advancement of the new science of science communication.

**Key Words:** science communication

**0454 Cracking the code: Making complex information understandable.** A. Perry*, *The Center for Food Integrity, Gladstone, MO.*

Consumer beliefs do not always align with the scientific consensus. Consumers may not accept an idea even though science says it is true. Consumers do not fully understand the science that individuals in animal agriculture find so simple. Our challenge is to find better ways to bridge the communication gap by using shared values to earn consumer trust. In partnership with Iowa State University, CFI was the first to build a research-based consumer trust model. Our peer-reviewed and published model for building consumer trust in today's food system shows that shared values are more important than skills and technical expertise in building consumer trust. The social decision-making process is complex. Building trust is step one. Explaining the complex scientific concepts around animal agriculture is step two. The ability to break down existing communication barriers is critical to fostering informed decision making that leads to consumer confidence.

**Key Words:** consumers, complex, communication, food

**0455 Communicating animal science effectively.** D. R. Williams*, *National Cattlemen's Beef Association, Centennial, CO.*

Having spent the past 25 yr of my career helping companies and organizations communicate during crises ranging from Alar in apples to Pink Slime in ground beef, I have learned a number of lessons about what works and does not work in communicating science effectively. The first lesson is to not lead with science! People react to issues that could impact their family's health and well-being with emotion. Responding with facts and figures is unlikely to calm their fears. So the first step in communicating effectively is to acknowledge their concerns, whether you believe they are rational or not. By acknowledging that their concerns are legitimate you open the door to sharing factual information. I have a formula for responding effectively I call the "Two Cs." We care, and we're capable. We care about the same things they do: the safety of our food, the care of animals, the future of our planet and the health and well-being of our families. Once you have established that common ground, you can focus on addressing differing viewpoints on the "facts" of the matter. In this panel discussion I will share real-life examples of how this technique has been used to communicate animal science effectively.

## CSAS GRADUATE STUDENT ORAL COMPETITION I

**0456 Ensiling barley varieties selected for varied levels of in vitro NDF degradability.** N. G. Preston*[1,2], J. Nair[1], P. Yu[1], D. A. Christensen[1], J. J. McKinnon[3], and T. A. McAllister[4], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, Agriculture and Agri-food Canada, AB, Canada, [3]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [4]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, AB, Canada.*

This study characterized the ensiling traits and digestibility of three barley varieties ranked for in vitro NDF degradability (NDFD). CDC Cowboy (H-NDF), CDC Copeland (I-NDF), and Xena (L-NDF) were ranked as high, intermediate, and low NDFD based on commercial silage samples ($n = 80$) collected over 2 yr. Barley varieties were planted the same day in one location and ensiled at the mid-dough stage in replicated mini or bunker silos. Silos were opened after 60 d of ensiling for chemical and microbial analysis. Silage from mini silos was exposed to air with temperature continuously measured and samples collected at 3, 7, 14, and 21 d. Silage was collected periodically from bunker silos during feed out. In vitro NDFD after 30 h of incubation in rumen fluid was estimated for silage collected after 60 d. Data were analyzed using the Proc Mixed procedure of SAS as a complete randomized design with fixed effect of variety and ensiling method, and random effect of silo within variety, and day as a repeated measure for aerobic stability. In vitro NDFD did not differ among varieties. Terminal pH was lowest ($P < 0.01$) for H-NDF in mini silos. The pH of H-NDF was higher ($P < 0.01$), and I- and L-NDF lower ($P < 0.01$) in bunker than mini silos. Lactate and acetate levels were higher ($P < 0.05$) in H-NDF mini silos, with acetate levels of all varieties being lower ($P < 0.01$) after ensiling in mini silos as compared with bunker silos. Day 60 I-NDF in mini silos had higher ($P < 0.01$) ADF and NDF levels, with method of ensiling affecting fiber levels ($P < 0.01$) with increased ADF and NDF in H-NDF and L-NDF in bunker as compared with the mini silos. The H-NDF silage was less aerobically stable than other silages as reflected by increasing ($P < 0.01$) temperature and pH ($P < 0.05$) and decreased levels of lactic acid ($P < 0.05$) and water-soluble carbohydrates ($P < 0.01$) over the exposure period. Using in vitro NDFD of field silage to select barley silage varieties for improved fiber digestibility proved difficult due to the effects of time of harvest and the fermentation process on this trait.

**Key Words:** barley silage, NDF degradability, aerobic stability0

**457 Characterization of the variation in the daily excretion of fecal constituents and digestibility predictions in beef cattle fed feedlot diets using near infrared spectroscopy.** L. J. Jancewicz*[1,2], G. B. Penner[3], M. L. Swift[4], J. J. McKinnon[1], C. L. Waldner[5], and T. A. McAllister[2], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, AB, Canada, [3]University of Saskatchewan, Saskatoon, Canada, [4]Hi-Pro Feeds, Okotoks, AB, Canada, [5]Department of Large Animal Clinical Sciences, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Canada.*

The 24-h variation in fecal nutrient excretion and accuracy of digestibility predictions using spot samples collected from feedlot cattle were evaluated using near infrared spectroscopy (NIRS). Six heifers were individually housed and randomly assigned to one of two feeding frequencies; once per day (0900), or twice per day (two equal feedings at 0900 and 1700), first over a backgrounding period, followed by a finishing period. Heifers were fed the backgrounding diet for 21 d, transitioned to the finishing diet over 20 d, which was fed for 21 d. During the last 4 d of both periods, total fecal collections were conducted at 4-h and 4-d-24-h intervals and NIRS calibrations were used to predict fecal organic matter (OM), starch, nitrogen (N), neutral detergent fiber (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL). Estimated total tract digestibility (eTTD) using NIRS predicted fecal nutrients and ADL and apparent total tract digestibility (aTTD) of DM, OM, starch, NDF, and ADF determined using previously derived NIRS calibrations were calculated at each 4-h interval as well as over 4 d. Fecal DM (%), NDF, and ADF varied among 4-h interval samples in the backgrounding period, and fecal DM, starch, NDF, ADF, and ADL varied in the finishing period. Fecal starch was able to predict aTTD during both feeding periods (backgrounding: R2 = 0.96, $P < 0.01$; finishing: R2 = 0.98, $P < 0.01$). Most 4-h interval samples could be used to predict eTTD of nutrients and aside from starch in the finishing period, there were no differences for eTTD using fecal samples collected at any of the 4-h intervals versus those collected over 4 d. The NIRS calibrations for predicting aTTD coefficients using the 4-h interval samples or the 4 d-24-h composite were least accurate for NDF and ADF. Spot fecal samples collected at any time point from multiple cattle have potential to predict digestibility. However, timing of sampling after feeding must be standardized to predict starch digestibility during the finishing period, with samples between 0–4 h and 8–16 h generating estimates of both starch concentration and digestibility that were closest to that derived from 4-d-24-h composite samples.

**Key Words:** fecal nutrients, fecal starch, 24-h variation, feedlot cattle, near infrared spectroscopy

**0458 Effect of energy substrate and days on feed on plasma insulin response in finishing beef heifers.** F. Joy*, K. M. Wood, and G. B. Penner, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to determine the effect of dietary energy source and days on feed (DOF) on plasma insulin concentration and insulin responsiveness when subjected to an arterial glucose challenge. Eight heifers were randomly allocated to 1 of 2 finishing diets consisting of a barley-based control (CON; $n = 4$; 75.2% barley grain, 6% barley silage, 9.8% canola meal and 9% vitamin and mineral supplement on a DM basis) or a diet where a high-lipid byproduct-pellet replaced 60% of the barley grain and canola meal relative to CON (HLP; $n = 4$). Diets were formulated to be iso-caloric and iso-nitrogenous, but the CON had greater starch (46.6 vs. 39.5%) and lower ether extract (3.8 vs. 5.7%) than HLP. The 160-d study period was divided into four 40-d periods (P1, P2, P3, and P4). On the final day of each period, 7.57 mmol/kg $BW^{0.75}$ of dextrose was infused and the insulin response was analyzed in plasma collected at 0, 5, 10, 15, 20, 25, 30, 45, 60, 90, and 120 min post-infusion. Data were analyzed using a mixed model (fixed effects of treatment, period, and the treatment × period interaction). Period was included as a repeated measure. The 12-h fasting plasma insulin concentration did not differ ($P = 0.40$) between the treatments averaging 1.51 μg/L. However, insulin concentration increased from P1 (1.17 μg/L; $P < 0.01$) to P3 (1.81 μg/L) and P4 (1.60 μg/L) with the latter not differing. Area under the curve for insulin following the glucose challenge tended ($P = 0.08$) to increase with DOF, but did not differ by diet. The peak insulin concentration following the glucose challenge increased from 8.42 during P1 to 11.3 μg/L during P3 ($P = 0.048$) and the time to attain the peak tended to increase ($P = 0.09$) with DOF, but was not affected by treatment ($P > 0.1$). A tendency ($P = 0.07$) for a treatment × period interaction was observed for peak insulin concentration with HLP attaining a greater peak than CON in all periods except P2. The results of this study indicate that insulin concentration and the insulin insensitivity to a glucose challenge in growing beef heifers increase with advancing DOF and this increase is independent of energy substrate fed. Increasing insulin resistance may be one factor leading to reduced energetic efficiency associated with advancing DOF in finishing cattle.

**Key Words:** beef, insulin, finishing

**0459 Effect of digestible fiber content of barley silage on lactation performance and chewing activity of lactating dairy cows in comparison with corn silage.** B. Refat[*1,2], D. A. Christensen[3], J. J. McKinnon[4], J. Nair[1], A. D. Beattie[5], T. A. McAllister[6], W. Yang[7], and P. Yu[1], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]Animal Production Department, Faculty of Agriculture, Zagazig University, Egypt, [3]University of Saskatchewan, Saskatoon, Canada, [4]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [5]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Canada, [6]Lethbridge Research and Development Centre, AAFC, AB, Canada, [7]Lethbridge Research and Development Centre, AAFC, AB, Canada.*

There is a limited knowledge on evaluating barley silage with different digestible fiber content on dairy cow performance. The objective of this study was to evaluate the effects of barely silage varieties selected for varying rates of in vitro NDF digestibility on DM intake (DMI), milk production, and total chewing activity of high-yield dairy cows in comparison with corn silage. Four early lactating multiparous Holstein cows (average body weight = 703 ± 78 kg; days in milking = 101 ± 25; parities = 2.75 ± 0.83) were used in a 4 × 4 Latin square design. The cows were fed diets that contained 49% barley-based concentrate and 51% forage (DM basis). The forage consisted of 10% alfalfa hay and 41% silage. The four whole plant silages were: corn silage (P7213R), CDC Cowboy barley silage, CDC Copeland barley silage, and Xena barley silage. The diets were formulated to meet the nutrient requirements by lactating dairy cows producing 40 kg of milk using NDS software. The in vitro 30 h NDF digestibility (NDFD) of CDC Cowboy, CDC Copeland and Xena varieties were 37, 31, and 29%, respectively. The experiment consisted of 18 d of adaptation and 5 d of data collection. Statistical analyses were performed using PROC MIXED procedure of SAS 9.4 with significance declared at $P < 0.05$. The results indicate that barley silage variety did not influence DMI, milk production and chewing activity ($P > 0.1$). The CDC Cowboy with higher NDFD did not result in an improvement in milk yield (averaged 35.3 ± 1.71 kg/d, $P > 0.1$), feed efficiency (averaged 1.37 ± 0.07 DMI/milk yield, $P > 0.1$), and total chewing activity (averaged 892 ± 23 min/d, $P > 0.1$) compared with other barley silage varieties. Cows fed the corn silage had similar DMI (averaged 26.3 ± 1.4 kg/d, $P > 0.1$) but produced more milk than those fed barley silage (40.1 vs. 35.3 ± 1.71 kg/d, $P < 0.05$). As a result, the cows fed corn silage had improved feed efficiency compared with those fed barley silage (1.57 vs. 1.37 ± 0.07 DMI/milk yield, $P < 0.05$). The results of this study indicate that feeding barley silage with higher digestible fiber content does not necessarily result in greater milk production performance. However, feeding corn silage has potential to produce more milk and better feed efficiency compared with barley silage.

**Key Words:** fiber digestibility, chewing activity, milk yield

**0460 Daytime pasture vs. free-stall barn access: What do dairy cows with year-long outdoor experience prefer?** E. R. Shepley[*1], E. Vasseur[2], and R. Bergeron[3], *[1]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [2]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [3]University of Guelph, ON, Canada.*

Provision of regular exercise to dairy cows is a topic that has received an increasing amount of interest in recent years. Pasturing cows not only addresses the current issue of restricted movement found in many production units, but also has positive effects on health and welfare. The objective of the current study was to investigate cow preference for day-pasture access or a free-stall barn under Eastern Canadian summer climatic conditions. Two important components were introduced in the current study: the use of a herd with year-round outdoor experience and the provision of the same feed options (fresh forage and silage) inside and on pasture. Thirty-two lactating organic Holstein cows were submitted to a 6-d preference cycle comprised of three 2-d phases. Cows were restricted to a free-stall barn (forced-indoor), restricted to pasture (forced-outdoor), or provided the choice between staying in a free-stall barn or going to pasture (free-choice) for a 7-h period in between morning and evening milking. Live observations of activities (feeding from the feeder, grazing, lying down, and other) were conducted every 2 min by scan sampling during the forced-outdoor and choice phases. A group level *t* test was used to test whether preference of cows to be outdoors differed from 0% (choice to stay in free-stall), 50% (indifference), and 100% (choice to go to pasture). An independent 2-sample *t* test was used to compare time spent in conducting the observed activities inside to those outside. Cows spent more time at pasture when provided the choice (range h 1 to h 6 across wk: 68.4 to 87.4%), displaying partial preference for the outdoors in h 1, and h 3 to h 6 (difference from 0%; $P < 0.01$) and complete preference for outdoor in h 2 (difference from 0 and 50%; $P < 0.01$), when the percentage of cows choosing to be outside was the highest. Cows conducted the same levels of activities on pasture as in the free-stall barn ($P > 0.05$), with cows grazing more than eating silage from the feeder on pasture (33.1 vs. 10.2%, respectively) and eating fresh forage over silage when indoors (33.6 vs. 4.2%, respectively). This study showed that when provided with year-long outdoor access, dairy cows

chose day-time pasture access over free-stall barn, and freshly-cut forage or pasture over silage.

**Key Words:** dairy cow, preference test, outdoor access

**0461 Can regular exercise and more comfortable stalls improve cleanliness and lameness in tie-stall dairy cows?** S. Palacio*[1,2], S. Adam[3], R. Bergeron[4], D. Pellerin[5], A. M. de Passillé[6], J. Rushen[6], D. B. Haley[7], T. J. DeVries[8], and E. Vasseur[1], *[1]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [2]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [3]Valacta, Ste.-Anne-de-Bellevue, QC, Canada, [4]University of Guelph, ON, Canada, [5]Universite Laval, Quebec, Canada, [6]Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada, [7]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Canada, [8]Department of Animal Biosciences, University of Guelph, ON, Canada.*

Tie-stall dairies are still one of the major housing systems around the world and with growing industry requirements to meet animal welfare standards, providing options to help producers meet these animal welfare standards is a priority. The objective of the study was to evaluate how minor stall modifications and/or regular exercise (access to pasture and winter exercise) affected the welfare of Holstein cows housed in tie-stalls. Twenty lactating cows/farm on 12 tie-stall farms were visited and assessed 4 times over 1 yr. Visit 1 was conducted toward the end of the pasture season, visit 2, 9–30 d after modifications were applied, visit 3, toward the end of the winter, and visit 4, 1 yr after visit 1. Stall modifications were applied to half of the study cows on each farm with most modifications being a re-adjustment of the tie-rail. Assessments of animal welfare consisted of animal and housing-based measures, as well as a management questionnaire. Farms were separated on whether they provided exercise (Exc) or not, as well as cows that were kept on modified (Mods) stalls or in unmodified stalls; differences in cow cleanliness, BCS and lameness were analyzed with a mixed model. Farm was nested in Exc and was included as a random effect and Exc, Mods and their interaction were treated as fixed effects. On visit 2 (in winter) 20% more cows had dirty udders when kept in modified stalls with exercise compared with unmodified stalls with exercise (30 vs. 10% respectively, $P < 0.05$). On visit 3, there were 20% fewer lame cows in the herds with exercise (18%) compared with herds with no exercise (38%) ($P < 0.05$). On visit 4, there were 9% more cows with dirty udders in modified stalls (16%) compared with unmodified stalls (7%) ($P < 0.05$). Results show that exercise can have a beneficial effect on lameness, especially during the winter months, and that modifications intended to improve stall comfort might cause some increase in cow dirtiness. However, this increase in dirtiness must be weighed against the potential benefits of a providing dairy cows with more adequate and comfortable stalls.

**Key Words:** regular exercise, tie-stall improvement, dairy cow

**0462 *Saccharomyces cerevisiae* boulardii improves acute phase response and phagocytosis during weaning in dairy calves.** B. Fomenky*[1,2], J. Chiquette[1], P. Y. Chouinard[3], and É. M. Ibeagha-Awemu[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada, [2]Département des Sciences Animales, Université Laval, Québec, Canada, [3]Département des Sciences Animales, Université Laval, Québec, Canada.*

The use of direct fed microbials (DFM) as alternatives to antibiotic growth promoters in farm animal production continues to stimulate research and commercial interest. During the early period of life, inadequate immune development and weaning stress contributes to increase susceptibility to infectious diseases in calves. Currently, it is less clear how DFM elicit acute phase immune response in calves. This study aimed to investigate the effect of *Saccharomyces cerevisiae* and *Lactobacillus acidophilus* on acute phase response and phagocytosis during the early period of calf growth.

Forty eight Holstein calves (2–7 d old) were grouped according to body weight and circulating IgG and randomly assigned to four treatments as follows; Control (CTRL)-fed milk replacer with starter diet introduced gradually in the third week of the experiment; CTRL supplemented with *Saccharomyces cerevisiae boulardii CNCM I-1079* ($7.5x10^9$ cfu/L milk replacer + $3x10^9$ cfu/kg feed) (SCB); CTRL supplemented with *Lactobacillus acidophilus BT1386* ($2.5x10^8$ cfu/L milk replacer + $1x10^9$cfu/kg feed) (LA); and CTRL supplemented with tetracycline (528 mg/L milk) and neomycin (357 mg/L milk) before weaning and chlortetracyclin (55 mg/kg) after weaning (ATB). After weaning calves received hay in addition to starter diet and their respective treatments. Serum samples on experiment d 29 and 43 (pre-weaning), 46, 49, 51, and 54 (weaning) and 58 and 65 (post-weaning) were used for measurements of C-reactive protein and haptoglobin. Likewise, polymorphonuclear neutrophils (PMN) were isolated from plasma on d 15 and 43 (pre-weaning), 47 and 54 (weaning), 59, 66, and 87 (post-weaning), stimulated with lipopolysaccharide and phagocytosis beads pH rhodo Green *E. coli* bio particles. Phagocytosis was then measured using flow cytometry. The effects of treatments were analyzed using a complete randomized block design with repeated measures and PROC MIXED of SAS with Tukey adjustments for multiple comparisons.

Serum concentrations of C-reactive protein and haptoglobin in SCB-treated calves increased during weaning (d 54; $P < 0.05$) when compared with CTRL, LA and ATB-treated calves. Concentrations of C-reactive protein tended to increase on d

65 (post weaning; $P < 0.10$) with SCB compared with CTRL or ATB. The PMN from calves on SCB increased ($P < 0.05$) phagocytosis during weaning (d 47) as compared with CTRL.

Data show that SCB has immunomodulatory effects in calves and a possible role in enhancing innate immune and inflammatory responses of calves during the critical stress period of weaning. Direct fed SCB might play a role in innate immunity as an early defense system against infections in calves.

**Key Words:** calf, *Saccharomyces cerevisiae*, C-reactive proteins, haptoglobin, innate immunity

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**0463 Effect of lipid supplementation and type of lipid on fatty acid composition of the ruminal epithelium and short-chain fatty acid transport.**

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

The objective of this study was to evaluate the effect of lipid supplementation and the type of lipid on the fatty acid (FA) composition of the ruminal epithelium and short-chain fatty acid (SCFA) transport. Twenty-one Holstein steers (194 ± 10.7 kg) were blocked by BW and randomly assigned to 1 of 3 treatments differing in FA supply and composition. The control treatment (CON) contained 2.9% ether extract whereas the FA treatments contained 6.2% ether extract with the lipid coming from saturated (SAT; tallow and palmitic acid) or unsaturated sources (UNSAT; flax and Megalac). All calves were fed at 3% BW on a DM basis. After a 30-d feeding period, steers were killed and samples of the ruminal tissue were collected for FA analysis and to evaluate SCFA uptake and flux in Ussing chambers. Data were analyzed as a randomized complete block design using a mixed model with orthogonal contrasts to evaluate the effect of FA supplementation and the type of the FA supplement. There was a tendency for increased FA concentration in ruminal tissue for supplemented calves ($P = 0.10$), and SAT calves tended to have less FA than UNSAT (15.1 vs. 20.1 g/100 g; $P = 0.06$). Ruminal tissue from SAT had a tendency for greater monounsaturated FA (37.5 vs. 32.0; $P = 0.08$) and had less polyunsaturated FA (17.0 vs. 23.0; $P = 0.03$) than UNSAT. The changes in major FA classifications were largely due to an increase for C16:0 (25.2 vs. 24.2%; $P = 0.02$), decrease in C16:1 (1.65 vs. 10.32%; $P = 0.02$), and a decrease in EPA (0.19 vs. 0.38; $P < 0.01$) for SAT relative to UNSAT. Acetate uptake was not affected by FA supplementation ($P \geq 0.25$), but providing supplemental FA increased propionate [0.61 vs. 0.37 nmol/(cm2 × min); $P = 0.05$] and butyrate uptake [0.82 vs. 0.45 nmol/(cm2 × min); $P = 0.03$)] by the ruminal epithelium. Moreover, feeding SAT increased butyrate uptake relative to UNSAT [1.06 vs. 0.59 nmol/(cm2 × min); $P = 0.01$)]. There was a tendency for an increase in propionate flux across the ruminal epithelium with FA supplementation [0.65 vs. 0.56 μ mol/(cm2 ×h)], but there were no differences between SAT and UNSAT. The results from this study indicate that providing supplemental FA may alter ruminal epithelial FA composition and enhance SCFA transport relative to non-supplemented calves.

**Key Words:** short-chain fatty acid, absorption, palmitic

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**0464 Degradation kinetics and bypassed nutrients of value added pellet products based on combination of new co-products from bio-fuel/bio-oil processing, low grade of peas, and lignosulfonate chemical compound at different levels for ruminants.**

V. Guevara*, D. A. Christensen, J. J. McKinnon, and P. Yu, *Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

New co-product, carinata meal, from bio-fuel processing is ready to be used as animal feed nowadays. Conventional co-product, canola meal, has high levels of methionine and cysteine, but limiting in lysine. Low grade of peas contains high starch content and also has high levels of lysine and tryptophan. There is little information available on nutrient profile, as well as degradation kinetics, especially when it blends with other feedstuff as a pellet. The aim of this project was to test and develop eight high value added pellet products (BPP) based on combination of co-products from bio-fuel/bio-oil processing, low grade of peas and lignosulfonate at different levels for ruminants. Statistical analyses were performed using PROC NLIN and PROC MIXED procedures of SAS 9.4 with significance declared at $P < 0.05$. The results showed that BPP1 (low level of carinata meal, high level of peas and no lignosulfonate), BPP2 (low level of carinata meal, high level of peas and lignosulfonate), BPP5 (low level of canola meal, high level of peas and no lignosulfonate), BPP6 (low level of canola meal, high level of peas and lignosulfonate) and BPP8 (high level of canola meal, low level of peas and lignosulfonate) had the higher rate of degradation (Kd) ($P < 0.05$). There were no significant differences between all blend pellet products (BPP) on soluble fraction in situ (S), insoluble but potentially degradable fraction in situ (D) and undegradable fraction in situ (U) ($P > 0.10$). BPP3 (high level of carinata meal, low level of peas and no lignosulfonate), BPP4 (high level of carinata meal, low level of peas and lignosulfonate) and BPP7 (high level of canola meal, low level of peas and no lignosulfonate) and BPP8 had the higher rumen undregradable dry matter (BDM) ($P < 0.05$); while BPP1, BPP2, BPP5 and BPP6 had the higher effective degradability of dry matter (EDDM) ($P < 0.05$). In conclusion pellet products with high level of co-products had the higher rumen undegradable dry matter. Further study on intestinal digestion of nutrients is needed.

**Key Words:** canola, carinata, lignosulfonate

**0465 The different effects of ferrous glycine chelate and ferrous sulfate to intestinal porcine epithelial cells.** Z. Zhuo*, *College of Animal Science, Zhejiang University, Hangzhou, China.*

This study was conducted to investigate the effects of ferrous glycine chelate and ferrous sulfate on cell proliferation and gene expression of iron related transporters in intestinal porcine epithelial cells (IPEC-J2). When IPEC-J2 cells covered 80~90% of the Petri dish, they were treated with different concentration of $FeSO_4$ and Fe-Gly (0, 50, 100, 200 μ mol/L as the low concentration; 16,000, 32,000, 64,000, 128,000 as the high concentration) for 12 h and 2 4h to determine the cell survival rate. Besides, IPEC-J2 cells were also treated with $FeSO_4$ and Fe-Gly (50 μ mol/L as iron) for 2 h, and then quantitative Real-time PCR was applied to detect the mRNA expression of DMT1, FPN1, Dcytb and PepT1. The results showed that both $FeSO_4$ and Fe-Gly nearly have no toxicity to cells in low concentration; however, high concentration of iron solution could significantly affect cell survival. The influence on cell viability caused by $FeSO_4$ was more obvious in high concentration compared with Fe-Gly. The qRT-PCR results revealed that Fe-Gly had significant lower expression of DMT1, FPN1 and Dcytb than FeSO4 ($P < 0.05$), while there was no difference on the expression of PepT1. For the physiological function of Dcytb, DMT1 and FPN1 are related with iron ions transportation, it reminded us that $FeSO_4$ may own more free iron ion than Fe-Gly in the same concentration. Fe-Gly had a better stabilization than FeSO4, which means it can prevent iron toxicity to cell when in a high concentration.

**Key Words:** ferrous glycine chelate, ferrous sulfate, IPEC-J2, cell proliferation, gene expression

**0466 The effect of SNPs in the promoter on expression of CYP2E1 gene and boar taint.** H. E. Archer*[1], M. Jafarikia[2], B. Lillie[3], F. Schenkel[2], and E. J. Squires[1], *[1]Department of Animal Bioscience, University of Guelph, ON, Canada, [2]Center for Genetic Improvement of Livestock, University of Guelph, ON, Canada, [3]Department of Pathobiology, Ontario Veterinary College, Canada.*

Boar taint, an unfavorable odor detected in the meat of intact male pigs, is caused by the accumulation of two compounds: androstenone and skatole. Despite mounting welfare concerns, surgical castration of all male piglets is still the most common control method in production systems. The need for new methods to control boar taint is therefore a necessity. Genetic selection represents one such alternative. Among the genes known to be involved in boar taint metabolism, CYP2E1 has repeatedly proven influential. The aim of this study was to identify SNPs within the CYP2E1 promoter affecting gene expression and boar taint. Genotypes were obtained from a previously developed list of 7 single nucleotide polymorphisms (SNPs) on 66 boars from three major swine breeds: Duroc, Landrace and Yorkshire. RNA was isolated from liver tissue and quantitative PCR was performed to measure CYP2E1 gene expression. Association analysis was run correlating genotype and CYP2E1 expression (ΔCT) using PROC GLM (SAS Version 9.4). Weight was included as a fixed effect. The effect of breed, androstenone and skatole concentrations on CYP2E1 expression were also tested. All SNPs had a MAF > 0.05. Results indicated that 1 SNP within the CYP2E1 promoter was significantly associated with CYP2E1 expression at $\alpha < 0.05$. An additional 3 SNPs demonstrated association at $\alpha < 0.10$. While weight was significantly associated with gene expression, breed was found to have no effect. Significant within breed variation in CYP2E1 expression was observed, indicating significant differences in gene expression among individuals. Androstenone and skatole were significantly associated, with means of 1.33 ug/g and 0.58 ug/g, respectively. Though SNPs were significantly associated with gene expression, no associations were observed between gene expression and androstenone or skatole in fat. Due to this lack of association between expression and boar taint, results indicate that CYP2E1 mRNA expression alone is not a key indicator for boar taint.

**Key Words:** boar taint, CYP2E1, SNP

**0467 Nutritional evaluation of barley varieties grown for silage.** J. Nair*[1], D. A. Christensen[2], P. Yu[1], A. D. Beattie[3], T. A. McAllister[4], D. Damiran[1], N. Preston[1,5], L. Fuhr[6], and J. J. McKinnon[7], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]University of Saskatchewan, Saskatoon, Canada, [3]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Canada, [4]Lethbridge Research and Development Centre, AAFC, AB, Canada, [5]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, AB, Canada, [6]Dairy Smart Nutrition, Saskatoon, SK, Canada, [7]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

This study evaluated the nutritional and neutral detergent fiber (NDF) digestibility characteristics of common barley varieties grown for silage by beef and dairy operations in western Canada. Of 135 silage samples collected over two crop years (2012 and 2013), 80 samples harvested at the mid-dough stage, representing seven varieties (Conlon, CDC Copeland, CDC Cowboy, Falcon, Legacy, AC Metcalfe and Xena) were selected for analysis. Chemical composition, NDF digestibility (NDFD) and indigestible NDF (INDF) content were analyzed as randomized complete block design with year as random blocking factor using mixed model procedure of SAS (9.4). Average pH

and dry matter (DM) were 4.05 ± 0.17 and 36.8 ± 4.1, respectively. AC Metcalfe had higher ($P < 0.05$) CP content relative to CDC Copeland and Xena with intermediate values for the other varieties. Acid detergent fiber (ADF) content was higher ($P < 0.05$) for CDC Cowboy and AC Metcalfe relative to Conlon. Similarly, CDC Cowboy had a higher ($P < 0.05$) NDF content relative to Conlon, Falcon and Legacy. AC Metcalfe had a higher ($P < 0.05$) lignin content than CDC Copeland. Starch content of Legacy and Conlon was higher ($P < 0.05$) than that of CDC Cowboy with intermediate values for the other varieties. Neutral detergent fiber digestibility (%NDF) after 6 ($NDFD_{6h}$) and 30 h ($NDFD_{30h}$) of incubation in an ANKOM Daisy$^{II}$ system indicated that Legacy and Falcon had a higher ($P < 0.05$) $NDFD_{6h}$ relative to the other varieties; while CDC Cowboy had the highest ($P < 0.05$) $NDFD_{30h}$ followed by CDC Copeland, AC Metcalfe, Falcon and Conlon with Xena and Legacy being the lowest. Rumen in situ incubation for 288 h to determine the INDF (% NDF) content of barley varieties indicated that CDC Cowboy had a higher ($P < 0.05$) potentially digestible NDF (pdNDF) content relative to AC Metcalfe with other varieties being intermediate. Silage fermentation parameters including VFA, lactate and ammonia concentrations did not differ among varieties. These results indicate that barley varieties grown for silage in western Canada vary with respect to chemical composition, NDFD and pdNDF content and suggest that nutritional as well as agronomic characteristics are important for producers to consider when selecting barley varieties for silage. Selection pressure by plant breeders for increased NDFD may help lead to new or improved forage barley varieties for ruminant production systems.

**Key Words:** barley silage, variety, NDFD

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**0468 The repeatability of gonadotropin releasing hormone-induced release of luteinizing hormone and its association with fertility in dairy cattle.**

M. Gobikrushanth*[1], P. A. Dutra[1], C. A. Felton[2], T. C. Bruinjé[1], M. G. Colazo[2], S. Butler[3], and D. J. Ambrose[1,2], *[1]Department of Agricultural Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Livestock Research Branch, Alberta Agriculture and Forestry, Edmonton, AB, Canada, [3]Animal & Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland.*

Objectives were to: (1) determine repeatability and variability of plasma LH concentrations in response to exogenous GnRH administration and (2) examine associations among categories of LH release, plasma estradiol, ovulatory response and first service conception rate in dairy cattle. Lactating Holstein cows (35 primiparous, 65 multiparous) received one injection of $PGF_2\alpha$ (cloprostenol, 500 µg, d 0) followed by GnRH (gonadorelin, 100 µg, d 3; Presynch) and were subjected to an Ovsynch protocol starting on d 10, with timed-AI (TAI) occurring at ~75 d postpartum. Blood samples were collected immediately before (0 h) and 2 h after the GnRH of Presynch and the second GnRH of Ovsynch to determine plasma LH concentrations. Cows were ranked based on LH concentrations after the second GnRH of Ovsynch, from highest to lowest, and those in the top ($n = 33$) and bottom ($n = 33$) thirds were classified into HIGH- and LOW-LH categories. Differences in plasma LH and estradiol concentrations among parity and LH categories were analyzed using MIXED procedure of SAS. Repeatability was analyzed using the CORR procedure and binomial data using the GLIMMIX procedure of SAS. Mean ( ± SEM) LH concentrations (ng/mL) before GnRH were 0.4 ± 0.04 and 0.6 ± 0.03, while, the mean LH 2 h after GnRH were 8.3 ± 0.7 (range 1.0 to 27.4, CV 80.7%) and 10.0 ± 0.7 (range 0.7 to 28.4, CV 67.3%), during Presynch and Ovsynch assessments, respectively. The correlation between GnRH-induced LH concentrations during Presynch and Ovsynch assessments was $r = 0.19$ ($P = 0.06$). The proportion of cows that remained in HIGH- and LOW-LH categories during both Presynch and Ovsynch assessments was 35.3 and 33.3%, respectively. The mean plasma LH concentration (ng/mL) after GnRH was significantly greater ($P < 0.01$) for HIGH-LH (17.6 ± 0.6) than LOW-LH (2.8 ± 0.6) category. Similarly, cows in the HIGH-LH category had greater plasma estradiol than those in LOW-LH category (2.7 ± 0.3 vs. 1.1 ± 0.3 pg/mL; $P < 0.01$). In addition, cows in the HIGH-LH category had greater ovulatory response (97.0 vs. 78.8%; $P = 0.03$) and increased first service conception rate (44.1 vs. 24.2%; $P = 0.04$) than cows in the LOW-LH category. The mean plasma LH concentration in multiparous cows was significantly greater at Presynch assessment (9.3 ± 0.8 vs. 6.3 ± 1.1; $P = 0.03$) and numerically greater at Ovsynch assessment (10.7 ± 0.8 vs. 8.7 ± 1.1; $P = 0.16$) than in primiparous cows. In summary, GnRH-induced LH concentrations were highly variable and weakly repeatable. However, cows with higher GnRH-induced plasma LH concentrations 2 h after second GnRH of Ovsynch had greater ovulatory response and conception rates.

**Key Words:** LH variability, repeatability, fertility

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**0469 Use of low-cost, non-nutritive adsorbents as intestinal binding agents to sequester the boar taint compound androstenone.**

P. Park*, I. B. Mandell, C. F. M. de Lange, and J. Squires, *Department of Animal Biosciences, University of Guelph, ON, Canada.*

Boar taint is an unpleasant odor and taste detected from pork of some intact males when cooked, caused by high accumulation of the testicular steroid androstenone and the indole skatole. Currently available research exploring dietary approaches to control androstenone is scarce. The objective of this study was to evaluate for the efficacy of binding agents in vivo against androstenone and its impacts on performance in intact male pigs, following up on previous works in vitro.

The study aims to capitalize on a hormone-recycling phenomenon which takes place in the gastrointestinal tract of animals, called enterohepatic circulation. Four adsorbents have been assessed for their binding effectiveness against androstenone in our laboratory; these were previously used in studies which successfully mitigated negative effects associated with mycotoxin ingestion in production animals. All additives bound androstenone in high efficacies in vitro, which warranted evaluation of the effectiveness of these binders in swine diets to reduce its levels in plasma and fat. Ninety ($n = 90$) purebred Duroc boars (123 ± 6 d of age at start of experiment) were equally allocated ($n = 18$) and fed 1 of 4 diets added with 2% bentonite (BNT), 3.5% diatomaceous earth (DE), 15% spent filter aid (SFA), or 0.7% hydrated sodium-calcium aluminosilicate (HSCAS) for at least 28 d followed by 14 d of recovery. All groups were compared with a control entire male group ($n = 18$) fed a typical corn-soybean meal finisher diet. Plasma samples and backfat biopsies were collected at d 0, 14, 28, 42, and 56 of trial. Pigs were weighed weekly and calculated for growth performance parameters. Estrone-1-sulfate in plasma was analyzed as a positive control for enterohepatic circulation. Analysis of trends during the treatment period were performed using the PROC MIXED repeated measures procedure in SAS (SAS Institute, Cary, NC, USA). There were no differences in ADG, ADFI, or FCR across diets ($P > 0.05$) throughout the treatment period. In addition, there were no significant decreases in backfat or plasma androstenone and estrone-1-sulfate across pigs fed treatment diets by d 28 ($P > 0.05$). However, there was a wide variation in plasma and fat androstenone concentration, which may result from the process of transporting the pigs into a novel environment and mixing. Further research using of crossbred pigs that will not be mixed and/or transported into unfamiliar groups is needed to conclusively evaluate the efficacy of these treatments.

**Key Words:** boar taint

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**0470 The effect of sorting wheat or barley, based on the predicted CP of individual seeds, on physical characteristics and in vitro dry matter digestibility.**

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Nutrient values are based on sample averages, ignoring variability among seeds. The objective of this experiment was to determine if fractions obtained by separating kernels based on predicted CP (PCP) have different physical characteristics and DM digestibility (DMD). Second, we determined if grinding method and intensity influence digestibility of each fraction. The BoMill TriQ (TriQ), which uses near infrared transmittance spectroscopy (NIT), was used to separate individual kernels based on PCP. In the first study, the TriQ was used to sort 6 wheat sources into 10 fractions. Sixty kernels from each fraction were randomly chosen for measurement of length, width, height, area, geometric mean diameter, perimeter, sphericity, color, and mass. Data were analyzed using a mixed model with the fixed effect of fraction. Physical characteristics were similar among fractions ($P > 0.10$), except color, where lower PCP content had greater L* (54.12 vs. 50.95; $P < 0.05$). In the second study, 2 fractions [high CP (HCP) vs. low CP (LCP)] were produced from 5 sources of wheat and barley. The unsorted grain and each fraction were ground through a hammer mill (0.188 or 0.375 mm screens) or a roller mill to produce coarse and finely ground treatments. The roller mill was adjusted to produce samples with a similar processing index (wt/v) to the hammer mill. In vitro DMD and total gas production (TGP) were determined after a 12-h incubation. Data were analyzed independently by grain source including the effect of fraction, grinder, degree of processing, and interactions. The TGP (ml) and DMD (%) were similar among fractions ($P > 0.10$). The TGP and DMD of barley ground using a hammer mill was greater ($P < 0.10$) than when processed using a roller mill (59.4 ± 2.0 and 24.0 ± 2.0; 41.8 ± 1.0 and 24.0 ± 1.0, respectively) and a similar response was observed for wheat ($P < 0.10$; 63.8 ± 1.4 and 27.8 ± 1.5; 42.3 ± 0.8 and 26.3 ± 0.8, respectively). Increasing the degree of processing increased TGP ($P < 0.10$; 47.4 ± 2.0 and 35.9 ± 2.0; 48.9 ± 1.5 and 42.7 ± 1.4, respectively) and DMD ($P < 0.10$; 36.2 ± 1.0 and 29.6 ± 1.0; 36.4 ± 0.8 and 32.2 ± 0.8, respectively) of barley and wheat. Sorting individual seeds for PCP produces fractions with comparable physical characteristics, DMD, and in vitro TGP.

**Key Words:** grinding, near infrared transmittance spectroscopy, single seed sorter

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**0471 The effect of binding feed emzymes to spores of *Bacillius subtlis* and *Bacillius coagulans* on in vitro NDF digestibility in ruminal batch cultures.**

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Immobilization of enzymes on *Bacillus* spores has been shown to enhance enzyme stability. Binding feed enzymes to spores may therefore protect them in the rumen environment and improve enzyme efficacy. The objective of this study was to determine whether a xylanase feed enzyme bound to the surfaces of *Bacillus subtilis* or *Bacillus coagulans* spores would improve in vitro ruminal NDF digestibility compared with free

enzyme. Three separate in vitro ruminal batch cultures were performed on different days using the following treatments: *B. subtilis* spore-bound enzyme (BsubE; $1.0 \times 10^9$ *B. subtilis* spores + 0.1 mg xylanase enzyme protein); *B. coagulans* spore-bound enzyme (BcoaE; $1.0 \times 10^9$ *B. coagulans* spores + 0.1 mg xylanase enzyme protein); free enzyme (ENZY; 0.1 mg xylanase enzyme protein); and control (CON; water). The treatments were applied to alfalfa hay (2-mm particle size) 4 h before incubations. Rumen fluid was collected from two cannulated heifers and mixed with Menke's buffer (3:1) under anaerobic conditions to make inoculant. Serum vials containing pre-treated alfalfa hay (0.5 g) were filled with 60 mL of inoculant and then incubated on a shaker (39°C) for 0, 3, 6, 12, 24, and 48 h. Triplicate vials were removed at each time point to measure gas production, methane emission, and alfalfa digestibility. Gas production (ml/g dry matter (DM)) at 48 h was not different between BsubE, BcoaE, or ENZY ($P > 0.05$); however, it was reduced in CON vials compared with the other treatments ($P < 0.001$). Methane emissions at 24 and 48 h (ml/g DM) were least for CON (25.2 and 29.8 mL/g, respectively), intermediate for the spore treatments (25.8 and 30.5 g/ml for BsubE; 25.9 and 30.7 g/ml for BcoaE), and greatest for ENZY (35.4 and 39.0 mL/g, respectively; $P = 0.011$). In vitro DM digestibility was not different at 24 h ($P = 0.36$), but at 48 h there was a difference between CON (78.9%) and BsubE, BcoaE and ENZY (average 80%; $P = 0.018$). There was a tendency for greater NDF digestibility at 48 h in the enzyme treatments, compared with CON ($P = 0.075$). These data showed that the feed enzyme enhanced digestion of alfalfa. However, there was no difference when the enzyme was applied in free-form or bound to spores. Protection of feed enzymes through absorption to *Bacillus* spores may be more effective when the enzymes are unstable in a ruminal environment.

**Key Words:** feed enzyme, rumen digestibility, spores

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**0472 Characterization of bovine nasopharyngeal lactic acid bacteria and their in vitro antimicrobial activities against the respiratory pathogen *Mannheimia haemolytica*.**

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Most research on bacteria in the bovine nasopharynx has focused on pathogens implicated in respiratory disease. There is limited information on commensals, such as lactic acid bacteria (LAB), which are important to mucosal health and have been investigated as probiotics to inhibit pathogens. The purpose of this study was to characterize the bovine nasopharyngeal LAB and their in vitro antimicrobial activities against *Mannheimia haemolytica*. The diversity of nasopharyngeal LAB was investigated in two separate studies using DNA– or culture-based techniques. In the first study, nasopharyngeal samples were collected from calves ($n = 14$) on a farm before shipment to a feedlot (d 0), and then 2, 7, and 14 d after feedlot placement. Swabs were processed for DNA extraction and the 16S rRNA gene was PCR-amplified and sequenced using the MiSeq platform. In the second study, nasopharyngeal swabs were collected from calves ($n = 70$) sampled at feedlot entry and 60 d afterward. The swabs were processed for the isolation of LAB using selective media. A subset of LAB ($n = 66$) was identified by sequencing the full-length 16S rRNA gene and isolates were subsequently screened for inhibition of *M. haemolytica* using the agar slab method. From the first study, high–throughput sequencing showed that the total LAB (defined as the order *Lactobacillales)* constituted 4.2% of the nasopharyngeal bacterial microbiota and consisted of 23 genera. Within LAB, 6 different families were identified that included *Streptococcaceae* (49.2%), *Carnobacteriaceae* (23.9%), *Aerococcaceae* (16.0%), *Enterococcaceae* (5.6%), *Lactobacillaceae* (5.3%), and *Leuconostocaceae* (0.26%). The relative abundance of total LAB increased by 97% from d 0 to 2 and remained greater for the 14 d of feedlot placement, compared with d 0 ( $P < 0.05$). Interestingly, however, the *Lactobacillaceae* family decreased ( $P < 0.05$) from d 0 to 2, demonstrating that not all *Lactobacillales* members increased after feedlot arrival. Using culture–based methods, only 6 genera of LAB were isolated: *Streptococcus* (39.2%), *Lactobacillus* (37.1%), *Enterococcus* (10.3%), *Aerococcus* (9.3%), *Corynebacterium* (3.1%), and *Pediococcus* (1.0%). Among the screened LAB isolates, species within *Lactobacillus* exhibited the strongest inhibition against *M. haemolytica*, with zones of inhibition ranging between 16 and 23 mm. Our results show that the relative abundance of nasopharyngeal LAB can change after cattle are transported to a feedlot and that some LAB are able to inhibit the respiratory pathogen *M. haemolytica*. These LAB may have potential as nasal probiotics for the mitigation of bovine respiratory pathogens.

**Key Words:** lactic acid bacteria, probiotic, bovine nasopharynx

**0473 Severity and prevalence of ruminal acidosis during the diet transition for commercial feedlot cattle.** B. I. Wiese*[1], S. Hendrick[2], J. J. McKinnon[3], J. Campbell[1], and G. B. Penner[4], *[1]Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, Canada, [2]Coaldale Veterinary Clinic, Coaldale, AB, Canada, [3]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [4]University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to determine the severity and prevalence of ruminal acidosis in commercial feedlot cattle during the transition to a finishing diet. Previously backgrounded steers ($n$ = 907) and heifers ($n$ = 998) were chosen as a source population and housed separately in 8 pens with an average of 227 ± 13 and 249 ± 6 hd/pen, respectively. Within the source population, 16 steers (mean BW ± SD = 435.1 ± 32.8 kg) and 16 heifers (mean BW ± SD = 382.7 ± 49.4 kg) were used to measure reticulo-ruminal pH using an orally administered pH measurement system; however, 3 systems were not recovered on slaughter. Cattle were fed 3 times daily and were transitioned from a diet containing (forage:concentrate; F:C) 62:38 to 20:80 (DM basis) over 40 d. Dry matter intake was assessed at the pen level. The effect of diet and day within diet were analyzed using the MIXED procedure in SAS, with diet and sex as fixed effects. Dry matter intake was greater for steers than heifers (10.2 vs. 9.3 kg/d; $P < 0.01$) and increased from diet 1 to diet 3, reaching a peak of 10.2 kg/d, before declining to 9.4 kg/d in diet 6. Mean reticulo-ruminal pH ($P < 0.01$) declined from pH 6.45 in diet 1 to pH 6.10 in diet 6. Heifers had greater mean pH than steers (6.38 vs. 6.33) when averaged over the diet transition ($P = 0.04$). Area (pH min)/d) and duration (min/d) that pH was < 5.6 increased with decreasing F:C ($P < 0.01$), as did the standard deviation from mean pH ($P < 0.01$). Over the entire transition period 24/29 study animals experienced at least one bout indicative of acidosis (pH < 5.6 for > 180 min) but the average daily prevalence was 5.4%. The prevalence of reticulo-ruminal acidosis increased with decreasing F:C (peak of 13.5%). When days within a diet were evaluated, lowest mean pH was observed 2-d post diet change ($P < 0.01$). Results indicate that daily prevalence for ruminal acidosis ranges between 1 and 13% with the risk increasing with decreasing F:C. The susceptibility to ruminal acidosis may differ between steers and heifers and the second day relative to a diet change appears to be the day with the greatest risk.

**Key Words:** diet transition, feedlot cattle, ruminal acidosis

**0474 Comparison of digestion and particle-associated bacteria after in situ incubation of different barley varieties in the rumen of cattle.** H. E. Yang*[1,2], C. A. Zotti[2], J. J. McKinnon[1], and T. A. McAllister[2], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, AAFC, AB, Canada.*

The chemical composition of barley grain, including the structure of starch, can vary among barley varieties and result in different digestion efficiencies. It is not known if compositional differences in barley can affect the particle-associated bacteria (PAB) involved in digestion. Therefore, the objective of this study was to characterize the in situ rumen digestion and PAB of four barley grain varieties. Three ruminally-cannulated cattle were fed a diet of 60% barley silage, 37% barley grain and 3% supplement. Four different barley varieties (Fibar, Xena, McGwire and Hilose) and corn as a control were included in the experiment. Ground grains (3 g) were placed in nylon bags and incubated in the rumen of cattle for 0, 2, 4, 12, 24, and 48 h. At each time point, triplicate bags were removed from each animal and analyzed for dry matter (DM), starch and crude protein (CP) disappearance. A second set of bags ($n$ = 3) containing 5 g of each grain were incubated for 2, 4, and 12 h and DNA was extracted to characterize PAB via 16S rRNA gene sequencing. McGwire had the highest effective degradability (ED) of DM ($P < 0.01$), followed by Xena, Fibar, Hilose, and corn, respectively. The ED of starch was highest ($P < 0.01$) for Xena, followed by McGwire, Fibar, Hilose, and corn, while CP disappearance was not affected by grain type. Overall, 15 phyla were identified after analysis of 16S rRNA genes. Barley variety did not affect the relative abundance of phyla however they did differ with incubation time. *Firmicutes* (19.2%), *Bacteroidetes* (18.27%) and *Proteobacteria* (8.89%) were the dominant phyla after 2 h of incubation. By 12 h, *Bacteroidetes* decreased to a relative abundance of 4.3%. In contrast, *Firmicutes* increased in abundance over time, accounting for 45.9 and 82.1% of PAB after 4 and 12 h of incubation, respectively. Principal Coordinate Analysis showed that bacterial populations clearly grouped according to incubation time. At the family level, *Lactobacillaceae* increased over time, with a relative abundance of 0.76, 6.49, and 76.3% at 2, 4, and 12 h, respectively, reflecting an increasing presence of lactic-acid producing bacteria. This study found that the diversity of PAB on barley grain was not affected by barley variety, despite there being differences in digestion kinetics. However, time affected PAB, illustrating that the bacterial biofilm involved in the digestion of grains clearly undergoes compositional shifts during ruminal digestion.

**Key Words:** barley, rumen, microbiota

**0475 Carbohydrate spectroscopic features of bio-oil co-products in relation to rumen degradation kinetics in ruminants.** X. Li[*1,2], W. Xu[1], J. Yang[1], Y. Zhang[1], and P. Yu[2], *[1]College of Animal Science and Technology, Northeast Agricultural University, Harbin, China, [2]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

The objectives of this study were to investigate the carbohydrate structure makeup associated with dry matter (DM) rumen degradation kinetics of three commonly used bio-oil co-products in ruminants. Three bio-oil products (rapeseed meal, canola meal and soybean meal) from three different sources in both Canada and China were collected in 2014. The carbohydrate spectral features were investigated using attenuated total reflectance-Fourier transform infrared spectroscopy instrument. The rumen degradation kinetics was determined according to the in situ nylon bag method with 3 rumen cannulated lactating Holstein cows at Rayner Dairy Teaching and Research Facility, University of Saskatchewan, Canada. The PROC MIXED procedure of SAS 9.3 was used for spectral data and degradation kinetics data analyses. The PROC CORR procedure of SAS was used to investigate the relationship between carbohydrate structure makeup and metabolic characteristics. Significances were declared at $P < 0.05$.The results showed that the peak area intensities of structural carbohydrate related region and its multiple peaks height were all lower in rapeseed meal and canola meal compared with soybean meal ($P < 0.05$). The cellulosic compound related spectral region had lower peak area and peak height intensities in rapeseed meal and canola meal than soybean meal ($P < 0.05$). Additionally, structural carbohydrate to total carbohydrate ratio and cellulosic compound to total carbohydrate ratio were all lower in rapeseed meal and canola meal than soybean meal ($P < 0.05$). For in situ DM rumen degradation kinetics, rapeseed meal had significantly lower soluble fraction than soybean meal. Rapeseed meal and canola meal had significantly lower potentially degradable fraction and higher undegradable fraction in comparison with soybean meal ($P < 0.05$). Compared with soybean meal, rapeseed meal and canola meal had higher rumen bypass DM content, and lower rumen effectively degradable DM content. There is a close relationship between carbohydrate spectral parameters and nutrient metabolic characteristics. The peak area intensity of functional group such as structural carbohydrate, cellulosic compound related region and their ratio to total carbohydrate were all positively related with DM degradable fraction and negatively correlated with DM undegradable fraction ($P < 0.05$). In conclusion, canola meal genetically developed from rapeseed meal shares similar carbohydrate structure and nutrition availability with rapeseed meal. The unique carbohydrate molecular spectral bands in the mid-IR region are highly associated with the nutrient utilization of bio-oil co-products in ruminants.

**Key Words:** carbohydrate molecular structure, vibrational spectroscopic profiles, nutrient metabolic characteristics

**0476 Low protein diets produce divergent effects on energy balance.** R. C. Zapata[*1], A. Pezeshki[2], A. Singh[1], N. J. Yee[1], and P. K. Chelikani[1], *[1]University of Calgary, AB, Canada, [2]Oklahoma State University, Stillwater.*

Background: The protein leverage theory postulates that diets low in dietary protein increase total energy intake due to overconsumption of carbohydrates and fat in an attempt to meet protein requirements. However, little is known of the mechanisms by which protein deficiency elicits such behavioral and metabolic adaptations, promotes positive energy balance and increases the risks for obesity and associated metabolic disorders.

Objectives: Our objectives were to determine the effects of graded degrees of protein restriction on (1) energy balance, body composition, glucose tolerance, gut hormones, (2) sympathetic signaling and, (3) key regulatory markers of thermogenesis in liver, skeletal muscle and brown adipose in diet-induced obese (DIO) rats.

Methods: The DIO rats were randomized to receive one of 4 isocaloric high-fat diets with graded concentrations of protein ($n$ = 8/group; 4.40 kcal/g): Control (15% protein, CON), 10% (10P), 5% (5P), 0% (0P) for 2 wk, followed by realimentation to CON for 2 wk. Food intake, energy expenditure, body composition, glucose tolerance, plasma hormone concentrations, and tissue gene and protein expressions were measured. Data were analyzed by linear mixed models or ANOVA.

Results: We found that during protein restriction, compared with CON, 0P decreased energy intake but increased energy expenditure which led to reduced body weight, fat and lean mass, 5P increased energy intake and energy expenditure which led to reduced body weight and lean mass, and 10P increased energy intake but did not affect body weight and composition. These diet-induced alterations in energy expenditure are in part mediated through enhanced β-adrenergic signaling coupled with upregulation of key thermogenic markers (UCP1, β-Adrenergic receptors, fibroblast growth factor-21, irisin) in the brown adipose, liver and skeletal muscle. The 0P decreased plasma peptide YY, leptin, insulin, C-peptide and tended to decrease amylin and glucose-dependent insulinotropic peptide. The 0P and 5P induced fatty liver, reduced energy digestibility, and decreased lean mass and body weight that persisted beyond the restriction period. In contrast, moderately low protein diets promoted gain in body weight and adiposity following the period of protein restriction.

Conclusion: In summary, our novel findings demonstrate that low protein diets produce divergent effects on energy balance by engaging sympathetic signaling. Importantly, moder-

ately low protein diets could exacerbate preexisting susceptibility to weight gain and obesity. Funding: NSERC, ALMA

**Key Words:** low protein, energy balance, obesity

## CSAS GRADUATE STUDENT POSTER COMPETITION

**0477 Effect of high dietary canola meal inclusion in lactating sows on nutrient digestibility and sow and piglet performance.** D. E Velayudhan* and C. M. Nyachoti, *University of Manitoba, Winnipeg, Canada.*

The aim was to determine the effects of high canola meal inclusion levels in sow lactation diets on nutrient digestibility, reproductive performance, milk composition and piglet performance. Forty five sows ($n$ = 15) with an average parity of 1.8 (SD = 0.83) were randomly assigned to 1 of 3 dietary treatments; corn soybean meal control diet with 0, 15, and 30% canola meal (Diet A, B and C, respectively). All diets were formulated to be similar in standardized ileal digestible amino acids and NE, and were formulated to meet or exceed NRC (2012) nutrient requirement recommendations for lactating sows with an average post-farrowing BW of 210 kg, an expected average BW loss of 5.8 kg, and an expected piglet ADG of 230 g. Sows were moved to farrowing rooms and given the experimental diets from d 111of gestation until weaning on d 21. All sows were weighed and backfat thickness measured on d 111 of gestation and also on d 0, 7, and 21 post-farrowing. Litters were weighed on d 0, 7, and 21. Weaning to estrous interval in sows was also recorded. Blood samples, 2 h post feeding and milk samples were collected from sows on d 0, 7, and 21 to analyze plasma urea nitrogen (PUN) and milk composition, respectively. Fecal samples were collected on d 10, 11, and 12 post-farrowing to determine energy and nutrient digestibility. All data were analyzed as a randomized complete block design using mixed procedures of SAS 9.3 (SAS Inst., Cary, NC). There were no effects of higher levels of dietary canola meal inclusion on lactation feed intake, sow BW and backfat change, and weaning to estrous interval ($P > 0.10$). Also, there were no dietary effect on piglet mortality and piglet ADG ($P > 0.10$). There were no differences in the sow milk composition among dietary treatments ($P > 0.10$). However, sows fed 15 and 30% canola meal had lower ($P < 0.05$) PUN values compared with those fed control diet, on d 0, 7, and 21 post-farrowing. Also, apparent total tract digestibility of DM, GE, CP and P declined ($P < 0.05$) with increasing levels of canola meal inclusion. It was concluded that inclusion of up to 30% canola meal in lactation diet can support satisfactory sow and litter performance.

**Key Words:** canola meal, performance, sow

**0478 Transcriptome analysis of the intestinal tissues of cattle suggests an association among host immune responses, lipid metabolism and the super-shedding of *E. coli* O157.** O. Wang*[1], T. A. McAllister[2], G. Plastow[3], B. Selinger[4], K. Stanford[5], and L. L. Guan[6], *[1]University of Alberta, Edmonton, Canada, [2]Lethbridge Research and Development Centre, AAFC, AB, Canada, [3]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [4]University of Lethbridge, AB, Canada, [5]Alberta Agriculture and Forestry, Lethbridge, Canada, [6]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Super-shedder cattle, which are defined as cattle shedding > 4 log of CFU of *Escherichia coli* O157 (O157) per g of feces, are responsible for the majority of O157 excretion into the farm environment. Colonization of the rectal anal junction by O157 is integral to super shedding. The objective of current study was to further understand the molecular mechanisms of colonization during super-shedding through investigating the transcriptome of the whole intestinal tract of cattle. We hypothesized that the difference in gene expression profiles between the anterior and distal part of intestine underlies the tropism of O157 toward the distal colon, and that transcriptomes of intestinal tissues differ between super-shedders and steers fecal-negative for O157 (non-shedders). RNA-sequencing (Illumina HiSeq 2000, 100 bp paired-end) was performed for intestinal tissues, including duodenum, proximal jejunum, distal jejunum, cecum, spiral colon and descending colon collected from 5 super-shedders and 5 non-shedders. Sequencing data were processed using a Tophat2, HTseq and edgeR pipeline, and gene function analysis was performed using Ingenuity Pathway Analysis. The number of genes detected in tissues ranged from 16,846 ± 639 (cecum) to 18,137 ± 696 (distal jejunum), and the functional analysis indicated that cell-mediated and humoral immune functions were enriched for the transcriptomes of small intestinal tissues, reflecting their greater immune activity. The number of differentially expressed genes between super-shedders and non-shedders ranged from 1 (duodenum) to 248 (distal jejunum) (false discovery rate < 0.05). Up-regulated genes in super-shedders, including F3, GPR123 and CCR9 in distal jejunum, and GP2 and CD36 in descending colon, indicated possible increased activation of cell-mediated immune responses in these two intestinal regions of super-shedders. Up-regulated APOA1, GPAM, PLIN1 and APOB in descending colon of super-shedders suggested altered lipid metabolism. This is the first report of transcriptome analysis for intestinal tissues of cattle, and our current findings indicate that the tropism of O157 toward the distal part of the colon may be due to less active immune protection in the large intestine. Furthermore, both host