CSAS GRADUATE STUDENT ORAL COMPETITION

0212 Effects of butyrate during subacute ruminal acidosis on VFA transport capacity in the rumen epithelium of holstein dairy cows. A. H. Laarman[*1], L. Dionissopoulos[1], O. AlZahal[2], S. L. Greenwood[3], M. A. Steele[4], and B. W. McBride[2], *[1]University of Guelph, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]University of Vermont, Burlington, VT, [4]Nutreco Canada, Guelph, ON, Canada.*

This study examined the effects of exogenous butyrate during subacute ruminal acidosis (SARA) on the membrane VFA-transport proteins in the rumen epithelium. Sixteen mid-lactation Holstein cows fed a TMR including a pelleted concentrate supplement consisting of 60% barley grain, 20% corn grain, and 20% wheat grain on a dry matter basis. For 2 pre-trial days, all cows were adapted to the full amount of concentrate supplement to increase the dietary NFC to 44.0%. Cows were blocked by DIM and assigned either a butyrate treatment or control treatment for 7 d. Cows assigned the butyrate treatment were ruminally dosed twice daily with a calcium butyrate salt at 2.5% of their pre-trial DMI. Cows assigned the control treatment were ruminally dosed with a carrier. On Days 1 and 7, blood, rumen fluid, and rumen biopsies were sampled for serum BHBA concentrations, VFA profiles, and transport protein abundance, respectively. Rumen pH was continuously measured on Days 6 and 7 using an in-dwelling pH-measuring device. There was no difference in SARA between control and butyrate treatments (rumen pH < 5.6 for 598 ± 97 min/d vs. 536 ± 89 min/d, $P = 0.65$). Ruminal butyrate concentration were higher in the butyrate treatment compared to control treatment on both Days 1 (9.88 vs. 22.60 ± 0.94 mM, $P < 0.05$) and 7 (8.60 vs. 21.60 ± 0.94; $P < 0.05$). Serum BHBA was also elevated in the butyrate treatment animals on Day 1 (910 vs. 4201 ± 265 μM, $P < 0.05$) and Day 7 (800 vs. 3262 ± 265 μM, $P < 0.05$) compared to control animals. Immunofluorescence showed an increase in the abundance of monocarboxylate co-transporter isoform 1 (MCT1), sodium/proton exchanger isoform 3 (NHE3) and sodium/bicarbonate co-transporter isoform 1 (NBC1) in all cows between Days 1 and 7. By Day 7, butyrate dosing increased the abundance of MCT1 (11,275 ± 953 vs. 14,747 ± 953 A.U., $P < 0.05$) and decreased the abundance of NBC1 (15,065 ± 992 vs. 11,122 ± 992 A.U., $P < 0.05$) compared to control cows. These results suggest SARA increases the capacity for proton expulsion from the cytosol as well as VFA export into the bloodstream. Butyrate increases the capacity for VFA uptake by increasing the abundance of MCT1 on the basolateral membrane and decreasing NBC1 to maintain intracellular pH.

Key Words: butyrate, epithelium, transport

0213 Nutrient composition and degradation characteristics of anthocyanidin containing alfalfa transformed with Lc, C1, and Lc × C1 regulatory genes. R. G. Heendeniya Vidanaral[*1], M. Y. Gruber[2], Y. Wang[3], D. A. Christensen[1], J. J. McKinnon[1], B. Coulman[1], and P. Yu[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Agriculture and Agri-Food Canada, Saskatoon, SK, Canada, [3]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Alfalfa (*Medicago sativa* L.) is rich in nutrients. However, utilization of its nutrients in ruminants is restricted due to rapid rumen degradation of protein. This may be prevented if adequate protein binding proanthocyanidins are present in the aerial part of the plant. Proanthocyanidins are synthesized by the flavonoid pathway. The Lc gene and C1 genes synthesize bHLH and MYB transcription factors associated with the flavonoid pathway regulation. The objective of this study was to investigate the influence of single gene (Lc and C1) and double gene (Lc × C1) transformation on chemical composition and degradation characteristics of protein and carbohydrate compared to non-transgenic (NT) parental plants. Samples were collected from plant populations of C1 genotype, two Lc genotypes (Lc1 and Lc3), two Lc × C1 genotypes (Lc1C1 and Lc3C1), NT and AC-Grazeland (ACGL) and maintained in a growth chamber. Plants were harvested at late-bud stage, freeze-dried and ground (1 mm). Chemical composition was determined by AOAC methods. Protein and carbohydrate sub-fractions were estimated according to Cornell Net Carbohydrate and Protein System (CNCPS ver. 6.1). Anthocyanidin was extracted with aqueous acetone and hydrolyzed with butanol-HCl to measure spectrometric absorbance. The extractable anthocyanidin contents in Lc alfalfa and Lc × C1 averaged 149 ± 85 and 185 ± 74 μg/g DM, respectively. The single gene had a higher total carbohydrate (CHO; 70% vs. 68%; $P = 0.03$) and non-fiber carbohydrate (NFC; 44% vs. 40%; $P < 0.001$) than double gene transformed alfalfa. There was no difference ($P > 0.05$) in structural carbohydrate (ADF and NDF) content. The single gene alfalfa had a lower CP (19% vs. 21%; $P = 0.02$) than double gene transformed alfalfa. The profiles of protein (PA, PB1, PB2, and PB3), and carbohydrate (CA, CB1, CB2, and CB3) varied among different genotypes, resulting in different degradation profiles. Double gene genotypes had a higher ($P < 0.01$) rumen degradable crude protein (RDCP) but lower ($P < 0.01$) RD-CHO than single gene genotypes. This caused an increase ($P < 0.01$) in total degradable N to CHO ratio in double gene transformation by 10 g N/kg CHO. In conclusion, the gene transformation influenced anthocyanidin accumulation in aerial parts as well as accumulation of nitrogenous compounds and non-structural carbohydrates, thereby changing chemical composition and degradation characteristics. The single gene transformed alfalfa had a lower N to CHO balance than double gene alfalfa.

The C1 gene influences nutrient composition of alfalfa differently, when co-expressed with two Lc lines (Lc1 and Lc3).

Key Words: alfalfa, Lc and C1 genes, gene transformation

0214 Comparative analyses of the bovine rumen microbiota using RNA and targeted DNA-based sequencing approaches. F. Li*[1], X. Sun[2], G. Henderson[3], F. Cox[3], P. H. Janssen[3], and L. L. Guan[2], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]University of Alberta, Edmonton, AB, Canada, [3]AgResearch Limited, Grasslands Research Centre, Palmerston North, New Zealand.*

The bovine rumen microbiota comprises diverse populations, including bacteria, archaea, protozoa, and fungi. Defining rumen microbiota structures and their activities can enhance our understanding of the role of microbes in regulating rumen fermentation. We hypothesized that sequencing total RNA without rRNA removal (RNA-Seq) can be used to study the active microbiota, avoiding potential biases introduced by PCR-amplification of bacterial and archaeal 16S rRNA genes before sequencing. Total DNA and total RNA were isolated from the rumen contents of five steers maintained on a feedlot diet. Partial amplicons of bacterial and archaeal 16S rRNA genes were sequenced (Amplicon-Seq). RNA-Seq was performed in parallel. The data were processed using a QIIME-based pipeline in combination with Greengenes and SILVA-derived taxonomic frameworks. In total, five major bacterial phyla, with a relative abundance greater than 0.1% in any one sample, were identified in both Amplicon-Seq and RNA-Seq datasets; namely *Proteobacteria*, *Bacteroidetes*, *Firmicutes*, *Spirochaetes*, and *Synergistetes*. *Bacteroidetes* was more abundant in Amplicon-Seq than RNA-Seq datasets (52.6 ± 8.8% versus 23.7 ± 7.7%, mean ± SEM), whereas *Proteobacteria* was predominant in RNA-Seq datasets (45.7 ± 14.1% versus 13.0 ± 7.7%). *Euryarchaeota* was the most abundant archaeal phylum in both Amplicon-Seq (100.0 ± 0.0%) and RNA-Seq (94.2 ± 2.5%) datasets. Despite some differences in individual animals, microbial community compositions obtained using Amplicon-Seq and RNA-Seq techniques were broadly comparable. Of particular interest is that *Proteobacteria* appear to be more abundant in RNA-Seq datasets. Whether they are indeed more active relative to their abundance (Amplicon-Seq) than other bacteria warrants further investigation. Our results suggest that total RNA sequencing without rRNA removal can be used to study the active rumen microbiota.

Key Words: Amplicon-Seq, RNA-Seq, rumen microbiota

0215 Effect of pelleting at different conditions on ruminal degradation kinetics and intestinal digestion of canola meal in dairy cattle. X. Huang* and P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

Pelleting has been adopted and widely used in the animal feed industry with its positive improvements in feed quality. Canola meal, an important protein source for ruminants in Canada, is usually prepared in mash or in pellets in feed mills. The objective of this study was to investigate the effects of pelleting at different conditions on in situ ruminal degradation kinetics and in vitro intestinal digestion of canola meal. Two batches of canola meal were pelleted after conditioning at different temperatures (70, 80, and 90°C) for different time (30s and 60s). Five rumen-cannulated lactating Holstein cows were used in an in situ trial to determine ruminal degradation kinetics. Intestinal digestibility was detected using a three-step in vitro method. Samples conditioned at 80°C had highest degradation rates (K_d) for crude protein (CP) and dry matter (DM) among pellets due to the quadratic effect of conditioning time ($P < 0.05$). The soluble fraction (S) of protein in pellets was greater than that in the unprocessed mash (9.84 vs. 5.68% CP, $P < 0.01$). The unprocessed mash had a greater content of bypass CP (BCP) but a lower content of effectively degraded CP (EDCP) than pellets (BCP: 44.20 vs. 39.30% CP; EDCP: 55.81 vs. 60.70% CP), indicating pelleting reduced ($P < 0.01$) BCP but increased ($P < 0.01$) EDCP contents of canola meal. However, bypass carbohydrates (BCHO) and effectively degraded CHO (EDCHO) were not affected by pelleting. The unprocessed mash had a lower ratio of effective degradability of N to carbohydrates (ED_N/ED_CHO) than pellets (126.17 vs. 142.85; $P < 0.01$). Conditioning temperature had a significant impact on ED_N/ED_CHO among pellets ($P < 0.05$). In the in vitro trial, intestinal digestible protein (IDP) content was greater in the unprocessed mash than in pellets (113.28 vs. 94.85 g/kg DM, $P < 0.05$), indicating that pelleting decreased IDP content of canola meal. There was no difference detected among samples on intestinal digestion characteristics for carbohydrates. In conclusion, pelleting increased ruminal degradation of protein while intestinal digestion of protein decreased in the current study. However, ruminal degradation and intestinal digestion characteristics of carbohydrates were not affected.

Key Words: pelleting, canola meal, rumen degradation, intestinal digestion kinetics

0216 Evaluation of corn and barley varieties in backgrounding grazing programs for beef calves.
S. A. McMillan*[1], B. Lardner[2], J. J. McKinnon[1], K. Larson[2], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

A study evaluated the effects of grazing either swathed barley (*Hordeum vulgare;* cv. Ranger*)* or standing corn (*Zea mays;* cv. Pioneer P7443R) as compared to drylot calves fed barley hay on forage quality, dry matter intake (DMI), calf backgrounding and feedlot performance, and backgrounding production costs. Each year, 120 spring born Angus calves (278.2 ± 5 kg) were fall weaned, stratified by body weight and randomly allocated to 1 of 3 replicated (n = 2) backgrounding systems: 1) field grazing standing whole plant corn (CORN); 2) field grazing swathed whole plant barley (BAR); or 3) dry lot (DL) bunk fed processed barley hay. CORN and BAR calves were limit grazed in 4-ha paddocks for 3 d grazing periods using electric fencing for 68 d, with all groups receiving a pelleted supplement (78% TDN, 16% CP) daily at 0.8% BW. Forage samples were collected every 21 d to determine CP, TDN, ADF, and NDF. DMI was estimated using the herbage weight disappearance method. After backgrounding, replicates of calves were divided into 2 and placed in a feedlot. Calves were fed a barley silage based diet with either barley or corn grain for 203 d to a target weight of 615 kg, at which point they were slaughtered and carcass data was collected. Data were analyzed as a one-way ANOVA using the Proc Mixed Model procedure of SAS. Protein content was greatest (P < 0.05) for DL and BAR (12.6% and 12.3%, respectively) compared to CORN (8.0%). Forage TDN, ADF, NDF, and forage DMI did not differ *(*P > 0.02) among backgrounding systems. Final BW and ADG were greatest (P < 0.05) for DL calves compared to CORN and BAR (331.7 vs. 311.9 and 311.2 kg, respectively) and (0.9 vs. 0.6 and 0.6 kg/d, respectively). There was no difference in costs of gain among systems but the total cost of production was greatest (P < 0.05) for DL calves ($2.20/calf/day). Feedlot performance and carcass characteristics did not differ among systems, suggesting that backgrounding calves by field grazing either standing whole plant corn or swathed barley can result in lower backgrounding production costs compared to feeding in drylot.

Key Words: backgrounding, barley, corn

0217 Transcriptomic analysis of rectal-anal junction tissue from super-shedders vs. cattle negative for *E. coli* O157:H7.
O. Wang*[1], G. Liang[1], X. Sun[1], B. Selinger[2], K. Stanford[3], G. S. Plastow[1], T. A. McAllister[4], and L. L. Guan[1], *[1]University of Alberta, Edmonton, AB, Canada, [2]University of Lethbridge, Lethbridge, AB, Canada, [3]Alberta Agriculture and Rural Development, Lethbridge, AB, Canada, [4]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

E. coli O157:H7 is a foodborne pathogen that causes hemorrhagic colitis and hemolytic uremic syndrome in humans. Cattle are the main reservoir for *E. coli* O157:H7 and individuals shedding > 10^4 CFU/g of feces are defined as super-shedders. To date, the molecular mechanisms responsible for the high level of carriage and shedding in super-shedders is unknown, but presumably is mediated by a host-microbial interaction. We hypothesized that changes in gene expression related to immune responses in tissues from the rectal-anal junction (RAJ) may be associated with the super-shedder phenomenon. In this study, we performed transcriptomic analysis of tissues from the RAJ, the reported main colonization site of *E. coli* O157:H7. Total RNA was extracted from RAJ tissues collected from five super-shedder steers and four non-shedder pen mates. RNA sequencing was done using Illumina sequencer Hiseq 2000 with average of 29.7 M ± 4.2 M paired-end reads generated from each sample. After mapping the reads to the bovine genome using Tophat, a total of 15,614 expressed genes (FPKM > 0.3) were detected at least once in at least one of the steers, with expression of 13,047 of genes (FPKM > 0.3) detected in non-shedders and 11, 846 (FPKM > 0.3) in super-shedders. The top functions of these genes enriched by GO terms include metabolic process, cellular process, and biological regulation which were not different between the two groups. In total, 20 genes were downregulated in super-shedders as compared to non-shedders (FDR < 0.1, using EdgeR). Of those genes downregulated in super-shedders, 11: CXCL13, CCL21, CCR7, IL2RA, LTB, S100A12, CD19, BANK1, CD19, MS4A1, KLHL6 were predicted to be associated with traits related to immune function; including movement of T cells, recruitment of leukocytes as well as the levels of B-cells and IgG. This is the first study to report transcriptomic analysis of the RAJ as it relates to the shedding status of the host. Our results suggest that immune homeostasis in super-shedders may play a role in the high levels of shedding observed in these individuals.

Key Words: *E. coli* O157, super-shedder, transcriptomic analysis

0218 Influence of steeping DDGS on growth performance and digestive function in liquid fed weanling pigs. M. Wiseman*, J. Zhu, D. Wey, and C. F. de Lange, *University of Guelph, Guelph, ON, Canada.*

Liquid feeding of high-fiber co-products with supplementary fiber-degrading enzymes may increase feeding value and influence gut development. This study assessed the effect of extended steeping of DDGS on performance and digestive function in newly-weaned pigs (weaned at 20 d) fed corn-soybean meal based liquid diets (28% DM). Enzymes (67.2 IU/g DDGS β-glucanase; 15.36 IU/g DDGS Xylanase; AB Vista) were used in both treatments: steeped (sDDGS; DDGS with enzymes fed between Day 5 and 14 of steeping in 39°C water at 16% DM) and unsteeped (usDDGS; DDGS and supplement mixed with water at time of feeding). Diet DDGS inclusion levels were 7.5% in phase 1 (d 0−7) and 25% in phase 2 (d 7-20) and 3 (d 21-35). The study was a randomized block design (n = 6 pens, 14 pigs/pen). Results are lsmean ± SEM (sDDGS vs. usDDGS, respectively), except fermentation characteristics (mean ± SD). On d 7, 14, and 35, 3 pigs per pen were euthanized for determination of liver, stomach, and small intestine (SI) weights, SI length, and digesta pH. VFA concentration was determined in d14 and d35 jejunal, ileal, and cecal digesta pooled among pigs in a pen. sDDGS batch (n = 5) characteristics (d5 and d14, respectively) revealed average pH 3.54 ± 0.16 and 3.04 ± 0.08, lactic acid 127.1 ± 22.3 and 72.5 ± 26.6 mM, and n-Butyric acid 38.7 ± 14.5 and 41.6 ± 27.1 mM. Unsteeped diets had pH 5.97 (n = 1), lactic acid 11.9 ± 11.8 mM (n = 3),and n-Butyric acid 7.1 ± 6.5 mM (n = 3). Steeping did not affect (P > 0.10) growth performance (Day 0-35 ADG 289 ± 15.8 and DMI 416.9 ± 10.3 g/d (n = 6) vs. ADG 290 ± 17.5 and DMI 415.7 ± 11.4 g/d (n = 5)), d7 physiological parameters (P > 0.10), or any gastrointestinal section weights (P > 0.05). Liver weight relative to BW was higher (P < 0.05) in sDDGS pigs on d14 while absolute liver weight was higher (P < 0.05) on d35 (30 vs. 27 ± 1 g:kg BW and 638 vs. 542 ± 21 g). sDDGS increased (P < 0.05) d14 jejunal formic and n-butyric acid (84.6 vs. 9.0 ± 16.8 and 61.8 vs. 42.1 ± 6.0 mM) without altering pH (P > 0.10). On d35 sDDGS increased (P < 0.05) cecal formic acid and decreased pH (P < 0.05) (71.7 vs. 153.7 ± 18.8 mM and 5.49 vs. 5.74 ± 0.07). No other VFA concentrations were affected (P > 0.05). sDDGS decreased (P < 0.05) d35 colon pH (5.64 vs. 5.85 ± 0.07) without altering pH elsewhere (P > 0.10). Results indicate steeping DDGS with enzymes results in altered enteric fermentation without affecting growth performance.

Key Words: digestive function, enzymes, liquid feeding pigs

0219 Selection of hybrid bromegrass for increased NDF digestibility. C. L. Rosser*[1], B. Coulman[1], and G. B. Penner[2], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The objective of this study was to determine whether selecting hybrid bromegrass for improved NDF digestibility would improve NDF digestibility and the performance of growing lambs. In 2010, 128-hybrid bromegrass (*Bromus riparius Rehm. × Bromus inermis Leyss.;* cv. AC Knowles) plants were clipped (5-cm stubble height) and used to determine 24-h in situ NDF digestibility (NDFd). Individual plants with the greatest (HNDFd; n = 20) and least (LNDFd; n = 20) digestibility values were selected (34.5 and 23.5%, respectively; P < 0.001) and polycrossed in isolation to produce seed. Seedlings were established in a field nursery June 8, 2011 and harvested July 23, 2012 and July 11, 2013 for in situ NDF digestibility determination. The DM yield tended to be greater for the LNDFd population (350 vs. 380 g/plant; P = 0.072) than HNDFd, while the degradable DM (37.2 vs. 33.6%; P = 0.098) and OM (39.8 vs. 35.7%; P = 0.092) fractions tended to be greater for HNDFd than LNDFd. Degradation rates for DM, OM, CP, NDF and ADF were not affected by treatment ($P \geq 0.398$). Additional plots of the HNDFd and LNDFd hybrid bromegrass populations were swathed on July 11, 2013, dried, and baled for an in vivo digestibility experiment. Twelve Suffolk × Canadian Arcott wether lambs were randomly assigned to the HNDFd or LNDFd treatments. The bromegrass hay was fed ad libitum and all lambs were supplemented with a pellet fed at 0.88% of initial BW. Total DMI and forage intake were not affected by treatment (P = 0.219). Nutrient intake (OM, CP, NDF, ADF, and ether extract; $P \geq 0.143$) was also not different between lambs fed LNDFd or HNDFd. However, NFC intake tended to be greater for HNDFd than LNDFD (0.34 vs. 0.29 kg/d; P = 0.070). Feeding the HNDFd or LNDFd bromegrass for 21 d did not affect final body weight or ADG ($P \geq 0.189$), but cumulative weight gain was greater for lambs fed HNDFd (P = 0.013). Total tract digestibility of DM, OM, NDF, ADF and NFC were not affected by treatment ($P \geq 0.328$), but CP and ether extract digestibility values tended to be greater for LNDFd than HNDFd ($P \leq 0.068$). These data suggest that although there were improvements in the degradable fractions of DM and OM and cumulative weight gain of the lambs fed HNDFd, the hybrid bromegrasses did not differ in NDF digestibility.

Key Words: digestibility, forage intake, hybrid bromegrass

0220 Effect of feeding different sources of nitrogen on performance of growing pigs fed diets deficient in non-essential amino acid nitrogen.

W. D. Mansilla[*1], J. K. Htoo[2], and C. F. de Lange[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Evonik Industries AG, Hanau-Wolfgang, Germany.*

When formulating diets with low nitrogen (N) content, the supply of dietary non-essential amino acids (NEAA) is reduced and essential amino acid (EAA) may be catabolized to supply N for endogenous synthesis of NEAA, which can lead to compromised pig performance. The objective of this study was to evaluate the effect of supplementing different sources of N in diets deficient in NEAA-N on performance of growing pigs. In total 36 barrows (BW 15.5 ± 1.0 kg) were randomly assigned to 9 different diets: a basal cornstarch and casein-based diet, not deficient in EAA but low in CP (N × 6.25; 8.01%); and the basal diet supplemented with 4 different sources of N (urea, ammonium citrate, glutamic acid and a mix of NEAA) at 2 levels each, supplying 1.37 and 2.75% additional CP, respectively. The mix of NEAA was based on body composition of NEAA of 20 kg pigs, and aimed to minimize endogenous synthesis of NEAA. Pigs were housed individually and fed at 3.0 × maintenance requirement for ME during 3 consecutive weeks. BW gain was monitored weekly. BW gain and gain:feed of pigs fed urea were lower than any other sources of N ($P < 0.05$), but they were similar across the other treatments ($P > 0.10$). As the level of N increased, BW gain and gain:feed increased ($P < 0.05$). Feeding ammonium to pigs is as efficient as supplementing glutamate or NEAA mix to support growth performance when diets are deficient in NEAA-N, while utilization of urea-N is lower.

Key Words: growth, nitrogen, pig

Table 0220. BW gain, feed intake and gain:feed in growing pigs fed a diet deficient in NEAA-N supplemented with different sources of N at different levels of N supplementation

		BW gain, g/d	Feed intake, g/BW$^{0.6}$/d	Gain:feed
Source	Urea	367[a]	169	0.381[a]
	Ammonia	399[b]	169	0.415[b]
	Glutamate	404[b]	169	0.421[b]
	NEAA mix	402[b]	169	0.418[b]
	SEM	7.5	0.1	0.008
Level	0.0	363[a]	169	0.378[a]
	1.37	387[b]	169	0.403[b]
	2.75	429[c]	169	0.445[c]
	SEM	6.4	0.01	0.007
P-value	Source	0.006	0.219	0.004
	Level	< 0.001	0.286	< 0.001
	Interaction	0.070	0.247	0.069

[a,b,c] Values in the same column followed by different superscripts differ ($P < 0.05$).

0221 Comparison of winter feeding systems for the evaluation of beef cow performance, reproductive efficiency and system costs.

D. Jose[*1], G. B. Penner[1], J. J. McKinnon[1], K. Larson[2] and, B. Lardner[1,2], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

Extensive winter grazing has been proven as a successful strategy to reduce production and labor costs in a cow-calf operation without much adverse effects on animal health and performance. Two experiments were conducted during the winter of 2012-2013, to evaluate 3 winter feeding systems: (i) field grazing standing whole plant corn (SC; TDN = 59.5%, CP = 7.8%), (ii) field grazing swathed barley hay (SB; TDN = 66.2%, CP = 8.5%) and, (iii) barley hay bales fed in drylot pens (DL; TDN = 60.1%, CP = 12.7%). The specific objectives were to compare beef cow performance, reproductive efficiency and system costs in experiment 1 (EXP 1), and ruminal pH parameters in experiment 2 (EXP 2). In EXP 1, dry pregnant Angus cows ($n = 60$, body weight (BW) = 651.2 ± 7 kg), stratified by body weight and days pregnant were randomly allocated to 1 of 3 replicated ($n = 2$) winter grazing treatments for 77 d. Cow BW, body condition score (BCS), and rib and rump fats were measured at the start and end of the trial. Increases in rump fat were greater ($P = 0.002$) for SC cows compared to DL cows (1.90 mm vs. 0.55 mm, respectively). Calves born to cows on SC were heavier ($P < 0.001$) at birth compared to calves from SB cows (42 vs. 40 kg respectively). In EXP 2, 9 cannulated beef heifers were cycled through the 3 winter systems concurrently within EXP 1, in a replicated 3 × 3 Latin square design, for 63d to evaluate effect of forage type on rumen pH. Results from EXP 2 indicated that SB heifers had the lowest ($P < 0.003$) mean, minimum and maximum rumen pH and greatest duration and area under pH < 5.8 ($P < 0.001$) compared to heifers on SC and DL winter systems. Economic analysis revealed that total costs were greatest for the DL ($2.29/head/d) compared to SC ($1.78/head/d) and SB ($1.65/head/d) systems. Results suggest that both SC and SB systems are cost effective alternatives to DL system, and do not negatively affect cow body weight or reproductive performance in winter.

Key Words: winter grazing, corn grazing, swath grazing, reproductive performance

0222 Dietary supplementation with excess leucine transiently improved whole body nitrogen retention in young pigs challenged with bacterial lipopolysaccharide.

M. Rudar* and C. F. de Lange, *University of Guelph, Guelph, ON, Canada.*

The increase in circulating pro-inflammatory cytokines following a bacterial lipopolysaccharide (LPS) challenge causes a disruption in normal nitrogen (N) and amino acid (AA) me-

tabolism. The reduction in whole body N retention during inflammation can be attributed to an increase in hepatic protein synthesis at the expense of muscle protein synthesis, which may be modulated by leucine (Leu) intake. The objective of this study was to explore the effect of excess dietary Leu on the dynamics of N retention in young pigs following an LPS challenge. A total of 24 starter pigs (13.93 ± 2.05 kg) were used in a 2 × 2 factorial design (n = 6). Pigs were fed isoenergetic and isonitrogenous diets formulated to contain all essential AA 10% above requirements for protein deposition (Con; 1.36% SID Leu) or Leu supplemented at twice that amount (+Leu; 2.72% SID Leu). Pigs were housed in metabolic crates and fed six times daily according to their body weight. Pigs were challenged with either saline (−LPS) or repeated and increasing doses of LPS (+LPS; 30 μg·kg^{-1} injected intramuscularly on Days 1, 3, 5, and 7 of a 7-d N-balance period). Blood was collected on Days 1 and 7 1 h after feeding to determine plasma AA concentrations. Whole body N retention was determined daily. Pigs fed +Leu had higher plasma Leu than pigs fed Con (319 vs. 159 μmol·L^{-1}, SE 10.3, $P < 0.01$). There was no effect of diet on N retention across the 7-d N balance period ($P > 0.10$). However, LPS reduced N retention during the first 3 d of the N balance period ($P < 0.05$). For +LPS pigs, the effect of diet on N retention changed over time ($P < 0.05$); on Day 2, N retention was lower in +LPS pigs fed Con than +LPS pigs fed +Leu (10.5 vs. 12.3 g/d, SE 0.66, $P < 0.05$). Moreover, N retention was higher in −LPS pigs than in +LPS pigs fed Con (13.0 vs. 10.5 g/d, SE 0.66, $P < 0.01$) whereas N retention was not different between–LPS pigs and +LPS pigs fed +Leu (12.3 vs. 12.3 g/d, SE 0.66, $P > 0.10$) on Day 2 post-challenge. In this study, excess dietary Leu partly attenuated the reduction in body protein gain after an LPS challenge.

Key Words: endotoxin, leucine, nitrogen retention

0223 The relationship between trailer motion and carcass bruising in market cows during transport.

C. E. Kehler[*1,2], K. H. Ominski[1], L. L. Connor[1], T. G. Crowe[3], and K. S. Schwartzkopf-Genswein[4], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Agriculture and Agri-food Canada, Lethbridge, AB, Canada, [3]University of Saskatchewan, Saskatoon, SK, Canada, [4]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Increased trailer motion, coupled with large accelerations and decelerations, have been associated with decreased carcass quality and increased stress indicators in cattle, sheep and hogs. However, motion of livestock trailers has not been measured in North-American cattle semi-trailers over long distances (> 1000 km). The objective of this study was to describe the acceleration within each of the 5 compartments of a cattle semi-trailer and to determine the relationship between trailer acceleration and bruising severity. The root mean square (rms) of acceleration was measured at a sampling rate of 200 Hz in 3 orthogonal axes; x (vertical, positive upward), y (front-to-rear, positive forward) and z (lateral, positive leftward as viewed from rear) by rigidly clamping an accelerometer to the cross beam below each of the five compartments of 8 trailers transporting 331 animals from assembly yard to a processing facility. Journeys ranged in duration from 780 min to 942 min. A bruise severity score was obtained before trimming for n = 291 carcasses using the number of bruises weighted by the size of bruise on a 3-point scale (1 $\leq$ 6.5 cm; 2 = 6.5 to 12 cm and 3 $\geq$ 12 cm). Due to limitations in the battery capacity of the sensors, the acceleration was only measured for the first half of the journey for all but 2 journeys. The percent difference in rms between the entire journey and the first half of those 2 journeys ranged from 7.22% to 14.54%. The mean rms of acceleration for all trailers (34 accelerometers) was 1.43 ± 0.42 m/s^2, 1.32 ± 0.53 m/s^2 and 1.67 ± 0.50 m/s^2 for x, y and z axes, respectively. Mean bruise number and severity per carcass were 4.52 ± 2.43 and 5.31 ± 2.84, respectively. When measured by trailer a quadratic relationship was observed between acc (rms) and bruise severity in the z-axis (r = 0.69, P = 0.09) however, no relationship was observed between either the x or y axes and bruise severity. Acceleration varied slightly between trailer compartments in the z (P = 0.10) and y-axes (P = 0.10) but not in the x axis. Bruising also varied slightly by trailer compartment (P = 0.11). Results indicate that reductions in side to side trailer movements could decrease bruising, thereby improving carcass quality and animal welfare. Extension and replication of this research is required to further understand the relationships between trailer motion, carcass bruising and overall animal welfare.

Key Words: cattle, transport, acceleration

0224 Impact of reducing dietary crude protein concentration on serum lysine concentration and lysine utilization efficiency in lactating sows.

L. A. Huber[*1], C. F. de Lange[1], U. K. Larsen[2], D. Chamberlin[3], and N. L. Trottier[3], *[1]University of Guelph, Guelph, ON, Canada, [2]Aarhus University, Foulum, Denmark, [3]Michigan State University, East Lansing*.

It was hypothesized that reducing dietary crude protein (CP) concentration while maintaining available Lys intake will improve Lys utilization efficiency for milk production in sows. Forty lactating multiparous Yorkshire sows were used to determine the effect of reducing dietary CP concentration and supplementing with crystalline amino acids on dietary Lys utilization efficiency during early (d3−7) and peak (d14-18) lactation. Sows were assigned to 1 of 4 diets: [1] 16.0% CP (as-fed; analyzed contents; HCP); [2] 15.7% CP (0.1% crystalline Lys; MHCP); [3] 14.3% CP (0.2% crystalline Lys; MLCP); [4] 13.2% CP (0.3% crystalline Lys; LCP); diet HCP was formulated using soybean meal and corn as the only Lys sources. Across diets, standardized ileal digestible (SID) content of Lys was 0.77%, based on analyzed

content and estimated SID. Other essential amino acids were included to exceed requirements. Litters were standardized to 10 piglets within 24h of birth. Milk yield was estimated based on litter size and growth rate. Blood was collected from fasted sows on d3, 7, 14, and 18 for free amino acid analysis. The efficiency of using SID Lys intake for Lys output in milk (Klys) was calculated according to NRC (2012), accounting for maternal maintenance requirements and the contribution of maternal body protein mobilization based on sow BW change. Sow feed intake and litter growth rate during the 21d lactation period did not differ between dietary treatments (overall means: 5670 ± 138 and 2263 ± 94 g/d, respectively). Serum Lys concentration was influenced by day in lactation ($P < .0001$); there tended ($P = 0.08$) to be a quadratic effect of dietary CP concentration (142.8, 105.6, 127.5, and 167.7 ± 22.7, and 84.8, 63.2, 61.7, and 79.6 ± 11.9 µmol/L; HCP, MHCP, MLCP, and LCP on d7 and d18, respectively). In early lactation, reduced dietary CP concentration did not affect Klys (67.5, 70.9, 64.2, and 66.7 ± 6.63%; HCP, MHCP, MLCP and LCP, respectively; $P > 0.10$). In peak lactation Klys was higher for MHCP than HCP ($P < 0.05$), but a further reduction in diet CP concentration did not affect Klys ($P > 0.10$; 59.8, 68.3, 65.1, and 67.6 ± 2.92%; HCP, MHCP, MLCP and LCP, respectively). There appears to be an association between plasma Lys levels and Klys, which needs to be explored further. In peak lactation the use of up to 0.1% crystalline Lys to replace protein bound Lys in the diet improved Klys.

Key Words: amino acids, lactating sows, lysine utilization

0225 Diurnal variations in enteric methane emissions from non-lactating dairy cows offered diets differing in forage to grain ratio. A. J. Kotz*[1], S. C. Li[2], E. J. McGeough[1], E. Khafipour[3], and J. C. Plaizier[2], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [3]Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, MB, Canada*.

This experiment determined how level of dietary grain inclusion affected daily enteric methane emissions and their diurnal variation in dairy cows. Six mature non-lactating Holstein dairy cows were offered one of three diets with forage to grain ratios of 100:0 (F), 75:25 (M), and 50:50 (H). The forage portion of the diet consisted of 80% grass hay and 20% alfalfa hay (DM basis). The concentrate was a barley-corn based ration (DM = 893 g/kg, CP = 198 g/kg DM). Feed was offered three times daily at 0900, 1300, and 1700. The experiment was a replicated 3 × 3 Latin Square Design, with each animal receiving each of the three diets over the course of the three 5-wk periods. Experimental diets were switched gradually during the first week of every period. This was followed by 3 wk dietary adaptation. Sample collection and enteric methane output measurement were conducted on two separate days during the fifth week of every period. Rumen fluid was collected using a stomach tube and a fecal grab sample was taken to determine pH at 0830 and 1500 on the day preceding enteric methane output. An open-circuit hood calorimetric system was used to determine methane output over a 24 h period. Increasing the grain content of the diet decreased rumen pH (F = 7.02, M = 6.82, H = 6.77, $P < 0.01$) and fecal pH (F = 7.09, M = 6.85, H = 6.66, $P < 0.01$) and increased DMI (F = 12.2, M = 14.3, H = 16.6 kg/d, $P < 0.01$). Increasing the dietary grain content increased daily enteric methane emissions (F = 361.6, M = 423.0, H = 445.0 L/Day, $P < 0.01$). However, when methane production was expressed per kilogram of DMI, increasing the dietary grain inclusion reduced daily emissions (F = 29.8 L/kg DMI, M = 29.7 L/kg DMI, H = 27.2 L/kg DMI, $P < 0.01$). Methane emissions clearly exhibited a diurnal pattern that coincided with feeding events, irrespective of diet offered. The highest rate of methane production observed was concurrent with afternoon feeding at 1300 (0.38 L/min); while the lowest rate of methane production was observed 2 h before morning feeding (0.20 L/min). The diurnal pattern differed among diets ($P < 0.01$). In conclusion, dietary grain inclusion increased daily methane production and altered the diurnal pattern of methane emission rate.

Key Words: cattle, enteric methane emission, grain to forage ratio

---

0226 Long-term supplementation of diets with 3-nitrooxypropanol resulted in a sustained reduction in methane production in beef cattle. A. Romero-Perez*[1,2], E. K. Okine[1], S. M. McGinn[2], L. L. Guan[1], M. Oba[1], S. M. Duval[3], and K. A. Beauchemin[2], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada, [3]DSM Nutritional Products France, Research Centre for Animal Nutrition and Health, Saint Louis Cedex, France.*

The objective was to evaluate whether long-term supplementation of diets with 3-nitrooxypropanol (NOP), a synthetic compound proven to reduce enteric CH_4 emissions in short-term studies, results in a sustained reduction in enteric CH_4 emissions in beef cattle. Eight ruminally cannulated heifers (637 ± 16.2 kg of BW) were used in a completely randomized design with 2 treatments: Control (0 g/d of NOP) and NOP (2 g/d of NOP). Treatments were mixed by hand into the TMR (60% forage, DM basis) at feeding time. Feed offered was restricted to 65% of ad libitum DM intake (DMI; maintenance energy intake) to avoid excessive growth. Duration of the experiment was 146 d, including an initial covariate period without NOP supplementation (18 d), 4 periods with NOP supplementation (28 d each), and a final recovery period without NOP supplementation (16 d). Methane was measured at the

end of each period for 3 d using metabolic chambers. Volatile fatty acid (VFA) concentration and microbial populations were measured using rumen samples collected 0, 3, and 6 h after feeding. Data were analyzed using the PROC MIXED procedure of SAS. Average DMI for the experiment was 7.0 ± 0.2 kg. Methane intensity was reduced by 60% when NOP was supplemented (22.6 vs. 8.9 g/kg DMI; $P < 0.01$) with no signs of adaptation (period × treatment, $P = 0.2$). Total VFA concentrations were not affected ($P = 0.12$); however, acetate concentration was reduced and propionate concentration increased when NOP was supplemented ($P < 0.01$), which led to a reduction in the acetate to propionate ratio (3.9 vs. 2.9; $P < 0.01$). NOP had no effect on the copy number of the 16S rRNA gene of total bacteria ($P = 0.5$) but the copy numbers of the 16S rRNA gene of methanogens ($P < 0.01$) were reduced and copy numbers of the 18S rRNA gene of protozoa ($P = 0.03$) were increased. All effects of NOP observed during the measurement periods were absent during the recovery period when supplementation was discontinued. These results showed that reduction of CH_4 production in ruminants is sustained with long-term dietary supplementation of NOP.

Key Words: 3-nitrooxypropanol, beef cattle, methane

0227 Measuring animal productivity and rumen efficiency from extensively overwintered beef cows on the Canadian prairies.

G. R. Donohoe*, K. M. Wittenberg, D. N. Flaten, B. D. Amiro, and K. H. Ominski, University of Manitoba, Winnipeg, MB, Canada.

Many producers in the Prairie region have adopted the use of low-cost, extensive overwintering strategies. Although the economic benefits of these practices are well-documented, rumen efficiency and animal productivity have not been fully characterized. Evaluation of such strategies is challenging because of our limited capacity to measure individual animal intake in extensive overwintering systems. In an attempt to address these knowledge gaps, sixty mature, non-lactating, pregnant beef cows were fed low-quality forage (8.8% crude protein and 4.3 Mcal kg^{-1} gross energy (GE), DM basis) ad libitum and monitored over two, 28-d periods. Cows were divided into three treatment groups: intensively overwintered (drylot; DL), extensively overwintered (bale grazed; BG) and extensively overwintered supplemented with dried distillers' grains with solubles (DDGS) at a rate of 8.31 kg DM every third day (BG+DDGS). Measurements included temperature, body weight, DM intake, enteric methane emission, and serum urea nitrogen (SUN). Average daily air temperature over the trial was -17.1 ± 6.5°C (± SD). Localized temperatures, measured with iButtons near the animal body surface, showed that cows in the extensive treatments were exposed to colder temperatures, at -14.7 ± 0.6°C, compared to cows overwintered intensively, at -11.9 ± 1.4°C (± SD). Average daily gain over the trial was greater ($P < 0.01$) for DL cows when compared to BG cows, but not different ($P > 0.20$) when comparing DL to BG+DDGS. Intake was greater ($P = 0.04$) in period one for DL cows compared to BG cows, measured using GrowSafe and alkane bolus techniques, at 13.4 ± 0.38 and 12.1 ± 0.44 kg DM d^{-1}, respectively (± SE). This resulted in greater ($P < 0.01$) enteric methane emission from the BG cows in period one, at 5.62 ± 0.49 and 8.46 ± 0.49%GEI, for the DL and BG treatments, respectively (± SE). The addition of DDGS every third day in the extensive treatment reduced enteric methane in both periods. Average SUN concentrations over the trial were below the acceptable range of 2.1 mmol L^{-1} at 1.00 ± 0.40 and 1.40 ± 0.60 mmol L^{-1} for cows in the DL and BG treatments, respectively (± SD). When measured at 24 and 72 h after feeding DDGS, SUN concentrations for cows in the BG+DGSS treatment were 5.14 ± 1.67 and 2.65 ± 0.57 mmol L^{-1}, respectively (± SD), indicating that supplemental DDGS was an effective strategy to increase SUN when feeding low-quality forage. This data demonstrates that animal nutrient requirements may differ in intensive and extensive overwintering environments, and therefore require further characterization to improve metabolic and production efficiency of cattle.

Key Words: enteric methane, beef cows, overwintering

0228 Adding sera enriched in PUFA with different n-6/n-3 ratio advanced bovine in vitro embryo development from both high- and inferior-quality oocytes.

R. Salehi*[1], A. Ruiz-Sanchez[1], M. G. Colazo[2], M. Oba[1], M. Dyck[1], and D. J. Ambrose[3], *[1]University of Alberta, Edmonton, AB, Canada, [2]Alberta Agriculture and Rural Development, Edmonton, AB, Canada, [3]Alberta Agriculture and Rural Development, Livestock Research Branch, Edmonton, AB, Canada.*

Diets containing sunflower (SUN; high linoleic acid, LA) or flaxseed (FLX; high α-linolenic acid, ALA) positively affect early embryonic development (EED) in dairy cows. Also, a FLX-based diet decreased the proportion of non-viable embryos in vivo. Oleic acid (OLA), abundant in canola (CAN), improves oocyte competence in vitro but its influence on EED is not known. Our objectives were to: (1) compare the effects of adding serum collected from cows fed CAN, SUN or FLX on in vitro development of bovine embryos derived from high-quality oocytes (Exp-1), and (2) determine the effect of FLX-fed-cow-serum on development of embryos derived from inferior-quality oocytes (Exp-2). Estrus-cow-serum was harvested from Holsteins fed hay (8.8 DM kg/d) and concentrates (3.8 DM kg/d) supplemented with 1 of 3 rolled oilseeds (8% of total DM) for ≥ 21 d: CAN ($n = 4$); SUN ($n = 4$); or FLX ($n = 4$). Cumulus-oocyte-complexes (COC) aspirated from abattoir ovaries were categorized into Grade 1+2 (high-quality) and Grade 3 (inferior-quality) for Exp1 and 2, respectively. The COC were matured and fertilized (Day-0) in vitro; presumptive zygotes ($n = 977$ from Grade 1+2, Exp-1; $n = 359$ from Grade 3 COC, Exp-2 in 5 replicates each) were cultured with corresponding sera (5%) until Day-8. Se-

rum fatty acid profile (% total fatty acid) were OLA 12.1, total polyunsaturated fatty acids (PUFA) 49.4, n-6/n-3ratio 4.7 (CAN); LA 52.5, PUFA 57.5, n-6/n-3ratio 10.5 (SUN); ALA 17.9, PUFA 54.3, n-6/n-3ratio 2.0 (FLX). In Exp-1, SUN (78.0) and FLX (78.8) increased ($P < 0.05$) % cleaved compared with CAN (65.0) but not with fetal calf serum (FCS; 72.1). Blastocyst (BL) developmental rate (%) was higher ($P < 0.05$) on Day-7 in FLX (15.5) and SUN (15.5) than in CAN (9.1) and FCS (9.2) treatments, but not on Day-8 (overall, 23.3). More ($P < 0.05$) advanced stage embryos (expanded- and hatched-BL, %) were present on Day-8 in SUN (85.0) compared to FLX (69.8), CAN (61.5) and FCS (64.0). In Exp-2, although % cleaved did not differ (41.8), FLX tended ($P = 0.12$) to increase BL developmental rate on Day-7 (6.73) compared to FCS (3.01). More advanced stage embryos (BL and expanded-BL) were present in FLX vs. FCS (84.6 vs. 0.0%). In Exp-2, BL developmental rate (11%) and advanced stage embryos (95%) did not differ on Day-8. In summary, adding serum from cows fed FLX or SUN enhanced BL developmental rate on Day-7 and the proportion of advanced stage embryos on Day-7, even from inferior quality oocytes.

Key Words: oilseed, embryo, serum