CSAS GRADUATE STUDENT POSTER COMPETITION

0979 (M057) Effect of dietary supplementation with linseed oil on the miRnome profile of the bovine mammary gland. R. Li[*1,2], F. Beaudoin[1], X. Zhao[3], C. Lei[2], and E. M. Ibeagha-Awemu[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, [2]Northwest A&F University, Xi'an, China, [3]McGill University, Ste Ann De Bell, PQ, Canada.*

Linseed is particularly rich in α-linolenic acid (C18:3n3) and its supplementation in diets induces an increase in milk unsaturated fatty acid content (along with decrease in milk saturated fatty acids) with potential milk fat depression. The specific role of microRNAs (miRNAs), important post-transcriptional regulators of gene expression, in this dietary adaption remains unknown. Using next generation sequencing, the miRnome of the bovine mammary gland in response to dietary supplementation with 5% linseed oil on dry matter bases was studied. Thirteen high-producing Holstein dairy cows in mid-lactation were fed a control ration (total mixed ration of corn and grass silages) for 28 d followed by a treatment period (control diet supplemented with 5% linseed oil) of 28 d. Milk component yields including fat (%) were measured on a weekly basis. Mammary biopsies on three cows were performed on d 14 (control period) and on d +7 and +28 (treatment period). Results show a significant decrease ($P < 0.0001$) in milk fat yield (%) during the treatment period (3.02 ± 0.17) as compared to the control period (3.62 ± 0.17). Nine libraries were constructed and subjected to 50bp smallRNA sequencing. A total of 103,796,305 raw reads were obtained and 93,218,009 retained after adaptor trimming and quality filtering. Of these, 69,210,197 (74.25%) were mapped to the bovine genome. A total of 338 known miRNAs (82.6% of mapped reads) were identified with more than one count per million in at least six libraries. Furthermore, 223 novel hairpins encoding for 212 novel miRNAs were identified. Five miRNAs (bta-miR-148a, miR-143, miR-26a, miR-30a-5p, and miR-10b) were most highly expressed, accounting for 54.93% of reads of identified known miRNAs. As compared to d 14 (control period), 10 miRNAs were significantly regulated (five up-regulated: bta-miR-4286, mir-199c, miR-199a-3p, miR-98, and miR-23b-3p; five downregulated: bta-miR-484, miR-96, miR-200a, miR-335, and miR-2299–5p) at d +28 ($P < 0.01$), while no significant regulation was detected at d +7 ($P > 0.01$). About 5541 genes were predicted to be targeted by differentially expressed miRNAs. Function enrichment analysis showed significant enrichment of target genes for functions related with lipid metabolism ($P < 0.01$). In conclusion, our study revealed that several miRNAs were differentially expressed during the milk fat depression introduced by linseed oil supplementation, suggesting that these miRNAs could be important regulators of mammary lipid synthesis. Furthermore, novel miRNAs identified in this study will greatly enrich the bovine miRnome repertoire and also act as targets for further study of bovine mammary gland biology.

Key Words: microRNA, linseed oil, bovine mammary gland

0980 (M058) Effect of co-expression of Lc and C1 flavanoid regulatory genes in alfalfa on nutritive value and ruminal methane production. 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, Canada, [2]Agriculture, and Agri-Food Canada, Saskatoon, SK, [3]Agriculture and Agri-Food Canada, Lethbridge, AB.*

An alfalfa progeny was developed by transforming Lc and C1 genes which are regulatory genes associated with flavonoid pathway in Zea maize. The transformation objective was to promote anthocyanidin accumulation in alfalfa leaves and stems, thus reducing the extent and rate of protein degradation in the rumen and potentially rumen methane production. The objective of this study was to evaluate the effect of co-expression of Lc and C1 genes on 1) protein, energy and feed milk values, and 2) methane gas production relative to single gene transformed alfalfa and non-transgenic parent plants. Alfalfa samples were collected at late-bud stage from populations of single gene transformed (C1, Lc1, and Lc3), double gene transformed (Lc1C1 and Lc3C1), parental non-transgenic (NT), and a commercial cultivar (AC-Grazeland: ACGL) maintained in growth chambers at the Saskatoon Research Centre, Agriculture and Agri-Food, Canada. Samples were chemically analyzed according to AOAC methods, and energy and protein values were determined using NRC (2001) and CNCPS (v.6.1) models. Fermentation gases were obtained from in vitro batch culture and analyzed by gas chromatography for methane. Rumen degradable protein was higher ($P < 0.01$) by 2% in double gene alfalfa comparing to single gene alfalfa, but no differences ($P > 0.05$) were observed in digestible rumen undegradable protein. In comparison to single gene alfalfa, co-expression of Lc and C1 genes increased ($P = 0.01$) net energy by 50 kcal for both lactation and growth and thereby increasing ($P < 0.01$) the feed to milk conversion efficiency by 80 g of milk per kg of alfalfa dry matter. The double gene alfalfa tended to have lower ($P = 0.07$) total gas production than NT alfalfa and significantly lower ($P < 0.05$) methane production by 3.5 L per kg DM than single gene alfalfa. In conclusion, C1 gene when co-expressed with Lc gene improved the feeding value of alfalfa and reduced in vitro methane production.

Key Words: Lc-C1 transgenic alfalfa, energy and protein, methane

0981 (M059) Predicting milk fat concentration from nutrient content and DCAD of the diet.

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The farm-gate price of milk in Canada is based on composition, which provides incentive for producers to increase fat content. The objective of this study is to determine the extent to which changes in nutrients and DCAD can predict milk fat percentage. Data recorded by Valacta (Dairy Production Center of Expertise Quebec-Atlantic) for the years 2009 to 2011 was used and originally comprised 3481,705 test-day records (275,758 cows and 3140 herds). Records used for the regression analysis were restricted to those from Holstein cows, between one and 305 DIM, taken during winter months, reducing the number of admissible records for the analysis to 306,191 (134,236 cows and 2658 herds). Lactations were divided into early (1 to 50 DIM), peak (51 to 100 DIM), and established lactation (101 to 305 DIM). Statistical analysis were performed using PROC HPMIXED of SAS with herd and cow (herd) as random effects. Independent variables were included in the final equation when $P \leq 0.05$. The variables used as covariates in the regression were: milk production (kg/day), DIM, and estimated breeding value for fat composition (EBV_FAT). Variables tested to explain milk fat concentration were: NDF from forage + 0.5 x NDF from concentrate (NDF_NRC), NFC, amount of buffers (BUFF; kg/day), amount of fat supplements with more than 80% of palmitic acid (PALM80; kg/day), and DCAD. In the final analysis for the 3 yr, multiple regression in early lactation (n = 24,987; R^2 = 0.44) included, in addition to the covariates, the following variables: NDF_NRC (quadratic) and PALM80. For peak lactation (n = 29,317; R^2 = 0.42) the variables were DCAD, NDF_NRC, BUFF and PALM80. For established lactation (n = 100,706; R^2 = 0.64) NDF_NRC, NFC (quadratic), BUFF and PALM80. All the equations accounted for a significant effect of year. When the regression was split by year, all the variables remained the same, while the DCAD (quadratic) was also added to the model for established lactation in all 3 yr, but with different optimal value (2009: > 330 mEq/kg MS; 2010: 210 mEq/kg MS; 2011: > 380 mEq/kg). In summary, the equations were able to predict up to 64% of milk fat variation based on the combination of different nutrients, especially NDF_NRC (quadratic) and PALM80. Based on the variations in optimal values between years, it could be concluded that the impact of the DCAD on milk fat concentration can be influenced by the nutritional quality of feed ingredients.

Key Words: lactating dairy cows, milk fat, DCAD.

0982 (M060) Evaluation of methane prediction equations for beef cattle fed high forage or high concentrate diets.

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Enteric methane (CH_4) emission is the major contributor to greenhouse gases from beef cattle farms. Many equations are available to predict enteric CH_4 emissions from beef cattle, but the predictions vary substantially amongst equations. The aims of this study were to: 1) construct a database of enteric CH_4 emissions for beef cattle fed forage and grain-based diets from published literature, and 2) identify the most precise and accurate extant CH_4 prediction models for beef cattle fed diets varying in forage content. The database was comprised of treatment means of enteric CH_4 production from in vivo beef studies published from 2000 to 2013. Criteria for selecting data to include in the database were: animal description, intake, diet composition, and measurement of enteric CH_4 production. Missing values were estimated using feed composition tables, nutritional software or by calculation from the diet description. Fifty-one equations that predict CH_4 production from diet composition were evaluated. Precision and accuracy of the equations was evaluated using the concordance correlation coefficient (r_c), bias correction factor (C_b) and root mean square prediction error (RMSPE, g/d), and then ranked highest to lowest based on r_c. Statistical analysis was performed using JMP and SAS. The final database contained 39 studies and 163 treatment means that were divided into two subsets: a subset comprised of data from diets containing 40% or more forage and a subset comprised of data from diets containing less than 40% forage (dry matter basis). Using the complete database, equations with highest r_c were: G (Ellis et al., 2009), IPCC (2006) and J (Ellis et al., 2009), with r_c: 0.71, 0.67, 0.63, C_b: 0.98, 0.98, 0.98, and RMSPE: 55.0, 57.7, 61.4, respectively. For the high forage dataset, equations with highest r_c were IPCC (2006), G (Ellis et al., 2009), and Nonlinear 2 (Mills et al., 2003) with r_c: 0.75, 0.75, 0.71, C_b: 0.96, 0.99, 0.95, and RMSPE: 47.9, 51.7, 52.5, respectively. For the low forage dataset, equations with highest r_c were 9b (Ellis et al., 2007), G and P (Ellis et al., 2009), with r_c: 0.52, 0.48, 0.47, C_b: 0.67, 0.81, 0.81, and RMSPE: 56.0, 64.0, 62.0, respectively. Ranking of extant CH_4 prediction equations for their accuracy and precision differed with forage content of the diet. When used for cattle-fed low-forage diets, extant CH_4 prediction models were generally imprecise and lacked accuracy.

Key Words: beef cattle, enteric methane emission, models

0983 (M061) Non-protein nitrogen improves feed efficiency of growing pigs fed a diet 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, ON, Canada,* [2]*Evonik Industries AG, Hanau-Wolfgang, Germany.*

In pig diets the balance between essential amino acids (EAA) and total N should be considered, especially when large amounts of crystalline EAA are supplemented and N levels are reduced. When lowering dietary N, the dietary supply of non-essential amino acids (NEAA) is reduced and the need of N for endogenous synthesis of some NEAA may be increased, requiring N from either catabolism of excess EAA and NEAA or non-protein nitrogen (NPN). The objective of the present study was to determine the effect of supplementing NPN, in the form of ammonium salts, in diets deficient in NEAA-N on performance of growing pigs. In total, 48 gilts (initial BW of 15.2 ± 1.3 kg) were randomly assigned to 4 diets: 1) positive control (PC; 13.39% CP), not deficient in EAA and NEAA-N, and all N was supplied from intact protein (casein and soybean meal) or crystalline EAA; 2) negative control (NC; 10.19% CP), supplying the same amount of potentially limiting EAA as PC, but deficient in NEAA-N; 3) NC with 3 g/kg added ammonium (Low NPN); and 4) NC with 6 g/kg added ammonium (High NPN), the latter containing the same amount of digestible N as PC. Pigs were grouped in two pigs per pen with six pens per treatment. BW gain and feed intake were monitored weekly during 3 wk, and blood samples were taken on d 14 and 21 to determine plasma urea concentration. Wk 1 yielded poor growth performance and was considered a week of adaptation. During wk 2 and 3, BW gain was not affected by NPN ($P > 0.10$), while feed intake tended to decrease with increasing dietary NPN ($P = 0.06$). Gain:feed improved linearly with supplementation of NPN in diets ($P < 0.05$; 0.45, 0.47, and 0.51 for NC, Low and High NPN during wk 2 and 3). Gain:feed for High NPN was similar to that for PC ($P > 0.10$: 0.51 and 0.52 for High NPN and PC; wk 2 and 3). Plasma urea concentration was Low and not different between diets ($P > 0.10$). Dietary supplementation with NPN, in the form of ammonium salts, can improve pig performance when pigs are fed diets deficient in NEAA-N.

Key Words: growth, nitrogen, pigs.

984 (M062) Impact of the fatty acids in the diet on milk fat content: Analysis from a database of commercial farms. H. Mannai*, P. Y. Chouinard, L. Fadul-Pacheco, D. Pellerin, and E. Charbonneau, *Université Laval, Québec, Canada.*

Controlled trials have shown that milk fat content can be affected by dietary fatty acids. The purpose of this study was to evaluate the impact of dietary fatty acids on milk fat content in commercial dairy herds using multiple regression procedure. Data recorded by Valacta (Dairy Center of Expertise, Québec-Atlantic) from 2009 to 2011 were used for the analysis. The fatty acid content in feed ingredients (16:0, 16:1, 18:0, *cis* 18:1, *trans* 18:1, 18:2 and 18:3), not originally in the database, were obtained from CNCPS V6.1, INRA Tables of Feed Composition, and peer-reviewed articles. Test-day records from Holstein cows in early- (1 to 50 DIM) and peak- (51 to 100 DIM) lactation during winter months were used, giving 2491 records over the 3-yr period from 1585 cows and 143 herds. Statistical analyses were performed using the PROC MIXED of SAS with herd and cows (herd) as random effects. Independent variables were included in the final equation when $P \leq 0.10$. The variables used as covariates in the regression were DIM and estimated breeding value for fat composition (EBV_FAT). Variables tested to explain milk fat concentration were: forage NDF + 0.5 × concentrate NDF content (NDF_NRC), NFC content, buffer intake (BUFF), and intake of previously listed individual fatty acids. Multiple regressions for data from early lactation records ($n = 390$; $R^2 = 0.43$) included, in addition to the covariates, the variables 18:0 (quadratic), *cis* 18:1 (quadratic), 18:2, and BUFF. For peak-lactation records ($n = 422$; $R^2 = 0.49$) the variables included were 16:0 (quadratic), 16:1, 18:0 (quadratic), *trans*18:1 (quadratic), 18:2 (quadratic), NFC (quadratic), NDF_NRC (quadratic), and BUFF. The nonlinear relationships observed for several fatty acids retained in the model could be explained by the heterogeneity of fatty acid sources on commercial farms (forages, cereal grains, oil seeds, fat supplements in the form of triglycerides, free fatty acids or calcium salts, etc.), and their interaction with numerous feed ingredients. The current study gives insight into the relationships between individual dietary fatty acids and milk fat content in the context of commercial milk production.

Key Words: dietary fatty acids, milk fat, lactating dairy cows

0985 (M063) Pregnancy and lambing rates in anestrous ewes bred to a new synchronization protocol and laparoscopic timed artificial insemination (TAI). S. B. Turner*[1], M. B. Gordon[1], T. Gowan[2], J. A. Small[2], and D. M. W. Barrett[1], [1]*Faculty of Agriculture, Dalhousie University, Truro, NS, Canada,* [2]*Agriculture and Agri-Food Canada, Truro, NS.*

Reproductive performance in seasonally anestrous ewes is poor even after the application of conventional controlled breeding techniques. Estradiol-17β (E_2) has been shown to synchronize follicular wave emergence in anestrous ewes treated for 12 or 14 d with a medroxyprogesterone acetate sponge. The objective of this study was to determine the effects of an E_2 treatment administered 6 d after CIDR insertion on E_2 concentrations, estrus, pregnancy rates, and lambing rates in ewes bred out of season. Ewes from three farms (Farm A: $n = 22$; Farm B: $n = 48$; Farm C: $n = 28$) received

CIDRs (d -12) followed by an injection of eCG (500 IU; d 0) at CIDR removal and an injection of sesame oil without (1 mL; Control) or with E_2 (350 µg; d −6) 6 d before CIDR removal. Treatments were balanced for breed, age, parity, and BCS. Blood samples were taken from half of the ewes on d −6 and 0 to determine E_2 concentrations. On d 1 ewes were exposed to rams to observe estrus. Ewes were subjected to laparoscopic TAI on d 2. Pregnancy was diagnosed by transabdominal ultrasonography on d 50. Estrus, pregnancy rates, and lambing rates were analyzed using logistic regression. Day of lambing and E_2 concentrations were analyzed using ANOVA. The percent of ewes observed in estrus within 36 h of CIDR removal was similar between treatments (E_2: 24.5%; Control: 34.7%; $P > 0.05$). Pregnancy rates were similar between treatments (E_2: 40.8%; Control: 40.8%; ± $P > 0.05$) and were higher on Farm C than Farm B (Farm A: 45.5%; Farm B: 22.9%; Farm C: 67.9%; $P < 0.05$). Lambing rates were also similar between treatments (E_2: 34.7%; Control: 34.7%; $P > 0.05$) and were higher on Farm C than Farm B (Farm A: 40.9% Farm B: 16.7%; Farm C: 60.7%; $P < 0.05$). Relative to CIDR removal, ewes lambed earlier on Farm B (Farm A: 141.7 ± 1.3 d; Farm B: 136.6 ± 1.4 d; Farm C: 143.2 ± 0.9 d; $P < 0.05$) and ewes treated with E_2 lambed earlier (E_2: 138.9 ± 1.0 d; Control: 142.2 ± 1.0 d; $P < 0.05$). Concentrations of E_2 were similar between treatments on d −6 (E_2: 1.5 ± 0.1 pg/mL; Control: 1.6 ± 0.1 pg/mL; $P > 0.05$) and d 0 (E_2: 1.6 ± 0.1 pg/mL; Control: 1.3 ± 0.1 pg/mL; $P > 0.05$). Differences were mainly observed among farms potentially due to differences in breed, BCS, semen, or management practices. The addition of an E_2 treatment during a CIDR-eCG heat synchronization protocol does not clearly increase pregnancy and lambing rates in seasonally anestrous ewes.

Key Words: anestrus, ewes, controlled breeding

0986 (M064) Effect of duration on feed and energy substrate on the digestive physiology of finishing feedlot cattle. F. Joy*, J. J. McKinnon, S. Hendrick, and G. B. Penner, *University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to determine the effect of dietary energy substrate and days on feed (DOF) on apparent total tract digestibility, rumen fermentation, short-chain fatty acid (SCFA) absorption and the arterial glucose clearance rate. Eight ruminally cannulated, cross-bred growing heifers were randomly allocated to one of the two dietary treatments. The control (CON) diet consisted of 75.2% barley grain, 9.8% canola meal, 9% mineral-vitamin supplement, and 6% barley silage (DM basis). To evaluate the effect of energy source, a high-lipid byproduct pellet was included to replace 60% of the barley grain and canola meal (HLP). Diets were similar in NEg (5.15 MJ/kg) and CP (13.7% DM). The study consisted of four consecutive 40-d periods with collections occurring in the last 6 d of each period. Dry matter intake did not differ among periods but the HLP group tended to eat less ($P = 0.09$). The ADG was greater for CON ($P < 0.05$) than HLP and ADG decreased with advancing DOF. The ADG of CON was greater than HLP during first and the last periods (Trt×Period; $P = 0.024$). Heifers fed HLP tended to have greater mean ruminal pH (6.10 vs. 5.96; $P = 0.07$) than CON, but pH was not affected by DOF. The CON heifers had a greater digestibility for DM, OM, CP and NDF ($P < 0.05$) and the digestibility for DM, OM, CP, NDF and starch increased with advancing DOF ($P < 0.05$). Crude fat digestibility of CON increased with DOF while that of HLP decreased (Trt × Period; $P < 0.05$). Total SCFA concentration in the rumen was greater ($P = 0.006$) for CON (141.5 vs. 128.08 mM/dL) than HLP and it tended to decrease with DOF ($P = 0.098$). The molar proportion of acetate increased and butyrate decreased with increasing DOF ($P < 0.05$) but propionate was not affected. The rate of SCFA absorption was not affected, but the passage rate of chromium over period was decreased ($P < 0.026$). The arterial clearance rate of glucose was not affected by treatment or DOF. These data suggest that replacing 60% of the barley grain and canola meal with high lipid byproduct pellets negatively affects total tract digestibility and performance. Moreover, regardless of diet, with advancing DOF digestibility increases and SCFA concentration decreases without corresponding changes in SCFA absorption and, as such, these changes do not explain the reduction in G:F with advancing DOF.

Key Words: beef, digestibility, feeding-duration

0987 (M065) A prepartum diet supplemented with rolled canola seed reduced pituitary sensitivity to GnRH in dairy cows during second week postpartum. *R*. Salehi*[1], M. G. Colazo[2], M. Oba[1], and D. J. Ambrose[2], [1]*University of Alberta, Edmonton, Canada,* [2]*Alberta Agriculture and Rural Development, Edmonton, Canada.*

Cows fed a prepartum diet supplemented with rolled canola seed (high in oleic acid, OLA) had longer interval from calving to first ovulation than cows fed diets supplemented with either linola (high in linoleic acid, LA) or flax (high in linolenic acid) (Colazo et al., 2009; JDS, 92:2562). We hypothesized that the delayed ovulation in canola-fed cows occurred through suppression of pituitary LH since adding OLA to culture medium suppressed GnRH-induced LH release from porcine pituitary cells in-vitro (Barb et al., 1995; JAS, 73:1416). To test our hypothesis, pregnant Holstein cows, blocked by BCS, were assigned to 1 of 3 prepartum diets supplemented with canola (high OLA, $n = 10$), sunflower (high LA, $n = 10$), or control (no oilseed, $n = 11$) from 35 d before expected calving date until parturition. The concentrate portion of OLA- and LA-diets contained 0.99 kg rolled oilseeds providing 0.27 kg/d OLA or 0.31 kg/d LA. Average DMI ± S.E. (kg/d) was higher in control (15.30 ± 0.63) than in canola (13.54 ± 0.54), sunflower (13.31 ± 0.57) diets. Blood was sampled during the

first (6 ± 1.00 d, n = 15) or second (9 ± 1.20 d, n = 16) week postpartum, every 15 min for 6 h to measure LH pulsatility. Thereafter, 100 μg GnRH was administrated im and blood was sampled for 4 h to measure induced LH release. Treatments did not affect LH pulsatility during the first and second week postpartum. Mean, minimum, maximum LH, pulse amplitude, and frequency were 0.30, 0.11, 0.82, 0.40 ng/ml, and 4.24 pulses per 6 h, respectively, and they were not affected by treatments or weeks. GnRH-induced LH release was not influenced by dietary treatments during the first week postpartum, but cows fed a prepartum diet high in OLA had lower mean LH (1.70 ± 0.20 ng/mL) than in control (2.40 ± 0.20 ng/mL; P = 0.02) during the second week postpartum, but it did not differ from LA (1.80 ± 0.20 ng/mL; P > 0.05); LA vs. control, P = 0.09. After GnRH administration, diets did not affect LH peak (3.39 ng/ml), interval to peak (47.40 min) or area under curve (7.01 ng/ml per 4h). In summary, although, prepartum diets did not affect pulsatile and GnRH-induced LH release during the first week postpartum, cows fed a prepartum diet supplemented with rolled canola had lower mean GnRH-induced LH than those fed no oilseed.

Key Words: oilseed, prepartum, luteinizing hormone

0988 (M066) Utilization of high lipid byproduct pellet in the finishing diet of feedlot steers to improve carcass traits and reducing feed costs.

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Two studies were conducted to evaluate the rate and timing of provision of a high-lipid high-fiber byproduct pellet (HLP) as a partial replacement for barley grain in diets for feedlot cattle. In study 1, steers (n = 288; BW = 378.4 ± 0.50 kg) were randomly allocated to one of 24 pens, and pens were assigned to one of four treatments. The study period was divided into three equal periods of 49 d each, namely P1, P2, and P3. A barley-based diet (CON; 75.2% barley grain, 9.8% canola meal, 9% mineral and vitamin, and 6% barley silage; DM basis) was compared to a diet where HLP replaced 60% of the barley grain and canola meal, relative to the CON. Steers received the HLP diet for 0 (CON147), 147 (HLP147), the last 98 (HLP98), or the last 49 d (HLP49). Steers fed CON had greater ADG (1.96 vs. 1.83 kg/d; P < 0.01), but DMI was not affected. The HLP147 had greatest DMI and least G:F during P1, but least DMI in P3 (Trt × Period; P < 0.01). Hot carcass weight of CON and HLP49 were the heaviest (P < 0.05), and HLP49 tended to have the greatest percentage of carcasses in yield grade 1 (P = 0.07). Carcass quality grade was not affected. In the second study, steers (n = 264; BW = 441.3 ± 0.19 kg) were randomly allocated to one of 24 pens and fed for 120 d. Diets were similar in composition to study 1 except that the HLP replaced 30% of the barley grain. Treatments included feeding steers the HLP diet for 0 (CON), 120 (HLP120), and the last 60 (HLP60), and the last 60 d along with additional canola oil (HLP60CO). There were no differences for DMI and ADG (12.6 and 2.0 kg/d, respectively). The G:F for HLP120 was less than the other treatments (0.149 vs. 0.158; P = 0.001). Hot carcass weight was greater for CON and HLP60 than HLP120 and HLP60CO (386 vs. 377 kg). The HLP120 tended to have the greatest proportion (P = 0.06) of yield grade 1, with HLP60CO tending to be the lowest (62.5 vs. 37.9%). Carcass quality was not affected. Partially substituting barley grain with HLP in the second half of the finishing period may improve carcass yield grade without negatively affecting growth performance and feed efficiency relative to a barley-based diet.

Key Words: beef, byproduct, pellet, carcass