Oshawa, Canada*

The objective of this study was to examine the interaction between marine oil supplement and management system on milk fatty acid (FA) composition. Forty-eight Holstein cows were blocked by parity and predicted calving date and deployed across pasture (PAS; n=23), or confinement (n=25) systems. Cows within each management system were assigned randomly to a control (no supplemental lipid) or one of two isolipidic supplements: rumen-protected fish oil (RPF) or rumen-protected microalgae (RPM) for 125±5 days starting 30 days pre-calving. Both lipid supplements provided similar amounts of long-chain polyunsaturated FA (LC-PUFA; ~ 65 g/d), but contained different proportions of EPA and DHA. The predominant LC-PUFA in RPF was EPA; whereas, DHA was the major LC-PUFA in RPM. Cows in both system groups were housed in a tie-stall barn from -30 until 28±10 DIM and were fed diets with similar formulations. The PAS group was then adapted to pasture and rotationally grazed on a perennial sward until the end of experiment (95±5 DIM). Milk samples were collected at 60 and 90 DIM for compositional analyses. Milk yield (kg/d) was lower (P=0.05) in grazing (34.0) compared with confined cows (40.1). Milk fat percent was reduced (P<0.05) with RPM compared with RPF (3.00 vs. 3.40) and the control (3.56). However, milk fat yield was not affected (P>0.1) by lipid supplementation. Compared with cows in confinement, cows on pasture produced milk fat with lower (-26%; P<0.05) content of atherogenic saturated FA (ASFA; 12:0+14:0+16:0) and higher (P<0.05) *cis*-9 18:1 (+32%), 18:3 n-3 (+30%) and CLA (+70%). Supplementation with RPF or RPM, regardless of management system, reduced (P<0.05) milk fat content of ASFA (-11%) and increased CLA (+28%) and n-3 LC-PUFA (+150%). Our findings show that compared to confinement, the milk produced in a pasture system has a more healthful FA composition. The healthfulness of milk fat from grazing cows can further be improved by marine lipid supplementation, which results in a several fold increase in the concentrations of beneficial FA as well as further reduction in the content of ASFA.

Keywords: dairy cow, marine oil, milk FA composition, pasture, TMR

O05-GS **Effects of frequency and level of energy supplementation on intake, rumen fermentation and digestibility of beef heifers fed low-quality forage.** F. Anez[1,*], G. B. Penner[1], P. G. Jefferson[1,2], H. A. Lardner[1,2], J. J. McKinnon[1], *[1]Animal & Poultry Science, University of Saskatchewan, Saskatoon, [2]Western Beef Development Centre, Humboldt, Canada*

The objective was to determine the effects of supplementing energy at 2 frequencies and levels on dry matter intake (DMI), rumen fermentation and nutrient digestibility of beef heifers fed low-quality forage. In a 4×4 Latin Square design, 4 rumen-cannulated Hereford heifers (339±12 kg) were fed low-quality grass hay (10.2% CP; 66.1% NDF; 42.2% ADF) and offered a pelleted supplement (30.3% NDF; 32.0% starch; 7.2% fat). Supplementation strategies were: no supplement (CON), daily supplementation at 0.6% BW (DLY), supplementation on alternate days at 0.9% (LA) and 1.2% (HA) BW. Three data sets were analyzed: 1) overall (average of all collection days), 2) day of supplementation (DS) and 3) day of no supplementation (DNS) to alternating treatments. Contrasts were used to determine: supplement effect (CON vs DLY), and to determine whether frequency and level of supplementation affected response (DLY vs LA and DLY vs HA). Overall, hay DMI (% BW) did not differ ($P \geq 0.13$) for DLY (2.0) vs CON (2.2) or LA (1.9), but tended to be higher ($P<0.10$) vs HA (1.8). On DS, hay DMI (% BW) differed ($P=0.01$) for DLY (2.0) vs HA (1.6), but not ($P=0.97$) on DNS (DLY=1.9; HA=1.9). Overall, total VFA concentration (mM) was lower ($P<0.01$) for CON (69.2) vs DLY (77.1); but not different ($P \geq 0.45$) for DLY vs LA (75.8) or HA (75.1). Rumen NH_3 (mg/dL) was lower ($P<0.01$) for CON (3.4) and higher ($P<0.01$) for LA (5.8) vs DLY (4.6), but not different ($P=0.37$) for DLY vs HA (4.3). Overall, ruminal pH was lower ($P \leq 0.04$) for DLY (6.65) vs CON (6.75) and HA (6.72), but similar ($P=0.18$) for DLY vs LA (6.70). On DS, ruminal pH was lower ($P=0.04$) for HA (6.59) vs DLY (6.64), but higher ($P<0.01$) on DNS for HA (6.85) vs DLY (6.67). Apparent DM, OM and GE digestibility coefficients were lower ($P \leq 0.03$) for CON and LA vs DLY, but not different ($P \geq 0.36$) for DLY vs HA. Results show that energy supplementation increases nutrient digestibility of beef heifers fed low-quality forage. Negative effects of alternate day supplementation on forage intake and rumen fermentation are reduced when a lower level is offered relative to simply doubling the daily amount of supplement.

Keywords: beef cattle, energy supplementation, frequency

O06-GS **Response of Different Types of Cereal Grains to Different Heating Methods in Ruminal and Intestinal Digestions in Dairy Cattle.** Y. Ying[*], D. A. Christensen, J. J. McKinnon, P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada*

Heat treatment could shift the proportion of protein degraded in rumen thus improve the utilization of nutrients. This study aimed to explore how dry and moisture heating would change the ruminal degradation kinetics, hourly effective rumen degradation ratio, potential N-to-energy synchronization and intestinal digestion of cereal grains. In this study, 2 batches of wheat, triticale and corn were processed in 3 treatments (control, dry heating and moisture heating at 121℃ for 80 min. Three dry Holstein cows with rumen cannula were used in an *in situ* trial. Then a three-step *in vitro* procedure was conducted to determine the intestinal digestibility. The results showed that moisture heating altered the digestion and shifted nutrient digestion from rumen to intestine and different types of cereal grains had different sensitivity to the heat treatments ($P<0.05$) while dry heating didn't produce significant differences. For all the 3 types of cereal grains, an increase of rumen bypass dry matter (BDM) and rumen bypass carbohydrates (BCHO) were detected due to the moisture heating ($P<0.05$). Bypass crude protein (BCP: wheat: 84 vs. 171; triticale: 53 vs. 86 g/kg DM) was also accreted in wheat and triticale ($P<0.05$). The ratio of effective degradability of N to carbohydrate was reduced (ED_N/ED_CHO: 45.9 vs. 17.9) in wheat ($P<0.05$). In the *in vitro* trial, intestinal digestible rumen bypass carbohydrates (IDBCHO) increased while total digestible starch (TDST) and total digestible carbohydrates (TDCHO) both reduced ($P<0.05$) in all the 3 cereal grains. For protein profiles, both intestinal degradable protein (IDP: wheat: 70 vs. 139 triticale: 36 vs. 61 g/kg DM) and intestinally absorbable feed protein (IADP: wheat: 36 vs. 71; triticale: 28 vs. 46 %CP) were increased in wheat and triticale, but total digestible protein didn't change. In conclusion, the moisture heating affected the nutrient digestion, shifted nutrient digestion from rumen to intestine, and have the potential to increase the nutrient availability of wheat and triticale in dairy cattle.

Keywords: rumen degradation and intestinal digestion, cereal grains, heat processing

O07-GS **The effect of malt characteristics on in situ digestibility of malt barley grain harvested in three years.** S. Ding[1,2,*], M. Oba[2], M.-L. Swift[3], W. Z. Yang[1], T. McAllister[1], *[1]Research Centre, Agriculture and Agri-Food Canada, Lethbridge, [2]Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, [3]Research Centre, Alberta Agriculture and Food , Lacombe, Canada*

In Canada, barley for malt production accounts for about 65% to 70% of annual barley production. However, over 70% of the barley produced in western Canada is used as livestock feed, thus a significant portion of this is malting barley. Although malting characteristics (MC) of barley are well defined, their relationship to feed value has not been examined. The objective of this study was to evaluate if select MC can be used to predict rumen digestibility of malt barley. Four MC, seed hardness, beta-glucan content, diastatic power and friability were measured for barley samples collected for three years from five sites in western Canada. Three samples with the lowest and highest MC values for each year were selected resulting in a total of 144 samples that were ground through a 6-mm screen for rumen in situ measurements. *In situ* incubation was conducted using 3 ruminally cannulated heifers fed a diet consisting of 70% silage and 30% barley concentrate (DM basis). Barley samples (5 g) were placed in (10 × 20 cm) polyester bags (pore size, 51 ± 2 μm) and heat sealed. Bags were introduced into the rumen through the rumen cannula and incubated for 4, 12 or 48 h. Data was analysed using MIXED procedures of SAS. Values for seed hardness (index), *β*-glucan (PPM), diastatic power (°L) and friability (%) ranged from 47.8 to 68.4, 10.6 to 433.8, 123 to 226, and 36.9 to 92.3, respectively. No significant difference ($P>0.1$) between the four MC on DMD was shown, regardless of the incubation time and year. However, DMD was slightly lower ($P<0.04$) for high (65.3%) than for samples with low (67.6%) diastatic power after 12 h of incubation. In contrast, increased friability was positively correlated with higher ($P<0.04$) DMD (Low vs. high; 66.6 % vs. 68.4 %) after 12 h incubation. Friability and seed hardness did differ ($P < 0.05$) among years after 48 h of incubation. Overall, *in situ* DMD (%) of malting barley differed ($P < 0.01$) with sampling year at 4 and 12 h of incubation, regardless of MC. These results suggest that several MC may be correlated to rumen fermentation of malt barley; however, most differences of the results appear to be due to year of production.

Keywords: in situ DMD, malting barley, malting characteristic

O08-GS **Evaluation of canola meal derived from Brassica napus versus Brassica juncea for growing and finishing cattle.** J. Nair[1,*], G. B. Penner[1], P. Yu[1], H. A. Lardner[1,2], T. McAllister[3], J. J. McKinnon[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK,* [2]*Western Beef Development Centre, Humboldt, SK,* [3]*Agriculture and Agri-Food Canada Research Centre, Lethbridge, AB, Canada*

A feedlot study was conducted to compare the feeding value of canola meal derived from two canola varieties, *Brassica napus* (*B. napus*) and *Brassica juncea* (*B. juncea).* The trial was run as a completely randomized design using 300 crossbred steers (323±23.5 kg BW; N=25 pens). The study consisted of a 56 d backgrounding period in which canola meal from two sources replaced barley grain at 15 and 30% of the control ration dry matter (DM) and a 152 d finishing period in which canola meal replaced barley grain at 10 and 20% of the control ration DM. The results indicate that during backgrounding there was a linear increase in average daily gain (ADG; $P < 0.01$), DM intake (DMI; $P < 0.01$) and gain:feed (G:F; $P = 0.01$) as the level of *B. juncea* meal increased. Steers fed *B. napus* during backgrounding exhibited a linear increase in ADG ($P = 0.02$) and quadratic increase in DMI ($P = 0.05$) and G:F ($P = 0.10$) as meal level increased. Backgrounding NEm and NEg values of the diet increased linearly ($P = 0.03$ and 0.04) as the level of *B. juncea* increased. During finishing, cattle fed *B. napus* had a quadratic increase ($P = 0.01$) in DMI and linear decreases in G:F ($P < 0.01$) and in dietary NEm ($P = 0.02$) and NEg ($P = 0.01$) content. Finishing cattle fed *B. juncea* exhibited a linear decrease in G:F ($P = 0.01$) and a tendency ($P = 0.08$) for increased DMI as meal level increased. Carcass characteristics were not ($P > 0.10$) affected by treatment. In summary, feeding canola meal from *B. juncea* and to a lesser extent *B. napus* at levels up to 30% as a replacement for barley grain (DM basis) resulted in superior performance relative to a barley-based backgrounding diet possibly as a result of higher protein content. However, with finishing cattle, performance suffered particularly with inclusion of meal derived from *B. napus* due to lower dietary NEg content.

Keywords: B. napus, B. juncea, canola meal, feedlot performance

O09-GS **Ruminal epithelium barrier function following abrupt change to moderately fermentable diet.** B. L. Schurmann[1,*], M. E. Walpole[1], P. Gorka[1,2], C. H. Ching[3], M. E. Loewen[3], G. B. Penner[1], [1]*Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada,* [2]*Animal Nutrition and Feed Management, University of Agriculture, Krakow, Poland,* [3]*Department of Biomedical Sciences, Western College of Veterinary Medicine, Saskatoon, Canada*

The objective of this study was to determine whether barrier function and inflammatory responses of the ruminal epithelium were affected following abrupt exposure to a moderately fermentable diet. Twenty-five weaned Holstein bull calves were assigned to 1 of 5 dietary treatments: the control diet (CON; 91.5% hay and 8.5% vitamin and mineral supplement) or were fed a moderately fermentable (MF; 41.5% barley grain, 50% hay, and 8.5% vitamin and mineral) diet for 3 (G3), 7 (G7), 14 (G14), or 21 d (G21). All calves were fed at 2.25% BW at 0800 h and killed at 1000 h on the last day of the respective feeding period. Ruminal epithelial tissue was collected from the caudal-dorsal blind sac and prepared for mounting in Ussing chambers under short circuit conditions, and rate of the serosal-mucosal flux of ^{3}H-mannitol ($J_{SM\text{-}mannitol}$; 74 KBq/15 mL) was measured across the ruminal epithelium. Tissue was also collected from the same region and stored at -20°C in RNAlater for quantitative real-time PCR for genes involved in the localized inflammatory response: ruminal calcium-activated chloride channel regulator-1 (CLCA1), tumor necrosis factor-α (TNFα), and interleukin proteins IL-1β, IL-4, IL-8, IL-10, IL-13, and IL-22. Data were analyzed as a randomized complete block design with polynomial contrasts used to evaluate whether adaptation to dietary change responded in linear, quadratic, or cubic patterns. Mannitol flux increased linearly (linear $P = 0.047$) from 0.45 for CON to 0.61 $\mu mol/(cm^2 \times h)$ for G21. The fold change of IL-1β increased linearly from 2.96 for CON to 9.22 for G21 ($P = 0.014$). However, there were no effects of treatment for the expression of target genes CLCA1, TNFα, IL-4, IL-8, IL-10, IL-13, or IL-22 ($P > 0.10$). These data indicate that adaptation to a moderately fermentable diet reduces barrier function of the ruminal epithelium and increases expression of IL-1β.

Keywords: Barrier function, Diet adaptation, Rumen epithelium

Graduate Student Competition - Oral (Session #2)

O10-GS **Interaction Effects Of Chiller Temperatures, Electrical Stimulation And Ageing On Beef Quality.** J. A. Puente[1,*], B. Uttaro[2], S. Samanta[3], J. Aalhus[2], A. Elezzabi[3], H. L. Bruce[1], [1]*Agricultural, Food and Nutritional Science, University of Alberta, Edmonton,* [2]*Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe,* [3]*Department of Electrical and Computer Engineering, University of Alberta, Edmonton, Canada*

The effects of early *post mortem* carcass temperature, muscle pH and ageing on beef quality measurements were investigated using a split-plot design. Whole carcass (n=20) from Angus crossbred steers were chilled at either -2°C or 2°C (TEMP) after the right side received electrical stimulation (ES) (450 volts for 90s). Following 48 h chilling, *longissimus thoracis* (LT) muscles were removed from each carcass side and divided into anterior and posterior roasts randomized to minimize location effect and assigned to 3 or 14 days ageing treatments (AGEING). Following ageing, three 2.5 cm thick steaks were taken from each LT muscle for objective color, cooking loss and Warner–Bratzler Shear Force (WBSF), and pH and drip loss measurements, respectively. Data were analyzed as a split-plot using the MIXED procedure in the Statistical Analysis System (SAS) software (Version 9.2, Statistical Analysis Systems, Cary, NC, USA). Analysis of variance was conducted using TEMP, ES and AGEING as fixed effects. Carcasses were blocked by replicate and block was included as a random source of variation. Treatment effects were considered significant at $P < 0.05$ and where treatment was significant least square mean differences were used to determine differences between means with significance at $P < 0.05$. Degrees of freedom were corrected using the Satterthwaite adjustment. Muscles from carcasses cooled at 2°C resulted in steaks with higher L* (P=0.03) and b* (P=0.02) values than those of -2°C. Roasts aged 14 days produced steaks with higher L* (P=<0.0001), a* (P=<0.0001), and b* (P=0.04) values and lower drip loss (P=<0.0001) and cook loss (P=0.01) values than 3 day aged. Steaks from ES sides had higher values of a* (P=0.0006), and b* (P=0.0009) than those of non-ES sides. Significant interaction between ES and AGEING suggested that ES steaks at 3 days aged had lower values of WBSF (P=0.0079) than those of non-ES, but this difference did not persist to day 14. This study showed that ES significantly improved meat appearance and tenderness but that this improvement declined with time *post mortem.*

Keywords: beef color, shear force, electrical stimulation, ageing

O11-GS **Does monitoring of animal welfare parameters through the supply chain predict pork meat quality variation?** L. M. Rocha[1,2,*], A. Velarde[3], A. Dalmau[3], L. Saucier[2], L. Faucitano[1], [1]*Agriculture and Agri-Food Canada, Sherbrooke,* [2]*Department of Animal Science , Université Laval, Quebéc, Canada,* [3]*IRTA, Monells Girona, Spain*

The objective of this study was to assess the relationship between the animal welfare conditions at the farm assessed through audit protocols and pork quality variation. A total of 6 farms (A, B, C, D, E and F; total of 855 pigs) were assessed according to the Welfare Quality protocol® (WQ®) based on 12 criteria organised in 4 welfare principles: good feeding (GF), housing (GH), health (HC) and appropriate behaviour (AB). A total of 720 pigs (60 pigs/farm) were randomly chosen at the abattoir over 6 slaughter days (two farms per day, 120 pigs) for meat quality evaluation. Meat quality was assessed in the *Longissimus Dorsi* (LD) muscle at 24 h post-mortem by measuring the ultimate pH (pHu), colour (CIE L*, a*, b*) and drip loss using the filter paper wetness method. The 4 principle scorings of each farm were calculated with the WQ® website calculator, whereas meat quality data were analyzed using the MIXED procedure of SAS. Spearman correlations were performed using SAS to determine relationship between the on-farm animal welfare audit scores per principle and meat quality traits. Spearman correlation showed that the LD muscle pHu was strongly influenced by GH ($r = -0.94$; $P < 0.001$), HC ($r = 0.72$; $P < 0.001$) and AB ($r = -0.62$; $P < 0.05$) at the farm. Drip loss was only affected by HC at the farm ($r = -0.65$; $P < 0.05$). The LD muscle from pigs originating from the farm E presented a lower ($P = 0.004$) pHu (5.65 *vs.* 5.72), a greater ($P = 0.002$) drip loss (5.21 *vs.* 3.03%) and was paler (50.16 *vs.* 48.70; $P = 0.03$) than the LD muscle of pigs from farm D. Accordingly, the score for HC principle was low in farm E (63.9) and was the second best (76.2) in the case of farm D. Therefore, these preliminary results demonstrate that the implementation of on-farm animal welfare auditing may help controlling the variation of important pork meat quality traits.

Keywords: Animal welfare, Audits, Meat quality

O12-GS **Validation of Rumination Collars for Beef Cattle.** C. A. Goldhawk[1,2,*], K. S. Schwartzkopf-Genswein[2], K. A. Beauchemin[2], [1]*Faculty of Veterinary Medicine, University of Calgary, Calgary,* [2]*Agriculture and AgriFood Canada, Lethbridge, Canada*

Two studies were conducted to evaluate the effect of housing, diet, and head posture on a wireless rumination monitoring system (Hi-Tag, SCR Engineers Ltd.; Netanya, Israel) used with Angus or Angus-Hereford yearlings. The Hi-Tag system outputs rumination time as

minutes per 2 h period, thus all observations were conducted over 2 h periods that matched the system output. Study 1 consisted of 7 yearling heifers housed in tie-stall housing and fed a high concentrate ration (TSHG) for 1 wk, and then a high forage ration (TSHF) for 1 wk. Video cameras were placed 1 m from the head of each animal to record rumination behaviour and head posture. Study 2 consisted of 6 yearling steers in a loose-housed pen, fed the high forage diet (FHF), with continuous live observations to record rumination behaviour and video recordings for head posture. Rumination data were collected from a total of 72, 47, and 44 periods for the TSHG, TSHF, and FHF treatments, respectively. The inter-observer correlation was high for video (r = 0.97) and live observations (r = 0.98), and for video intra-observer correlation (r = 0.99). A high correlation was found between live and video observation (r = 0.97). A subset of 15 periods from each treatment were randomly selected to evaluate the relationship between the proportion of an observation period with the head raised and the difference between the Hi-Tag system and observer estimates of rumination. When all data were pooled, the correlation between Hi-Tag and observer estimates of rumination time were low, r = 0.41 (P < 0.001). Correlation by housing type and diet was also low as the correlation for TSHG was r = 0.39 (P< 0.001), TSHF was r = 0.46 (P = 0.001), and for FHF the correlation was r = 0.08 (P = 0.595). The difference between the Hi-Tag system and observer estimates of rumination were not correlated with proportion of a period that the head was raised (r = -0.02, P = 0.89). In conclusion, the Hi-Tag system did not accurately measure rumination in yearling beef cattle.

Keywords: automation, beef, cattle, rumination

O13-GS **Agents of Bovine Respiratory Disease in North American Feedlots.** C. Klima[1,*], R. Zaheer[2], S. Hendrick[1], T. W. Alexander[2], T. A. McAllister[2], [1]*University of Saskatchewan, Saskatoon,* [2]*Agriculture Agri-Food Canada, Lethbridge, Canada*

Bovine respiratory disease (BRD), continues to be a primary health problem in newly received feedlot calves. The objective of this study was to analyze nasal swab and lung tissue samples from BRD mortalities for the prevalence of BRD-associated viral and bacterial pathogens and to characterize the recovered bacterial isolates for their genetic profiles, antimicrobial susceptibility and the genetic nature of antimicrobial determinants. Samples from 68 BRD mortalities originating in Alberta (n=42), Texas (n=6) and Nebraska (n=20) were screened by PCR for bovine virus diarrhoea virus (BVDV), bovine respiratory syncytial virus, bovine herpes virus 1, parainfluenza type 3 virus, *Mycoplasma bovis, Mannheimia haemolytica* (MH)*, Pasteurella multocida* (PM) and *Histophilus somni* (HS), with all being detected with the exception of bovine herpes virus 1. The most prevalent agents were MH and BVDV (81% and 71% of samples respectively). If recovered, single isolates of MH (n=55), PM (n=9) and HS (n=10) from each lung tissue sample were profiled by pulsed-field gel electrophoresis. A highly virulent, clonal subpopulation of MH isolates (n=8) was detected from Nebraska. In isolates of MH (n=16), PM (n=1) and HS (n=1) from either Texas or Nebraska an integrative conjugative element (ICE) harbouring multidrug resistance towards to >7 antimicrobials (i.e., aminoglycoside, β-lactam, fluoroquinolone, lincosamide, macrolide, pleuromutilin, tetracycline) was identified. Whole genome sequencing of 3 of the multidrug resistant MH confirmed the presence of full or partial ICE sequences. It appears that the ICE plays a significant role in the antimicrobial profile of *M. haemolytica* and could be a major determent to many of the therapeutic antimicrobial strategies currently employed against this important respiratory pathogen.

Keywords: bovine respiratory disease, feedlot cattle

O14-GS **Effects of an esterase-producing inoculant and chop-length on silage fermentation, ruminal fermentation, growth performance and carcass characteristics of finishing feedlot steers.** W. Addah[1,2,*], J. Baah[2], E. E. K. Okine[1], T. A. McAllister[2], [1]*Agricultural, Food and Nutritional Science, University of Alberta, Edmonton,* [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Canada*

Forage chop length may affect silage fermentation and animal performance. Inoculation of silage with fibrolytic inoculants has been shown to improve fermentation and fibre digestibility. This study determined the effects of chop length and a fibrolytic inoculant on silage fermentation, and the growth performance and carcass characteristics of finishing feedlot steers. Whole-crop barley (*Hordeum vulgare* L.; 31% DM) was chopped to theoretical lengths of 1.0 cm (SC) or 2.0 cm (LC) and ensiled with or without an esterase-producing inoculant containing *L. buchneri* LN4017, *Lactobacillus plantarum* LP7109 and *Lactobacillus casei* at a rate of 2.8 × 105 CFU/g forage) in farm-scale silos. After 311 d of ensiling, the silage was used to formulate four finishing diets (inoculated SC, uninoculated SC, inoculated LC and uninoculated LC) for feedlot steers. Data were analyzed using the mixed procedure of SAS as a 2 × 2 factorial design. Inoculation increased the concentration of acetic acid in both SC (45.7 *vs* 24.3 g/kg DM) and LC (54.3 *vs* 15.9 g/kg DM), and decreased NDF by 10% (473.1 *vs* 527.3) and 6% (469.1 *vs* 501.1) in the SC and LC, respectively. Steers fed the inoculated LC diet had lower (*P*=0.024) ruminal propionic acid concentration whereas this parameter was not altered (*P*=0.758) by inoculation of SC silage. Ruminal isovaleric (*P*=0.022) and butyric acids (*P*=0.043) were greater in the LC but these did not differ (*P* ≥ 0.140) in steers fed either the inoculated or uninoculated SC diet. Neither inoculation, chop length nor their interaction affected the growth performance of steers but the rib eye area and proportion of saleable meat were greater (*P*≤0.035) for the steers fed SC than for those fed LC diets. This study suggests that whole-crop barley silage could be chopped up to 2.0 cm and inoculated with this ferulic acid-producing inoculant without impeding fermentation or animal performance. The economic benefits of greater saleable meat yield and *longissmus* muscle area for SC should be weighed against the operational cost of chopping silage to shorter chop length prior to ensiling.

Keywords: Barley silage, carcass characteristics, esterase-producing inoculant, feedlot steers, rumen fermentation

O15-GS **Dynamics of whole body nitrogen retention and blood urea nitrogen in young pigs challenged with bacterial lipopolysaccharide is not affected by diet complexity.** M. Rudar*, C. de Lange, *Animal and Poultry Science, University of Guelph, Guelph, Canada*

Reduced use of milk and plasma proteins in pig diets can decrease both feed costs and growth performance during the starter phase. The long-term consequences of this practice are unclear because it may alter disease resistance. The objective of this study was to explore the effect of diet complexity on the dynamics of nitrogen (N) retention and blood urea nitrogen (BUN) in young pigs following a bacterial lipopolysaccharide (LPS) challenge. Weaned pigs (6.51 ± 0.78 kg) were fed either simple (plant protein, 21.7% crude protein, n = 4) or complex (milk and plasma proteins, 19.8% crude protein, n = 4) diets that were formulated to be similar in available nutrient content. One week post-weaning, catheters were surgically inserted into a jugular vein. Seven days post-surgery, pigs were moved to metabolic crates and fed 450 g/d split equally between two meals. On day 10 post-surgery, LPS was infused intravenously for 20 h (5 $\mu g \cdot kg^{-1} \cdot h^{-1}$, day 1) and an N balance was conducted. Feces, urine, and blood were collected daily until the end of the 8 day N balance period. There was no difference in mean N retention between pigs fed simple and complex diets over the 8 day period (7.93 vs 7.70 g/d, SE 0.41, $P > 0.05$). However, N retention increased in pigs fed both diets from days 1 to 3 (3.22 vs 8.96 g/d, SE 0.42, $P < 0.001$) and was constant from days 3 to 8 ($P > 0.10$). BUN increased in pigs fed both simple and complex diets following the LPS challenge (20.0 vs 9.5 mg/dL, SE 1.3 on day 1, $P < 0.05$ to 79.7 vs 71.5 mg/dL, SE 24.0 on day 2, $P > 0.10$). BUN subsequently declined but remained elevated relative to pre-challenge levels from days 5 to 8 (36.2 vs 20.8 mg/dL, SE 3.5, $P < 0.01$). The higher BUN in pigs fed simple opposed to complex diets corresponds to an increase in mean N intake (13.77 vs 12.30 g/d, SE 0.50, $P < 0.05$) and to an increase in mean urinary N excretion (3.33 vs 2.06 g/d, SE 0.13, $P < 0.001$). In this study, diet complexity did not affect the response of young pigs to an endotoxin challenge.

Keywords: Endotoxin, nitrogen retention, pigs

O16-GS **Mechanisms of urea transport across the isolated ruminal epithelium in bison (Bison bison) and beef cattle (Bos taurus).** M. Walpole[1,*], P. Gorka[1,2], M. Woodbury[3], L. L. Guan[4], G. Penner[1], [1]*Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada,* [2]*Department of Animal Nutrition and Feed Management, University of Agriculture in Krakow, Krakow, Poland,* [3]*Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon,* [4]*Department of Animal Nutrition and Feed Management, University of Alberta, Edmonton, Canada*

The objective of the study was to determine the effect of *in vitro* rumen NH_3 on total and aquaporin (AQP, Ni^{2+}-sensitive) mediated urea flux across the ruminal epithelium in yearling Angus cross bulls (BOVINE) and 2-yr old Plains bison bulls (BISON). Twenty-four BISON and BOVINE bulls were blocked by BW and randomly assigned to either a backgrounding (50% barley silage, 40% barley grain, 10% mineral and vitamin supplement) or finishing (15% barley silage, 75% barley grain, 10% mineral and vitamin supplement) diet with 3 hd/pen. Two animals/pen were killed each week and ruminal epithelial tissue was collected from the caudal dorsal blind sac and mounted in Ussing chambers under short-circuit conditions. The serosal buffer contained 7 m*M* urea and was adjusted to a pH of 7.4, while the mucosal buffer lacked urea, and contained either 0 or 7 m*M* $(NH_4)_2CO_3$ and was adjusted to a pH of 6.2. AQP were inhibited through the addition of 1m*M* $NiCl_2$ to both serosal and mucosal buffers. The serosal-to-mucosal fluxes of urea ($J_{sm\text{-}urea}$) and mannitol ($J_{sm\text{-}mannitol}$) were measured using ^{14}C-labelled urea and ^{3}H-labelled mannitol, respectively, with $J_{sm\text{-}mannitol}$ being used as an indicator of hydrophilic transport. Ruminal NH_3 was unaffected by species ($P = 0.60$) or diet ($P = 0.27$) while plasma urea nitrogen tended ($P = 0.055$) to be higher for BISON (12.5 mg/dL) than BEEF (10.8 mg/dL), but was not affected by diet ($P = 0.22$). The $J_{sm\text{-}urea}$ tended to decrease with addition of Ni^{2+} ($P = 0.065$), while mucosal ammonia had no affect ($P = 0.41$). $J_{sm\text{-}urea}$ and $J_{sm\text{-}mannitol}$ were not affected by species ($P = 0.41$) or dietary treatment ($P = 0.29$), however $J_{sm\text{-}urea}$ was lower in animals killed second ($P = 0.011$). These results indicate AQP play a role in urea transport in both bison and beef cattle.

Keywords: ammonia, aquaporin, ruminal epithelium

O17-GS **Genome wide association for human nose score of boar taint using single-snp analysis.** Y. G. Tesfayonas[1,2,*], [1]*Animal Breeding and Genomics Center, Wageningen University, Wageningen, Netherlands,* [2]*Animal Breeding and Genetics, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden*

Human nose score (HNS) is one method used to reduce boar taint without castration. It involves the scoring of the level of boar taint in boars by sensory panel. The objective of this study was to identify single nucleotide polymorphisms (SNPs) associated with HNS and to determine the phenotype variation explained by the SNPs. Boar taint is the unpleasant odor released when cooking meat from entire male pigs. It is mainly caused by increased accumulation of androstenone and skatole in adipose tissue. Producers castrate male pigs to remove boar taint, however, this practice has raised animal welfare concerns from consumers. HNS of 1835 intact boars from five purebred (1,438) and three crossbred (397) lines genotyped with Porcine 60K SNP Bead chip, and 46,751 SNPs were used for the genome wide association study; boars that were part of the purebred and crossbred both contained sire and sow lines. The design of the study was population based. GRAMMAR approach in R package-GenABEL was employed for the genome wide association analysis. This study revealed genome wide significant SNP (FDR ≤0.05) on pig chromosome SSC5. The SNP had minor allele frequency of 0.04% and it explained 19% of the phenotype variation. In addition, Boars heterozygous for the SNP had a mean score (0.72) higher than the two homozygous genotypes (0.56 and 0.63) which suggests over dominance.Moreover, chromosome wide significant SNPs (FDR ≤0.05) were found on SSC2, SSC7 and SSC17. Some of the SNPs correspond to quantitative trait locus (QTL) of androstenone and skatole. Therefore, HNS can be used to alleviate boar taint through breeding.

Keywords: Boar taint, Human nose score, Single nucleotide polymorphism

O18-GS **Genetic influence of host animals on fatty acid composition in beef cattle tissues.** C. Ekine[1,*], L. Chen[1], M. Vinsky[1], Z. Wang[1], P. Stothard[1], E. Okine[1], N. Aldai [2], M. Dugan[1], T. McAllister[3], C. Li[1], *[1]Agriculture Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Lascaray Research Centre, University of the Basque Country (UPV-EHU), Vitoria-Gasteiz, Spain, [3]Agriculture and Agri-Food Canada, Lethbridge, Canada*

The fatty acid composition in beef has emerged as an economically relevant trait to the beef industry due to increasing consumer awareness of the health implications of fat intake associated with red meat consumption. The aim of this study was to investigate the genetic variability of fatty acids in beef tissues and to identify DNA markers associated with the fatty acids. Comprehensive fatty acid profiles were analyzed in the brisket adipose tissue of 223 Angus based commercial crossbred steers. The steers were also genotyped on 948 single nucleotide polymorphisms (SNP) of lipid metabolism related genes. Estimation of direct heritability of fatty acids and SNP effects were conducted using an animal model with the relationship matrix among steers defined based on the SNP genotypes. The results showed a wide range of heritability estimates for the fatty acids analyzed from 0.03 for branched-chain fatty acids to 0.51 for 9*c*-14:1. The SNP association identified a panel of 25 to 46 gene SNPs that had significant associations with each of the fatty acids ($P < 0.05$), and the amount of phenotypic variance jointly explained by the significant SNPs was from 0.89% for the health index to 3.41% for 9*c*-14:1. Our results indicate that fatty acids in beef brisket adipose tissue had a low to moderate heritability depending on individual fatty acids, and there is a potential to improve the fatty acid profile in beef cuts through genomic evaluation and selection.

Keywords: Beef cattle, Fatty acid composition, Heritability, SNP association

O19-GS **Bovine microRNAs: genomic organization and expression in subcutaneous adipose tissue.** J. M. Romao[1,*], W. Jin[1], M. He[2], T. McAllister[2], L. Guan[1], *[1]AFNS, University of Alberta, Edmonton, [2]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Canada*

Adipose tissue plays a major role in energy metabolism and is an important determinant of beef quality and animal productivity. The molecular regulation of bovine adipose tissue is not fully understood. MiRNAs are a new class of regulators reported to be involved in adipogenesis. The objective of this study was to characterize the expression profile and genomic organization of miRNAs in bovine subcutaneous adipose tissue. Adipose tissue samples (n=24) were collected from 8 British-continental crossbred steers at 12, 13.5 and 15 months of age. Total RNA was extracted from biopsy samples and miRNA expression was profiled using miRNA microarray. Approximately 30% of the known bovine miRNAs were detected in subcutaneous adipose tissue (n=224) of which 155 miRNAs were expressed in all steers in at least one age, representing the core miRNAs in bovine adipose tissue. A total of 45.2% of the core miRNA genes were organized in clusters (distance between miRNAs is less than 10kb on the genome) and 54.8% were non-clustered on the chromosomes. MiRNAs encoded in clusters had higher expression than non-clustered ones (p=0.002). Of the core miRNAs identified in beef cattle adipose tissue a total of 49% were associated with highly conserved miRNAs among different vertebrate species, 14.2% were associated with moderately conserved miRNAs and 36.8% with poorly conserved miRNAs. Highly conserved miRNAs had higher expression (p<0.001) than moderately or poorly conserved miRNAs. The expression of core adipose miRNAs changed according to genomic context characteristics such as cluster organization and miRNA conservation status, which enhances our knowledge on miRNA expression patterns in adipose tissue. These findings will improve our understanding on the roles of miRNAs in the regulation of bovine adipogenesis.

Keywords: adipogenesis, adipose tissue, Beef cattle, genomic context, microRNA

O20-GS **Predicting residual feed intake in beef bulls by measuring radiated heat loss through infrared thermography.** S. Thompson[1,*], A. Schaefer[2], G. Crow[3], J. Basarab[4], J. Colyn[2], K. Wittenberg[3], V. Baron[5], C. Fitzsimmons[6], K. Ominski[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, [2]Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, [3]Animal Science, University of Manitoba, Winnipeg, [4]Lacombe Research Centre, Alberta Agriculture and Rural Development, Lacombe, [5]Agriculture and Agri-Food Canada, [6]Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, Canada*

Between 65-75% of the total dietary energy required for beef production is used by the cow herd. Residual feed intake (RFI) has been used to select metabolically efficient cattle in beef breeding programs, particularly for sire selection. Adoption of genetic selection using RFI has been limited due to the high cost and difficulty of measuring individual feed intake for a 76-day period. An alternative method of predicting RFI is to measure radiated heat loss using infrared thermography (IRT). Previous studies have shown promise using IRT to predict metabolic efficiency in mature cows, heifers, and growing bulls. The objective of this study was to explore use of IRT to predict RFI in growing beef bulls. Sixty bulls were fed either a forage-based or a grain-based ration as part of an RFI study. Infrared images of the head were collected over a total of 8 sample days using a FLIR S60 camera and cheek temperature (Ck) was calculated. Daily feed intake (FI) measured by the GrowSafe feeding system was regressed against average daily gain, metabolic mid-weight and final ultrasound backfat to obtain an expected feed intake (EFI) value. RFI was calculated as the difference between FI and EFI. Bulls were grouped into low, medium and high classes based on ±0.5 of RFI standard deviation. RFI values ranged from -1.15 to +1.44 kg day^{-1} dry matter (avg=0.0; SD=0.577). Sample day Ck values were calculated and RFI was regressed against average Ck temperatures. Trial-average Ck temperatures for low (27.75°C; SE=0.273; n=20), medium (27.60°C; SE=0.184; n=23), and high RFI groups (27.79°C; SE=0.236; n=17) were not significantly different (P>0.05). However, there were individual days where RFI and Ck values were significantly related (P<0.05). Data suggests that under certain environmental conditions, Ck measurements exhibit a positive relationship with RFI. Temperature deviations associated with extremes in ambient temperature (placing animals outside their thermoneutral zone) or underlying subclinical health problems could bias results in IRT measurements and RFI ranking. Investigation into these conditions is needed to standardize IRT collections and improve predictions.

Keywords: beef bulls, Infrared thermography, residual feed intake

O21-GS **Residual feed intake, enteric methane and carbon dioxide emissions in growing beef bulls.** T. R. Ullenboom[1,*], G. H. Crow[1], J. A. Basarab[2], K. M. Wittenberg[1], V. Baron[3], K. H. Ominski[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, [2]Western Forage Beef Group, Alberta Agriculture, Food and Rural Development, [3]Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, Canada*

Residual feed intake (RFI) is a measure of metabolic efficiency. Cattle selected for low RFI are expected to produce less methane (CH_4) than do high RFI cattle. Methane is a greenhouse gas and a reduction of methane emissions from cattle would be both environmentally and economically beneficial to the cattle industry. The objective of this study was to determine the relationship between RFI and enteric CH_4 as well as carbon dioxide (CO_2) emissions (as an indication of energy expenditure and efficiency) from growing beef bulls. Sixty Angus bulls (307±43 kg, 281±27 days of age) were randomly assigned into four pens of 15 animals in a completely random design with repeated measures. Following a 21-d adaptation period, two pens received a high forage diet, and two pens received a high grain diet. The forage diet consisted of alfalfa hay 50.7%, corn silage 49%, mineral 0.2%, and salt 0.2% on a dry matter basis. The grain diet consisted of alfalfa silage 36.2%, corn silage 24.8%, corn grain 32.3%, dried distillers grains 6.3%, mineral 0.2%, and salt 0.2% on a dry matter basis. Intake was measured using the GrowSafe® System for a 76-d period. Enteric gas emissions were measured using the sulphur hexafluoride technique in four 24-h sampling events at the beginning (BG, n=50) and in three 24-h sampling events at the end (END, n=12) of the feeding period. The effects of diet and group (BG and END) on CH_4 and CO_2 were analysed. From the beginning to the end of the feeding period, enteric CH_4 emissions ($P < 0.0001$) increased from 227±9 to 351±20 L hd^{-1} d^{-1}, as did CO_2 emissions ($P < 0.0001$) which increased from 4274±246 to 6753±533 L hd^{-1} d^{-1}. This increase in emissions was expected as body weight (BW) and daily dry matter intake (6.34±0.17 to 7.19±0.55 kg d^{-1}) increased over time. Enteric CH_4 emissions per unit of gross energy intake (%GEI) did not differ between diet or group (overall mean=8.03±0.12%). Few of the correlations between 76-day RFI_{fat} and measures of enteric CH_4 emissions were significant. These findings are contrary to previous studies and suggest that RFI ranking may be associated with metabolic mechanisms in addition to fermentation efficiency.

Keywords: Methane, RFI

Animal Health and Emerging Issues

O22 **Mucosal Vaccination: Using *Bacillus* Spores for Antigen Delivery.** S. M. Cutting*, *School of Biological Sciences, Royal Holloway, University of London, Egham, UK.*

Spores of the Gram-positive bacterium *Bacillus subtilis* have utility as vehicles for mucosal vaccination using the oral, nasal or sub-lingual routes. Spores carry natural adjuvant properties, are used as probiotics in humans and in animal feed products and, of course are very robust surviving exposure to desiccation, heat and gastric fluids. As vaccines, spores can be used for antigen expression using genetic modification and expression of proteins on the spore surface. Surprisingly, inactivated, and therefore killed spores can also be used as carriers and both GM and non-GM forms spore vaccines have been used to confer protection to a number of human and animal pathogens including *C. tetani, B. anthracis, Influenza, Rotavirus, C. difficile*, *C. perfringens* and *M. tuberculosis*. The first ever human clinical study of a novel oral vaccine to *C. difficile* using bacterial spores will commence this year and this may indicate the future potential of spores as novel vaccines that are safe and straightforward to use. This presentation will summarize the status of spore vaccines and their applications in the veterinary arena.

O23 **Welfare management practices to increase beef production and sustainability.** K. S. Schwartzkopf-Genswein*, *Agriculture and Agri-Food Canada, Lethbridge, Canada*

Common on-farm management practices include weaning, handling, transport, castration, and dehorning which can have significant negative impact on animal health and well-being if conducted with disregard for animal welfare. The relationship between animal stress, injury, reduced immune function and animal health is well established. Therefore any management practice that can cause stress has the potential to increase herd morbidity and mortality which are directly related to reduced profitability. For example, there is significant evidence rough handling can reduce weight gain, increase handling time and carcass bruising. In fact, many slaughter facilities are investing significant capital into video monitoring systems to access handling quality on-site. Most North American trucking companies now require that drivers have a certification which includes training on proper animal handling and driving quality. Recent studies have shown that transport durations without feed and water exceeding 30 h are associated with increased shrink related to water and tissue loss, mortality, becoming non-ambulatory and lame. In addition, calves given a combination of a local anesthetic and analgesic prior to castration had improvements in feed intake and average daily gain as well as reduced pain associated behaviours compared to calves not provided pain control. In the years to come, sustainable and profitable beef production will only be accomplished through welfare friendly management practices. Sustainability and profit will not only be linked to improved animal performance but increased market access and consumer acceptance. Increasing use of in house and third party on-farm welfare audits will focus on ensuring all routine management practices are conducted in accordance with achieving good animal welfare.

Keywords: beef production, profit, sustainability, welfare

O24 **Microbial Biodegradation Of Recalcitrant Beta-Sheet Rich Protein By Shifting Communities Of Bacteria And Fungi During Composting.** T. Reuter[1,*], B. H. Gilroyed[2], W. Xu[3], T. A. McAllister[4], K. Stanford[1], [1]*Livestock Research Branch, Government of Alberta, Lethbridge,* [2]*School of Environmental Sciences, University of Guelph, Ridgetown, Canada,* [3]*Department of Medicine, Karolinska Institute, Stockholm, Sweden,* [4]*Ruminant Nutrition & Microbiology, Agriculture and Agri-Food Canada, Lethbridge, Canada*

Both microbial endospores and prions causing transmissible spongiform encephalopathies (TSE) are reported to persist in environmental reservoirs, remaining either viable or infectious over decades. The bioactivity and physiochemical conditions within these environmental reservoirs might determine the fate of these persistent biomolecules.

The microbial activity during the composting process efficiently degrades a wide range of organic substrates over time. Recalcitrant organic matter such as beta-sheet rich proteins pose a marginal metabolic return of energetic and nutritional profit for microflora compared to readily biodegradable substrates. Hooves, either black or white, containing different amounts of melanin were used as a surrogate protein to gain information on the potential degradation of prions during composting of manure and livestock mortalities.

The biodegradation of bovine hooves placed into porous nylon bags was monitored over time at day 0, 7, 14, 28, 56, 112 and 230. Bacterial 16S and fungal 18S DNA fragments were amplified by PCR and profiles were separated by sequence differences using denaturing gradient gel electrophoresis. Sequence analysis of separated fragments revealed simultaneously a number of bacterial and fungal identities at different time points during composting. Our data revealed that the microbial diversity was affected by a time-temperature interaction and by the hoof color. Our physicochemical and molecular data, supported by scanning electron microscopy, suggest the formation of biofilms composed of a complex and shifting community of bacteria. These bacterial biofilms along with a more static population of fungal species collaborate in degradation of recalcitrant organic matter over time.

Keywords: biodegradation, prion, DGGE, sequencing, bacteria, funghi

O25 **Compost Temperatures Reduce Bacillus Endospore Viability,** A. Harvey[1,2,*], T. Reuter[3], B. Selinger[2], A. Kingsley[4], T. A. McAllister[1], [1]*Agriculture and Agri-Food Canada,* [2]*University of Lethbridge,* [3]*Agriculture and Rural Development ,* [4]*Animal Disease Research Institute , Lethbridge, Canada*

Outbreaks of transmissible pathogens in wildlife and domestic animals represent a potential risk to food safety and security, human health and socioeconomic status. Anthrax, a lethal infectious disease, affecting primarily herbivores, is caused by an endospore-forming bacterium, Bacillus anthracis (BA). Endospores from BA pose a communicable risk as a bio-warfare agent. Endospores are extremely resistant to environmental stresses and remain viable in soil for decades. Composting is an effective disposal method for infectious materials, but has not been investigated for the ability to inactivate BA endospores. This study examined the impact of sporulation temperature and composting temperature exposure on Bacillus endospore viability. Four surrogate strains, two Bacillus thuringiensis and two Bacillus licheniformis were chosen for their similarity to BA, and sporulated at 25, 30 or 37°C to reflect temperature variations during natural sporulation. Endospores were inoculated (10^8 CFU) into triplicate vials containing sterile silica beads or autoclaved compost and placed inside an oven. The oven was adjusted to mimic a temperature profile of a previously conducted long-term (>150 d) field-scale composting study. Control vials, inoculated with endospores produced at 37°C ,were maintained at 21°C. The experiment was duplicated in two ovens. Viable endospores were enumerated by serial dilution and spread plating after 0, 25, 50, 100 and 150 d of incubation. In both compost and silica samples, oven exposure resulted in a $\geq 4 \log_{10}$ decline in endospore viability, compared to room temperature controls, suggesting that temperature and not compost residuals is the primary factor responsible for endospore inactivation. Our results suggest that composting represents a viable method for the disposal BA contaminated materials and related mortalities.

Keywords: anthrax, Bacillus, composting, disease, livestock

O26 **Boosting Molecular Assays To Detect Pathogenic Escherichia Coli In Cattle.** C. C. Conrad[1,*], K. Stanford[2], T. A. McAllister[3], J. E. Thomas[1], T. Reuter[2], [1]*Biological Sciences, University of Lethbridge,* [2]*Livestock Research Branch, Government of Alberta,* [3]*Ruminant Nutrition & Microbiology, Agriculture & Agri-Food Canada, Lethbridge, Canada*

Shiga toxin-producing *Escherichia coli* (STEC) are food borne pathogens responsible for outbreaks and lethal human diseases worldwide. Cattle, the main reservoir for STEC, harbor unknown numbers of STEC serotypes in the intestinal tract with the potential to compromise the safety of food and water. As a serious public health concern; traditional microbiology and/or molecular biology based detection methods used to monitor STEC in cattle related sources and products are mandated, but current protocols are limited. Molecular assays with greater sensitivity for the detection of pathogenic STEC in cattle prior to harvest and human consumption are required. A collateral requirement for detection assays related to perishable products is specificity in addition to a fast and reliable high throughput performance.

In comparison to traditional approaches, sample processing and molecular methods were evaluated using a multi-factorial Latin square design. The design involved fresh feces, rather than freeze drying and ball grinding samples prior to DNA extraction. A portion of feces were autoclaved prior to testing as a control to exclude active background microflora for precise detection and enumeration of target serotypes. Autoclaved *versus* non-autoclaved feces were spiked with STEC (Serotype O26 and O157) dilutions (10^{-1} to 10^{-6} per gram), and enriched for up to 6 hour. Each hour, enriched aliquots were analyzed comparing data from traditional culture methods *vs.* optic density *vs.* quantitative polymerase chain reaction (qPCR). In addition, efficiency of two common DNA extraction methods was compared. After 3 hours of enrichment, less than 100 CFU of inoculated STEC per gram feces could be traced using qPCR. Based on the results of this study, freeze drying and ball grinding following a minimum of 3 hours of enrichment in combination with a silica membrane based DNA extraction provided a reliable and fast performance optimal for the detection of STEC in feces. In conclusion, the optimization of current protocols to monitor emerging STEC can improve the evaluation of potential food safety risks with focus on the proportion of isolates possessing toxin genes with known impacts on human health.

Keywords: detection, food safety, non-O157:H7 E.coli, pathogen

Nonruminant Nutrition

O27 Egg Production and Quality of Laying Hens fed Leaf Composite Mix as Alternative Premix for Commercial Premix.

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A 16-week feeding trial was conducted to evaluate the effects of partial and total replacement of commercial layer premix with the leaf composite mix (LCM) produced from the mixture of five edible tropical leafy vegetables; Moringa, African basil, cassava leaf, fluted pumpkin and bitter leaf on production performance and some internal egg qualities. Three hundred Isa brown point of lay birds were randomly allotted to 6 dietary treatments of 50 birds per treatment having 5 replicates in a completely randomized design. The commercial premix in the basal diet was reduced by 0, 20, 40, 60, 80 and 100% and replaced with 0, 1, 2, 3, 4 and 5% LCM and designated diets 1, 2, 3, 4, 5 and 6 respectively. Growth indices were significant ($P<0.05$) influenced by the dietary treatment with birds fed 2% LCM-based diet having the best FCR (1.71) but not statistically different from those fed 60-80% LCM-based diets. The Hen-day production (74-89%) of birds fed LCM-based diets was significantly higher than those fed the control diet (61%). The cholesterol levels of birds fed on LCM-based diets were reduced by 88.3-92.8% over those fed control diet while egg yolk colouration increased progressively with increased LCM inclusion level in the diets. The egg pH though significantly ($P<0.05$) affected by the dietary treatments do not follow a particular trend. Thus, it could be suggested that inclusion of leaf composite mix from the 5 leafy vegetables understudy could be a veritable substitute for commercial premix in laying birds in developing countries and this could increase egg production and consumption among the limited resource poor in the third world countries.

Keywords: Leaf Composite Mix, Commercial Premix, Performance, cholesterol and egg pH

O28 Effects of graded corn cob levels on physicochemical properties of digesta and the size of visceral organs in weaner pigs.

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The objective of the study was to investigate the effects of graded levels of corn cob (CC) meal incorporated in the diet on the physicochemical properties of digesta and sizes of gastrointestinal (GIT) organs of growing pigs. Understanding changes in physicochemical properties of digesta assists feed compounders to identify appropriate fibre inclusion levels that minimize nutrient losses through excretion or overfeeding. A total of 18 pigs with initial body weight (BW), 14 ± 1.2 kg were allocated each to one of the five corn cob levels (80, 160, 240, 320 and 400 g/kg DM) and a control diet. The control diet contained 18.09 MJ/kg DM and crude protein of 24.78 g/kg DM. After four weeks, weights of the GIT compartments were recorded and the contents were sampled for analyses of water concentration, water holding capacity (WHC), swelling capacity, nutrient contents, neutral detergent fibre (NDF), acid detergent fibre (ADF) and short chain fatty acids (SCFA) concentrations. Proc GLM (SAS, 2009) was used to determine the effects of inclusion level of CC on physicochemical measures of digesta and size of GIT organs and means were compared using PDIFF. The sizes of visceral organs of pigs feeding diets with less than 240 g/kg DM were not different. Pigs fed on diets containing at least 240 g/kg CC diets had higher ($P < 0.001$) stomach and the colon weights, compared to the control. Water holding capacity was lowest in the stomach and highest in the caecum. From the stomach to the distal colon, the WHC of digesta was higher compared to the control diet ($P < 0.05$). The NDF, ADF and WHC of diets containing less than 240 g/kg DM of CC did not change markedly along the digesta. Propionic and acetic acid concentration was higher ($P < 0.05$) in the colon of pigs that consumed a diet based on 80 and 160 g/kg DM of CC. In conclusion, high increment levels of CC beyond 240 g/kg DM increase the size of GIT organs as well as bulkiness of digesta during transit in the gut of growing pigs.

Keywords: bulkiness, dietary fiber, water holding capacity

O29 Prediction of scaled feed intake in finishing pigs using physicochemical properties of bulky feeds.

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The objective of the present study was to determine the physicochemical properties that predict scaled feed intake (VFI) of bulky diets in finishing pigs. A total of 84 pigs weighing 65 ± 1.37 kg body weight (BW) were given, *ad libitum*, each of the 21 diets containing a basal feed diluted with 80, 160, 240, 320 and 400 g/kg of alfalfa hay, corn cob, sawdust or sunflower husks. The basal feed contained 12.3 MJ digestible energy and 160 g of CP/kg DM. Physicochemical properties of the feeds measured were dry matter (DM), crude protein (CP; g/kg DM), ether extract (g/kg DM), ash (g/kg DM), water holding capacity (WHC; g water/g DM), bulk density (g DM/ml), crude fiber (CF; g/kg DM), neutral detergent fiber (NDF; g/kg DM) and acid detergent fiber (ADF; g/kg DM). Each of the 21 diets was given to four pigs, in

individual pens, for 31 days, inclusive of a 10 d adaptation period. The feed intake and live BW were determined for each pig, every week. Mixed model procedures for repeated measures was used to analyse the dataset (SAS, Version 9.1). Stepwise regression was used to identify significant physicochemical properties that affect SFI and relationships between measured parameters were determined by the response surface option of regression (SAS, Version 9.1). Neutral detergent fiber ($R^2 = 0.86$; $P < 0.05$), CF ($R^2 = 0.76$; $P < 0.05$), CP ($R^2 = 0.75$; $P < 0.001$) and WHC affected ($R^2 =0.74$; $P<0.01$) SFI. There was a quadratic relationship between SFI and NDF given by the function SFI = 82.0 (sem 5.30) - 0.18 (SEM 0.03) NDF + 0.0002 (SEM 0.00004) NDF^2 ($P < 0.01$). The SFI was related to CF and CP by quadratic functions; SFI = 63.4 (SEM 2.22) - 0.16 (SEM 0.03) CF + 0.0003 (SEM 0.00007) CF^2 ($P <0.001$) and SFI = 61.8 (SEM 9.68) - 0.39 (SEM 0.16) CP + 0.002 (SEM 0.0006) CP^2 ($P < 0.01$), respectively. The SFI was related to WHC by linear function; SFI = 77.3 (SEM 4.37) - 7.43 (SEM 1.77) WHC ($P < 0.001$). In conclusion, although threshold values were not identified, WHC, NDF and CF content provide relationships with SFI that can be used to predict voluntary feed intake in finishing pigs.

Keywords: bulky content, dietary fiber, water holding capacity

O30 **The effects of crude glycerol dietary inclusion level on pig growth performance, carcass and meat quality.** P. L. McEwen[1,*], C. F. M. de Lange[1], I. B. Mandell[1], K. de Ridder[1], G. Simpson[2], [1]*University of Guelph, Guelph,* [2]*Hypor Inc., Regina, Canada*

Crude glycerol (CG) is a co-product from the bio-fuel industry. The feeding value of CG was examined using 120 pigs (initial BW 37.7 ± 2.5 kg), randomly assigned to one of five dietary CG treatments with 4 pens per treatment of either six barrows or gilts. Pigs were fed according to a three-phase feeding program. Diets were formulated to meet nutrient requirements according to NRC (1998). The CG was manufactured from waste vegetable oil using the Ridgetown Campus biodiesel facility and contained 70.5% DM. Dietary treatments represented 0 (Con), 2.5($CG_{2.5}$), 5(CG_5), 10(CG_{10}) or 15 (CG_{15}) % crude glycerol (90% DM basis). Pigs were slaughtered at 115 kg BW for carcass and meat quality evaluation. The ADG (kg/d) were similar (P>0.30) across treatments (1.08, 1.11, 1.07, 1.07 and 1.10 for Con to CG_{15}, respectively; SE=0.03). On a dry matter basis, feed:gain was also unaffected (P>0.30) by treatment (2.44, 2.40, 2.44, 2.51 and 2.53 for Con to CG_{15}; SE=0.07). Ultrasound fat and lean depths were similar (P>0.10) across treatments at 50 kg BW. In contrast, fat depth at 80 kg BW was lower (P<0.05) for $CG_{2.5}$ than CG_5 to CG_{15}, while lean depth was unaffected (P>0.65) by treatment. At slaughter, hot carcass weight, dressing percentage, probe back fat and loin depth, ruler loin width and length, loin eye area, amount of lean in the loin as measured by dissection, and belly flex measurements were not affected (P>0.08) by treatment. Meat quality evaluation of longissimus muscle included subjective assessment of colour (Japanese & NPPC scales), wetness and firmness, and objective measurements for pH, colour (CIE, L^* a^* b^*), drip loss, and shear force (2 and 7 day aged chops). Most meat quality measurements were not affected (P>0.08) by treatment while loin firmness was higher (P<0.02) for CG_5 than CG_{10} and CG_{15} and was less for CG_{15} than CG_{10}. Therefore crude glycerol can be an effective dietary ingredient for growing-finishing pigs without affecting carcass and meat quality.

Keywords: Crude glycerol, meat quality, pig performance

O31 **Effects of butyrate glycerides on the lipid metabolism of broilers: a mechanistic study.** J. Gong[1,*], F. Yin[1], X. Yang[1], C. Yang[1], H. Yu[1], X. Shi[2], Y. Hou[3], Y. Yin[4], S. Leeson[5], K. de Lange[5], [1]*Agriculture and Agri-Food Canada, Guelph,* [2]*the UHN/MSH Gene Profiling Facility, Mount Sinai Hospital, Toronto, Canada,* [3]*Wuhan Polytechnic University, Wuhan,* [4]*Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China,* [5]*University of Guelph, Guelph, Canada*

Butyrate plays vital roles in the animal intestinal health, including inhibition to bacterial pathogens. However, its application in animal production is limited by its offensive smell and virtual absorption in the upper digestive tract. Butyrate glycerides have no such limitations and their butyrate can be released by lipase in the small intestine, thus providing a novel delivery vehicle to the animal intestine. Our recent studies have demonstrated their moderate antimicrobial activity. In addition, dietary supplementation with 3,000 ppm butyrate glycerides has significantly improved the feed efficiency towards young broilers (up to 20 d) and chicken intestine development. More interestingly, the dietary treatment can reduce chicken body fat deposition, which closely correlates to the level of three key enzymes in the lipid metabolism in the serum and liver, jejunum, and abdominal adipose tissues. The mRNA-Seq analysis has identified 229 and 84 differentially-expressed genes in the jejunum and liver, respectively, between treated and untreated birds. The Integrity Pathway Analysis has revealed the involvement of these genes mainly in thelipid metabolism, molecular transport, and small molecular biochemistry. In particular, the PPARα pathway is the major one affected by the dietary treatment. Our data support the application of butyrate glycerides as a feed additive, particularly as an alternative to dietary antibiotics, for chicken production although further studies are required.

Keywords: Broilers, Butyrate glycerides, Intestine, Lipid metabolism, PPARα pathway

O32 **Whole body retention of 18:3n-3 and apparent conversion of 18:3n-3 to n-3 highly unsaturated fatty acids in pigs fed flaxseed or fish oil diets.** H. R. Martínez-Ramírez[1,*], J. K. Kramer[2], C. F. de Lange[1], [1]*Animal and Poultry Science, University of Guelph,* [2]*Agriculture and Agri-Food Canada, Guelph, Canada, Guelph, Canada*

A total of 56 pigs (4 barrows and 4 gilts per treatment, Landrace×Yorkshire×Duroc) were used in a serial slaughter study to determine the whole body retention efficiency (**RE**) of 18:3n-3 and the apparent conversion (**AC**) of 18:3n-3 to HUFAs (18:4n-3, 20:3n-3, 20:4n-3, 20:5n-3, 22:5n-3, 22:6n-3) in pigs fed either flaxseed (**FS**) or fish oil (**FO**) containing diets over three different time periods (**G**, **F**, or **C**; 25-65, 85-120 or 25-120 kg BW, respectively), yielding six treatments. A 7th treatment, a diet free of FS and FO served as control (**CON**). Eight pigs were slaughtered at 25 kg BW to determine initial body composition. Empty BW (i.e., carcass plus viscera) was analyzed at 25 and 120 kg BW for fatty acid (**FA**) content. Within FS or FO treatments, cumulative n-3 PUFA intakes were similar across treatments ($P>0.10$; 7 and 2 kg of FS and FO, respectively). Growth performance and carcass characteristics were not influenced by dietary treatments ($P>0.10$). The content (mg/100 g empty BW) of the sum of n-3 PUFA was independent of FS treatments ($P>0.10$; 1112, 1231, 1057 for FSG, FSF, and FSC; respectively), higher ($P<0.001$) than FO treatments (620, 647, 635 for FOG, FOF, and FOC, respectively), and the lowest for CON (212). Expressed as a proportion of 18:3n-3 intake, RE of 18:3n-3 was similar for FSG, FSF, FSC, FOC, and CON ($P>0.10$; 60, 75, 68, 60, and 71%, respectively) and lower ($P<0.05$) than FOG and FOF (88 and 90%, respectively). Pigs fed FS had a lower n-6:n-3 PUFA ratio than FO ($P<0.05$; 2.6 vs. 4.4); both were lower than CON ($P<0.001$; 13). The AC of 18:3n-3 to sum of 20:5n-3 and 22:6n-3 was similar for FSG, FSF, FSC, and CON ($P>0.10$; 1.3, 1.1, 1.4, 1.8%, respectively), whereas no detectable AC of these FA were observed for FO treatments. These results suggest that the content of n-3 PUFA from FS and FO reflects both the amount and type of FA deposited in the pig`s body. Within FS and FO treatments, the n-3 PUFA content and AC to n-3 HUFA was independent of BW, which provides flexibility as to when n-3 PUFA can be fed to produce n-3 PUFA enriched pork.

Keywords: apparent conversion, n-3 PUFA, pigs

O33 **Influence of physicochemical properties of fibrous diets on behavioural reactions of individually housed pigs.** A. G. bakare, P. S. Ndou, M. Chimonyo[*], *Animal and Poultry Science, University of KwaZulu-Natal, Pietermaritzburg, South Africa*

The objective of the study was to predict time spent on different behavioural activities of individually housed growing pigs from physicochemical properties of feeds. Maize cob, maize stover, sunflower hulls, veld grass, sawdust and lucerne were used to provide a wide range of physicochemical properties. The fibre sources were included at 0, 80, 160, 240, 320, 400 g/kg inclusion levels in pig diets. Time spent eating, drinking, lying down, sitting/standing and other activities was observed using video cameras. Pigs spent most of their time lying down (71.4 %) followed by time spent eating (23 %), drinking (3.2 %) and sitting/standing (2.4 %). Bulk density (BD), acid detergent fibre (ADF) and water holding capacity (WHC) were the most important variables for predicting time spent on different behavioural activities ($P < 0.001$). Bulk density and ADF produced linear responses with time spent eating and drinking ($P < 0.001$). There was a quadratic response between time spent lying down and ADF content of feed ($P < 0.001$). Water holding capacity was the most important physicochemical property of feeds for predicting number of visits made by the pig to the feeder. Total time spent on each visit by a pig per day was best predicted by ADF. In conclusion, physicochemical properties of diets alter behaviour of caged growing pigs.

Keywords: Dietary fibre; Feeding Behaviour; Growing Pigs

Ruminant Production and Management

O34 **The Interaction Between Cow Nutrition and Neonatal Calf Health**. G.P. Lardy and G.L. Stokka, *Department of Animal Sciences, North Dakota State University, Fargo, ND*

Cow production costs continue to increase and costs related to nutrition (including harvested and grazed forages) account for 60 to 70% of the total production costs in cow herds in North America. We also know that nutrition plays a critical role in animal health. In the beef industry in North America, millions of dollars are spent annually treating diseases which have interactions with nutrition (or improper nutrition as the case may be). Recently, more research has been conducted which indicates in utero nutrition has impacts on the developing offspring which continue long after the offspring are born. This phenomenon is referred to as developmental programming. This may be further defined as the process through which a stimulus or insult establishes a permanent response. Developmental programming has been studied in humans and in a variety of animal species. There is some data in beef cattle, but the relatively long gestation length and long generation interval make long term studies very costly and more difficult to conduct. In beef cattle, gestational nutrition programs affect cow body condition score at calving, subsequent reproductive performance (including the percentage of cows cycling at the initiation of the breeding season, pregnancy rates, and calving percentages). Gestational nutrition also has impacts on calf vigor, immunoglobulin concentration and absorption, and subsequent calf health. In recent work conducted in Nebraska, calf growth, carcass traits, and subsequent reproduction of heifer calves was affected when their dams received gestational protein supplementation. Additional work is needed to further investigate the underlying mechanisms by which these effects occur and how they might be managed to improve productivity and profitability of beef cattle operations.

O35 **Adaptation and Recovery of the Ruminal Epithelium.** G. B. Penner[1,*], J. R. Aschenbach[2], [1]Animal and Poultry Science, *University of Saskatchewan, Saskatoon, Canada,* [2]*Veterinary Physiology, Free University of Berlin, Berlin, Germany*

There is no doubt that the rumen epithelium plays a critical role to facilitate mineral and nutrient absorption, secretion of bicarbonate and urea, and as a barrier preventing the translocation of antigens and pathogens from the ruminal contents into systemic circulation. Moreover, it is clear that the fermentability of the diet influences the above-mentioned functions. Past studies have largely focused on strategies to adapt the rumen epithelium to enhance absorptive capability focusing on proliferation of the rumen papillae but have not comprehensively established the timeline for these responses. Recent studies have demonstrated that the adaptive response includes functional changes at the cellular level in addition to the traditionally measured hypertrophic and hyperplasic responses. In fact, large increases in short-chain fatty acid (SCFA) absorption occur within 7 d of dietary change, as do increases for the net absorption of Na^+. Corresponding to an increase in the net absorption of Na^+, increases in the mRNA abundance of Na^+/H^+ exchangers have been reported. Secretory processes also adapt rapidly including marked increases in urea secretion when low protein diets are fed following a period of being fed high protein diets. While the adaptive response has largely been investigated from a proliferation standpoint, it should be acknowledged that adaptation also represents regression of epithelial function. For example, short-term feed restriction and induction of ruminal acidosis both act to acutely reduce SCFA absorption across the reticulo-rumen. Barrier function of the total tract is also compromised with severe short-term feed restriction and complete feed deprivation. Currently available data indicates that recovery of epithelial function from nutritional insults (feed restriction and rumen acidosis) is dependent on the severity of the insult itself and functionality of the rumen epithelium prior to the insult.

Keywords: Adaptation, Barrier function, Rumen epithelium, Short-chain fatty acid absorption

O36 **Effect of rested grazing and alfalfa inclusion in bromegrass pastures on cow-calf productivity.** H. C. Block[1,*], O. N. Durunna[1], C. D. Robins[2], M. H. Entz[3], M. Khakbazan[1], S. L. Scott[4], [1]*Brandon Research Centre, Agriculture and Agri-Food Canada,* [2]*Manitoba 4H Council, Brandon,* [3]*Department of Plant Science, University of Manitoba, Winnipeg,* [4]*Alberta Livestock and Meat Agency, Edmonton, Canada*

A six-year randomized complete block grazing study used 224 cow-calf pairs and 40 paddocks per year to evaluate conventional vs. rested grazing and alfalfa inclusion in bromegrass pastures on cow-calf production. Experimental units consisted of 28 cow-calf pairs, four perennial paddocks (4.61 ± 0.29 ha) for rotational grazing and one annual (alternating oat and barley) paddock (4.79 ± 0.31 ha) for swath-grazing. Grazing occurred in three phases. Phase 1 (June-July) involved five grazing events in each experimental unit with no separation of conventional and rested grazing groups. Phase 2 (August-September) consisted of an additional four grazing events for conventional grazing and early-seeded swath-grazing, to avoid perennial grazing during the critical pre-frost period, for rested groups. For Phase 3 (October-December), conventional grazing groups were on late-seeded swath-grazing and rested grazing groups on perennial pastures. Weaning occurred at the end of Phase 2. Cow and calf weights and cow body condition scores were collected at the start and end of each phase. Animal unit days per ha were determined from average cow and calf weight in each phase and paddock areas. All data were evaluated using the mixed models procedure of SAS with year as a repeated measure. There was a grazing treatment by year interaction ($P<0.01$) for total AUD per ha where the rested grazing was greater ($P<0.01$) in four years, there was no grazing effect ($P=0.67$) in one year, and conventional grazing was greater ($P<0.01$) in one year. There was also a forage by year interaction ($P=0.03$) where AUD per ha increased ($P<0.01$) with rested grazing regardless of forage, but forages only differed ($P=0.03$) when rested grazing occurred. However, the grazing treatment by year interaction ($P=0.01$) for combined cow and calf weight gain per ha had greater ($P\leq0.01$) gain per ha in four years for conventional than rested grazing, and no difference ($P=0.16$ to 0.81) in two years. The greater grazing yield of rested grazing treatment was offset by lower cattle weight gains indicating optimal grazing system selection is dependent upon additional economic and management considerations.

Keywords: Alfalfa, Beef cattle, Bromegrass, Rested grazing, Swath grazing

O37 Effect of harvest maturity and crop on forage yield and the productivity weaned beef calves strip-grazing annual swaths.

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A 56-d (August-October) randomized complete block factorial swath-grazing study evaluated the effect of crop (Desperado barley vs. Souris oat) and early (head emergence) vs. late (barley at soft dough; oat at late milk) harvest on forage yield and productivity using 4.5-month old weaned beef calves (n=160, 189 ± 25 kg) and 16 paddocks (1.85 ha). Experimental units (one paddock and ten calves) were blocked in groups of four to account for land gradient, calf gender and weight. Seeding was from 10 to 14 May. Quadrat (0.25 m^2) clippings were collected just prior to swathing for initial crop yield and just prior to strip grazing advances for regrowth. Calves were weighed twice on and off trial, and every two weeks during grazing. Ultrasound backfat was measured at the start, mid-point, and end of the grazing study. Calves were supplemented with ground barley grain and soybean meal to equalize estimated total protein intake (based on initial swath protein content and expected intake) and supplement energy intake. Animal unit days were calculated using average calf weight and actual grazed paddock area. All data were analyzed with the mixed models procedure of SAS. Harvest was 3 July (early barley), 5 July (early oat), and 20 July (late barley and oat). There was a crop by harvest interaction (P=0.01) for the combined initial swath and regrowth yield per ha with early barley being deficient (P<0.01) relative to early oat or late barley. There were more (P=0.04) animal unit days per ha for late than early harvest and no effect (P=0.46) of crop. Animal gain per ha and per day was subject to a crop by harvest interaction (P<0.01) with early barley being deficient (P<0.01) relative to early oat or late barley. Ultrasound backfat loss was subject to a crop by harvest interaction (P=0.01) with calves on late swathed barley retaining more (P<0.01 to 0.04) backfat. These results suggest unsupplemented swath-grazing is insufficient to maintain calf condition and that although later harvest increases weaned calf productivity, the potential impact of regrowth on overall forage yield and quality need consideration with early season swath-grazing.

Keywords: Barley, Beef calves, Harvest maturity, Oat, Swath grazing

O38 Milk fatty acid profile of organic dairy farms in Ontario.

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The objective was to compare seasonal differences in feed and milk fatty acid (FA) profiles from organic (Org) and conventional (Con) dairy systems in ON. Milk from the bulk tank and the major forage fed to cows were sampled Sept. to Nov. 2011 (F) and April to May 2012 (S) from 12 Org and 24 Con farms which employed a variety of management systems. Only farms with complete data for feed and milk in both seasons were used. Feed composition was determined at the SGS AgriFood Laboratory (Guelph, ON). Bulk milk and feed samples were sent to Dalhousie University for FA analysis. Variation in feed composition was largely due to the wide range in feeds used within and across systems. Dry matter (DM) and crude protein (CP) content of feed averaged 43.50 and 14.32% of DM. Forage content (% of total FAs) of alpha-linolenic acid (ALA) was decreased in the following order (P<0.05): Org -F (25.8±4.0), Con -F (8.6±4.5), Org -S (5.7±3.2), Con -S (3.70±1.36). The ALA content in forages was typical of values of fresh forage compared with those of corn and prolonged feed storage. There was a season x system interaction (P<0.05) for milk content (% of total FAs) of rumenic acid (RA) and vaccenic acid (VA), which were highest (P<0.05) in Org-F milk (5.19, 0.68 and 1.79) compared with Org-S milk (4.09, 0.45 and 0.91), and Con-F (4.33, 0.45 and 0.90) or Con-S (4.51, 0.47 and 0.89). Org milk had a higher (P<0.05) content of stearic acid (10.94 vs. 9.82) and ALA (0.88 vs. 0.57) compared with Con while level of atherogenic saturated FAs (ASFA; 12:0, 14:0 and 16:0) was reduced (P<0.05) for Org compared with Con (49.8 vs. 47.8 % of milk FA). Differences in milk FA profile between Org and Con were small. However, since Org milk contained more of the beneficial FAs (VA, RA and ALA) and less ASFA we concluded that milk during fall and spring from Org farms was more healthful than that of Con and related to differences in the main forage fed.

Keywords: conventional, dairy, fatty acid, milk, organic

Food Safety and Meat Science

O39 Improving food safety in the live animal.

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Food animals are colonized by a complex microbiome within their gastrointestinal tract and skin/hide which can be penetrated by foodborne pathogenic bacteria, such as *Salmonella*, *Campylobacter* and enterohemorrhagic *E. coli* (EHEC). These pathogens pose a significant threat to human consumers directly through contaminated foods and indirectly through alternative transmission routes such as water and contaminated crops. In-plant pathogen-reduction strategies (e.g., carcass rinses) have been successful at reducing direct foodborne illness from meat products, but have not eliminated foodborne illnesses from foods or environmental contamination. Because foodborne pathogenic can be found on the farm and in live animals, pathogen reduction strategies for use in live food animals are viable adjuncts to public health improvement. Modeling studies have indicated that pre-harvest reduction of pathogens could have the greatest impact on human illnesses. Thus recent years have seen the development of a variety of live animal treatments to improve food safety. In general, these can be broken down into strategies that: 1) utilize the native microbiome, or an introduced microorganism to exclude or "push out" pathogens (e.g., probiotics, prebiotics, DFM); 2) utilize direct action against the pathogen (e.g., antimicrobials, phage, sodium chlorate); 3) harness the immune system (e.g., vaccination, specific immune proteins); and 4) focus management strategies on reducing horizontal and vertical spread of pathogens. The wide variety of strategies being investigated will be discussed, including limitations of use and mechanisms of action. Economic feasibility of implementation of strategies will also be discussed. While complete elimination of foodborne pathogens from the environment is not possible, the animal industry is presented with an array of near- or in-market strategies that can reduce foodborne pathogenic bacterial carriage and shedding in food animals.

Keywords: food safety

O40 Modern Technology: current and possible future applications in the pork industry.

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The 'modern' in 'modern technology' is constantly changing. Techniques that were once new are now taken for granted or have been replaced by more recent ones. Centuries ago, new technology could have meant a mechanical way of keeping track of the time of day, or of measuring temperature. Today, new technology is usually heavily computer-dependent and often offers an increase in recording speed, and in measurement sensitivity or depth. These new technologies are often developed in and by other fields of study, then adopted and adapted to suit specific aspects of pork production. Ultrasound for live animal or hot carcass fat measurements, for example, was adopted from human medicine, and the equipment adapted for on-farm and on-line use. More recently the old technology of reflectance spectroscopy has been combined with the newer technology of digital imaging to create hyperspectral imaging. This was developed for remote sensing in the field of Earth Sciences but has been successfully applied to detection of marbling in pork. Some of the most recent advances in technology include extreme miniaturization of mechanical components, very fine control of tools, and equipment which was once restricted to benchtop use being made portable. With understanding of the components of meat or fat and their properties, and of the underlying principles and limits of new technologies, new pairings to quickly and accurately answer specific questions to meet industry needs can become possible.

O41 Variable efficacy of a vaccine and direct-fed microbial for controlling Escherichia coli O157:H7 in feces and on hides of feedlot cattle.

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To evaluate efficacy of a type-III secreted protein vaccine and a *Lactobacillus-acidophilus*-based direct-fed microbial for controlling *E. coli* O157:H7, feces from cattle were screened for *E. coli* O157:H7 prior to allocating animals (n=864) to one of three experimental groups: **DFM**, fed standard finishing diet containing 10^9 CFU/animal/day direct-fed microbial; **VAC**, fed standard finishing diet and given a 2 ml intramuscular injection of vaccine at allocation and 28 days later; or **CON**, fed standard finishing diet only. Experimental groups were balanced by initial levels of *E. coli* O157:H7, with 30 pens allocated June 15, 2011 (allocation set 1, AS1), 18 pens allocated June 28, 2011 (allocation set 2, AS2) and 18 cattle per pen. All cattle had rectal fecal samples collected at 28 day intervals until slaughter (103 to 145 days on trial). In addition, a subset of cattle had perineal swabs collected at 28 day intervals until shipment to slaughter. Number of fecal samples with enumerable *E. coli* O157:H7 ($\geq$ 1.6 CFU/g feces) was reduced in AS1 and AS2 by VAC (*P* =0.008), although VAC and DFM had no impact on numbers of *E. coli* O157:H7 shed by cattle positive for the organism. For AS1, VAC reduced (*P* =0.02) detection of *E. coli* O157:H7 throughout the study, with an efficacy of 55.2% during the feeding period, and 72.1% at shipment to slaughter. In contrast, incidence of *E. coli* O157:H7 in AS2 was similar for VAC and CON. During the feeding period in AS1, DFM reduced detection of *E. coli* O157:H7 in perineal swabs (P=0.01) compared to CON , although increased *E. coli* O157:H7 was detected ($P = 0.03$) in both perineal swabs and feces of DFM-fed AS2 cattle. Differences in efficacy for controlling *E. coli* O157:H7 among allocation sets may be a reflection of differing feedlot origins of animals and a two week difference in sample collection dates. Of the two interventions, VAC shows the most potential for pre-harvest control of *E. coli* O157:H7, but due to the variable efficacy of DFM and VAC in this and other studies, additional product development to ensure more consistent control of *E. coli* O157:H7 would be welcomed.

Keywords: E. coli O157:H7, vaccine, direct-fed microbial, cattle, feedlot

O42 **Effect Of Forms Of Feed On Performance And Carcass Characteristics Of Broiler Chickens.** A. O. Onakomaiya[*], O. S. Akinola, *Animal Production and Health, Federal University Of Agriculture Abeokuta, Nigeria, Abeokuta, Nigeria*

The aim of this experiment was to compare the effect of dry, wet and fermented feed on the performance and carcass characteristics of broiler chicks. Three experimental diets were used in the study. Diet 1, was conventional dry mash. Diet 2 was conventional mash in a 1:1.3 dilution with water. Diet 3, was conventional mash in a 1: 1.3 dilution with water and fermented for 24 hours. 20- day old Marshal strain of broiler chicks were randomly assigned to the experimental diets in a completely randomized design (CRD). Each treatment group was replicated four times with 16 birds per replicate. Results showed that final weight, were significantly higher ($P<0.05$) in birds fed fermented and wet mash compared to dry mash. Birds fed fermented and wet mash had significantly ($P<0.05$) higher total weight gain than those fed dry mash. Birds receiving fermented and wet mash showed significantly ($P<0.05$) superior weight gain over the group fed dry mash. There was significant ($P<0.05$) difference between the birds fed fermented and wet mash in the gizzard. The results also indicated that the treatments had significant ($P < 0.05$) differences on the abdominal fat of the birds with fermented and wet mash having superior abdominal fat than dry mash. The results of this experiment showed that feeding fermented and wet mash improved the performance of the broiler chickens.

Keywords: carcass, broiler chickens, fermented feeding, performance, wet feeding

O43 **Sensory qualities of pork from Large White and Windsnyer gilts prepared by different cooking methods.** J. Madzimure[1,*], M. Chimonyo[2], V. Muchenje[3], [1]*Animal Production and Technology, Chinhoyi University of Technology, Chinhoyi, Zimbabwe,* [2]*Discipline of Animal and Poultry Science, University of KwaZulu-Natal, Pietermaritzburg,* [3]*Department of Livestock and Pasture Science, University of Fort Hare, Alice, South Africa*

The objectives of the current study were to determine sensory characteristics of Large White and Windsnyer gilts' pork cooked by either microwaving or boiling. Pork from 12 pigs of each breed (aged 21 weeks) was served to a semi-trained panel of 66 participants. Windsnyer pork had higher ($P < 0.05$) scores on initial and sustained impression of juiciness than Large White pork. Microwaved pork had higher ($P < 0.05$) scores for aroma, first bite impression, sustained juiciness, and the amount of connective tissue, fibre and overall flavour intensity when compared to boiled pork. Most sensory attributes were positively correlated ($P < 0.05$) to each other with higher coefficients being found in microwaved Windsnyer pork than in microwaved Large White pork. Gender affected sensory attributes with female consumers giving higher scores than male consumers for aroma intensity, initial impression of juiciness and a-typical flavour. The results may suggest that Windsnyer pork cooked by microwave method could be more acceptable to consumers than Large White pork.

Keywords: Aroma, Flavour, Juiciness, Pork quality, Tenderness

O44 **The Phenomic Challenge – Integrating performance, carcass and meat quality data with genomics.** J. Aalhus[1,*], J. Basarab[2,3], I. Larsen[1], O. López-Campos[1,3], M. Dugan[1], N. Prieto[1,4], B. Uttaro[1], A. Schaefer[1], N. Cook[5], G. Plastow[3,4], C. Li[1,3,4], C. Calkins[6], M. Juárez[1], [1]*Lacombe Research Centre, Agriculture & Agri-Food Canada,* [2]*Livestock Research Branch, Alberta Agriculture & Rural Development, Lacombe, AB,* [3]*Livestock Gentec,* [4]*Department of Agricultural, Food & Nutritional Sciences, University of Alberta, Edmonton, AB,* [5]*Livestock Welfare Unit, Alberta Agriculture & Rural Development, Lacombe, AB, Canada,* [6]*Goldfinch Solutions LLC, Lincoln NE, United States*

Over the past 15 years, the development of molecular genomic technologies has been rapid and has outpaced the development of accelerated technologies to assess the phenotypic characteristics of livestock. In particular, traits of economic importance such as performance, carcass composition and meat quality (e.g. tenderness, fatty acid composition) are complex traits and their measurement requires significant knowledge and/or control of environmental influences along the value chain (e.g. biotype, diet, pre-slaughter management, *post-mortem* temperature, storage, cooking method, etc.). Most research methods to measure these characteristics were developed with a high level of accuracy and precision that was necessary to find differences when experimental power was limited by numbers of animals. Some success has been had by using these traditional methods of evaluation, however infrastructure, manpower and time constraints have limited these databases to thousands of samples evaluated over multiple years, rather than the tens of thousands evaluated in the same timeframe through genomic technologies. However, during this time, researchers at AAFC-Lacombe have been focusing their efforts on developing rapid analytical methods and sophisticated database management to improve the speed of phenotypic data collection and accessibility. While some loss in accuracy is inevitable, the methods show reasonable precision and the increase in statistical power through evaluation of increased numbers maintains statistical validity. In the future we hope to integrate the use of these technologies into genomics research and begin to integrate their use into large industry databases such as the Beef Information Exchange system (BIXS).

Keywords: Phenomics, new technologies, performance, carcass composition, meat quality

O45 **Extended storage reduces n-3 PUFA content in trimmed pork loins and bellies.** H. R. Martínez-Ramírez[1,*], J. K. Kramer[2], C. F. de Lange[1], [1]*Animal and Poultry Science, University of Guelph,* [2]*Agriculture and Agri-Food Canada, Guelph, Canada*

Rancidity and peroxidation of fatty acids (**FA**) in pork products may reduce the content of n-3 PUFA and affect functional food attributes. The aim of this study was to determine the effect of extended storage on content of n-3 PUFA in ground trimmed loins (**LO**) and bellies (**BE**). A total of 56 pigs (4 barrows and 4 gilts per treatment, Landrace×Yorkshire×Duroc) were fed either flaxseed (**FS**) or fish oil (**FO**) containing diets during three different time periods (**G**, **F**, or **C**; 25-65, 85-120 or 25-120 kg BW, respectively), resulting in six treatments. A 7th treatment consisted of a diet free of FS and FO that served as control. The LO and BE were stored at – 20°C immediately after slaughter. Crude fat was extracted from LO and BE at 7 and 180 d of storage. Stability of fat and FAs was expressed as the percentage change in content within DM during storage. The cumulative n-3 PUFA intake was similar within the FS and FO treatments (*P*>0.10; 7 and 2 kg/pig of FS and FO, respectively). Within FS and FO treatments, crude fat content in BE did not change during storage (*P*>0.10; -1.20 and 1.47%, respectively), whereas crude fat content in LO tended to decrease (*P*<0.10) during storage for FS (6.99%) but not for FO (4.77%) treatments. Regardless of source and the time of feeding n-3 PUFA, total content of FAs decreased during storage (*P*<0.001; 61.0 and 29.4% for BE and LO, respectively). This coincided with reductions (*P*<0.001) in content of n-3 PUFA (64.9 and 38.5%) and n-6 PUFA (61.0 and 28.7%) in BE and LO, respectively. Extended storage reduces contents of FA in pork products, which may be attributed to peroxidation reactions and will influence functional food attributes, and possibly consumer acceptance, of pork.

Keywords: n-3 PUFA, peroxidation, pigs

Breeding and Genetics

O46 **Improvement of tenderness in Canadian Beef through genomics.** S. P. Miller[1,2,3,*], G. VanderVoort[1], B. D. Lu[1], I. B. Mandell[4], J. E. Squires[4], J. A. Basarab[5], J. L. Aalhus[6], C. Li[6], P. Stothard[2], Z. Wang[2], G. S. Plastow[2], S. S. Moore[3], [1]*Centre for the Genetic Improvement of Livestock, University of Guelph, Guelph,* [2]*Livestock Gentec, University of Alberta, Edmonton, Canada,* [3]*Centre for Animal Science, University of Queensland, Brisbane, Australia,* [4]*Animal and Poultry Science, University of Guelph, Guelph,* [5]*Lacombe Research Station, Alberta Agriculture and Rural Development,* [6]*Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, Canada*

Genomic selection refers to the use of dense marker panels to estimate breeding values of selection candidates, particularly for traits of economic importance, which are difficult to record. Selection criteria accuracy is important to maximize genetic response. The objective of this study was to measure the accuracy of genomic prediction with a high-density SNP panel. Phenotypic measurements were Warner-Bratzler shear force of the *longissimus dorsi* muscle seven days post mortem (LM7D) on 1395 crossbred cattle. The observed mean was 5.3 ± 0.09 kg for data ranging from 2.35 kg to 9.4 kg based on six 1.27 cm cores. For each LM7D record an animal model was fitted to estimate breeding values (EBV). EBV were then de-regressed. Genotype data were imputed using FImpute 2.2 to a panel containing the Affymetrixâ BOS1 High-Density markers added with 3871 custom SNP markers, previously evaluated for tenderness for a combined panel of 643,806 single nucleotide polymorphisms (SNP). The overall average imputation accuracy obtained was 95.2%. Genotype data were converted to AB format and subsequently coded as 0,1,2. A subset of 960 crossbred cattle with both genotype and de-regressed EBV were divided into training (860 from University of Guelph research herd) and validation (100 purchased cattle) datasets. Genomic breeding value (GBV) estimates were calculated using Kernel Partial Least Squares (KPLS) and GBLUP algorithms. Division of data was performed to minimize pedigree influence on breeding value prediction in the validation data.

Observed correlations of de-regressed EBV and their predicted values in validation data were 0.65 and 0.61 for KPLS and GBLUP, respectively. There was close agreement with the two methods. This level of correlation indicated the panel could be used effectively for selection, although further validation is required before industry adoption.

Keywords: Genetic Selection, Meat quality

O47 **Effects of within-litter birth weight variation of piglets on performance at three weeks of age and at weaning in a Large White × Landrace sow herd.** T. J. Zindove[1,*], E. F. Dzomba[2], A. T. Kanengoni[3], M. Chimonyo[1], [1]*Animal and Poultry Science,* [2]*Genetics, University of KwaZulu-Natal, Pietermaritzburg,* [3]*Animal Production Institute, ARC, Irene, South Africa*

The effect of piglet birth weight variation on subsequent weight variations and litter performance in Large White x Landrace sows is not well understood. The objective of the current study was to determine the relationship between within-litter birth weight coefficient of variation (CVB) and performance of piglets at three weeks and at weaning. A total of 1,836 litter records from 746 sows, collected between January 1998 and September 2010 at the Agricultural Research Council (ARC), Irene, were used. The PROC REG (SAS, 2008) was used to test the relationship between CVB and within-litter weight coefficient of variation at three weeks (CV3), survival at three weeks (SURV3), mean litter weight at three weeks (MWt3), litter weight at three weeks (LWt3), within-litter weaning weight coefficient of variation (CVW), percent survival to weaning (SURVW), mean weaning weight (MWWT) and litter weight at weaning (LWWT). The CVB had a linear relationship withSURV3 (b = -0.20; $P < 0.05$) and CV3 (b = 0.50; $P < 0.05$). Litters with high CVB had more deaths at three weeks ($P < 0.05$). Increase of CV3 with CVB varied with parity ($P < 0.05$). The rate of increase of CV3 with CVB was highest in Parity 1 (b = 0.41) followed by Parity 2 (b = 0.36) then middle aged (Parity 3-5) sows (b = 0.32). There was no significant relationship between CVB and LWt3 or MWt3 ($P > 0.05$). Weight variation at weaning was positively skewed (skewness value of 0.81). The SURV3 ranged from 13.3 to 100 % with a mean of 87.6 %. The CVB had a linear relationship with both CVW (b = 0.50; $P < 0.05$) and SURVW (b = – 0.04; $P < 0.05$). There was an unfavorable positive relationship between CVB with both CVW and SURVW. It can be concluded that litter performance at weaning is related to CVB.

Keywords: Coefficient of variation, Parity, Piglets, Survivability

O48 **Preadjustment of Body Weight Growth and Ultrasound Body Tissue Development Traits and Genetic Parameters in Three Seedstock Pig Breed populations in Korea.** Y. H. Choy[*], J. G. Choi, Y. L. Choi, A. Mahboob, *Animal Breeding & Genetics, National Institute of Animal Science, Chonan, Republic of Korea*

This study was conducted to compare the effects of body weight growth adjustment methods on genetic parameters of body growth and tissue by three different models. Performance data with pedigree information collected from swine breeder farms in Korea were collected. Performance data collected were body weights on test day and ultrasound measures of backfat thickness (**BF**), rib eye area (**EMA**) and retail cut percentage (**RCP**). Breeds were Landrace, Yorkshire and Duroc. Days to 90kg body weight (**DAYS90**) were estimated with linear function of age and ADG calculated from body weight on test day. Preadjusted BF and EMA and RCP (**ABF, AEMA, ARCP**) were calculated with formula of Korean Swine Performance Recording Standards (KSPRS). Number of performance records after censoring and keeping records of pigs born from year 2000 were of 78,068 Duroc, 101,820 Landrace and 281,411 Yorkshire pigs. Models included contemporary groups defined by herd-year-season of birth and the effect of sex for all traits. In Model I, DAYS90 and ultrasound measures of BF, EMA and RCP without preadjustment were fit with final weight at the test day as linear covariates. Model II fit DAYS90 and preadjusted ultrasound measures (ABF, AEMA and ARCP) with contemporary group effects and linear covariates of final weight. And Model III fit DAYS90 and preadjusted ultrasound measures with contemporary group effect but without any linear covariates. REML estimation was processed with REMLF90 program. Heritability estimates were 0.42, 0.43, 0.22 0.45 for **DAYS90**, **BF**, **EMA**, **RCP**, respectively for Landrace population from Model I. Those estimates were little different for the other two breeds from all three different models. Noticeable differences by models were found in genetic and environmental correlation structure between DAYS90 and ultrasound measure traits. Genetic (environmental) correlation coefficients between DAYS90 and BF of three breeds were in the ranges of -0.29~-0.38 (-0.35~-0.36) in Model I. However, those between DAYS and ABF in Model II and Model III were in the ranges of -0.04~-0.11 (-0.02~-0.07) and 0.01~0.08 (0.06~0.12), respectively.

Keywords: Pig, Genetic Parameter, Growth, Ultrasound

O49 **Gene expression patterns in spleen of mink inoculated with the Aleutian mink disease virus.**

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Aleutian mink disease virus (AMDV) is a global problem for the mink industry. There is no vaccine or a treatment for this disease and little information is available on the underlying mechanisms of the host response during the early stages of AMDV infection. The objective of this study was to investigate the effects of inoculation of mink with AMDV on the expression of genes in the spleen during the early phase after inoculation. Four full-sib black male mink from each of three families were used. Three mink from each family were sedated and inoculated intra-nasally with a spleen homogenate containing a local strain of AMDV. One mink from each family was euthanized on days 1, 2 and 7 post-inoculation (pi) and its spleen was aseptically harvested into tubes containing RNAlater®. One mink from each family was not inoculated (naïve control), and sampled on day 0. Libraries were prepared from total RNA using the Illumina TruSeq™ RNA kit, and were sequenced using HiScanSQ, producing 100 bp reads from each end. A total of 1,008,653,162 paired-end reads were generated from the 12 animals, ranging from 59.7 M to 174.9 M reads per sample. The reads were aligned to the dog genome, the closest species to the mink with complete genome sequence, using the Burrows-Wheeler Aligner method. Only 8.27% of the reads were aligned to exons of 15,962 genes of the dog genome with coverage depths of up to 948,248 reads. Compared with naïve controls (t-test), 460, 563 and 94 of the mapped genes were up-regulated and 21, 22 and 26 genes were down regulated ($P<0.05$, fold change ≥ 2) on days 1, 2 and 7 pi, respectively. The level of expression of four of the up-regulated genes remained at least 2 fold higher than that of the controls on all sampling occasions after inoculation. The DC38 gene had the greatest fold increase of 4.3, 6.3 and 5.9 in days 1, 2 and 7 pi, respectively, followed by the Integrin alpha-D (ITGAD) gene with 3.5, 2.7 and 3.8 fold increase in expression. An elevated level of the DC38 seems to be a common response of host to infection with many viruses.

Keywords: Aleutian mink disease virus, Gene expression, Mink, Next generation sequencing

O50 **Genomic prediction for residual feed intake and carcass merit traits in Angus and Charolais beef cattle.**

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Accuracies of predicting genomic breeding values (GEBV) for residual feed intake (RFI) and carcass merit traits were investigated based on 522 Angus and 395 Charolais steers genotyped on single nucleotide polymorphisms (SNP) with the Illumina Bovine SNP50 Beadchip. Three training population forming strategies of within breed, across breed, and pooling data from the two breeds were used to estimate SNP effects for genomic prediction. The results showed that the accuracy of the GEBV prediction was the highest when the prediction was within breed and when the validation population had greater genetic relationships with the training population, with a maximum of 0.58 for Angus and 0.64 for Charolais for RFI and 0.17 to 0.64 for carcass merit traits. The within breed prediction accuracies dropped to 0.29 and 0.38 for RFI and 0.26 to 0.43 for carcass merit traits in the Angus and Charolais populations, respectively, when the validation populations had a minimal pedigree link with the training population. When the training population of a different breed was used to predict the GEBV of the validation population, i.e., across breed genomic prediction, the accuracies were further reduced to 0.10 to 0.22 for RFI and near 0 to 0.10 for carcass merit traits, depending on the prediction method used. Pooling data from the two breeds to form the training population resulted in accuracies increased to 0.31 and 0.43 for RFI and 0.22 to 0.40 for carcass merit traits, respectively, for the Angus and Charolais validation populations. The results suggest that the genetic relationship of selection candidates with the training population has a greater impact on the accuracy of GEBV using the Illumina Bovine SNP50 Beadchip. Pooling data from different breeds to form the training population will improve the accuracy of across breed genomic prediction for RFI and carcass merit traits in beef cattle.

Keywords: beef cattle, SNP, genomic prediction, residual feed intake, carcass merit traits

POSTER PRESENTATIONS

Animal Health and Behaviour

P01 **Non Invasive Surveillance of Bovine Respiratory Disease Using Infrared.** A. Schaefer[1,*], C. Bench[2], N. Cook[3], K. Wynne-Edwards[4], M. Jelinski[5], R. Lewis[6], R. McCorkell[7], [1]*Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe,* [2]*AFNS, University of ALberta, Edmonton,* [3]*Lacombe Research Centre, Alberta Agriculture, Lacombe,* [4]*Vet Med, University ot Calgary, Calgary,* [5]*Vet Agri-Health, Airdrie,* [6]*Westlock Vet, Westlock,* [7]*Vet Med, University of Calgary, Calgary, Canada*

Bovine respiratory disease (BRD) is an economic and welfare challenge for the beef industry. The early detection and treatment of cattle at risk of BRD is desirable. However, current identification methods are often not effective until later stages of the disease. The objective of the present study was to examine the use of infrared thermography (IRT) to non invasively identify the onset of BRD in cattle. Forty two calves (300 kg) were studied over a 28d period. The animals were transported from an auction site to the Lacombe Research Centre where they were placed into feedlot pens. The calves were bunk fed a silage ration and had free access to water. An infrared scanning system was placed at the water station which non invasively captured facial thermal data. All calves were assessed for body weight, rectal temperature (RT), white blood cell counts (WBC), neutrophile/lymphocyte ratio (N/L) and clinical scores (CS) upon arrival, departure and when trained handlers deemed an animal to be ill. The true positive (TP) identification of BRD was defined when a calf displayed ≥ 3 of: RT > 40 ° C; WBC > 10 X 10^6/L or < 7 X 10^6 /L; N/L > 0.8 or < 0.1 and a CS >3/20. A true negative animal (TN) was defined as displaying ≤ 1 of these biometric measures. Values for TP calves (n=20) for RT, WBC, N/L and CS were 40.7±0.3 (SD), 9.1±2.5, 0.9±0.4 and 3.5±0.6 respectfully. For TN calves (n=22) these values were 39.2±0.2, 8.9±1.6, 0.34±0.16 and 1.1±0.8. All mean biometric values were significantly different between TP and TN animals P<0.01 with the exception of WBC counts which for TP animals were either low (neutropenia) or high (neutrophilia). The orbital IRT temperatures for TP calves were significantly higher (P<0.01) with greater variance (35.27°C ±0.39) for the entire pre BRD period compared to TN calves (34.67°C± 0.27) with a peak difference between these two groups of over 1°C. This would have identified TP calves on average three days earlier than clinical scores. The analysis of ROC curves identified an optimal cut off value for IRT that displayed a sensitivity of 76.2% and a specificity of 85%. The data suggest that IRT may serve as a useful adjuvant in the identification of BRD.

Keywords: bovine respiratory disease infrared thermography

P02-GS **Age-dependent and site-specific effects on intestinal miRNA expression in young dairy calves.** G. Liang[1,*], N. Malmuthuge[1], P. Stothard[1], P. Griebel[2], L. Guan[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton,* [2]*Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatoon, Canada*

The health of the gastro-intestinal tract in newborn calves is one factor that contributes significantly to health and productivity in adult cows. . MicroRNAs (miRNAs) are a large family of small, ~ 22-nucleotide non-coding RNAs that have emerged as key regulators of gene expression involved in numerous biological processes, including innate and adaptive immunity. We hypothesized that miRNA expression in the intestine varies with age and among intestinal region and these differences may influence development of local innate and acquired immune responses to enteric pathogens in young dairy calves. In this study, the miRNA expression profiles and their potential targeted genes in the small intestine were characterized using tissues collected from the ileum, mid-jejunum and distal-jejunum. Tissues were collected from 1-week (n=6), 3-week (n=6), and 6-week (n=6) old healthy calves and miRNA expression analyzed with next-generation sequencing. This analysis revealed both age-dependent and intestinal region specific expression patterns for a subset of miRNAs known to be involved in regulating immune functions. For example, the expression of miR-211, miR-486 and miR-96 were significantly different (FDR<0.05) at different time-points when comparing throughout the intestine. These miRNAs are predicted to regulate host genes encoding cytokine-related signaling pathways as well as functions related to development and differentiation of lymphocytes. In addition, miR-196 families, which may play a crucial role in regulating the proliferation of lymphatic endothelial cells, were uniquely expressed in ileum. Our data suggests that intestinal miRNAs display age-dependent and intestinal region specific expression patterns during the early life of dairy calves. Specific miRNA families may play an important role in regulating the development of the local mucosal t immune system.

Keywords: dairy calves, microRNA, ruminant gut health

P03 Infrared thermography of groups of pigs detects thermal responses to vaccination.

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An automated, non-invasive system for monitoring of thermoregulation has the potential to mitigate swine diseases through earlier detection. Measurement of radiated temperature of groups of animals by infrared thermography (IRT) is an essential component of such a system. This study reports on the feasibility of monitoring group radiated temperature as a biomarker of immune response using vaccination as a model. A total of 315 weaned pigs were used in 15 replications of an experiment in which groups of 7 pigs per pen were either treated with an intramuscular vaccine (FarrowSure Gold), a sham injection of 0.9% saline, or left as untreated Controls. An infrared camera (Flir A320) was fixed to the ceiling directly above the pen of animals, and recorded infrared images of the groups at 5 minute intervals. The order of treatments was balanced over the 15 replications. Infrared images were analysed for temperature data including the maximum image temperature. The effect of the distribution of the pigs within the pen on the temperature parameters was assessed by analysis of variance for temperature differences between pig distributions and was significant ($P < 0.0001$). Higher temperatures were recorded when pigs were grouped together into a single cluster, which represented 47% of all images. The average daily maximum image temperature following vaccination (38.46°C) was significantly higher ($P<0.05$) than the Control animals (38.02°C) and the Sham treated group (37.96°C), and was significantly higher than for the same animal's temperature recorded 24-hours prior to vaccination (37.62°C). Increased temperature in the Vaccination group occurred from approximately 5 hours post-vaccination, reached peak elevated temperature at approximately 10 hours post-vaccination, and remained elevated above control day values for up to 23 hours post-vaccination. Infrared thermography detected significant changes to the radiated temperature of a group of animals following vaccination. The experiment suggests that IRT technology would be a useful screening tool for febrile diseases in pig barns.

Keywords: Infrared thermography, Radiated heat, Swine, Vaccination

P04 Comparison between a needle-free injection device (NFID) and a needle-syringe (NS) for vaccinating beef calves against infectious bovine rhinotracheitis (IBR) and Clostridium chauvoei.

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This study was conducted to compare the effectiveness of a needle-free (NF) injection device and needle syringe (NS) when used to vaccinate two-month old calves against infectious bovine rhinotracheitis (IBR) and *Clostridium chauvoei.* Two independent trials were conducted in the spring and fall with 96 crossbred beef calves (106.24 ± 16.68 kg) and 98 calves (101.46 ± 16.96 kg), respectively, in separate cow-calf herds in Manitoba, Canada. The calves were vaccinated with a modified-live virus (MLV) combination vaccine containing IBR, BVDV (types 1 and 2), parainfluenza-3 virus (PI-3), and bovine respiratory syncytial virus (BRSV). The same group of calves was also vaccinated with a clostridial vaccine containing *C. chauvoei*, *C. septicum*, *C. novyi*, *C. sordelli*, *C. perfringens* types B, C and D. Calves in each herd were vaccinated with either a NFID or NS. Visible vaccine residue at the skin surface was recorded immediately following vaccination. Serum IBR antibody levels were analyzed by a semi-quantitative IBR enzyme-linked immunoassay (ELISA). Serum *C. chauvoei* antibody levels were analyzed by a modified indirect immunofluorescence technique. Post-vaccination skin reactions were recorded on days 21, 42, 119 and 140 post-vaccination. Visible vaccine residue was apparent in NF-vaccinated calves following both the primary and booster IBR and *C. chauvoei* vaccinations. Initial immune response to IBR vaccination in NF- and NS-vaccinated calves was similar ($P<0.05$), resulting in progressively declining IBR antibody levels, which closely followed those of unvaccinated control calves. Levels of IBR antibodies in NF- and NS-vaccinated calvesincreased in a similar ($P>0.05$) mannerfollowing the booster vaccination. Needle-free and NS vaccinations elicited similar ($P>0.05$) immune response in spring-born and fall-born calves as both vaccination techniques increased *C. chauvoei* antibody levels following primary and booster vaccinations. Needle-free vaccination was as effective as NS vaccination in eliciting IBR and *C. chauvoei* protective antibody response in calves.

Keywords: Clostridium chauvoei, infectious bovine rhinotracheitis, needle-free vaccination, needle-syringe

P05 **Altered immune response in bovine paratuberculosis.** P.-L. Dudemaine[1,*], G. Fecteau[2], M. Lessard[1], G. Côté[3], O. Labrecque[3], S. Buczinski[2], E. Doré[2], J.-P. Roy[2], N. Bissonnette[1], *[1]Agriculture et Agroalimentaire Canada, Sherbrooke, [2]Faculté de médecine vétérinaire, Université de Montréal, [3]Ministère de l'Agriculture, Pêcheries et de l'Alimentation du Québec, St-Hyacinthe, Canada*

Paratuberculosis (PTB, also called Johne's disease) is nowadays viewed as one of the most serious chronic enteritis diseases of ruminants. The etiologic agent of PTB is *Mycobacterium avium* subsp. *paratuberculosis* (MAP). The economic impact of PTB on the national cattle industry is substantial. The disease is currently incurable and considered to be a hidden threat because detection of subclinical cows is difficult. At present, diagnostic tools such as direct pathogen culture from feces and serological detection (ELISA) are more efficient during the later phases of the disease. A series of analyses was carried out to better understand the immune response as the PTB disease progresses. The proliferative capacity of immune cells incubated with serum from infected cows (n=29) was reduced by 15% compared with lymphoproliferation in the presence of serum from healthy cows (n=31). Analysis of the plasma cytokines (interleukin [IL] 10, IL‑17, interferon-gamma [IFN‑γ], IL‑4, and osteopontin) also provided interesting information about the systemic immune response established during PTB progression. Concentrations of IL‑10 and IL‑4 were not affected by infection status. However, upregulation of IL‑17, IFN‑γ, and osteopontin showed that a proinflammatory state is established as the disease progresses. Gene expression analysis of macrophages infected by MAP supported the hypothesis of lymphocyte T helper 17 (T_{h17}) immune response. High upregulation of tumor necrosis factor-alpha (TNF‑α), IL‑1β, IL‑23, and transforming growth factor-beta (TGF‑β), which are cytokines associated with the establishment of a T_{h17} immune response, was observed as early as 6 h postinfection. These results suggest a strong T_{h17} response in the later stages of the infection, as has been observed for similar chronic diseases such as inflammatory bowel disease and Crohn's disease. Johne's disease entails significant economic losses, especially for the dairy industry. Given that immune-based diagnostics (e.g. serum ELISA) are disappointing for some cows, these results provide important clues concerning the systemic immunity established during PTB disease progression and will contribute to the development of more effective diagnosis tools.

Keywords: Immune system, Lymphocyte T helper 17, Paratuberculosis, Plasmatic cytokines

Breeding and Genetics

P06 **Estimation Of Genetic Parameters For Ultrasound Measurement Traits And Carcass Traits In Hanwoo.** S. H. Roh[1,*], C. Y. Kim[1], J. H. Ro[1], J. K. Park[1], J. S. Shin[1], J. H. Seo[2], Y. H. Choy[3], B. H. Park[3], T. J. Choi[3], S. H. Na[3], J. G. Lee[4], *[1]Hanwoo Improvement Center, Seosan, [2]Livestock policy division, SaeJong, [3]National Institute of Animal Science, CheonAn, [4]GyeongSang National University, JinJu, Republic of Korea*

Hanwoo cow is a breeding ground for quality calves and an importance resource to realize economic profits for farms. Therefore, farms would like to breed entities generating substantial benefits in an economic breeding in the aftermath of corn prices and also desire to confirm such capacity in an earlier manner.

This study conducted its research to determine its quality based on record of ultrasound measurement for heifer among measures to early identify carcass traits of heifers so as to be utilized for selection and culling of quality heifer.

As for data used for analysis, ultrasound measurement traits (Backfat thickness, Longissimus muscle area, Intramuscular fat, Rump fat) which are conducted by Hanwoo breeding farm, and carcass traits (Backfat thickness, Longissimus muscle area, Carcass weight, Marbling score) were used. For ultrasound measurement traits, 3899 units measured for heifers at the age of 9-17 months by using Esaote AquilaVet 3.5Mhz and for carcass traits, carcass records for those discharged after being born from heifers and 7486 units of performance test and progeny test were used.

The generic parameters were estimated at 0.36, 0.53, 0.57, and 0.14 for backfat thickness, longissimus muscle area, intramuscular fat, and rump fat of ultrasound measurement traits and 0.35, 0.34, 0.26, and 0.52 in backfat thickness, longissimus muscle area, carcass weight, and marbling score of carcass traits, in respectively. The genetic correlation analysis between ultrasound measurement traits and carcass traits were recorded at 0.83 in ultrasound backfat thickness and carcass backfat thickness, 0.80 in ultrasound longissimus muscle areaand carcass longissimus muscle area, 0.93 in ultrasound intramuscular fat and marbling score and 0.65 in rump fat and carcass backfat thickness.

As for Hanwoo, breeding is made by focusing on marbling score which is a great source for economic profits so that ultrasound intramuscular fat is considered as being possible to be used for selection and culling of heifer in farms considering high generic correlation in ultrasound intramuscular fat and marbling score.

Keywords: Hanwoo, Ultrasound measurement traits, Carcass traits, Heritability, Genetic correlation

P07 Genetic relationship between live animal ultrasound scanned traits and carcass traits in Korean native cattle (Hanwoo).

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The objective of this study was to estimate genetic parameters for live animal ultrasound scanned traits and carcass traits in Hanwoo steers. Genetic parameters for ultrasound scanned traits and carcass traits measured from 184 bulls and 1,648 steer progeny were estimated by derivative-free restricted maximum likelihood method. Genetic variance components were estimated with ASREML program and the heritability estimates were calculated by the ratio of phenotypic variance and additive genetic variance. Live animal ultrasound measurements were percentage of intramuscular fat (UFAT12/UFAT24), longissimus muscle area (UEMA12/UEMA24), backfat thickness (UBF12/UBF24), at yearling and at 24 months of age. Carcass measurements were intramuscular fat (FAT), longissimus muscle area (EMA), backfat thickness (BF) of steer carcasses slaughtered at 24 months of age. Models included fixed factors of birth year-season and linear covariates of age at measurements for ultrasound measures or age at slaughter for carcass measures, and random factors of animal effects and residual effects. Heritability estimates for UFAT12, UEMA12 and UBF12 were 0.38, 0.35, and, respectively. Heritability estimates for UFAT24, UEMA24 and UBF24 were 0.37, 0.36, 0.31 and 0.56, respectively. Genetic correlations between UFAT12 and FAT, between UEMA12 and EMA and between UBF12 and BF were estimated to be 0.78, 0.62, and 0.80, respectively. Genetic correlations between UFAT24 and FAT, between UEMA24 and EMA and between UBF24 and BF were estimated to be 0.85, 0.93 and 0.84, respectively. Heritability estimates for carcass traits were moderate to high ranging from 0.31 to 0.57, highlighting the potential for genetic improvement of these traits. Results indicate that live animal ultrasound scan measures on young breeding animals and carcass traits are highly correlated genetically to make earlier selection of young bulls effective for genetic improvement of meat quality of Hanwoo cattle.

Keywords: Genetic Parameter, Hanwoo, Carcass, Ultrasound, Progeny test

P08 Comparison of genetic parameters from station test records or from commercial farm records for growth and carcass traits in Hanwoo (Korean beef cattle).

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This study was conducted to compare the genetic parameters of growth and carcass traits of Hanwoo cattle, the records of which were collected from station test steers and from steers raised in commercial farms. Station test data were consisted of 8,479 yearling body weights and carcass trait records from station tests. And 387,561 carcass records of steers from commercial farms were collected from slaughter houses in Korea from 2008 to 2011. Carcass measures from station records and from commercial field records were treated as different traits as their ages at slaughter were different: carcass weight (CWT_S from station tests, CWT_F from commercial farms), eye muscle area (EMA_S, EMA_F), backfat thickness (BFT_S, BFT_F), and marbling score (MS_S, MS_F). Yearling weights (YWT_S) were collected only from station test animals. Multiple trait sire models were fit for estimation of genetic parameters. In the models for field carcass traits, two fixed group effects of province-birth year-birth month, slaughter house-slaughter year-slaughter month with covariates of slaughter ages (linear, quadratic, cubic) were considered. In the models for station test animals, batch-tested location-slaughter date effect and slaughter age covariates (linear, quadratic, cubic) were considered for carcass traits. Heritability estimates of field carcass traits were 0.05 for CWT_F, 0.04 for EMA_F, 0.07 for BFT_F, and 0.12 for MS_F with little differences by linear to cubic covariates in the models. Carcass traits from station tests showed higher heritability estimates than those from commercial field records. The ranges of the estimates were 0.22~0.26 for CWT_S, 0.23~0.28 for EMA_S, 0.25~0.31 for BFT_S, and 0.56~0.65 for MS_S. Quadratic covariance models showed highest heritability estimates for all carcass traits from station tests. Genetic correlation coefficients between carcass traits from different information sources were in the ranges of 0.83~0.87 between CWT_S and CWT_F, 0.69~0.73 between EMA_S and EMA_F, 0.75~0.81 between BFT_S and BFT_F, 0.46~0.54 between MS_S and MS_F depending on the covariates structure in the models.

Keywords: field record, genetic parameters, Hanwoo, station test

P09 **Functional analyses of SNPs in the promoter regions of bovine genes.** M. Vinsky[1,*], X. Zhu[1,2], X. Zhang[2], C. Li[1,3], [1]*Beef Genomics, Agriculture and Agri-Food Canada, Edmonton, Canada,* [2]*Animal Science College, South China Agricultural University, Guangzhou, China,* [3]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*

Single nucleotide polymorphisms (SNP) in gene promoter regions may affect the binding of transcription factors and thus the gene expression. In this study, we performed functional analyses of SNPs in the promoter regions of bovine CRH, PCDH7, PADI2, NEUROD1, MUSK and TSHR genes. SNPs that are predicted to cause the changes in the binding site of transcription factors were selected for this functional analyses. DNA fragments of about 150 bp that span the promoter SNP region were amplified from animals carrying the alternative homozygous genotypes of each SNP. The amplified DNA fragments were sequenced to confirm the identity of each SNP allele. The SNP allele-specific promoter fragments were cloned into the vector pGL4.17 and the promoter constructs were then transiently transfected into 3T3-L1 cell lines. Promoter activity was quantified using a dual luciferase reporter assay. The results of the reporter assay showed significant difference in promoter activity between the two SNP alleles or SNP haplotype alleles for CRH, PCDH7, and TSHR ($P<0.05$). However, no significant difference in promoter activity was found between the SNP alleles examined for genes PADI2, NEUROD1 and MUSK ($P>0.05$). The SNP allele-specific promoter reporter assay has the potential to validate significant SNP-trait associations at a molecular level and to identify the causative SNPs for genome selection.

Keywords: promoter, bovine, functional analysis, reporter assay, Single nucleotide polymorphisms (SNP)

P10 **Effects of niche-market genotypes on pig performance traits.** H. Zhang[1,2], J. L. Aalhus[1], I. L. Larsen[1], S. Nelson[1], J. Ye[2], M. Juárez[1,*], [1]*Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, Canada,* [2]*Department of Livestock Production, Inner Mongolia Agricultural University, Hohhot, China*

Pork production is a major industry in Canada but over recent years, we have lost our world leading position on the export market. Experts agree on the need for differentiation and development of new high quality products, as well as for adaptability/flexibility within the Canadian pork industry to successfully compete in priority markets. Genotype-based high quality products are produced and marketed in numerous countries. The use of different genotypes could be one of the alternatives to create variation in the final quality of Canadian pork. However, the impact of using unique genotypes on animal performance, as well as their interactions with different production systems, needs to be evaluated. Thus, 30 Large White×Landrace F1 dams were inseminated with Duroc, Lacombe and Iberian semen (10 dams per breed). Reproduction traits were recorded and 72 piglets (36 males and 36 females) from each genotype were selected for the animal performance study. When the animals reached ~85 kg of weight, they were assigned to two slaughter weights (120 and 140 kg) and three different diets (control, 10% ExtraPRO or 10% LinPRO, for the last three weeks before slaughter) in a balanced 3×2×3×2 design. Individual weights were recorded from birth to slaughter. Fertility was lower for Iberian (80 *vs.* 90%), as expected when using frozen semen. Average litter size was slightly lower for Lacombe (10 piglets), while the number of weaned piglets was highest for Iberian (11.2). For both males and females, ADG was always higher ($P<0.05$) for Duroc and Lacombe than for Iberian (0.9 *vs.* 0.8 for males, and 0.8 *vs.* 0.6 for females), a less selected breed. At heavier weights, that difference increased as Iberian growth rate started to plateau, requiring several extra weeks to achieve the targeted slaughter weights. No difference was observed among dietary treatments. Hence, in the present study, the use of less selected genotypes to produce high quality niche-market pork may have a direct impact on pig performance traits.

Keywords: Duroc, Iberian, Lacombe, Pork

P11-GS **Possible involvement of epigenetic modifying enzymes in the regulation of nutrient effect on bovine milk fat synthesis.** R. Li[1,2,*], F. Beaudoin[1], X. Zhao[3], E. M. Ibeagha-Awemu[1], [1]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Canada,* [2]*College of Animal Science and Technology, Northwest A&F University, Xi'an, China,* [3]*Animal Science, McGill University, Ste-Anne-De Bellevue, Canada*

Diets rich in unsaturated fatty acids (USFAs) can be used to modify the fatty acid composition of milk in favor of health promoting isomers. However, such diets usually lead to marked decrease in milk fat yield and the expression of key lipogenic genes. The aim of this study was to examine the involvement of epigenetic modifying enzymes in the regulation of the effect of diets rich in USFAs (safflower oil and linseed oil) on milk fat synthesis.

Eighteen Canadian Holstein dairy cows in mid lactation were randomly assigned to one of two dietary treatments (Trts): Diet SF (Safflower) (a control diet [diet CT] composed of total mixed ration of corn and grass silages + 5% safflower oil on DM bases) or diet LS (linseed) (diet CT + 5% linseed oil). The Trt period (9 cows on diet SF & 9 cows on diet LS) lasted for 28 days preceded by a control period (all cows on diet CT) of 28 days. After Trt, cows were returned to diet CT for another 28 days (post-Trt period). Milk samples were collected on a weekly bases and samples of day -1

(control period), +6 and +27 (Trt period) and +54 (post-Trt period) were used to measure gene expression levels of two DNA methyltransferases (DNMT1 and DNMT3A) and four histone acetyltransferases (HAT1, KAT2, KAT5 and CREBBP) by real-time qPCR and milk fat yield. Paired T-test in Excel 2010 was used to evaluate the differences in gene expression levels between Trts at different time-points (+6, +27 and +54) and control time point (-1), as well as milk fat yield.
Milk fat yield decreased significantly during the Trt period with both diets as compared to control and post-Trt periods (P<0.001). HAT1 expression was significantly down regulated (P<0.05) at day +27 by both Trts as compared with day -1 while KAT2 was only significantly down-regulated (P<0.05) in response to linseed oil. The expression of other genes studied showed reduced trends in response to Trts but did not reach significant levels. In summary, our results show alteration of two epigenetic modifying enzymes which suggest that epigenetic events might participate in the regulation of nutrient effect on milk fat synthesis.

Keywords: DNA methyltransferase, gene expression, histone acetyltransferase, milk fat, safflower/linseed oil

P12-GS **Estimation of growth pattern and gene expression analyses of Korean native steer (Hanwoo) using the genomic breeding value of Korea.** C.-D. Jeong[1,*], L. L. Mamuad[1], S.-H. Kim[1], Y.-J. Choi[1], A. P. Soriano[1], K.-C. Nam[1], J.-J. Kim[2], S.-S. Lee[1], [1]*Animal Science and Technology, Sunchon National University, Suncheon,* [2]*School of Biotechnology, Yeungnam University, Gyeongbuk, Republic of Korea*

The objective of this study is to early diagnose the hereditary endowment which will lead to the establishment of a short-term feeding program based on the results predictions. A total of 140 Hanwoo steers were equally distributed to four treatments based on their parents' breeding values from highest to lowest (T1, T2, T3, T4). The experimental animals were fed in group pens (five animals/pen) with similar amount of feed depending on the growth stage. Rice straw was given on *ad libitum* while concentrate feed were fed with 4-7 kg (DMI of 3.2-5.2 kg/d) for growing period (6-16mos.) and 7-9 kg (DMI of 5.52-7.2 kg/d) for middle fattening period (17-24mos.). Body weight gain (BWG) was measured every two months while carcass weight was determined upon slaughtering the animals at about 31mos. Data were analyzed using Statistical Analysis Systems version 9.1 (2002). Results showed that BWG after 6mos. was highest (*P*<0.05) in T1 (190.77kg) than T3 and T4 while T2 had comparable weights with T1 and T3 but significantly higher than T4. After 16 and 24mos, BWG of T1 was the highest (*P*<0.05) and thus slaughtered the earliest (*P*<0.05). Carcass weight was significantly higher in T1 and T2 followed by T3 and T4, respectively. T1 backfat meat size was highly correlated to carcass weight and marbling score.Using High-Density Bovine SNP array analysis, we identified the meat quantity-related gene BTB-01280026 in blood and showed 2.9% expression rate, which was found in 9 steers. Furthermore, the steers to which the gene was expressed had the higher slaughter weight of about 12kg than other animals.

Keywords: Breeding value, Growth pattern, Hanwoo steer, Meat quantity-related gene

P13 **Repeated measures of residual feed intake in growing beef bulls fed forage and grain-based diets.** S. Thompson[1,*], T. Ullenboom[1], G. Crow[1], J. Basarab[2], K. Wittenberg[1], V. Baron[3], C. Fitzsimmons[4], K. Ominski[1], [1]*Department of Animal Science, University of Manitoba, Winnipeg,* [2]*Lacombe Research Centre, Alberta Agriculture and Rural Development, Lacombe,* [3]*Agriculture and Agri-Food Canada,* [4]*Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, Canada*

Residual feed intake (RFI) has been used to select metabolically efficient cattle in beef breeding programs. Cattle are traditionally performance tested on concentrate-based diets, and this is assumed to reflect performance regardless of diet composition. The objective of this experiment was to determine if beef bulls change their RFI ranking when fed a forage-based (F) as compared to a grain-based (G) diet. Sixty bulls, 280 days of age (SD=27) at the start of test were randomly assigned into four pens, with 2 pens receiving F treatment and 2 pens receiving G during period 1 (76 d). Thereafter, diets were switched for one of the forage (F-G) and one of the grain pens (G-F), while the remaining two pens continued their original diet treatment (F-F and G-G) during period 2 (63 d). Daily feed intake, DM basis, (FI), as measured by the GrowSafe feeding system, was regressed against average daily gain (ADG), metabolic mid-weight and final ultrasound backfat to obtain an expected feed intake (EFI) value, with RFI calculated as the difference between FI and EFI. Bulls in each pen (n=15) were grouped as either low RFI (more efficient, RFI rank ≤7), or high RFI (less efficient, RFI rank >7). RFI values ranged from -0.96 to +0.97 kg d^{-1} dry matter (SD=0.44) and -1.15 to +1.44 kg d^{-1} dry matter (SD=0.58) for periods 1 and 2, respectively. Across all pens approximately 27% of bulls remained in the low RFI group, 33% remained in the high RFI group, 20% of the bulls moved from low to high RFI rank and 20% moved from high to low RFI rank. The rank correlation for RFI between period 1 and period 2 was found to be low, with r=0.04, 0.20 and 0.34 (P>0.05) for F-G, G-F and F-F, respectively. However, the rank correlation for G-G was significantly positive, r=0.71 (P<0.05). The data reveals the inherent variability of individual measurements of RFI, suggesting many factors, including diet and environmental conditions, may account for the observed variability.

Keywords: beef bulls, reranking, residual feed intake

Carcass Quality & Carcass Evaluation

P14 **Energy partitioning in fat depots and the relationship between marbling score and whole carcass intramuscular fat relative to biological type and harvest age.** N. P. Welegedara[1,*], E. K. Okine[1], J. A. Basarab[2], Z. Wang[1], C. Li[1], H. Bruce[1], S. Markus[2], J. Stewart-Smith[3], J. Aalhus[4], R. W. Seneviratne[2], L. Goonewardene[2], *[1]Agricultural, Food and Nutritional Science, University of Alberta, [2]Alberta Agriculture and Rural Development, Edmonton, [3]BeefBooster Inc., Calgary, [4]Agriculture and Agri-Food Canada, Lacombe, Canada*

The objective was to determine the pattern of energy partitioning into the fat depots: body cavity (BC), subcutaneous (SC), intermuscular (IM) and intramuscular or marbling (MA) in steers of five (M1, M2, M3, M4 and TX) Beefbooster® biological types (BT) that were serially harvested at approximately 274, 347, 372, 399, 427 and 456 d in the feedlot and study the relationship between marbling score as determined at slaughter and whole carcass intramuscular fat. BC, SC and IM were determined by dissection of the left side of the carcass and MA determined chemically. Energy requirements were highest for IM and lowest for BC fat in all BT's with requirements for SC and MA fat being similar and intermediate. On average, 7%, 23%, 48%, 22% of the total fat energy was deposited as BC, SC, IM and MA respectively during the 182 d study. The rate of energy deposition in the MA depot was always lower in M3 (early maturing, small breeds) compared to the other BT's. The energy deposition ratio of other fat (SC, BC and IM) to MA fat increased from 2.8 (274 d) to 3.9 (456 d) pooled for all BT's. The correlation between marbling score and MA fat was 0.69 ($P < 0.01$) pooled for all BT's. The regression of marbling score on intramuscular fat pooled for all BT's was: intramuscular fat = 2.43 + 0.025 marbling score ($P < 0.01$, SE = 0.0020, $R^2 = 0.48$). The energy used for MA fat production in the whole carcass follows a pattern that is similar to SC fat in all BT's and is a depot that develops gradually over time and contrary to the view that MA is a late developing fat depot.

Keywords: energy partitioning , intramuscular marbling fat, marbling score

P15-GS **Factors Affecting the Prediction of Saleable Meat Yield in Lamb Carcasses Using Electronic Probe Technology.** C. Mikel[*], C. Campbell, B. McDougall, I. Mandell, *Animal and Poultry Science, University of Guelph, Guelph, Canada*

The current system for grading lambs in Ontario is based on a subjective visual scoring system which may provide inaccurate information for determining carcass value. The pork industry currently uses optical grading probes to determine carcass value; this information is then used to determine payouts for producers. The current study investigates the accuracy of electronic probe technology for evaluating saleable meat yield in Ontario lambs and how variation in management factors for lamb production impacts saleable meat yield and prediction of saleable meat yield. 203 lambs sourced from a variety of farms were probed using the Viewtrak PG-207 between the 11th and 12th rib, 3.5 cm from the midline on both the hot and cold carcass. Carcasses were broken into 4 primal cuts and dissected into lean, fat and bone. Ruler measures were taken at the probe site to evaluate accuracy of probe. Ram and ewe data were analyzed separately with data evaluated based on specific carcass weight ranges within a gender. There was extensive variation when examining Pearson correlation coefficients and multiple regression equations between probe and equivalent carcass measures for each gender. The R^2 for models incorporating hot carcass weights and hot probe measurements for muscle and fat depths for predicting saleable meat yield ranged from 0.046 to 0.360 for rams and 0.342 to 0.691 for ewes. Using cold probe data, R^2 ranged from 0.114 to 0.232 for rams and 0.403 to 0.664 for ewes. In this study, the electronic probe did not appear to be an accurate predictor of saleable meat yield across the diverse ranges of fatness and carcass weight found with Ontario lamb production.

Keywords: Carcass, Fat Depth, Lamb, Probe, Saleable Meat Yield

P16 **Potential of near infrared reflectance spectroscopy to predict fatty acid composition in subcutaneous fat from pigs fed reduced-oil corn dried distillers grains with solubles.** N. Prieto[1,*], B. Uttaro[2], C. Mapiye[2], M. Dugan[2], V. Zamora[3], M. Young[3], E. Beltranena[4], *[1]CSIC, Leon, Spain, [2]AAFC, Lacombe, [3]Gowans Feed Consulting, Wainwright, [4]Alberta Agriculture and Rural Development, Edmonton, Canada*

Recently, the oil content of corn dried distillers grains with solubles (cDDGS) for livestock feeding has been reduced from 10–12 to 6–9%, concomitantly reducing its dietary net energy (NE) value. The high proportion of unsaturated fatty acids (FA) in cDDGS results in soft pork fat that can affect the quality of processed pork products. The objective of this study was to test the ability of near infrared reflectance spectroscopy (NIRS) to predict FA composition from intact subcutaneous pork fat when animals were fed 30% cDDGS. Animals used were a subset of a larger study where the NE value of cDDGS was measured using 1056 pigs housed in 48 pens, split by gender, and fed diets containing cDDGS with assumed NE values of 1.70, 1.85, 2.00, 2.15, 2.30 and 2.45 Mcal/kg. A subset of 96 animals was slaughtered (124.9 kg) and the outer layer of subcutaneous fat was collected and scanned both warm (35 °C) and cold (4 °C) over a NIR spectral range from

400 to 2498 nm using benchtop equipment, and then analyzed for FA profile by gas chromatography. NIRS accurately predicted the proportion of SFA, MUFA, PUFA, omega-3 and omega-6 FA with R^2 (RMSECV, % FA) of 0.86 (1.37), 0.82 (1.31), 0.86 (1.08), 0.80 (0.26) and 0.83 (1.03), in warm samples. When the fat samples were scanned cold, slightly higher NIRS predictability was observed for SFA, MUFA, PUFA, omega-3 and omega-6 FA content, where R^2 (RMSECV, % FA) were 0.89 (1.11), 0.86 (1.11), 0.89 (0.97), 0.82 (0.25) and 0.86 (0.94), respectively. Further research applying NIRS to estimate FA composition in subcutaneous pork fat would logically be with portable equipment directly on the carcass due to the evident advantages in speed of analysis.

Keywords: DDGS, fatty acid, NIRS, pork, subcutaneous fat

Contemporary & Emerging Issues

P17 **Reliability and variability of 16S rRNA for microbial profiling of cattle feces.** Y. Xu^{1,*}, E. Dugat-Bony^{1,2}, K. Munns^{2}, L. Selinger^{2}, T. A. McAllister^{3}, B. Selinger^{1}, ^{1}*Department of Biological Sciences, University of Lethbridge,* ^{2}*Agriculture and Agri-Food Canada,* ^{3}*1Agriculture and Agri-Food Canada, Lethbridge, Canada*

Previous 16S rRNA profiling studies have identified substantial variation in fecal microbial communities among cattle. Frequently, the overlap of OTUs among samples is exceedingly low. We designed an experiment with a series of technical replicates to test the hypothesis that the pyrosequencing method contributes to some of this variation observed in microbial communities. We found that identification of abundant taxa was highly repeatable, but more than 80% OTUs were members of the “rare biosphere” (less than 0.01% of taxa). Repeat identification of these taxa was infrequent, even with deep sequencing (>10,000 pyrotags) among technical replicates. There was no significant difference within replicates in diversity index. All repeat samples (n=32) except one clustered together, demonstrating the high reliability of 16S rRNA as a profiling technique. There is a similar clustering pattern based on the rare OTUs and that based on all OTUs suggests that the rare organisms do not occur by change alone. The rare biosphere in cattle feces is biologically significant in that it contains several important pathogens such as *Mycobacterium tuberculosis and Campylobacter jejuni.* We conclude that pyrosequencing of 16S rRNA profiling is a reliable method for profiling bacterial communities in cattle feces and that rare taxa are important members of this community

Keywords: 16S rRNA, pyrosequencing, rare biosphere, Reliability

Food Safety

P18 **Characterization of selected lactic acid bacterial isolates for controlling Salmonella infection in broilers.** J. Gong^{1,*}, X. Yang^{1}, J. Brisbin^{2}, Q. Wang^{2}, F. Yin^{1}, H. Yu^{1}, S. Sharif^{2}, ^{1}*Agriculture and Agri-Food Canada,* ^{2}*University of Guelph, Guelph, Canada*

Salmonella contamination of poultry and poultry products remains to be a significant food safety issue. The present study has investigated the potential of 15 previously-selected lactic acid bacterial isolates, both *in vitro* and *in vivo*, in application for *Salmonella* control in broilers. *In vitro* characterization includes the determination of susceptibility to antibiotics and tolerance to low pH (2.0) and high bile salt (0.3-1.5%). Three chicken infection trials were subsequently conducted to evaluate four of the isolates for reducing the burden of *Salmonella enterica* serovar *typhimurium* (phage type 193) in broilers. Chicks were gavaged *Lactobacillus* cultures (10$^{6-7}$ CFU/chick) or PBS at 1 day of age followed by a *Salmonella* challenge (10^{4} CFU/chick) next day. Samples of cecal digesta, spleen, and liver were collected on day 1, 3, or 4 post-challenge. In Trial 1, four isolates (LB1, S8, S33, and S64) were assessed individually and *Salmonella* counts in cecal digesta were determined. In Trials 2 and 3, LB1 and a mixed culture of LB1, S8, and S64 were tested. Their effects on *Salmonella* counts in both cecal digesta and the organs of spleen and liver, and on *Salmonella* virulence gene expression were assessed. The results of chicken trials indicate that tested *Lactobacillus* isolates were unable to reduce *Salmonella* burden in the chicken cecum, but *Salmonella* infection to the spleen and liver. Among ten virulence genes that promote *Salmonella* intestinal invasion, nine of them demonstrated a decreased expression in *Salmonella* cells from the cecal digesta of *Lactobacillus*-treated birds. The probability analysis suggests that the genes of *hilA, hilD, sptP, and arvA* and genes of *hilC* and *sipC* contribute significantly to the spleen and liver infection, respectively.

Keywords: Chickens, Lactobacillus, Probiotics, Salmonella infection, Virulence genes

P19 **Rapid Determination of Total CLAs in Canadian Cheese by 1H NMR Spectroscopy.** D. Prema*, J. L. Pilfold, J. Krauchi, J. S. Church, K. K. Donkor and B. Cinel, *Faculty of Science, Thompson Rivers University, Kamloops, British Columbia, Canada*

Canadian consumers are becoming increasingly health conscious, and choices in the dairy case in the supermarket have expanded dramatically in recent years to include organic product lines, which are now widely available. Organic dairy products may contain higher levels of conjugated linoleic acids (CLAs), but to date there have been few scientifically sound studies in Canada to illustrate the difference in organic versus conventional dairy products. Organic dairy production standards dictate differences in the forage levels fed to the cows, which likely result in variation in the nutritional composition, including levels of CLAs, of the end products. CLAs are defined as a group of linoleic acid isomers that have received considerable attention over the last two decades due to their potential health benefits. The application of nuclear magnetic resonance (NMR) spectroscopy to measure CLAs in the lipid fraction of cheese is both novel and an alternative over traditional methods such as gas chromatography (GC), which can require time-consuming sample derivatization and the use of copious amounts of reagents and solvents. In this work, NMR spectroscopy was employed as a simple, efficient, and non-destructive method for measuring total relative CLA levels in store-bought cheese. We have analyzed a variety of organic ($n = 8$) and conventional ($n = 8$) cheeses (Gouda, Cheddar, Feta and Mozzarella) for CLA levels. The organic cheeses contained a mean relative CLA value of 0.403 ± 0.050, while the conventional products showed relative CLA values of 0.305 ± 0.021. A two-way analysis of variance (ANOVA) test showed that these levels do not differ statistically between the type of cheese ($P = 0.981$) or its method of processing ($P = 0.177$). Additionally, grass-fed Gouda and Feta cheeses were shown to contain significantly higher CLA levels than either of their conventional or organic counterparts. The mean relative value of CLAs in grass-fed Gouda and Feta was 0.973 ± 0.079, compared to 0.321 ± 0.023 and 0.396 ± 0.100 for similar conventional and organic products, respectively. While organic standards suggest that the cattle are fed more forage than with conventional dairy, our results show that this does not always translate into higher levels of CLAs in the final cheese products.

KEYWORDS: conjugated linoleic acids (CLAs), organic dairy products, nuclear magnetic resonance (NMR)

Foods and Food Products

P20 **Enriching hamburger with PUFA biohydrogenation products by supplementing steers fed high forage diets with either flaxseed or sunflower seed: Effects of adipose tissue source on palatability and fatty acid composition.** T. D. Turner[1,*], J. L. Aalhus[1], C. Mapiye[1], D. C. Rolland[1], I. L. Larsen[1], J. A. Basarab[2], V. S. Baron[1], T. A. McAllister[3], H. C. Block[4], B. Uttaro[1], M. E. R. Dugan[1], [1]*Agriculture & Agri-Food Canada,* [2]*Alberta Agriculture and Rural Development, Lacombe,* [3]*Agriculture & Agri-Food Canada, Lethbridge,* [4]*Agriculture & Agri-Food Canada, Brandon, Canada*

Influence of diet and fat source in hamburgers on sensory attributes and fatty acid (FA) composition, emphasising biohydrogenation intermediates (BHI), were evaluated. Sixty-four cross-bred steers were fed for 205 days on a grass hay or red clover silage based diet supplemented with concentrates (70:30 DM) containing flaxseed or sunflower seed to provide 5.4% dietary oil. Post-slaughter, hamburgers were made from *triceps brachii* ground with perirenal or subcutaneous fat (80:20 wt/wt). Data were analysed using forage, oilseed and tissue type as fixed effects and all interactions, with animal and slaughter day as random effects. Fatty acid composition was chiefly affected by fat source, with few effects due to oilseed or forage type. Perirenal fat increased 18:0 ($P<0.05$), total *trans*(*t*)-18:1, mainly *t*11-18:1 ($P<0.05$) and n-3 FA ($P<0.05$), but lowered *cis(c)*-monounsaturated FA, mainly *c*9-18:1 ($P<0.001$) content. Oilseed effects related to major FA found in oilseeds and their biohydrogenation rates. Feeding sunflower seed increased content of total *t*-18:1, mainly *t*11-18:1, and *c*9,*t*11-conjugated linolenic acid (CLA) ($P<0.01$), whereas feeding flaxseed increased n-3 FA ($P<0.001$) and 18:3n-3 BHI, including *c*9,*t*11-CLA, *t*11,*c*13-CLA and non-methylene interrupted non-conjugated dienes ($P<0.05$). Diet and tissue type influence on sensory attributes were small and may not be detected by the average consumer. Hamburgers containing perirenal fat enhanced tenderness and juiciness preferences, but gave a negative impression for residual mouth coating ($P<0.05$), which may relate to the higher SFA content. Flavour properties were more positive for hamburgers made with sunflower seed ($P<0.05$), possibly related to lower 18:3n-3 content, aiding oxidative stability. Overall, feeding oilseeds in forage based diets increased the BHI content in hamburger. Perirenal fat can enhance content of BHI with potential bioactive properties, i.e. *t*11-18:1, and represents a value added opportunity to maximise underutilised and undervalued fat depots coupled with potential health benefits.

Keywords: Beef, Biohydrogenation intermediates, Flaxseed, Sensory evaluation, Value added

Forages and Pastures

P21 **Comparison of target breeding weight and development system for beef heifers.** H. B. Lardner[1,2,*], D. Damiran[1,2], S. Hendrick[3], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon,* [2]*Western Beef Development Centre, Humboldt,* [3]*Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, Canada*

A 2-yr study was conducted with spring-born Black Angus beef heifers (n=174) to determine the effects of developing heifers to either 55 or 62% of mature body weight (MBW) at breeding on growth and reproductive efficiency. Each year, heifers (251 kg±4 kg) were randomly allocated to 1 of 2 levels of nutrition and developed to a targeted body weight (BW) of either (1) 55% (low gain, LG) or 62% (high gain, HG) of MBW (637 kg). Each group was further assigned (4 subgroups) to 1 of 2 replicated (n=2) development systems (1) bale graze bromegrass-alfalfa round bales in field paddocks (BG); or (2) fed bromegrass-alfalfa round bales in drylot pens (DL). High gain and LG heifers were supplemented with rolled barley (TDN=86.4%; CP=12.4%) at 0.7 and 0.5% of BW, respectively. Pregnancy rates through the second pregnancy were determined. During the winter development period (203 d), HG heifers had greater ($P < 0.05$) average daily gain than LG heifers (0.79 vs. 0.49 kg/d; SEM = 0.02), final BW (396 vs. 353 kg; SEM = 5.5), rib fat (3.1 vs. 2.3 mm; SEM = 0.09), rump fat (2.6 vs. 1.4 mm; SEM = 0.10), and frame score (3.2 vs. 2.8; SEM = 0.08). Heifers from either HG or LG development systems were not different ($P > 0.05$) for first or second pregnancy rate (88.5 vs. 85.9 %; SEM = 4.03; 94.5 vs. 97.3 %; SEM = 4.03, respectively), calf birth weight (36.2 vs. 35.3 kg; SEM = 1.22) and calving pattern. Low gain heifers achieved similar BW ($P > 0.05$) to HG heifers (494±6 kg; 78% MBW) at first calving. These results suggest developing heifers to 55% of MBW do not adversely affect reproductive efficiency compared with developing heifers to reach 62% of mature body weight.

Keywords: beef cattle, bale grazing, replacement heifers, target body weight

P22 **The ensilage dynamics and nutritive value of alfalfa silage produced using fibrolytic enzymes and a silage inoculant.** J. P. Lynch[1,*], L. Jin[1], E. C. Lara[2], J. S. Church[3], J. Baah[1], K. A. Beauchemin[1], [1]*AAFC, Lethbridge, Canada,* [2]*São Paulo State University, São Paulo, Brazil,* [3]*Thompson Rivers University, Kamloops, British Columbia, Canada*

The objective of this study was to determine the effect of applying fibrolytic enzymes at ensiling, either alone or in combination with a bacterial silage inoculant, on the silage conservation characteristics and nutritive value of alfalfa. Second-cut alfalfa (35% DM) was harvested, wilted, chopped and sub-sampled into 24 batches. Samples were randomly allocated in triplicate to one of four enzyme products (control; Dyadic Xylanase/Cellulase PLUS; Econase RDE; Rovabio Excel LC) applied alone or in combination with Pioneer 11GFT silage inoculant. All enzyme treatments were applied at 2 ml enzyme product / kg herbage DM, and inoculant was applied at 1×10^5 cfu /g fresh herbage. Samples were packed into laboratory-scale silos and were stored at 20°C for 70 days and analysed for dry matter (DM) losses, aerobic stability, chemical composition and *in vitro* ruminal digestibility. Data were subjected to ANOVA using the PROC MIXED procedure of the SAS statistical program. The use of enzymes did not affect ($P>0.05$) ensilage DM losses or lactic or acetic acid concentrations, compared to the control silage. Silage produced using Dyadic had lower NDF ($P=0.031$) and ADF ($P=0.021$) concentrations than control silage. However, no difference ($P>0.05$) was observed between the control silage and silage produced with Dyadic for NDF or ADF digestibility (NDFD, ADFD). Silages produced with 11GFT had higher DM losses ($P=0.015$) and pH ($P<0.001$) and a lower NDFD ($P=0.040$), ADFD ($P=0.038$) and proportion of lactic acid in the total fermentation products ($P=0.009$), compared to uninoculated silages. The use of fibrolytic enzymes did not alter the ensilage dynamics of alfalfa, either ensiled alone or with an inoculant. No advantage in ruminal DM or fiber digestibility was observed for silages produced with fibrolytic enzymes. The reduced nutritive value for alfalfa silages produced with 11GFT, compared to uninoculated silages, likely reflects a higher loss of digestible carbohydrates from a more heterolactic ensilage fermentation.

Keywords: Alfalfa, Fiber, Fibrolytic enzymes, ruminant, Silage

Growth and Development

P23 **Impact of maternal nutrition during gestation on fetal longissimus dorsi muscle transcriptome in beef cattle.** F. Paradis[1,2,*], J. R. Grant[1], K. M. Wood[3], K. Swanson[4], I. Mandell[3], S. P. Miller[3], B. McBride[3], C. Fitzsimmons[1,2], [1]*Agricultural, Food, and Nutritional Science, University of Alberta,* [2]*Agriculture and Agri-Food Canada, Edmonton, AB,* [3]*Animal and Poultry Science, University of Guelph, Guelph, ON, Canada,* [4]*Animal Science, North Dakota State University, Fargo, ND, United States*

Influences of nutrition during pregnancy on offspring performance have been established in many mammalian species, and could represent a window of opportunity to ensure/enhance genetic potential via dietary means in beef cattle. To investigate the impact of maternal nutrition on fetal development in the latter half of pregnancy, 22 mature (3-6 yrs old) multiparous pregnant Angus-Simmental cross-bred cows were divided into 2 groups (of 11 cows each), and fed one of 2 levels of nutrition; 1) ad-libitum intake (~140% above maintenance; HIGH), and 2) restricted to 85% maintenance intake (LOW). The diet consisted of a haylage-based total mixed ration containing 20% wheat straw. All cattle started the feeding trial simultaneously at 147±15 days of gestation and were slaughtered over 6 weeks (blocks), in groups of 4 (2 cows from both groups/week) at 247±10 days of gestation. Cows were weighed throughout the feeding period. Cow total weight gain (53 vs 104 kg; $P<0.001$) and ADG (0.53 vs 1.07 kg/day; $P<0.01$) were significantly different between treatments indicating nutritional restriction impacted the dam. At slaughter gross fetal phenotypes were collected but no differences were observed. Longissimus dorsi (LD) muscle samples were collected and a global transcriptome analysis was performed using Illumina RNA sequencing. Prior to differential expression (DE) analysis, low quality reads were removed and the remaining were aligned to the Bos Taurus reference genome (UMD_3.1) using TopHat. Gene read counts were analyzed for DE using edgeR and significantly differentially expressed genes were selected using a FDR of <0.05. A total of 256 genes displayed DE between the LD muscle of HIGH and LOW fetuses. Gene ontology analysis in DAVID revealed enrichment of 10 biological processes related to metabolic and catabolic pathways, which could have implications for future post-natal growth, development, and metabolic efficiency. Our results clearly illustrate that restricted feed intake during pregnancy can alter gene expression in the muscle and could be detrimental to the fetus even if no obvious phenotypes are observed.

Keywords: Fetal programming, Maternal nutrition, Muscle development

P24 **Non steady state thermal profiles used to rank RFI in cows.** A. Schaefer[1,*], J. Basarab[2], J. Colyn[1], J. Webster[3], M. Stewart[3], [1]*Lacombe Research Centre, Agriculture and Agri-Food Canada,* [2]*Lacombe Research Centre, Alberta Agriculture, Lacombe, Canada,* [3]*Ruakura Research Centre, AgResearch, Hamilton, New Zealand*

The determination of metabolic efficiency is economically important in the animal industries. This information can be used to cull or retain breeding stock thereby reducing feeding costs. Conventional methods for ranking efficiency utilize primarily either long term feeding regimes used to determine metabolizable energy (ME) requirements or respiratory gas collections which can be used to determine energy expenditure. The purpose of the current study was to use a time off feed induction method with the simultaneous measurement of radiated energy loss in order to rank metabolic efficiency. The hypothesis was that cattle displaying a greater metabolic efficiency will conserve energy more effectively during times of feed deprivation. Twenty cross bred commercial cows containing British genetics were used in the present study. All cows were monitored for residual feed intake (RFI) using a conventional 100 day feeding period during which time ME feed intake and growth (weight gain) were measured. RFI was determined as the difference between actual and expected feed intake. The animals were subsequently taken off feed for 24h and scanned for infrared radiated heat loss (IRT) using a FLIR A300 camera system located at a water station. The animals were divided into low RFI (-1.1, n=6), medium (-0.14, n=8) and high (+1.03, n=6) RFI groups. Corresponding mean infrared thermography cheek values were seen as low (12.2 C), medium (14.3 C) and high (15.7 C) for these groups. Spearman ranking indicated that the IRT for these animals was significantly ranked with RFI using this process ($P<0.05$). This data suggests that it may be possible to rank metabolic efficiency within a two day period by using this non invasive procedure.

Keywords: residual feed intake, infrared, cattle

P25 **Investigating RFI and diet interactions on ADG, body weight, rib and back fat thickness in pregnant Angus heifers.** C. Straathof[1,*], F. Paradis[1,2], H. Block[3], M. Colazo[4], B. Yaremcio[4], C. Li[1,2], H. Bruce[1], C. Fitzsimmons[1,2], [1]*Agricultural, Food & Nutritional Science, University of Alberta,* [2]*Agriculture and Agri-Food Canada, Edmonton, Alberta,* [3]*Agriculture and Agri-Food Canada, Brandon, Manitoba,* [4]*Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada*

Selection for residual feed intake (RFI) has the potential to alter inherent metabolism and energy partitioning which may impact other physiological processes such as longevity and reproductive efficiency. Our aim is to investigate the interaction between the genetic potential for RFI, and the impact of maternal nutrition during pregnancy on important production parameters in beef calves. Sixty-three Angus heifers were tested for RFI, split into high (32) and low (31) RFI groups, and then bred to either high or low RFI sires respectively in order to produce calves with the genetic potential for either high or low RFI. After 30d of pregnancy half of each RFI group was fed a diet formulated for an average daily gain (ADG) of 0.5 kg/d (L-diet), while the other half was fed a diet that would allow 0.7 kg/d ADG (H-diet). The diets were fed until 150d gestation, after which all heifers consumed the same diet. During the course of the trial and after, body weight, rib and back fat thickness were obtained, and were analyzed for diet and RFI effects, plus their interactions, using PROC MIXED of SAS. The H-diet heifers were heavier ($P<0.01$) at the end of the feed trial than those fed L-diet (456 ±8.5 vs 415 ±7.0 kg resp.), a difference that was also observed in ADG (0.59 ±0.03 vs 0.44 ± 0.02 kg/day resp., $P<0.05$). Back and rib fat thickness differed between diet groups at the end of trial ($P<0.01$), but only rib fat changed over the course of the trial (average increase of 2.3mm H-diet, and1.7mm L-diet; $P<0.01$). At approximately 220d gestation, body weights between heifers previously fed H-diet and L-diet were still different (488 ±8.0 vs 458 ±7.0 kg resp., $P<0.01$), though ADG from the end of trail until 220d was not different between diet groups. No differences were observed between high and low RFI heifers, nor was there evidence of significant interaction between RFI and diet. These results demonstrate the effects of maternal diet on the heifers' physical traits such as ADG, body weight and fat thickness. In the future we will investigate these effects, along with genetic capacity for RFI, on post-natal growth and development of the calves of these heifers.

Keywords: bovine, Fetal programming

P26 **Modeling carcass dressing percentage in market weight pigs.** H. R. Martínez-Ramírez[1,*], P. C. Morel[2], C. F. de Lange[1], [1]*Animal and Poultry Science, University of Guelph, Guelph, Canada,* [2]*Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand*

When using models to optimize management strategies for growing-finishing pigs the prediction of carcass dressing percentage (**CDP**) is critical, especially when evaluating the use feed ingredients that contain high levels of non-starch polysaccharides (**NSP**). A total of 87 CDP observations (representing treatment means; range: 75.8-83.8%) from 17 different studies were used to develop CDP prediction equations. The following variables were considered: BW at slaughter (101-139 kg), pre-slaughter (7-day) feed intake (2.71-3.55 kg/d), pre-slaughter diet ME content (12.9-15.2 MJ/kg), pre-slaughter diet NSP content (8.96-29.4%), pre-slaughter NSP intake (**NSPi**; 0.25-0.91 kg/d), probe carcass loin depth (51.6-65.4 mm) and probe carcass backfat depth (**Fat**, 13.3-29.2 mm). Diet nutrient contents were recalculated according to NRC (2012) and the standard NRC (2012) ME intake curve was used to estimate pre-slaughter feed intake from reported feed intake. Gut fill was predicted based on previously conducted analyses using empty BW (**eBW**) and NSPi: Gut fill (kg) = $(0.379 + 0.486 \times \text{NSPi}) \times \text{eBW}^{0.463}$. To account for systematic differences between US and Canadian CDP, US CDP were increased by 5.8%. For the variables linear, quadratic and interactive effects were considered. The mixed procedure of SAS was used for parameter estimation, using study as a random effect. Based on Akaike's information criterion (**AIC**), Table 1 describes the best model fit ($R^2=0.9536$). This study indicates that the best predictors for CDP were eBW, probe fat, and NSPi. A relatively simple model can be used to estimate CDP in market weight pigs, and may be expanded to represent effects of gender (e.g. entire males and immune castrate males) and feeding ractopamine.

Table 1. Predicting algorithms to represent carcass dressing percentage.

Item	**Coefficients**	**SE**	***P***
Intercept	55.6461	24.10	0.0242
eBW	0.6519	0.381	0.0912
eBW^2	−0.00357	0.002	0.0309
Fat	−1.4459	0.591	0.0166
Fat×NSPi	0.3942	0.124	0.0022
eBW×FAT	0.01151	0.005	0.0211
eBW×NSPi	−0.09031	0.022	<0.001

Keywords: carcass dressing percentage, Modeling, pigs

Meat Science and Muscle Biology

P27 **Influence of carcass chilling rate on quality characteristics of pork loin meat.** D. A. Omana[1,*], E. Goddard[2], G. Plastow[1], Z. Pietrasik[3], S. Anders[2], S. Moore[4], H. Bruce[1], *[1]Department of Agricultural, Food & Nutritional Science, [2]Department of Resource Economics and Environmental Sociology, University of Alberta, Edmonton, [3]Leduc Food Processing Centre, Alberta Agriculture and Rural Development, Leduc, Canada, [4]Queensland Alliance for Agriculture & Food Innovation, The University of Queensland, St Lucia, Australia*

Pork texture is affected by carcass early postmortem chilling conditions; therefore, the meat quality of pork loins (m. *longissimus dorsi*, LD) from two hundred pork carcasses chilled with (conventional chilling (CC)) or without (traditional chilling (TC)) a cold tunnel ($n = 100$) were investigated. LD were frozen following fabrication and then thawed at 4°C for 72 h prior to analysis. Data were subjected to analysis of variance using the MIXED procedure of SAS. Differences between means were determined using Tukey's Honestly Significant Difference test and were reported as significant at the $P < 0.05$ level. Proximate analysis revealed higher mean moisture content and lower mean intramuscular fat for CC than for TC pork. The mean LD pH value for CC pork was significantly ($P<0.05$) higher than that for TC pork, but mean L*, a*, b* and chroma values for CC pork were significantly lower than for TC pork, indicating that the increased fat content of the TC pork may have lightened its colour. Drip loss overall was lower than expected but was increased for CC pork most likely due to its increased moisture content. CC pork showed significantly lower mean cook loss and higher mean shear force values than TC pork. The significantly higher shear force values for CC pork may be due to decreased early post mortem muscle temperatures reducing calpain activity. Results indicated that cold tunnel chilling improved pork moisture and colour and reduced cooking loss but increased cooked pork toughness slightly. The true significance of this toughening remains to be determined with sensory testing as the benefits of increased moisture, reduced cook loss and improved colour associated with rapid chilling may outweigh any detriment to shear value.

Keywords: Conventional, Pork loin meat, Quality, Traditional

P28 **Composition of biohydrogenation intermediates in intramuscular fat of yearling steers fed forage-based diets with supplemental flaxseed or sunflower-seed.** C. Mapiye[1,*], T. D. Turner[1], D. C. Rolland[1], J. A. Basarab[2], V. S. Baron[1], T. A. McAllister[3], H. C. Block[4], B. Uttaro[1], J. L. Aalhus[1], M. E. R. Dugan[1], *[1]Agriculture and Agri-Food Canada, [2]Alberta Agriculture and Rural Development, Lacombe Research Centre , Lacombe, [3]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, [4]Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, Canada*

Supplementing forage-based diets with oilseeds can increase proportions of polyunsaturated fatty acid (FA) biohydrogenation intermediates in beef, however, effects of forage type have not been extensively investigated. This study evaluated the effects of feeding 70:30 forage:concentrate diets to yearling steers for 205 days, with either grass hay (GH) or red clover silage (RC) as the forage source, and concentrates containing either sunflower-seed (SS) or flaxseed (FS), each providing 5.4% oil to diets. Two pens of eight animals were fed per diet. At slaughter, a *longissimus thoracis* (LT) steak of each animal was collected from the 12th rib, methylated separately with methanolic hydrochloric acid and sodium methoxide, and analyzed using a combination of GC (100 m highly polar column) and Ag^+-HPLC. All the data were analyzed using PROC MIXED procedure of SAS including fixed effects of oilseed, forage and oilseed × forage interaction and random effects of slaughter date and pen nested within the oilseed × forage interaction. Compared to FS, beef from steers fed SS containing diets had greater LT proportions of total *trans*-18:1, chiefly *t*11-18:1 (vaccenic acid, 3.55-4.14% of total FA), total conjugated linoleic acids (CLA), chiefly *c*9,*t*11-CLA (rumenic acid, 0.65-0.69%), and *n*-6 FA ($P<0.05$). A forage × oilseed type interaction ($P<0.05$) was found for total *n*-3 FA, α-linolenic acid, and conjugated linolenic acid (CLNA), with their greatest LT proportions produced when feeding the RC-FS diet. Steers fed diets containing GH compared to RC or diets containing FS compared to SS had higher ($P<0.05$) LT proportions of non-conjugated, non-methylene interrupted dienes (*i.e.,* atypical dienes, AD). Overall, feeding diets containing SS increased LT proportions of vaccenic acid, rumenic acid and *n*-6 FA whereas feeding FS enriched levels of *n*-3 FA, CLNA and AD. Feeding diets containing GH versus RC also influenced LT FA composition, but generally, forage effects on FA profiles were limited compared to effects of oilseed.

Keywords: Beef, Forage, Rumenic acid, Vaccenic acid

P29 **Beef production and quality of yearling steers fed high-forage diets with flaxseed or sunflower-seed.** C. Mapiye[1,*], T. D. Turner[1], D. C. Rolland[1], J. A. Basarab[2], V. S. Baron[1], T. A. McAllister[3], H. C. Block[4], B. Uttaro[1], J. L. Aalhus[1], M. E. R. Dugan[1], *[1]Agriculture and Agri-Food Canada, [2]Alberta Agriculture and Rural Development, Lacombe Research Centre , Lacombe, [3]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, [4]Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, Canada*

Feeding cattle high-forage diets combined with oilseeds can result in large absolute increases in polyunsaturated fatty acid biohydrogenation intermediates in beef, particularly vaccenic and rumenic acids which have potential human health benefits. Increasing the degree of fatty acid unsaturation in beef, however, enhances the potential for fat oxidation, which can in turn result in undesirable alterations in eating quality. The aim of this work was to evaluate beef production and quality of yearling steers fed 70:30 forage:concentrate diets with either grass hay (GH) or red clover silage (RC) as the forage source, and concentrates containing either sunflower-seed (SS) or flaxseed (FS), each providing 5.4% oil to diets. Two pens of eight animals were fed per diet. At slaughter, the *longissimus thoracis* muscle was sampled at the 12th rib for meat quality analyses. All data were analyzed using PROC MIXED procedure of SAS including the fixed effects of oilseed, forage, oilseed × forage interaction and random effects of slaughter date and pen nested within the oilseed × forage interaction except for shear force and retail display data that were analyzed as repeated measures over time. Feeding diets containing SS as opposed to FS improved growth, carcass and sensory attributes ($P<0.05$). Feeding diets containing FS versus SS produced darker and redder meat ($P<0.05$). Feeding GH compared to RC also improved growth and carcass attributes, and sensory tenderness. Overall, steers fed diets containing SS versus FS or GH versus RC had improved beef production and quality attributes, but effects of oilseeds were generally greater than effects of forage type.

Keywords: Beef, Grass hay, Oilseed, Red clover silage

P30 **Effects of electrical stimulation and nitrite film packaging on colour stability of bison steaks and ground meat.** A. R. Rodas-González[1,*], O. López-Campos[1], J. Galbraith[2], B. Uttaro[1], M. Juárez[1], D. Siegel[3], J. Aalhus[1], *[1]Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, [2]Alberta Agriculture, Livestock Business Development Branch, Government of Alberta, Camrose, Canada, [3]Division of Bemis, Curwood Inc, Wisconsin, United States*

Previous studies have shown that bison meat discolours rapidly during retail display. This study was to determine if high voltage electrical stimulation (HVES) or nitrite film packaging (FreshCase®) could improve display-colour stability of bison steaks and ground meat. *Longissimus lumborum* (LL) and *rhomboideus* (RH) muscles were obtained from both bison carcass sides (right side HVES), vacuum packaged and aged (LL = 6, 13 and 20 d; RH = 14 d) at 2 °C. At the end of each aging period, LL steaks were obtained and evaluated for metmyoglobin reducing activity (MRA) and oxygen consumption (OC); while RH muscles were ground (80% lean:20% fat) and formed into 140g patties. Steaks and patties were then assigned to PVC-overwrapped packaging (PVC) or nitrite film packaging (NFP) and displayed in retail cases for 4 d at 3 °C. HVES had no effect on MRA and OC values in steaks ($P > 0.5$) nor on colour traits in steaks or patties during retail display ($P > 0.05$). At each ageing period, PVC-steaks and -patties deteriorated in colour during retail display from a “bright cherry red” at 0d to a “moderately dark red” after 4d ($P < 0.05$). In contrast, NFP-steaks and –patties improved in colour from “moderately dark red” to “slightly dark red” ($P < 0.05$). NFP-steaks and -patties showed no evidence of discolouration; while PVC-steaks and -patties exhibited more than 50% surface discoloration during retail display ($P < 0.05$). Similar results were observed for instrumental color. Additionally, NFP-patties had lower lipid oxidation than PVC-patties ($P < 0.05$). NFP shows promise for improving retail colour stability of bison steaks and patties; while HVES had no effect.

Keywords: bison, color stability, electrical stimulation, nitrite film packaging

P31 **Effects of electrical stimulation on meat quality of Bison strip-loin steaks.** A. R. Rodas-González[1,*], Ó. López-Campos[1], J. Galbraith[2], B. Uttaro[1], M. Juárez[1], J. Aalhus[1], *[1]Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, [2]Livestock Business Development Branch, Alberta Agriculture, Camrose, Canada*

High voltage electrical stimulation (HVES) has been shown to improve colour characteristics at grading and subsequent meat quality in beef. Since bison is characteristically dark in colour this study was conducted to determine the effects of HVES on bison meat quality characteristics. Twenty bison bull carcasses were split and the right sides were HVES (400 V peak, 5 ms pulses at 15 pulses per second for 30s) at 45 min postmortem then chilled at 2°C. Carcass pH and temperature were measured over 48 h. At 48 h postmortem, instrumental colour evaluation was obtained from the grade site (11-12th thoracic vertebrae) on both sides and *longissimus lumborum* (LL) muscles were removed, vacuum packaged and aged (6, 13 and 20 d) at 2°C. At the end of each aging period, purge loss was determined and steaks were obtained for myofibrillar fragmentation index (MFI). Additional steaks were packaged and displayed in retail for 4 d at 3 °C. Steaks were then evaluated for drip loss and Warner-Bratzler shear force (WBSF). No differences were observed between HVES groups in carcass pH and temperature at 48 h ($P > 0.05$). Lean colour was slightly darker in HVES sides (decreased *L*a*b*; P* < 0.05). Bison steaks from HVES sides did not show differences in MFI, WBSF, cooking traits or moisture loss (purge and drip loss) values (*P* > 0.05). As expected, WBSF and drip loss values diminished, and purge loss and MFI increased as days of post-mortem aging increased (*P* < 0.05). Based on these results, HVES did not offer any improvement on meat quality attributes of bison most likely due to glycogen depletion during shipping and transport.

Keywords: Bison, high voltage electrical stimulation, lean colour, shear force

P32 **Estimation of pork loin fatty acid composition from pigs fed reduced-oil corn dried distillers grains with solubles using near infrared reflectance spectroscopy and two sample treatments.** N. Prieto[1,*], B. Uttaro[2], C. Mapiye[2], M. Dugan[2], V. Zamora[3], M. Young[3], E. Beltranena[4], *[1]CSIC, Leon, Spain, [2]AAFC, Lacombe, [3]Gowans Feed Consulting, Wainwright, [4]Alberta Agriculture and Rural Development, Edmonton, Canada*

Corn dried distillers grains with solubles (cDDGS) are often used as dietary energy source in the feeding of pigs. Recently, partial removal of its oil content (4-6%) has resulted in a need to re-establish both its feeding value and effects on carcasses and pork quality. The high proportion of unsaturated fatty acids (FA) in corn oil can affect intramuscular fat which, in turn, may affect pork quality. The aim of this study was to compare the efficacy of near infrared reflectance spectroscopy (NIRS) to predict FA composition from both intact and homogenized loin samples when animals were fed 30% cDDGS. Animals used were a subset of a larger study where the net energy (NE) value of cDDGS was measured using 1056 pigs housed in 48 pens, split by sex, and fed diets assuming cDDGS NE values of 1.70, 1.85, 2.00, 2.15, 2.30 and 2.45 Mcal/kg. A subset of 96 pigs was slaughtered at 124.9 kg. At 24 h post mortem, a chop from the grading site was scanned both intact and homogenized from 400 to 2498 nm using benchtop equipment and analyzed for FA composition by gas chromatography. Accurate NIRS predictions were found for SFA, MUFA and CLA in homogenized samples expressed as mg FA/g muscle [R^2 (RMSECV): 0.95 (0.41), 0.95 (0.50) and 0.85 (0.002), respectively] and PUFA and omega-6 FA expressed as % total FA [R^2 (RMSECV): 0.84 (1.33) and 0.93 (1.22), respectively], although omega-3 FA predictability was less reliable (R^2: 0.60, RMSECV: 0.21% FA). When the samples were scanned intact, NIRS predictability was lower although still acceptable for SFA, MUFA and CLA expressed as mg FA/g muscle [R^2 (RMSECV): 0.81 (0.85), 0.87 (1.03) and 0.72 (0.003), respectively] and PUFA and omega-6 FA expressed as % total FA [R^2 (RMSECV): 0.73 (2.28) and 0.75 (1.99), respectively], but not reliable for omega-3 FA content (R^2: 0.44, RMSECV: 0.24% FA). These results suggest that a next step of NIRS validation would be to estimate pork FA composition on-line on carcasses. If successful, such approach would have evident advantages in speed of analysis and therefore opportunities for pork product differentiation.

Keywords: DDGS, fatty acid, NIRS, pork

P33 **Canadian Atlantic salmon quality characteristics.** C. Ding[1,2,*], M. Juárez[1], I. Larsen[1], B. Swift[3], S. Fukui[4], P. McKenzie[4], J. Ye[2], J. Aalhus[1], *[1]Lacombe Research Centre, Agriculture & Agri-Food Canada, Lacombe, Canada, [2]Department of Livestock Production, Inner Mongolia Agricultural University, Hohhut, China, [3]TRI-GEN Fish Improvement Ltd., Ponoka, [4]Mainstream Canada, Campbell River, Canada*

Canada ranks fourth in the world production of Atlantic salmon (120 million metric tons in 2011) and maintenance of end-product quality is increasingly important. As a baseline to monitor current salmon quality, net-farmed fish were harvested, gutted, and filleted (with weights obtained at each stage) from two separate locations on two different dates (n=40), packed on ice and transported by air to the AAFC Lacombe Research Centre. The following day, fish were removed from packaging, side weights recorded to determine shipping loss, separated into fillets (Anterior, Scottish and Norwegian), weighed, and measured for depth, pH, colour (L*a*b*), drip loss, shear force and proximate analyses. Whole fish weights ranged from 2.8-7.3 kg and averaged 5.3 kg. Fish from location A were heavier but had lower dressing percents and lighter fillet weights than fish from location B (P<0.05) and subsequently dressed weight was used as a covariate for further quality analyses. Heavier fish from location A had almost twice the moisture loss during transport (1.37 vs. 0.71), had similar pH, higher fat content (119.0 vs. 92.3 $mg.g^{-1}$), a lighter, paler red colour (higher L*a*b* values) and lower shear values (2.15 vs. 4.15 kg) than fish from location B (P<0.05). These differences were perceptible during handling as the fillets were oily with a softer texture. In contrast, during subsequent retail display, fish from location A had lower drip losses than fish from location B (15.7 vs. 25.7 $mg.g^{-1}$). These results indicate a fairly large range in quality in Atlantic salmon which may be influenced by production and harvest methods. Some of the quality deficiencies were similar to the pale, soft, exudative condition observed in other species caused by early post-mortem protein denaturation.

Keywords: Atlantic salmon quality

P34-GS **Relationship between animal sex, production and carcass characteristics and the incidence of dark cutting beef.**

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Beef carcasses that have a very dark rib eye muscle are graded Canada B4 and their value is reduced by about $0.5 per lb because the beef is unattractive to consumers and is prone to microbial growth. Recent research has suggested that carcasses with reduced muscling and weight are prone to cutting dark; therefore, the relationships between carcass or animal weight, rib eye area (REA), marbling, back fat, average daily gain (ADG), dry matter intake (DMI), feed conversion ratio (FCR) and sex of animal and the incidence of dark cutting was investigated. A data set of 845 cattle was used to test the effect of sex (steer, heifer) on the incidence of dark cutting while a sub-set of 100 cattle that graded AAA (n =28), AA (n =29), and A (n =15) was drawn from this database and matched by lot and date of birth to dark cutting animals (n = 28). The Statistical Analysis System (SAS) (Version 9.2) was used to perform CATMOD, Binomial and Multinomial Logistic regression. Both binomial and multinomial logistic regression indicated that the probability of a carcass grading B4 decreased as carcass weight and marbling score increased. CATMOD results indicated a trend for increased frequency of dark cutting in heifers (P=0.11), most likely because of the lighter weight of heifers than steers. Cattle producing Canada B4 carcasses had similar mean ultrasound fat cover, carcass weight and marbling to those producing Canada AA carcasses. Overall, production measurements predicted dark cutting best as dark cutting cattle had a mean DMI of less than 6 kg/day, a mean ultrasound REA greater than 80 cm^2, a mean ultrasound back fat depth less than or equal to 7 mm, a carcass marbling score less than or equal to 400 and a mean carcass weight of about 300 kg. Mean values of residual feed intake (RFI) were positive for cattle producing AA and AAA carcasses and negative for cattle producing B4 and A grade carcasses but were not significantly different between the grades. Results indicated that cattle that were likely to produce a B4 carcass were a specific physical type that potentially may be detected by producers using ultrasound, weigh scales and monitoring of feed intake.

Keywords: beef, carcass, dark cutting

P35 **Modification of pyridinoline concentration in m. Gluteus medius with steer age at slaughter, breed cross and growth promotants.**

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The influences of slaughter age, breed cross and growth promotants on the concentration of pyridinoline (PYR) in bovine m. *Gluteus medius* were investigated. Muscles (n = 112) from a 2 × 2 × 2 factorial with breed (Hereford-Aberdeen Angus, n = 64, or Charolais-Red Angus, n = 48) included as a sub-plot in a split-plot design were used. Experimental treatments involved steers grown to a back fat of 8 to 10 mm being killed at either 12 to 13 or at 18 to 20 months of age. Hormonal growth implants were administered or not and ractopamine hydrochloride fed (RAC) or not (NORAC). PYR was isolated by hydrolysis of perimysium in 6 M HCl and purification of hydroylsates using size exclusion and ion exchange chromatography. PYR was quantified using HPLC and comparison to a commercial PYR standard. Results indicated that there was no effect of animal production treatment on mg of collagen/g raw muscle although there was a trend (P = 0.11) toward RAC to increase muscle collagen concentration. There was no effect of treatment on nmol PYR/g raw muscle; however, administration of RAC significantly reduced the mol PYR/mol collagen (P = 0.0003) and there was a trend (P = 0.1) for hormonal growth implants to increase mol PYR/mol collagen. Pearson correlations indicated that PYR concentration in collagen increased as the concentration of collagen in muscle decreased (r = -0.50, P < 0.0001), although muscle PYR concentration was positively correlated with the amount of collagen in in the raw muscle (r = 0.33, P = 0.0004). PYR concentrations in muscle or collagen were not correlated to Warner-Bratzler shear force, suggesting that other collagen cross-links or myofibrillar proteins were more influential than PYR on cooked beef toughness. These results indicated that intramuscular collagen without PYR was being deposited in response to supplementation with the ß-adrenergic agonist but that long-term hormonal growth promotant use encouraged the formation of PYR.

Keywords: Collagen, Cross-link, Pyridinoline, Shear force

P36-GS **Effect of Suckler Beef Production in British Columbia on Tenderness.** I. Hartling*, J. S. Church, C. R. Friedman, B. Cinel, and K. K. Donkor, *Faculty of Science, Thompson Rivers University, Kamloops, British Columbia, Canada*

As consumers become more concerned with the nutritional value of the food they eat it is important for the beef industry to produce healthy meat without sacrificing quality. Grass or pasture raised beef generally has a higher nutritional value, but at the cost of real or perceived decreases in beef tenderness. We propose suckler beef production, which is rare in North America, as a solution to this problem. Suckler beef cattle are commonly raised in Europe on pasture, and in particular have been shown to have high levels of both omega-3 fatty acids and conjugated linoleic acid. Suckler cattle are also slaughtered at a younger age (10 months) with minimal finishing compared to the majority of cattle produced in North America, which may help produce more consistently tender beef. Warner-Bratzler shear force (WBS) tests were used to measure the tenderness of steaks from suckler raised beef raised in BC (nine cuts, n = 5; rib eye, n = 7), typical grass fed beef (18 months old; rib eye steaks, n = 18), and conventional grain fed beef (rib eye n = 17). Muscle fiber and connective tissue diameter of suckler steaks were measured by light microscopy. Analysis of variance (ANOVA) tests of WBS results showed the rib eye steaks from suckler, grain fed, and grass fed beef was equally tender (P = 0.439). A t-test comparison of ten cuts of suckler beef with industry standards showed that the tenderness of each suckler steak was equal to (3 cuts, P = 0.185 – 0.787) or greater than (7 cuts, P = 0.001 – 0.008) the same cut from grain fed beef. This research clearly demonstrates that tenderness does not need to be sacrificed in order to have healthier meat; and that producing suckler beef may provide tender steaks from additional muscles not typically used by the beef industry that were previously thought to be unsuitable for steaks due to lack of tenderness.

Keywords: suckler beef production, tenderness, nutritional value

Nonruminant Nutrition

P37 **Determination of the Efficacy of Feeding Yellow-Seeded Canola Products to Laying Hens.** J. L. MacIsaac [1], D. M. Anderson[2,*], R. Savary[2], [1]*Atlantic Poultry Research Institute,* [2]*Plant & Animal Sciences, Dalhousie University, Faculty of Agriculture, Truro, Canada*

Lower fibre, yellow-seeded canola holds potential as a feed ingredient in layer diets. In addition to feeding as an intact full-fat seed, meals produced by mechanically-pressing that retains 6-20% of the oil, may provide an alternative method of inclusion into laying hens diets. A 16-week trial was conducted using 240 27-wk old white Lohmann Lite laying hens to evaluate the effect of feeding yellow-seeded canola included as full-fat seeds (FFYS) or a high residue oil mechanically-pressed meal (MPCM) on production performance and egg fatty acid profiles. The experiment was a 2 X 4 factorial in a completely randomized design with processing method (FFYS and MPCM) and dietary inclusion level (0, 8, 16, 24%) as the main factors. Feed consumption for FFYS and MPCM decreased (P≤0.05) after the first 4-wk period (123.0, 116.8, 118.3, 118.5 and120.7, 113.0, 114.1, 111.3 g hen^{-1} day^{-1}; FFYS and MPCM 1-4, 5-8, 9-12, 13-16 wks, respectively). Inclusion of the yellow-seeded canola products at 24% resulted in lower (P≤0.05) body weights (1779, 1722, 1699, 1664 g hen^{-1}; 0, 8, 16, 24%). Egg production was not affected (P≥0.05) by processing or inclusion level. Cholesterol level of the eggs did not differ (P≥0.05) among the levels at wks 4 (231.9, 224.3, 218.6, 224.2 mg egg^{-1}; 0, 8, 16, 24%) or 16 (211.8, 211.9, 209.3, 209.0 mg egg^{-1}; 0, 8, 16, 24%). The FFYS increased (P≤0.05) egg EPA at 16% and 24%. Egg DHA levels increased (P≤0.05) at 8, 16 and 24% at wks 4 (50.6, 58.0, 62.7, 64.5 mg egg^{-1}; 0, 8, 16, 24%) and 16 (48.9, 58.7, 61.5, 67.5 mg egg^{-1}; 0, 8, 16, 24%). MPCM produced higher (P≤0.05) omega-3 levels at 16% (86.1 mg egg^{-1}) and 24% (89.5 mg egg^{-1}). FFYS increased (P≤0.05) omega-3 content of the eggs at all levels with 24% producing the highest (P≤0.05) content (69.2, 84.7, 98.2, 118.3 g egg $^{-1}$; 0, 8, 16, 24%). Yellow-seeded canola products could be fed to laying hens up to 24% of the diet without negative effects on production performance. Hens were able to deposit omega-3 fatty acids into egg yolks, in particular EPA and DHA.

Keywords: fatty acids, full-fat seeds, laying hen, mechanically pressed meal, Yellow canola

P38 **Apparent digestibility of gross energy, crude protein, crude fat and amino acids in camelina seed, mechanically extracted camelina meal and prepress solvent extracted camelina meal by Rainbow trout (Oncorhynchus mykiss).** D. Anderson*, M. Fu, *Animal Science, Dalhousie University, Faculty of Agriculture, Truro, Canada*

Prepress solvent extracted (SE) camelina meal (CM), mechanically extracted (ME) CM and camelina seed (CS) can potentially be used as plant-based ingredients in fish diets. This study evaluated the apparent digestibility coefficients (ADC) of crude protein (CP), dry matter (DM), crude fat (CF), gross energy (GE) and amino acids in SECM, MECM and CS. One hundred and eighty Rainbow trout (initial weight 570g ± 9g) were randomly assigned to six 500 l tanks (30 fish·tank^{-1}) in a fresh water recirculation system maintained at 12.4 ± 0.6 C. All diets were pelleted and contained chromic oxide (0.5%) as an inert fecal marker. Control diet was fed for one week to all tanks. On day seven all fish were stripped for fecal collection. After stripping all tanks were randomly assigned one of the test diets containing 69.5% control diet, 0.5% chromic oxide and 30% of one of SECM, MECM or CS. Diets were fed for the next two weeks with feces stripping commencing after five days of feeding test diets. Stripping was conducted every three days until two independent 90 g samples were collected per tank. The experimental design, a completely randomized experiment was subjected to analysis of variance of ADC and digestible nutrient content for test ingredients. If significant differences were found $P \leq 0.05$, Tukey Kramer test was used to differentiate the means ($P \leq 0.05$). The ADC for DM and GE were similar among SECM, MECM and CS. For CP the ADC in CS (76.2%) was higher ($P \leq 0.05$) than SECM (60.1%) while the ADC of CF in SECM (95.1%) and MECM 92.2%) were higher than CS (66.6%) ($P \leq 0.05$). The digestible energy in CS (3630 Kcal·kg^{-1}) was higher ($P \leq 0.05$) than SECM (1997 Kcal·kg^{-1}) and MECM (2522 Kcal·kg^{-1}). The ADC (%) in SECM, MECM and CS for lysine, methionine and threonine were 74.0, 79.7, 91.1, 85.8, 84.6, 97.9, 57.6, 70.1, 79.0 respectively. Large variation in the ADC of other amino acids were observed.

Keywords: digestibility, camelina meal, amino acids, rainbow trout, stripping method, digestible nutrient content

P39 Nutrient digestibility in different fish meals available in Atlantic Canada fed to Rainbow trout (Oncorhynchus mykiss).

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Fish meal, a significant ingredient in trout diets, is variable in nutrient content, cost·tonne^{-1} and nutrient digestibility depending on source and species of fish used to produce the meal. The apparent digestibility of crude protein (CP), gross energy (GE), dry matter (DM) and crude fat (CF) were determined for Capelin (C), herring (H), menhaden (M) and prime (P) (a blend of meals) fish meals using the indirect method with chromic oxide (0.5%) in all diets as a marker. Two hundred and forty Rainbow trout (initial weight 256 ± 9g) assigned randomly to eight 500 l tanks in a recirculating fresh water system (30 fish·tank^{-1}) at 12 ± 0.6 C. All fish were fed control diet initially for seven days with feces collected on day seven using the stripping technique. Beginning on day eight diets containing 69.5% control diet, 30% of one of the four fish meals and 0.5% chromic oxide were randomly assigned to the eight tanks. Fecal collection per tank was carried out after fish were on test diets for four days. The experiment was a completely randomized experiment with four fish meals each tested in two replicate tanks with two independent 90g samples collected from fish in each tank. Apparent digestibility coefficients (ADC) and digestible nutrient content of the four fish meals were subjected to analysis of variance. If significant differences were found among meals, Tukey Kramer test was used to differential means ($P \leq 0.05$). The ADC of CP in C (98.3%) was higher than M (89.7%) and P (92.4%) ($P \leq 0.05$). The ADC of CP in H (96.9%) was similar to all other meals. The ADC % of DM and GE respectively in C (91.2, 98.5) were higher ($P \leq 0.05$) than in M (75.6, 90.8) and P (82.5, 92.2). H was similar to all other meals for ADC of GE (95.3%). No differences were found ($P \leq 0.05$) in ADC of CF among fish meals. The digestible energy (DE) content of H (4995 Kcal·kg^{-1}) was greater ($P \leq 0.05$) than M (4625 Kcal·kg^{-1}). Both were higher in DE ($P \leq 0.05$) than C (4361 Kcal·kg^{-1}) and P (4207 Kcal·kg^{-1}).

Keywords: capelin meal, herring meal, menhaden meal, prime meal, digestibility, digestible nutrient content, rainbow trout

Physiology & Endocrinology

P40 Dietary adaptation of the gastrointestinal tract of calves involves changes in the mass of forestomach tissues and length of the small intestine.

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The objective of this study was to determine the rate of change in digesta content of the forestomach and gastrointestinal tissue weight in calves in response to dietary change. Twenty-five Holstein steer calves were stratified by BW and within strata assigned to 1 of 5 treatments. Calves received the control treatment (CON; 92% chopped grass hay and 8% mineral and vitamin supplement on DM basis) or received a moderate grain diet containing 50% chopped grass hay, 42% rolled barley grain, and 8% mineral and vitamin supplement for 3 (G3), 7 (G7), 14 (G14), or 21 d (G21). Calves were then killed and digesta mass, tissue weights, and intestinal length were determined. Data were analyzed using the Mixed Model of SAS and contrasts were used to determine whether linear, quadratic, or cubic responses occurred to advancing days on the moderate grain diet. Rumen content mass decreased quadratically ($P = 0.02$) from CON (41.0 kg) to G7 (34.3 kg) and G14 (34.4 kg) and increased for G21

(36.5 kg). The DM content of rumen digesta increased (quadratic $P = 0.02$) from CON (15.3%) to G7 (17.6%) reaching a plateau thereafter. Reticulo-rumen tissue weight was not affected ($P > 0.10$). Omasal digesta weight and tissue weight decreased linearly ($P < 0.01$) with advancing days on the moderate grain diet. Abomasal digesta and tissue weights were not affected ($P > 0.10$). Weight of the duodenum, jejunum, and ileum were not different among treatments ($P > 0.10$); however, jejunum length tended to decrease and then increase with advancing days on the moderate grain diet (cubic $P = 0.08$) and the length of the ileum increased linearly from CON (1.1 m) to G21 (1.6 m). These data indicate that adaptation to a moderate grain diet involves changes in the mass and length of tissues and that these changes respond gradually over time.

Keywords: Abomasum, Adaptation, Omasum, Reticulo-rumen, Small intestine

Production, Management & the Environment

P41-GS **Use of Principal Component Analysis to investigate relationships between methane emissions and nutrient composition of diets of beef cattle.** C. Escobar[1,*], K. Beauchemin[2], M. Oba[1], *[1]University of Alberta, Edmonton, [2]Agriculture and Agri Food Canada, Lethbridge, Canada*

Methane (CH_4) is the contributor to greenhouse gas emissions from cattle and its emissions can vary depending upon diet composition. Principal component analysis (PCA) is a technique that reduces the dimensionality of data into a set of uncorrelated variables, retaining as much variation as possible. Our aims were to: 1) build a database of enteric CH_4 emissions based on published literature, and 2) evaluate the relation between CH_4 emissions and nutrient composition of diets using PCA. A database was constructed using treatment means from research published (2000 to 2012), representing beef production systems from different diets. Criteria for selecting data to include in the database were measurement of enteric CH_4 production, dry matter intake (DMI) and diet chemical composition. Missing values for diet chemical composition were generated using values from feed composition tables or by calculation from the diet description provided. Statistical analysis was performed using JMP© (SAS Institute, NC) and the analysis included test of Mahalanobis for outliers. Relationships between CH_4 and chemical composition of diets were evaluated by PCA based on the correlation matrix. Factor extraction was made by the Varimax method. The database considered 23 studies and 89 records. Variables positively correlated ($P < 0.05$) to CH_4 (g/d) were DMI (kg/d) (r = 0.73) and forage intake (kg/d) (r = 0.64). Correlations between CH_4 (g/d) and organic matter (%) (r = 0.06), crude protein (%) (r = 0.05), neutral detergent fibre (%) (r = 0.30), and fat (%) (r = -0.45) were low ($P > 0.05$). Two factors explained 59.6% (PC1=43.6% and PC2=16.0%) of the total variation. The PC1 was associated with the chemical composition of the diets and monensin content (mg/kg DM). The PC2 was associated with the quantity of feed and methane (g/d). The loading plot indicated a strong relationship between CH_4 and DMI (kg/d) and to a lesser degree with forage intake (kg/d), and an inverse relationship between CH_4 and dietary fat content (%). In summary, DMI and forage intake both showed greater influence on CH_4 emissions than variables of dietary chemical composition.

Keywords: Methane, nutrient composition , PCA

P42 **Greenhouse gas emissions from dairying in Eastern Canada – Effects of varying dairy cow replacement rate.** E. J. McGeough, S. M. Little, H. H. Janzen, T. A. McAllister, S. M. McGinn, K. A. Beauchemin[*], *Agriculture and Agri-Food Canada, Lethbridge, Canada*

A partial life cycle assessment (LCA) was conducted to estimate the effect of varying replacement rate on GHG emissions from a typical non-grazing dairy production system in Quebec. Additionally, as dairying generates both milk and meat, a number of methods of allocating emissions between these co-products were employed. The LCA considered 65 female Holstein calves, of which 60 heifers survived to first calving at 27 mo of age. Progeny were also included in the analysis, with bulls and heifers in excess of replacement requirements finished as grain-fed veal. All animals were housed indoors and fed forages and grains produced on-farm. Replacement rates were based on commercial farm survey data compiled by Valacta, the dairy production centre of expertise for Quebec and the Atlantic provinces, with the mean, 10th and 90th percentile replacement rates employed. Replacement rates were; a) 10th percentile: 50.8%, b) mean: 36.7%, and c) 90th percentile: 22.4%. Pre-farm gate GHG emissions and removals were quantified using Holos, a whole-farm model developed by Agriculture and Agri-Food Canada and based on IPCC Tier 2 methodology tuned to Canadian conditions. Results were expressed as CO_2 equivalent per kg of fat and protein corrected milk (FPCM). Various allocations of emissions between meat and milk were considered: a) no allocation to meat, b) economic product value, c) dairy vs veal, and d) the International Dairy Federation (IDF) equation using feed energy demand for meat and milk production.

Decreasing dairy cow replacement rate, decreased the GHG intensity of milk production irrespective of allocation method. The largest reduction (17.3%) was observed where there was no allocation to meat, (1.10, 0.97 and 0.91 kg CO_2e/kg FPCM, respectively). The relative proportion of the individual gases remained relatively unchanged irrespective of replacement rate. Decreasing replacement rate increased (18%) the milking and dry stock contribution to total GHG emissions. Reducing dairy cow replacement rate reduced the GHG footprint of milk production, which would also be expected to improve farm profitability providing an economically attractive GHG mitigation strategy.

Keywords: Dairy, Greenhouse gases, Life cycle assessment, Replacement rate

P43-GS **Farm-based life cycle assessment of greenhouse gas emissions from beef cattle fed dried distillers' grains plus solubles.** M. Hünerberg[1,2,*], S. Little[1], K. Beauchemin[1], S. McGinn[1], O. Harstad[3], E. Okine[2], T. McAllister[1], [1]*Agriculture Agri-Food Canada , Lethbridge,* [2]*University of Alberta, Edmonton, Canada,* [3]*Norwegian University of Life Sciences, Ås, Norway*

Previous research has shown that feeding high fat corn distiller' grains plus solubles (CDDGS; ~10% fat, dry matter [DM]) reduces enteric methane (CH_4) emission from beef cattle. However, feeding CDDGS (~30% crude protein [CP] DM) and wheat distillers' grains plus solubles (WDDGS; ~40% CP, DM) resulted in increased N excretion that could offset reductions in CH_4 through formation of nitrous oxide (N_2O). The objective of this study was to evaluate the impact of CDDGS and WDDGS inclusion on greenhouse gas (GHG) emission from the beef life-cycle using a life cycle assessment (LCA) approach. The LCA was conducted using primary data for diet composition, CH_4 emission and N excretion generated in two studies using growing and finishing beef cattle. A representative model farm, which included 40% DM CDDGS or WDDGS in growing and finishing feedlot diets, was simulated using the Holos GHG model (www.agr.gc.ca/holos-ghg). The simulation was made relative to the standard practice of using barley grain as the main supplemental energy source in western Canadian beef cattle diets (control). Feeding CDDGS (24.8 kg CO_2 equivalent [CO_2eq]/kg beef) and WDDGS (25.4 kg CO_2eq/kg beef) resulted in 5.3 and 8.0% higher GHG intensity compared to the control scenario (23.5 kg CO_2eq/kg beef). Using high-fat distillers' grains may decrease CH_4, but if incorporated at high levels in the diet, it will increase N excretion resulting in an increase in net GHG emission.

Keywords: Beef cattle, dried distillers' grains plus solubles, greenhouse gas emissions, methane, nitrous oxide, carbon dioxide, life cycle assessment

Ruminant Nutrition and Microbiology

P44 **Effects of protein sources on growth performance of backgrounded steers.** W. Yang[1,*], L. Xu[1,2], C. Li[3], K. Beauchemin[1], [1]*AAFC, Research Centre , Lethbridge, AB, Canada,* [2]*College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia,* [3]*College of Animal Science and Technology, Inner Mongolia University for the Nationalities, Tongliao, Inner Mongolia, China*

Optimizing protein formulation in the diet of growing beef cattle is one of the most effective and practical methods of improving feed efficiency and growth performance. It also helps reduce N excretion and potential N pollution from feedlots. Dried distillers grain with solubles (DDGS) is commonly fed to beef cattle as protein and energy source. A growing study was conducted to investigate the effects of protein source on growth performance of backgrounded steers. Two hundred crossbred steers (initial BW, 274 kg) were blocked by weight, grouped into 20 pens, and then randomly allotted to one of five treatments. The treatments were: 1) the basal diet consisted of 60% barley silage and 40% barley-based concentrate (Control); or diets supplemented with an additional 2% CP in the form of 2) canola meal (CM), wheat DDGS (wDDGS), corn DDGS (cDDGS) or high-protein DDGS (hDDGS). The experimental diets supplemented with protein were formulated to be isonitrogenous (14.2% CP), while the control diet had 11.9% CP. Steers fed CM had higher (P < 0.01) DMI (8.5 kg/d) than steers fed the other diets (averaged 8.1 kg/d). Diets supplemented with CM, cDDGS or hDDGS, respectively, improved (P < 0.01) final BW (447, 441 and 441 kg), ADG (1.57, 1.51 and 1.52 kg/d), and gain:feed (185, 188 and 189 g/kg) compared to control (final BW, 427; ADG, 1.39; and gain:feed, 174). However, steers fed wDDGS diet had only a numerical improvement (P = 0.12) in final BW (434) and ADG (1.46). There were no differences (P > 0.05) in ADG or gain:feed between CM and cDDGS or hDDGS, whereas steers fed wDDGS had lower (P < 0.05) ADG than steers fed CM, and were less efficient (P < 0.05) than steers fed cDDGS or hDDGS diets. These results indicate that inclusion of protein ingredients in barley-based diets is necessary to improve growth performance of backgrounded steers. Several protein ingredients can be used effectively in the diets fed to backgrounded cattle depending upon availability and cost of feed ingredients, providing flexibility to producers wanting to minimize feed costs and maximize profits.

Keywords: backgrounded beef cattle, protein source, growth performance

P45 **Effect of Substituting Oat Grain by Wheat-based Dried Distillers Grains with Solubles on Nutritional Profiles, Energy Values, Rumen Degradation Kinetics and Balance, and Metabolizable Protein Supply in Cattle.** D. Damiran[1], A. Jonker[2], J. McKinnon[1], T. McAllister[3], D. Christensen[1], M. Yari[1], H. B. Lardner[1,*], P. Yu[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada,* [2]*Grasslands Research Centre, Palmerston North, New Zealand,* [3]*Agriculture and Agri-Food Canada, Lethbridge, Canada*

Oat (*Avena sative* L.) grain may be used by the western Canadian feedlot industry as an alternative feed when the cost of barley is high. The objective of this study was to estimate effects of inclusion of wheat based dried distillers grains with solubles (wDDGS) in oat-based diets on nutritive value for ruminants in terms of detailed (1) nutritional profiles, (2) energy values, (3) protein and carbohydrate sub-fractions, (4) in situ rumen degradation kinetics, (5) ruminal protein to energy degradation ratios, and (6) protein supply in the intestine.Two sources of oat grain were mixed with two sources of wDDGS in ratios of 100:0, 75:25, 50:50, and 25:75% (DM% basis; denoted O0, O25, O50, and O75, respectively; $n = 2$ for each mixture). The study revealed that increasing wDDGS inclusion level increased the concentration of most nutrients linearly ($P < 0.05$) except for starch and neutral detergent fiber (NDF) which were linearly decreased (from 43.6 to 12.0% and from 34.5 to 29.1% of DM for the starch and NDF, respectively). Using CNCPS, soluble and undegradable fractions of protein and carbohydrate increased linearly ($P < 0.05$) with increasing inclusion level of wDDGS, while the medium degradable fraction of CP, true protein, nonstructural carbohydrate, and the rapidly degradable fraction of carbohydrate linearly decreased ($P < 0.05$) with increasing inclusion level of wDDGS. With increasing inclusion of wDDGS, the extent of rumen degradability (g/kg DM) increased for OM (from 467 to 532 g/kg) and CP (75 to 231 g/kg), but decreased for starch (from 332 to 74 g/kg); while predicted protein supply in small intestine and degraded protein balance in rumen increased ($P < 0.05$). In conclusion, oat has reasonable optimal rumen N to energy fermentation ratios. However, the inclusion of 25% wDDGS in oat-based diets improved the ratio between nitrogen and energy supply in the rumen for microbial growth and improved absorbable protein supply to the small intestine, and decreasing NDF content of feed without altering energy value of the grain portion of whole diet.

Keywords: Cattle, oat, ruminal and intestinal digestion, hourly effective degradation ratio, wheat-based dried distillers grains with solubles

P46 **Methane emissions in response to various Propionibacterium strains in beef heifers fed a high grain diet.** D. Vyas[1,*], E. J. McGeough[1], S. M. McGinn[1], T. A. McAllister[1], K. A. Beauchemin[1], A. H. Smith[2], [1]*Agriculture and Agri-Food Canada, Lethbridge, Canada,* [2]*Dupont Nutrition and Health, Waukesha, United States*

The study was aimed at determining the efficacy of different *Propionibacterium* strains in mitigating methane (CH_4) emissions in beef heifers fed a high grain diet. Twenty ruminally cannulated beef heifers were used in a randomized block design with 28-d periods. The heifers were blocked in 5 groups on the basis of body weight (BW). Dietary treatments included 1) Control (10 g/head/d maltodextrin), 2) *Propionibacterium* strain P169 (10 g/head/d maltodextrin containing P169 at 5×10^9 CFU), 3) *Propionibacterium* strain P5 (10 g/head/d maltodextrin containing P5 at 5×10^9 CFU), and 4) *Propionibacterium* strain P54 (10 g/head/d maltodextrin containing P54 at 5×10^9 CFU), and were randomly allotted to each group. Each treatment was dosed into the rumen in a gel capsule. All heifers were fed the basal diet (10:90 forage to concentrate, dry matter basis). Rumen contents were collected on d 15 and d 18, ruminal pH was measured continuously from d 15-22, enteric CH_4 emissions were measured from d 19-22 and diet digestibility was measured from d 25-28. No treatment effects were observed for ad libitum dry matter intake (DMI, $P = 0.77$) or DMI in the chambers ($P = 0.48$). Mean ruminal pH averaged 5.91 and was not affected by treatments ($P = 0.80$). No treatment differences were observed for other ruminal pH variables, including minimum pH ($P = 0.89$) and maximum pH ($P = 0.60$). Likewise, total and major volatile fatty acid (VFA) profiles were similar among all treatments. Total enteric CH_4 production (g/d) was not affected by *Propionibacterium* strains and averaged 139 g/d ($P = 0.89$). Similarly, enteric CH_4 emission intensity, indicated as ratio of g CH_4/kg of DMI, was similar for all treatments ($P = 0.69$). No major treatment effects were observed for total tract digestibility of nutrients. In conclusion, pre-existing high propionate production in rumen due to elevated levels of starch fermentation and abundance of lactate utilizers might have reduced the efficacy of *Propionibacterium* strains to further increase molar proportion of propionate and subsequently reduce CH_4 emissions.

Keywords: Beef heifers, Methane, Propionibacterium

P47 **Methane emissions in response to various Propionibacterium strains in beef heifers fed high forage diet.** D. Vyas[1,*], E. J. McGeough[1], S. M. McGinn[1], T. A. McAllister[1], A. H. Smith[2], K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, Canada,* [2]*Dupont Nutrition and Health, Waukesha, United States*

The objective of this study was to test the efficacy of various *Propionibacterium* strains in mitigating methane (CH_4) emissions in beef heifers fed high forage diet. Twenty ruminally cannulated beef heifers were used in a randomized block design with 28-d periods. Dietary treatments included 1) Control (10 g/head/d maltodextrin), 2) *Propionibacterium* strain P169 (10 g/head/d maltodextrin containing P169 at 5×10^9 CFU), 3) *Propionibacterium* strain P5 (10 g/head/d maltodextrin containing P5 at 5×10^9 CFU), and 4) *Propionibacterium* strain P54 (10 g/head/d maltodextrin containing P54 at 5×10^9 CFU), and were randomly allotted to each group. Each treatment was dosed into the rumen in a gel capsule. All heifers were fed the basal diet (70:30 forage to concentrate, dry matter basis). Ruminal pH was measured continuously from d 15-22, enteric CH_4 emissions were measured from d 19-22 and diet digestibility was measured from d 25-28. No treatment effects were observed on ad libitum dry matter intake (DMI) ($P = 0.81$). In chambers, the DMI was dropped to 71, 88, 82 and 83% of ad libitum DMI for control, P169, P5, and P54 treatments, respectively. No treatment differences were observed for total volatile fatty acids (VFA), or molar proportion of individual VFA ($P > 0.10$). However, the molar proportion of isobutyrate was reduced ($P < 0.03$) by P5 and P54. Total enteric CH_4 production (g/d) was similar with all treatments and averaged 178 g/d (P = 0.67). However, enteric CH_4 emission intensity, indicated as ratio of grams of CH_4/kg of DMI, was reduced ($P = 0.02$) by 12, 8 and 13% with P169, P5 and P54 respectively. No major treatment effects were observed for total tract digestibility of nutrients. In conclusion, the strains were effective in reducing enteric CH_4 emission intensity (g CH_4/kg of DMI). With no changes in molar proportion of propionate, it is difficult to explain reduced CH_4 emission intensity. However, the effects might be intake mediated as heifers supplemented with *Propionibacterium* strains were able to maintain high DMI during stressful conditions in chambers as compared to control.

Keywords: Beef heifers, Methane, Propionibacterium

P48 **In vitro effects of echium oil and flaxseed oil on major rumen bacterial populations.** L. Jin[1,2,*], M. He[1], Y. Wang[1], T. Alexander[1], J. Kraft[3], C. Li[1], Y. Zhang[2], T. McAllister[1], [1]*AAFC, Lethbridge, Canada,* [2]*Northeast Agricultural University, Harbin, China,* [3]*University of Vermont, Burlington, United States*

Echium oil was refined from the seeds of *Echiumplantagineum*, a plant native to northern Africa and Europe. It contains high levels of γ-linolenic acid (*c*6, *c*9, *c*12; GLA) and stearidonic acid (*c*6, *c*9, *c*12, *c*15; SDA). The position of double-bonds differs from that of traditional oils rich in polyunsaturated fatty acid (PUFA), such as flaxseed oil (*c*9, *c*12, *c*15)and biohydrogenation of echium oil could manipulate rumen fermentation and alter rumen bacteria. An *in vitro* study was conducted to assess the effect of echium and flaxseed oil on rumen microbial populations. The control diet consisted of barley grain, barley silage and supplement in a ratio of 25:72:3 on dry matter (DM) basis. Oils in the diets were included at a level of 6% dietary DM. Serum vials containing 0.5g of each diet were retrieved after 0, 3, 6, 24 h of incubation. Whole genomic DNA was extracted and subjected to quantitative real-time PCR. The methane emission was reduced by both oil treatments at all-time points except 3 h of incubation ($P < 0.01$). Proportion of acetic acid was decreased, but propionic acid was increased in both oil treatments after 24 h of incubation ($P < 0.05$). Compared to non-cellulolytic bacteria, copy numbers of *16S rRNA* for *Fibrobacter succinogenes* and*Ruminococcus albus* with echium oil and *Ruminococcus albus* with flaxseed oil were lower than that in control at 3 h of incubation ($P < 0.05$). However, copy numbers of *16S rRNA* of *Ruminococcus albus* in both oil treatments were higher than control after 24 h of incubation ($P < 0.05$). Copy numbers of *16S rRNA* of three non-cellulolytic bacteria (i.e., *Streptococcus bovis*, *Prevotella bryantii*, and *Selenomonas ruminantium*) did not differ among treatments over the incubation period and *Ruminobacter amylophilus* was high in both oil treatments after 24 h of incubation ($P < 0.01$). Overall, the results demonstrated that the cellulolytic rumen bacteria were readily affected by PUFA from both oil sources, but these detrimental effects may have become less pronounced at later points in the incubation as PUFA were biohydrogenated.

Keywords: echium oil, rumen cellulolytic bacteria, real-time PCR, in vitro

P49 Effect of reduced-fat dried distillers grains with solubles on rumen fermentation, intestinal flow of microbial nitrogen and nutrient digestibility in Holstein cows.

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The objective was to evaluate the effect of reduced-fat dried distillers grains with solubles (RFDG) on rumen fermentation, intestinal flow of microbial N and nutrient digestibility. Four multiparous Holstein cows (mean and SD, 112 ± 41 DIM; 590 ± 61.14 kg BW) were fitted with ruminal and intestinal fistulae and randomly assigned to 1 of 4 treatments in one 4 × 4 Latin square. Treatments (DM basis) were 1) CONTROL, 0% RFDG; 2) 10% RFDG; 3) 20% RFDG and 4) 30% RFDG. Milk yield was recorded daily and samples were collected on d 18 to 21 of each period. Rumen pH was measured; samples of rumen fluid, duodenal digesta and feces were collected on d 18 to 21 of each period. Intestinal flow of microbial N was estimated with purines or DNA as microbial markers. Data collected were analyzed using the MIXED procedure of SAS, rumen VFA and ammonia concentrations were analyzed as repeated measures. Milk yield was not affected by treatment ($P = 0.65$) and averaged 31.43 ± 2.81 kg/d. Percent of milk protein was not affected ($P = 0.35$) and averaged 3.02 ± 0.07%. Percent milk fat ($P = 0.28$) was not affected and averaged 3.25 ± 0.14%. Total ruminal VFA ($P = 0.40$) and ammonia ($P = 0.18$) concentrations were not affected by treatment and averaged 135.18 ± 6.45 mM and 18.66 ± 2.32 mg/dL, respectively. Intestinal flow of microbial N was not affected by treatment when estimated using purines ($P = 0.47$) or DNA ($P = 0.65$) markers. However, when averaged across treatments purines yielded higher ($P < 0.01$) microbial N flow compared to DNA markers, averages were 303.0 and 218.0 ± 18.0 g N/d, for purines and DNA markers, respectively. The digestibility of dry matter ($P = 0.14$), organic matter ($P = 0.14$), neutral detergent fiber ($P = 0.11$) non-fiber carbohydrates ($P = 0.07$) and N ($P = 0.06$) tended to increase with RFDG inclusion. Results indicate that dairy rations can be formulated to include up to 30% RFDG with no negative effect on ruminal VFA concentration, intestinal supply of microbial N and major nutrient digestibility.

Keywords: distillers grains, rumen fermentation, intestinal microbial N, nutrient digestibility

P50 Differential effects of nitrogen sources including Optigen®II on in vitro rumen ammonia release.

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An *in vitro* study was conducted to examine differences in ammonia release from urea, Optigen®II (Alltech Inc.), soybean, and canola meal in forage (low energy) and concentrate-based (high energy) diets. Diets consisted of a mixture of barley grain - barley silage (25:75) for the growing diet and (80:20) for the finishing diet. Each diet was incubated with rumen fluid in the presence of each nitrogen source, three times over a period of three weeks. N-sources were added to diets to ensure that they were isonitrogenous at each specific inclusion level based on addition of soybean meal at 2, 6 and 10% of diet dry matter. Substrates (1.2 g) were incubated with 120 ml of mixed rumen fluid over a period of 24 h and the samples were retrieved for ammonia analysis after 0, 3, 9, 12 and 24 h of incubation. The results clearly show that the release of ammonia from Optigen®II was moderated as compared to urea, particularly after 3 and 9 h of incubation in the growing diet at 6 and 10% inclusion levels and in the finishing diet at the 10% level ($P < 0.01$). Ammonia concentration in incubations containing Optigen®II did not differ from that in soybean meal and canola meal with both diets after 3 and 9 h of incubation. This implies that the inclusion of Optigen®II would result in synchronization of carbon and nitrogen utilization by rumen microorganisms in a manner that is similar to that of soybean and canola meal and Optigen®II could be an effective partial substitute for soybean meal and canola meal.

Keywords: Optigen®II, urea, ammonia release, in vitro

P51 The effect of pregnancy on proteins relating to energy metabolism in mature beef cows.

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In mid- to late-gestation, nutrient demand increases to meet the growth requirements of the conceptus. The pregnant cow may be able to alter metabolism in response to energy demands of pregnancy. Eighteen non-lactating, mature Simmental/Angus crossbred cows, pregnant (PREG; n = 9) and non-pregnant (OPEN; n = 9) in a replicated randomized complete block design were used to investigate the impact of pregnancy on abundance of proteins relating to energy balance. Cows were individually fed a ration containing high grass haylage and 30% wheat straw to ad libitum intake. The first block was slaughtered at d 89 of the feeding period and each block every 7 d thereafter, such that PREG

cows in the block were slaughtered 4-5 wk prior to parturition. Tissue samples from liver, kidney, sternomandibularis muscle, ruminal papilli (ventral sac), pancreas, and small intestinal muscosa were collected at slaughter and snap frozen in liquid N_2. Western blots from these tissues were conducted to quantify abundance of: PCNA, ATP synthase, ubiquitin, and Na+/K+ ATPase for all tissues; PGC1-α, PPARγ, AMPKα and pAMPKα for liver, muscle, and rumen; PEPCK for liver and kidney; and UCP2 for liver. Data were analyzed using Proc Mixed of SAS as a replicated randomized complete block with pregnancy, cow age, and block nested within replicate as fixed effects. DM intake and ADG did not differ ($P \geq 0.2$) between OPEN and PREG cows. Hepatic Na+/K+ ATPase abundance was greater ($P = 0.04$) in PREG cows. In rumen papillae, abundance of pAMPKα was increased ($P = 0.006$) in PREG cows. No other differences ($P \geq 0.08$) were observed in targeted proteins for any tissues measured. These data suggests that differences in metabolic proteins occur during pregnancy that could have an influence on metabolic efficiency.

Keywords: Beef Cow, energy partitioning, feed efficiency, pregnancy

P52 **Effect of wheat vs barley and processing index on growth performance, eating behavior and carcass quality of finishing feedlot steers.**

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This study compared inclusion of wheat vs barley grain processed to two different indexes on the growth performance of finishing beef cattle. Cross breed steers (n=160, BW=538±36 kg) were allocated to 16 feedlot pens (10 steers per pen and 4 pens per treatment) and fed wheat or barley grain at 89% of diet DM with a processing index (PI) of either 75 or 85 for 12 wk prior to slaughter. Remaining dietary ingredients included 6% barley silage and 5% supplement. Average daily gain (ADG) was not affected ($P > 0.05$) by either grain type or PI. Dry matter intake (DMI) and ratio of gain: intake (G:I) were affected ($P < 0.05$) by PI but not grain type. A PI of 85 increased ($P = 0.05$) DMI but reduced ($P = 0.04$) feed efficiency as compared to PI75. Wheat reduced ($P < 0.05$) eating time, meal duration and size but increased ($P < 0.05$) eating rate compared to barley. A PI of 85 increased ($P < 0.05$) meal duration compared to PI75. Carcass traits and incidences of liver abscess were not affected ($P > 0.05$) by treatments with the exception that percentage of saleable meat was higher ($P < 0.05$) with PI75 as compared to PI85. In conclusion, grain PI could affect eating behavior, growth performance and carcass traits of finishing feedlot steers, whereas feed wheat and barley grain resulted in similar performance and carcass traits in finishing beef steers.

Keywords: barley, feedlot cattle, processing index, wheat

P53 **Effect of replacing barley grain with wheat on rumen fermentation in finishing beef cattle.**

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This study investigated effect of substituting barley grain with feed wheat in a finishing diet on rumen fermentation in beef cattle. An experiment was designed as a replicated 4x4 Latin square using 8 rumen cannulated steers (742±44kg) fed diets in which wheat replaced 0, 30, 60 or 89% wheat of the barley grain on a dry matter (DM) basis and with a constant processing index of 80. The remaining ingredients consisted of 6% barley silage and 5% supplement. Duration of rumen pH under 5.8 linearly increased ($P = 0.04$) with increasing levels of wheat, whereas average, minimum and maximum pH, time and area under pH 5.5 and 5.2, total VFA, mol (%) of individual VFA, protozoal populations and apparent digestibility were not affected ($P > 0.05$) by wheat inclusions. Copy numbers of 16S rRNA per g DM from *Ruminococcus amylophilus* as well as total bacteria linearly increased ($P < 0.05$) with increasing wheat, whereas those associated with *Fibrobacter succinogenes* decreased ($P < 0.05$) with levels of 30 or 60% wheat in the diet. In conclusion, replacing barley with wheat in feedlot diets appears to have no negative impact on rumen function or nutrient digestibility, suggesting that levels of wheat included in finishing diets could be higher than that typically used in the feedlot industry.

Keywords: barley, cattle, rumen fermentation, wheat

P54 **Fatty acids profile of goat meat fed diets with palm kernel cake derived from biodiesel production.**

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The objective of this study was to determine the optimal level of palm kernel cake in the diet of growing ½ Boer kids by analyzing the fatty acids profile of their meat. A total of 40 non-castrated ½ Boer kids with a mean age of 90 days and initial weight of 15.01 kg were used in this study. The animals were fed Tifton-85 hay and a concentrate mixture containing 0, 7.0, [1]4.0 and 21.0% palm kernel cake in the dry matter. Confinement lasted 72 days, and the animals were fasted and slaughtered on the last day. The left loin were used for the analyses and after the extraction of lipid content, the fatty acids were methylated and the identification and quantification of the fatty acid esters were obtained through analysis using a gas chromatograph coupled with a flame ionization detector. The fatty acid profile was not significantly influenced by the addition of palm kernel cake, except by the myristic acid levels (C14:0), this lack of influence most likely occurred due to the small change in the lipid profile of the total diets. Palm oils and their by-product derivatives possess an elevated content of lauric acid and myristic acid compared to soy, which is rich in linoleic acid. Comparing the ingredients separately, it can be inferred that, by possessing a higher polyunsaturated fatty acid content, soybean meal would provide a better fatty acid profile for the meat. However, it is important to consider that these ingredients compose, at most, 21% of the total diet and that their lipid characteristics were thus diluted by the characteristics of the other ingredients. The increase in myristic acid was caused by high levels in this fatty acid in palm derivatives. Myristic acid are considered an atherogenic fatty acid, but this modification was not sufficient to promote increase in an atherogenicity index, therefore wasn't impairment meat quality. Palm kernel cake can be added to the diet of ½ Boer kids at a ratio of up to 21.0% without causing any damage to the fatty acids profile of the resulting meat.

Keywords: by-products, kid, ruminant

P55-GS **Relationship of sorting behavior with chewing activity, rumen fermentation and milk production in lactating dairy cows fed diets differing in the dietary forage-to-concentrate ratio.** X. Gao[1,*], M. Oba[2], [1]*AFNS, University of Alberta, Edmonton,* [2]*AFNS, University of Alberta, Edmonton, Canada*

The objective of this study was to evaluate the relationship of sorting behavior with chewing activity, rumen fermentation and milk production in lactating dairy cows when fed two diets with different forage-to-concentrate ratios. Sixteen ruminally cannulated late lactating Holstein cows (DIM = 261 ± 33.8; BW = 601 ± 75.9 kg) were fed a high-forage diet (**HF**, 60% forage) for 21 days, then a high-grain diet (**HG**, 35% forage) for the following 21 days. Penn State Particle Separator was used for particle size analysis. The separator contained 3 screens (18, 9, and 1.18 mm) and a bottom pan to determine the proportion of long, medium, short, and fine particles, respectively. Sorting index (SI) was calculated as the ratio of actual intake to the expected intake for particles retained on each sieve. Cows sorted ($P < 0.05$) against long ration particles and for short and fine particles, and SI of short particles was positively correlated to chewing time/DMI ($P < 0.01$) and negatively correlated to DMI ($P < 0.05$) regardless of the dietary forage-to-concentrate ratio. When cows were fed the HF diet, although ruminal pH was not associated with the extent of sorting, the SI of short particles were negatively correlated to yields of milk (r = -0.63, $P < 0.01$), milk fat (r = -0.54, $P = 0.03$) and milk protein (r = -0.66, $P < 0.01$). However, when cows were fed the HG diet, there was negative correlation between SI of fine particles and minimum ruminal pH (r = -0.66, $P < 0.01$). In addition, milk and milk component yields were not correlated to the extent of sorting for the HG diet. These results suggest that the extent of sorting for short particles is negatively correlated to milk production for the HF diet or ruminal pH for the HG diet without decreasing chewing time.

Keywords: Chewing, Forage-to-concentrate ratio, Sorting

P56 **Feeding tannins to reduce ammonia emissions from feedlot cattle fed high protein finishing diets containing corn distillers grains.** K. M. Koenig[*], S. M. McGinn, K. A. Beauchemin, *Agriculture and Agri-Food Canada, Lethbridge, Canada*

The objective of the study was to investigate the effect of dietary condensed tannins (CT) on NH_3-N emissions from feedlot cattle fed high protein finishing diets containing corn dried distillers grains and solubles (DDGS). Four pens of 10 steers that were part of a larger study to determine the effect of CT in high protein diets on growth performance were moved from research feedlot pens to isolated pens for measurement of NH_3-N emissions. The 4 dietary treatments included 0% DDGS (0DGGS), 20% DGGS (20DGGS), 40% DGGS (40DGGS), and 40% DGGS with 2.5% CT extract from *Acacia mearnsii* (40DGGSCT), and contained 13.3, 15.9, 20.4, and 19.4% CP, respectively (DM basis). The DDGS was substituted for grain in a barley-based diet that contained 91% concentrate and 9% silage. In four 3-wk periods, NH_3-N emissions were measured from 2 pens of cattle using the integrated horizontal flux technique with passive NH_3 samplers. Emissions were measured from cattle fed 0DDGS and 20DDGS, 40DDGS and 40DDGSCT, 0DDGS and 40DDGS, and 0DDGS and 40DDGSCT in period 1, 2, 3, and 4, respectively, from Apr 30th to Jul 3rd. Manure accumulated in the pens for 14 d. Samplers were mounted to vertical masts at heights of 0.5, 1, 2, and 3 m located in the middle of the north, east, south, and west perimeters of the pen every 24 h for 4 d. Data for daily NH_3-N emissions from the 2 pens in each period were analyzed using a mixed linear model. The NH_3-N emissions were higher from steers fed 40DDGS (113.7 vs. 70.8 ± 7.2 g N/(steer·d), $P = 0.006$), but were only numerically higher from steers fed 20DDGS (51.3 vs. 26.3 ± 11.6 g N/(steer·d), $P = 0.18$) compared to 0DDGS. Steers fed 40DDGSCT tended to have lower NH_3-N emissions compared to steers fed 40DDGS (60.7 vs. 92.4 ± 9.4 g N/(steer·d), $P = 0.07$ and 17.1 vs. 25.7 ± 2.6 % N intake, $P = 0.08$) for 3 of the 4 d, although NH_3-N emissions from steers fed 40DDGSCT tended to remain higher than from steers fed 0DDGS (46.8 vs. 32.0 g N/(steer·d), $P = 0.08$). Feeding CT reduced NH_3-N emissions by 34% in feedlot cattle fed high protein diets although the effectiveness may depend on environmental conditions.

Keywords: cattle, condensed tannins, corn distillers grains

P57 **Analysis of probiotic bacteria to inhibit the respiratory pathogen Mannheimia haemolytica and adhere to bovine bronchial epithelial cells in vitro.** S. Subramanian[1,*], T. A. McAllister[1,1], J. Baah[2], T. W. Alexander[1], [1]*Beef Physiology,* [2]*Ruminant Nutrition and Microbiology, Lethbridge Research Centre, Lethbridge, Canada*

In North American feedlots, prevention and treatments of bovine respiratory disease (BRD) are aimed primarily at bacterial pathogens, through the use of antimicrobials. As an alternative to antimicrobials, this study investigated the *in vitro* potential of probiotic bacteria to inhibit growth of the BRD bacterial pathogen, *Mannheimia haemolytica*. The probiotic strains tested were *Lactobacillus acidophilus*(ATCC 4356),*L. rhamnosus* GG (ATCC 53103), *L. casei* (ATCC 393), *L. lactis* (DSM 20250), *L. helveticus* Lh12 (ATCC 15009),*L. plantarum* NCDO 1193 (NCIMB 8299), *Paenibacillus polymyxa* (strains ATCC 842, ATCC 10401, and JB) and *Streptococcus thermophilus* (DSM 20617). A serotype 1 strain of *M. haemolytica* (LRC24A) isolated from the respiratory tract of a feedlot steer that succumbed to BRD was used for inhibition assays. The antimicrobial activities of probiotic bacteria were analyzed by spotting 50 µL of cell-free filtrate isolated from overnight liquid cultures onto a plated lawn of *M. haemolytica*. The plates were then incubated for 24 h at 37°C and clearance zones were measured. The adhesion of bacteria to a bovine bronchial epithelial cells was also assessed by microscopy and direct plating. Filtrates from all bacteria with the exception of *S. thermophilus* inhibited *M. haemolytica* with inhibition zones ranging from 0.2 cm (*L. plantarum*) to 1.3 cm (*P. polymyxa* JB). The highest epithelial adherence rate was observed for *M. haemolytica* (86%). Among probiotic bacteria, adherence ranged from 0.34% (*P. polymyxa*) to 68% (*L. lactis*). This investigation showed that probiotic bacteria are able to inhibit the respiratory pathogen *M. haemolytica* and adhere to respiratory epithelia. These properties suggest that probiotic bacteria may have potential to mitigate this pathogen in the respiratory tract of cattle.

Keywords: Probiotic, Immunomodulation, Bovine Respiratory Disease, Mannhemia haemolytica

P58 **Interactions of cattle leptin genotype and dietary oilseeds and dried distiller's grain on fat accumulation, adipocyte size, and body fatty acid profile.** M. He[1], L. Jin[1,*], T. A. McAllister[1], F. Marquess[2], [1]*Agriculture and Agri-Food Canada, Lethbridge,* [2]*Quantum Genetix Canada Inc., Saskatoon, Canada*

Cattle leptin genotypes can be identified as TT, CT and CC based on single nucleotide polymorphisms (SNP) with differences in genotypes influencing fat metabolism and deposition. The present study examined interactions between leptin genotype and oilseed – dried distillers' grain diets (DDGS) on adipocyte size and fatty acid profile in British cross breed steers (n=40, BW=460±27kg). Steers were housed in individual pens and sorted into 8 groups in a 2×2×2 factorial experiment which included the CT or TT genotype, -10% flaxseed (FS) or high oleate sunflower seed (SS) in the diet with or without 30% triticale DDGS. Diets consisting of 90% concentrate and 10% barley silage were fed for 15 weeks prior to slaughter. Measurements included growth performance, ultrasound backfat thickness, cellularity of backfat biopsies, and fatty acid profiles of plasma and adipose and *longissumus thoracis* muscle samples. Gain:feed of steers with TT genotype was higher ($P = 0.02$) than steers with the CT genotype. Neither genotype nor diet affected ($P > 0.1$) back fat thickness, but inclusion of DDGS decreased ($P = 0.04$) the percentage of adipocytes with a diameters ranging from 151-175 µm whereas FS increased ($P < 0.01$) it. Cattle with TT genotype were higher ($P < 0.05$) in plasma total n-3 fatty acids compared to CT cattle, but similar differences were not observed in adipose tissue. However, in the LT muscle total n-3 fatty acids were higher ($P < 0.05$) in CT cattle compared to TT cattle consuming the FS+DDGS diet. Inclusion of FS alone increased ($P < 0.05$) total omega-3 fatty acids in fat and muscle tissue a response that was further increased ($P < 0.05$) with inclusion of f DDGS in this diet. The results indicated that cattle leptin genotype may affect omega-3 fatty acids level in plasma and intramuscular fat with these profiles been further influenced by inclusion of oilseed and DDGS in the diet.

Keywords: cattle, flaxseed, leptin gene, omega-3 fatty acid, triticale dried distiller's grain

P59-GS **An optimal method for microbial total RNA isolation from rumen contents.** F. Li[*], M. Zhou, X. Sun, L. Guan, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*

Ruminal fermentation is a vital process of feed digestion and is conducted by rumen microbes. Measuring gene expression of the rumen microbiome will reveal the activity of the whole microbial community and thus will enhance our understanding of the fermentation process from the biological view. Extraction of high-quality RNA from rumen contents is the first and essential step for microbial transcriptome analysis. Previous RNA extraction methods on frozen samples did not work effectively on RNA*later*® preserved rumen samples. Therefore, the objective of this study was to develop an optimal procedure to isolate microbial total RNA from rumen contents reserved in RNA*later*® reagent. In our study, sixteen bovine rumen content samples that were stored in RNA*later*® reagent at -20 °C since 2007 were subjected to microbial total RNA extraction. Our procedure was based on the acid guanidinium-phenol-chloroform method with modifications. Further optimization procedures included changing the volume of TRIzol®, Chloroform, Isopropanol and Saline solution used in the extraction procedure. More specifically, ~0.2 g rumen content sample corresponded to 1.5 ml of TRIzol®, 0.4 ml of Chloroform, 0.3 ml of Isopropanol and 0.3 ml of Saline solution. Our results showed that total RNA was effectively isolated from all sixteen rumen content samples with the quantity of total RNA ranged from 11.06 µg to 73.33 µg per gram of rumen content and the RNA integrity number (RIN) ranged from 8.2 to 10 with rRNA ratio (23S/16S) ranged from 1.7 to 2.0. These results suggest that RNA*later*® reagent can efficiently preserve microbial RNA in rumen contents, and our modified RNA isolation method can provide high-quality RNA for downstream transcriptome profiling analysis using next generation sequencing.

Keywords: microbial transcriptome, rumen contents, total RNA isolation

P60-GS **In-Vitro Efficacy of Bacteriophages T5, T4, T1 and O1 against E. coli O157:H7.** H. Liu[1,*], Y. Niu[2], J. Li[1], K. Stanford[2], T. A. McAllister[3], [1]*College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China,* [2]*Alberta Agriculture and Rural Development,* [3]*Agriculture and Agri-Food Canada, Lethbridge, Canada*

Cocktails of bacteriophages are frequently advocated as a means of avoiding phage resistance, but such an approach can also reduce efficacy via competitive interference. Thisstudy compared efficacy of cocktails of phage of different families and/or genera to single phage against *E. coli*O157:H7 (EC) in broth culture. Four phages (*Siphoviridae*phages T5 and T1, *Myoviridae*phages T4 and O1) as well as phage cocktails (T5+T1, T4+O1, T5+T4, T5+O1, T1+T4, T1+O1 and T5+T1+T4+T1) were assessed for their activity against 7 EC strains (E318N, CO281-31N, R508N, E32511, 3081, H4420N and EDL933) both individually and as a mixture. Single phage (>10^8PFU/ml) and cocktails were serial diluted and incubated at 37°C with diluted overnight EC culture (~10^4CFU/ml) at multiplicity of infection (MOI) of 0.01, 0.1, 1, 10, 100 and 1000. Optical density at 600 nm (OD_{600}) was measured at 2 h intervals for 10 h .When MOI was greater than 0.01, phage cocktails T1+T4 and T5+T1+T4+O1 showed higher activity (Avg. OD_{600}=0.067±0.008,*P*<0.05) against individual strains and the EC mixture, followed by T5+T1, T4 and T5. Growth of the EC mixture was almost completely inhibited by T5 or T5+T1 at each MOI and sampling times >4 h. There was no competitive interference (*P*>0.1) observed in 2 phage combinations targeted against CO281-31N, 3081 or EDL933. In contrast, T5+T4, T4+O1 and T5+T4+T1+O1 were less effective (*P*<0.001) than T5 or T4 against R508N and the EC mixture. At a MOI of 0.01, T5+T4 were less effective (*P*<0.001) than T5 alone against H4420N, but at MOI>10, the mixture was more (*P*<0.05) effective against this strain than T4 alone. Phage cocktails may exhibit slightly higher effectiveness against EC strains than single phage treatments at higher MOI (≥0.1) over time. At lower MOI (<0.1), competitive interference may reduce the effectiveness of phage cocktails against some EC strains.

Keywords: Bacteriophage, E. coli O157:H7

P61-GS **Heat-Induced Changes in Chemical and Nutrient Profiles of Different Types of Cereal Grains: Comparison of Control vs. Dry Heating vs. Moist Heating.** Y. Ying[*], D. A. Christensen, J. J. McKinnon, P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada*

The objective of this study was to find out how different heating methods would affect the chemical composition, energy value and nutrient profiles of three types of cereal grains. These grains were wheat, triticale and corn. The grain seeds were divided into 3 groups (control, dry heating and moist heating) and processed at 121℃ for 80 min in 2 batches. Significant (P<0.001) differences were found between the cereal grains in chemical characteristics, protein and carbohydrate fractions and energy values. Composition of NDF, NDICP and hemicellulose were increased while moisture and SCP were decreased in all three types of cereal grains (P<0.05). Compared to dry heating, moist heating had more impact on altering the nutrient profile. Among the protein fractions, PB1 fraction was decreased by moist heating (wheat: 27.1 vs. 10.1; triticale: 41.2 vs. 15.0; corn: 29.0 vs. 13.9, % CP) and both PB3 (wheat: 6.2 vs. 27.0; triticale: 9.1 vs. 35.3; corn: 8.1 vs. 29.5, %CP) and PC (wheat: 0.0 vs. 0.4; triticale: 0.0 vs. 0.2; corn: 0.0 vs. 5.2, %CP) fractions increased (P<0.05). Only CB3 of the 8 CHO fractions was changed by moisture heating (P<0.05). The results showed different types of cereal grain reacted differently to heat effect. For example, moist heating decreased the cellulose content (2.4 vs. 2.1, %DM) of triticale and ADF content (2.1 vs. 2.6, %DM) of corn (P<0.05). Total digestible FA was accreted in wheat (tdFA: 0.3 vs. 0.5, %DM) and total digestible NDF was reduced in triticale (tdNDF: 7.0 vs. 5.5, %DM) in response of moist heating (P<0.05). But none of DE, ME and NE in these two grains were significantly changed. For corn, total digestible NFC (tdNFC: 78.2 vs. 76.5, %DM), DE (3.8 vs. 3.7, Mcal/kg), ME (3.13 vs. 3.06, Mcal/kg), NE_m (2.13 vs. 2.08, Mcal/kg) and NE_g (1.46 vs. 1.42, Mcal/kg) were all decreased (P<0.05). In conclusion, heating induced changes in nutrient profiles and different heating methods had different impact and response sensitivity to heating differed among the cereal grain.

Keywords: cereal grains, chemical composition, Heat-induced changes, protein and carbohydrate fractions

P62 **Alteration of Modeling Nutrient Supply of Different Types of Cereal Grains to Dairy Cattle through Different Heating Methods.** Y. Ying*, D. A. Christensen, J. J. McKinnon, P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada*

Cereal grains have different degradation kinetics. Heat treatments are known to be able to change the nutrient values of the feed but the effect could be equivocal. The objective of this study was to evaluate the heat-induced changes in potential protein supply using NRC-2001 model and DVB/OEB model. Three types of cereal grains (wheat, triticale and corn) were either autoclaved or dry roasted in 2 batches. Including a control group, the experiment was a 3 by 3 factorial design. In the DVE/OEB model, autoclaving increased ($P<0.05$) the total protein supplied to the small intestine (TPSI: 148 vs. 222 g/kg DM) in wheat, as well as rumen bypass feed crude protein (BCP: wheat: 84 vs. 171; triticale: 53 vs. 86 g/kg DM) and truly absorbed bypass protein in the small intestine (ABCP: wheat: 77 vs. 154; triticale: 40 vs. 67, g/kg DM) in wheat and triticale. However, microbial protein synthesized in the rumen based on available nitrogen (N_MCP: wheat: 109 vs. 24; triticale: 77 vs. 46, g/kg DM) in wheat and triticale was decreased after autoclaving. Thus, in wheat, truly digested protein in the small intestine (DVE: 126 vs. 190 g/kg DM) was accreted and degradable protein balance (OEB: 23 vs. -44, g/kg DM) was reduced. According to NRC-2001 model, parameters such as truly absorbed rumen-synthesized microbial protein in small intestine (AMCP), truly absorbed rumen-undegraded feed protein in small intestine (ARUP), total truly absorbed protein in small intestine (MP: wheat: 136 vs. 165; triticale: 85 vs. 95 g/kg DM) and degraded protein balance (OEB: wheat: 3 vs. -60; triticale: -32 vs. -73 g/kg DM) in wheat and triticale were all decreased by autoclaving ($P<0.05$). Rumen endogenous protein (ECP) and truly absorbed rumen endogenous protein in the small intestine (AECP) were increased ($P<0.05$) by autoclaving while dry roasted samples had even higher values ($P<0.05$). In summary, wheat and triticale were more sensitive towards heat effect compared to corn and autoclaving had larger impact than dry roasting on the protein supply of dairy cattle.

Keywords: Modeling nutrient supply, cereal grains, heat treatment methods

P63 **Ensiling properties of whole crop barley and intercropped barley-oat-spring triticale.** L. Jin*, J. P. Lynch, L. Duniere, Y. Wang, J. Baah, K. A. Beauchemin, T. A. McAllister, *AAFC, Lethbridge, Canada*

Two laboratory silo experiments were conducted in two consecutive years to determine the effect of mixed cereal crops on silage conservation characteristics. Whole-crop silage was prepared from a single cultivar of barley (BA), a mixture of three cultivars of barley grown together (seeding ratio 1:1:1; BV), and intercropped barley, oats and spring triticale (seeding ratio: 1:1:1; BI). The materials were harvested from three areas of each field at the mid-dough stage, wilted to a dry matter (DM) content of 33-35% and chopped to a theoretical length of 1.0 cm. The chopped plant materials were packed into laboratory scale mini-silos without preservatives and stored at room temperature. Triplicate mini-silos of each treatment were opened on d 7 and d 90 of ensiling and samples were collected for determination of pH and concentrations of volatile fatty acids (VFA) and lactic acid. Samples collected from d 90 were also enumerated for lactic acid producing bacteria (LAB). The pH of BI and BV silage was lower ($P<0.05$) than that of BA silage at d 7 and d 90 in the first year. However, pH was lower ($P<0.05$) for BV silage than for BA and BI silage at d 90 in the second year. Lactic acid and succinic acid concentrations were higher ($P<0.05$) in BI than in BA and BV on d 90 in the first year. Total VFA and acetic acid concentrations were not affected by treatment. LAB was higher in BI and BV than BA in the second year ($P<0.05$). All silages had similar dry matter disappearance during the 90 days ensiling period in both years. The increased lactic acid production and reduced pH of BI suggest that mixing barley, oat and triticale during ensiling enhanced fermentation during ensilage and could be a potential method to improve silage quality.

Keywords: crop mixture, mini silo, silage conservation, fermentation

P64 **Effect of inoculant containing L.buchneri on ensiling fermentation of whole barley crop.** L. Jin*, J. P. Lynch, L. Duniere, Y. Wang, J. Baah, K. A. Beauchemin, T. A. McAllister, *AAFC, Lethbridge, Canada*

A mini silo study was conducted to determine the effect of applying bacterial inoculants (a mixture of *Lactobacillus buchneri*, *Lactobacillus plantarum*, *Lactobacillus casei*, BI) and BI plus exogenous enzymes (Rovabio Excel LC, BIE) at ensiling on fermentation of barley. Whole-crop barley (cv. Sundre) was harvested from three areas of the field, wilted to a dry matter content of 33-35% and chopped at a theoretical length of 1.0 cm. The chopped plant material was sprayed with de-ionized water (Control), de-ionized water containing 11GFT (BI1), 11G22 (BI2) or a mixture of 11G22 and exogenous fibrolytic enzymes (BIE). The BI was applied at 1.0×10^5 cfu / g fresh forage and the enzyme product was applied at 2.0 ml / kg fresh forage. The treated ensiling materials were packed into mini-silo and stored at room temperature. Triplicate mini silos were opened on d 7, d 28 and d 90 and silage samples were taken for measurements of fermentation products and chemical composition. The pH of BI1, BI2 and BIE was lower than that of control at d 7 but higher than control at d 28 and d 90 and the BI1 was the highest at d 90 ($P<0.01$). Acetic acid (g/kg DM) and total volatile fatty acid concentrations were higher for all treatments than for the control at d 28 and d 90 ($P<0.01$). Methanol and ethanol concentrations were higher for all treatments than for control at d 90 ($P<0.05$). Concentration of 1-propanol was higher in BI1 and BI2 than control and BIE at d 90 ($P<0.05$). Lactic acid bacteria were higher for all treatments than the control at d 90 ($P<0.01$). Overall, the BI and BIE enhance the fermentation characteristics during the ensiling process and possibly improved the aerobic stability of barley silage.

Keywords: L.buchneri, enzyme, silage conservation, fermentation

P65-GS **Whole genome sequencing of Escherichia coli O157:H7 isolates from super-shedder and non-super-shedder cattle.** K. Munns[1,2,*], Y. Xu[2], K. Stanford[3], L. B. Selinger[2], T. A. McAllister[1], *[1]Agriculture and Agri-Food Canada, [2]Department of Biological Sciences, University of Lethbridge, [3]Agriculture and Rural Development, Lethbridge, Canada*

Escherichia coli O157:H7 is a major foodborne human pathogen that causes disease worldwide. Healthy cattle are the primary reservoir of this bacterium. The term 'super-shedder' (SS) has been applied to cattle that shed high levels of *E. coli* O157:H7 cells in their feces ($>10^4$ cfu/g feces). Targeting SS cattle for mitigation strategies has been proposed as a means of reducing the incidence and spread of *E. coli* O157:H7 in feedlots. Presently, it is not known what factors contribute to SS. The objective of this study was to determine if there are genetic differences between *E. coli* O157:H7 isolates obtained from SS and non-SS cattle. Ten representative isolates were selected for whole genome sequencing (Illumia MiSeq) on the basis of a range of genetic and phenotypic characteristics. Four isolates were obtained from non-SS steers and six isolates from SS steers (shedding levels from 4.01 -8.45 log CFU/g feces). The isolates were 52.7%>100% related based on pulsed field gel-electrophoresis. Four isolates were typed as lineage I using a PCR lineage-specific polymorphism assay, three as lineage II and two as lineage I/II. Some isolates (n=4) were susceptible to all antimicrobial agents tested using the disk diffusion assay, while others (n=6) were resistant to one or more antimicrobials. Paired-end 100 bp sequencing yielded 29-30× coverage, and generated 231 to 368 contigs per isolate, representing 94.1 to 96.6% of the total predicted bases within the genomes. An average of 1600 single nucleotide polymorphisms (SNPs) was identified when compared to the reference strain (EC4115). The phylogenetic tree based on SNPs; however, did not support the genetic segregation between isolates from SS or non-SS cattle. Ongoing analysis is underway to identify if there are unique genetic components within the isolates that account for the SS phenotype. Further analysis may identify factors such as temperate phage, indels or other proteins that may enable some strains to proliferate to the SS state.

Keywords: cattle, E. coli O157:H7, single nucleotide polymorphism, super-shedder, whole genome sequencing

P66 **Replacement of dietary starch with strategically blended byproduct pellets for beef cattle.** P. Gorka[1,2], F. Joy[1,*], G. E. Chibisa[1], G. B. Penner[1], *[1]Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [2]Animal Nutrition and Feed Management, University of Agriculture in Krakow, Krakow, Poland*

The objective of this study was to determine whether the replacement rate of barley grain and canola meal with high-lipid byproduct pellets (HLP; 14.6% of CP, 29.8% of NDF and 9.0% of fat and 5.52 MJ NE_g/kg in DM) affect DMI and ruminal fermentation. Four ruminally cannulated Hereford × Gelbvieh heifers with an initial BW of (mean ± SD) 631.9 ± 23.3 kg were used in a 4 × 4 Latin square design. Prior to the start of the study, heifers were gradually adapted to a diet consisting of 89% concentrate, 6% barley silage, and 5% mineral and vitamin supplement (CON). Dietary treatments consisted of a CON or diets where 30 (HLP30), 60 (HLP60), and 90% (HLP90) of the barley grain and canola meal were replaced with HLP ensuring diets were isonitrogenous and isocaloric. Periods consisted of 28 d including 10 d for ration transition, 11 d for dietary adaptation, with the last 7 d of each period used for measurement of voluntary DMI and rumen pH. Rumen fluid was sampled for measurement of short-chain fatty acid (SCFA) concentration on d 23 and 24 of each period. At the end of each period digesta was evacuated, weighted, and representative samples were collected for DM determination. Dry matter intake was not affected by treatment ($P > 0.10$) averaging 12.9 kg/d. Digesta mass decreased linearly ($P < 0.01$) from 48.8 kg for heifers fed CON diet to 40.1 kg for heifers fed HLP90. Total SCFA concentration did not differ ($P > 0.10$) averaging 129.7 m*M*. The molar proportions of individual SCFA did not differ among treatments ($P \geq 0.09$). Rumen ammonia concentration increased linearly from 5.3 mg/dL for CON to 10.1 mg/dL for HLP90. Mean ruminal pH increased linearly ($P < 0.01$) from 5.44 to 5.86 with increasing inclusion rate of HLP while the duration (13.7 to 7.2 h/d) and area (4.9 to 1.9 (pH × h)/d) that pH were below pH 5.5 decreased linearly with increasing HLP inclusion. The results of this study indicate that including HLP at the expense of barley grain and canola meal does not affect DMI or SCFA concentration, but improves ruminal pH for cattle fed diets containing a low proportion of forage.

Keywords: barley grain, by-products, feedlot cattle, rumen fermentation

P67 **Effects of feeding dry- or steam-rolled barley or corn in diets containing lactose on the performance of dairy cows.** G. E. Chibisa[1,*], G. Penner[1], P. Gorka[2], T. Mutsvangwa[1], R. Berthiaume[3], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [2]Department of Animal Nutrition and Feed Management, University of Agriculture in Krakow, Krakow, Poland, [3]Valacta, Quebec City, Canada*

The objective of this study was to determine the effects of feeding dry- (DR) or steam-rolled (SR) barley or corn in diets containing lactose (as dried whey permeate; DWP) on DMI, milk yield and composition and ruminal fermentation characteristics. Eight lactating dairy cows were used in a replicated 4 × 4 Latin square design with 28-d periods (18 d of dietary adaptation and 10 d of measurements) and a 2 × 2 factorial arrangement of dietary treatments. Four cows in one Latin square were ruminally-cannulated for the measurement of ruminal fermentation characteristics. The treatment factors were source of starch (barley vs. corn) and extent of grain processing (DR vs. SR). The dietary inclusion level of DWP was 6%. Diets contained 16.6 ± 0.17% CP, 7.2 ± 0.18% sugar and 25 ± 0.76% starch. Dry matter intake was higher when cows were fed DR corn compared to DR barley (28.8 vs. 26.2 kg/d), but there were no differences in cows fed SR barley compared to SR corn (interaction $P = 0.01$). Milk yield tended to be higher in cows fed DR compared to SR barley (40.5 vs. 37.9 kg/d), whereas it did not differ in cows fed DR compared to SR corn (interaction $P = 0.05$). There was no diet effect ($P > 0.05$) on milk fat and protein concentrations. However, milk lactose concentration was numerically higher in cows fed DR barley compared to SR barley, whereas it was numerically lower in cows fed DR corn compared to SR corn (interaction $P = 0.05$). There was no diet effect ($P > 0.05$) on ruminal acetate, propionate, butyrate and total short-chain fatty acid (SCFA) concentrations, and severity of ruminal acidosis. However, total absolute ruminal absorption rates of acetate, propionate, butyrate and total SCFA were numerically higher in cows fed DR compared to SR barley, whereas they were numerically lower in cows fed DR compared to SR corn (interaction $P \leq 0.03$). In conclusion, although feeding DR or SR barley or corn in diets containing lactose resulted in differences in production performance and ruminal rates of SCFA absorption, it did not have an effect on ruminal SCFA concentration and severity of ruminal acidosis.

Keywords: lactose, production performance, starch

P68 **Simultaneous Inhibition of E. coli O157:H7, O26:H11, O145:NM and Salmonella Using a Single Bacteriophage.** Y. D. Niu[1], H. Liu[2,3], J. Li[3], T. A. McAllister[2], K. Stanford[1,*], *[1]Alberta Agriculture and Rural Development, [2]Agriculture and Agri-Food Canada, Lethbridge, Canada, [3]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China*

We previously isolated a bacteriophage (T5) with strong lytic activity against *E. coli* O157:H7 (EC157) strains. This study assessed efficacy of T5 at multiplicity of infection (MOI, 0.01, 0.1, 1, 10, 100 and 1000) against EC157, *E. coli* O26:H11 (EC26), O145:NM (EC145), *Salmonella* I 4,[5],12:i:- (SL15) and *S. typhimurium* (SL28), individually and as mixtures (EC26+EC157, EC145+EC157, EC26+EC145+EC157; SL15+EC157, SL28+EC157, SL15+SL28+EC157; EC26+SL28+EC157, EC26+SL15+EC157, EC145+SL28+EC157) at ~10^4CFU/ml in broth culture. Across sampling time and MOI, T5 inhibited growth of all mixtures ($P < 0.001$). Interestingly, at MOIs (0.1−10), T5 tended to exhibit greater activity against mixtures than at MOIs > 10, although this response reached significance ($P<0.01$) only for EC157+SL28 and EC157+EC145+SL28. Moreover, T5 at MOI < 100 was more efficient at lysing EC145 ($P < 0.01$) in mixtures than on its own, whereas at MOI = 0.01, T5 activity against EC26 was also increased ($P < 0.0001$) in mixtures. T5 showed less activity against *Salmonella*, inhibiting growth of SL15 at MOI > 10 ($P < 0.001$) and having no effect on SL28. However, in mixtures activity of T5 against *Salmonella* was enhanced reducing growth of SL15 ($P < 0.05$) at MOI < 1000 and SL28 ($P < 0.0001$) at all MOI. At a T5 (MOI = 10^4), enumeration of individual and mixed EC157, EC26 and SL28 cultures at 4h, 7h and 10h that T5 was able to simultaneously reduce ($P < 0.01$) number of each bacteria in mixtures by 2−8 $\log_{10}$ CFU/ml. Moreover, both EC157 and EC26 in the mixture were undetectable at each sampling time, indicating that they were more vulnerable to T5 ($P < 0.05$) in a mixture. Phage T5 was able to simultaneously reduce number of EC and SL in mixtures, and exhibited enhanced activity in mixed cultures.

Keywords: Bacteriophage, E. coli O157:H7, O145:NM, O26:H11, Salmonella

P69-GS **Accuracy of Predicting Feed Efficiency from the Starch Concentration in the Feces of Feedlot Cattle.** L. J. Jancewicz[1,2,*], G. B. Penner[1], M. L. Swift[3], J. J. McKinnon[1], K. A. Beauchemin[2], T. A. McAllister[4], [1]*Animal and Poultry Science, University of Saskatchewan, Saskatoon,* [2]*Ruminant Nutrition, Agriculture and Agri-Foods Canada, Lethbridge,* [3]*Livestock Research Branch, Agriculture and Rural Development, Lacombe,* [4]*Ruminant Nutrition and Microbiology, Agriculture and Agri-Foods Canada, Lethbridge, Canada*

A study was conducted to determine the accuracy of predicting cumulative feed efficiency (gain:feed; G:F, kg/kg DM) from fecal samples. Crossbred beef steers (160; 406 ± 30.1 kg) were allocated to one of four finishing diets consisting of 90% grain, 10% silage (4 pens/treatment, 10 steers per pen) in a 2 × 2 factorial arrangement. Treatments consisted of two types of grain (barley and wheat) at two processing indexes (PI) (75 vs. 85%). After 28 d of dietary adaptation, fecal samples were collected from the rectum of five steers from each pen, and from three fecal pats from the pen floor of each pen, every 28 d for three periods.Each period, the samples were pooled by sampling method (rectum versus pen floor) and by pen, dried and ground (1-mm) and analyzed for fecal starch concentration (FS, %). The samples were analyzed in two data sets, based on grain type. Period of rectal sampling had no effect on FS. When averaged over three periods, barley processed to PI85 resulted in 49.7% more starch in the feces than when processed to PI75 ($P < 0.01$). Wheat processed to PI85 had 58.0% more starch than when processed PI75 ($P < 0.01$). At the end of the study, cumulative G:F was determined for each pen. A negative correlation between FS and G:F was observed for the wheat-based diets (r = -0.74, P=0.049; however, no correlation was observed for the barley-based diets. The G:F for wheat could be predicted as G:F = -0.00034FS + 0.15 (r^2=0.55; P=0.035). Rectal sampling only at period 1 or 2 resulted in an r^2 of 0.50 for both (P=0.049 and 0.050, respectively); however, combining the FS concentration from period 1 and 2, increased the r^2 to 0.58 (P=0.027). When comparing the two collection methods, rectal and pen floor, no differences in FS were found (P=0.88), or in the ability to predict G:F from FS. For the wheat fed animals, fecal sampling for FS determination at any time during the feeding period can be a good predictor of cumulative G:F. However with barley, processing did not result in differences in FS large enough to achieve this relationship. The ability to sample from the pen floor negates the need to handle cattle to derive these results.

Keywords: fecal starch, feed efficiency, feedlot cattle, processing index, wheat

P70-GS **Apparent nutrient digestibility and rumen fermentation characteristics of finishing diets supplemented with canola meal derived from Brassica napus or Brassica juncea.** J. Nair[1,*], G. B. Penner[1], P. Yu[1], H. A. Lardner[1,2], T. McAllister[3], J. J. McKinnon[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK,* [2]*Western Beef Development Centre, Humboldt, SK,* [3]*Agriculture and Agri-Food Canada Research Centre, Lethbridge, AB, Canada*

A metabolism trial was conducted to evaluate nutrient digestibility and rumen fermentation characteristics of heifers fed finishing diets supplemented with canola meal derived from two canola varieties, *Brassica napus* (*B. napus*) and *Brassica juncea* (*B. juncea)*. The trial was designed as a 5 x 5 Latin square using five ruminally cannulated heifers (420 ± 11.5 kg BW). The control diet consisted of 89% barley grain, 4% barley silage and 7% supplement (DM basis). Canola meal from *B. napus* and *B. juncea* replaced barley grain at 10 and 20% of the ration DM in the 4 treatment diets. There was no ($P > 0.10$) effect of treatment on DM intake. Apparent DM digestibility tended ($P = 0.08$) to decrease when *B. napus* inclusion level increased, but not with *B. juncea*. Apparent CP digestibility linearly increased ($P = 0.04$) with increasing level of *B. juncea* meal. There was no effect ($P > 0.10$) of treatment on digestible energy (DE) content of the diet. Propionate tended ($P = 0.06$) to decrease as *B. napus* level increased while isobutyrate linearly increased as the level of *B. napus* ($P < 0.01$) and *B. juncea* ($P = 0.02$) increased. Mean rumen pH averaged 5.71 ± 0.11and was not influenced ($P > 0.10$) by treatment. The duration that pH was under 5.2 increased ($P = 0.05$) as the level of *B. juncea* increased and tended ($P = 0.10$) to increase with *B. napus* inclusion level. Total nitrogen (N) intake ($P < 0.04$) and urinary N ($P < 0.05$) linearly increased with increasing level of both meal sources. Nitrogen retention was not ($P > 0.10$) influenced by treatment. The results indicate that inclusion of canola meal from *B. napus* or *B. juncea* at levels up to 20% (DM basis) in the finishing diet does not negatively influence nutrient digestibility or DE content and has minimal influence on rumen fermentation.

Keywords: B. napus, B. juncea, canola meal, cattle, rumen fermentation