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.

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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 immunity and lipid metabolism may play a role in the interaction between the cattle host and O157. The identified genes may be potential genetic indicators for O157 super-shedding in cattle.

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

0479 Determination of standardized total tract digestibility of phosphorus in flaxseed meal fed to finishing pigs without or with phytase supplementation.

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This experiment was conducted to determine the phosphorus (P) digestibility of flaxseed meal (FM) fed to finishing pigs and effect of phytase supplementation on P digestibility for finishing pigs. A total of 18 growing barrows [(Yorkshire × Landrace) × Duroc] with an average body weight (BW) of 78.7 ± 2.4 kg (mean ± SD) were randomly allotted to 3 treatments to give 6 replicates per treatment. Pigs were housed for 10 d in adjustable metabolism crates (1.80 × 0.6 m) with 5 d of adaptation periods and 5 d of total collection periods in a temperature-controlled room (22 ± 2°C). A semi-purified diet based on corn starch-sucrose containing 320 g/kg of FM as the sole source of P was fed without or with phytase supplementation at the level of 500 FTU/kg. A P-free diet mainly based on corn starch, sucrose, and gelatin was also prepared to estimate the endogenous P losses (EPL). Pork gelatin was added to the diets for maintaining similar crude protein in all experimental diets. Vitamins and all minerals except P were included in the diets according to requirements for finishing pigs (NRC, 2012). Pigs were fed at 40 g/kg BW at the beginning of experiment. The daily feed allowance was offered in two equal portions at 0800 and 1600 h. Pigs had free access to water. Results indicated that total feed and P intake were not different between diets without or with phytase supplementation. However, phytase supplementation increased ($P < 0.01$) apparent total tract digestibility (ATTD) and standardized total tract digestibility (STTD) of P in FM diet. The ATTD of P and STTD of P were increased from 31.4% to 45.8% and from 37.3% to 51.8%, respectively. Phytase supplementation also decreased ($P < 0.05$) P concentration (1.95 vs. 1.62%) in feces. Total P output was tended to decrease ($P = 0.08$) in pigs fed diets containing FM with phytase. The basal EPL was calculated at 151 ± 20 mg/kg of DMI in pigs fed the P-free diet. In conclusion, dietary phytase supplementation may increase P digestibility in FM fed to finishing pigs.

Key Words: flaxseed meal, phosphorus, phytase

Table 0479.

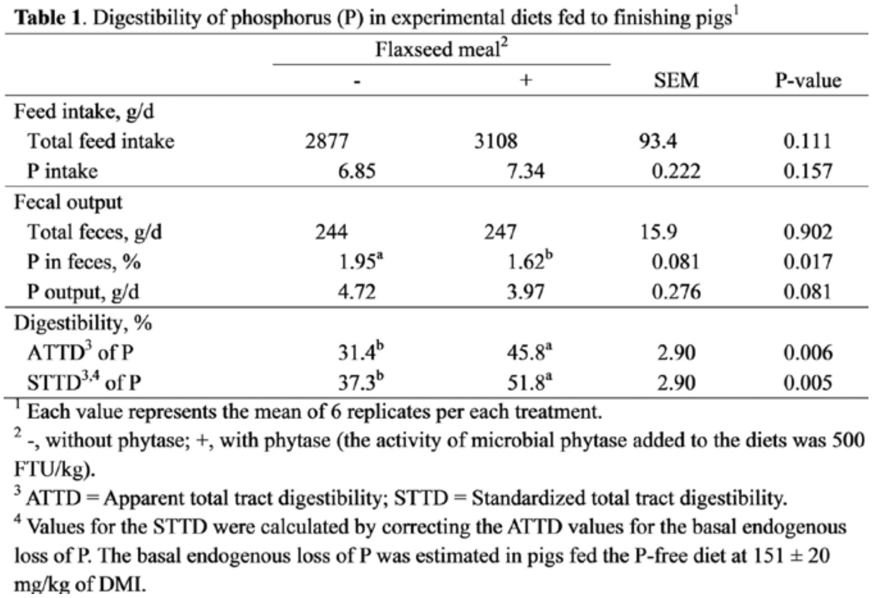

Table 1. Digestibility of phosphorus (P) in experimental diets fed to finishing pigs[1]

	Flaxseed meal[2]			
	-	+	SEM	P-value
Feed intake, g/d				
Total feed intake	2877	3108	93.4	0.111
P intake	6.85	7.34	0.222	0.157
Fecal output				
Total feces, g/d	244	247	15.9	0.902
P in feces, %	1.95^a	1.62^b	0.081	0.017
P output, g/d	4.72	3.97	0.276	0.081
Digestibility, %				
ATTD[3] of P	31.4^b	45.8^a	2.90	0.006
STTD[3,4] of P	37.3^b	51.8^a	2.90	0.005

[1] Each value represents the mean of 6 replicates per each treatment.

[2] -, without phytase; +, with phytase (the activity of microbial phytase added to the diets was 500 FTU/kg).

[3] ATTD = Apparent total tract digestibility; STTD = Standardized total tract digestibility.

[4] Values for the STTD were calculated by correcting the ATTD values for the basal endogenous loss of P. The basal endogenous loss of P was estimated in pigs fed the P-free diet at 151 ± 20 mg/kg of DMI.

0480 The effects of partial replacement of barley starch with lactose on production and ruminal fermentation characteristics in dairy cows.

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Previous studies have reported improved DMI and milk production when dietary starch was replaced with sugars in corn-based diets, but there is limited work with barley-based diets. Because corn and barley starch differ in their rates and extents of ruminal degradation, it is important to determine if replacement of barley starch with sugars is beneficial as has been reported for corn. The objective of this study was to determine the effects of partial replacement of barley starch with lactose (as dried whey permeate; DWP) on DMI, milk yield and composition, and ruminal fermentation characteristics. Eight lactating Holstein cows (97 ± 10 d-in-milk; 733 ± 63 kg BW)

were used in a replicated 4 × 4 Latin square design experiment with four dietary treatments. Experimental periods consisted of 18 d of adaptation and 10 d of measurements. Four cows in one Latin square were ruminally cannulated. Cows were fed a barley-based diet (3.6% total sugar [TS]; control), or diets that contained 6.6, 9.6 or 12.6% TS on a DM basis. Dietary TS content was increased by the replacement of barley grain with DWP, which contained 83% lactose. Diets were isonitrogenous (17.2% CP) and starch contents of the control, 6.6, 9.6, and 12.6% TS diets were 24.3, 22.2, 21.2 and 19.1%, respectively. The inclusion of DWP did not affect DMI (mean = 26.6 kg/d) and milk yield (34.3, 35.0, 35.6, and 34.6 kg/d for the control, 6.6, 9.6, and 12.6% TS diets, respectively); however, milk lactose content tended to increase quadratically ($P = 0.07$) as TS content increased. There was a linear decrease ($P = 0.03$) in ruminal NH_3–N concentrations as TS content increased. Ruminal pH tended to decrease linearly as TS content increased ($P = 0.06$; 6.32, 6.31, 6.34, and 6.22 for the control, 6.6, 9.6, and 12.6% TS diets, respectively). Total ruminal VFA concentrations were not affected ($P > 0.05$) by diet; however, there was a linear increase ($P = 0.04$) in butyrate concentration as TS content increased. Plasma urea-nitrogen concentrations were not affected by diet, but milk urea-nitrogen concentrations tended to change in a cubic manner as TS content increased ($P = 0.08$; 14.1 15.1, 14.0, and 13.7 mg/dL for control, 6.6, 9.6, and 12.6% TS diets, respectively). These results suggest that partial replacement of barley starch with lactose improves ruminal N efficiency by decreasing ruminal NH_3–N concentration, but production performance was unaffected

Key Words: barley starch, lactose, production, ruminal fermentation

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0481 Potential to improve fiber digestion in the rumen of cattle through inoculation with bison rumen contents.

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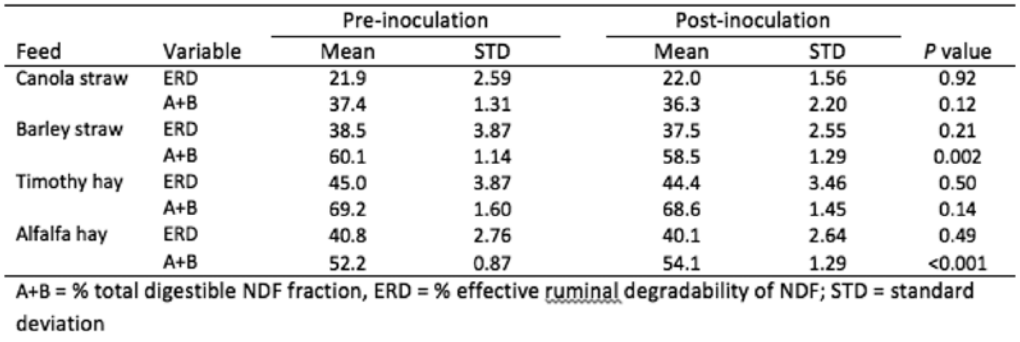
We hypothesized that inoculating the rumen of cattle with bison rumen contents would improve the ruminal degradability of forage by enhancing the cellulolytic capacity of the rumen microbiome. Sixteen ruminally cannulated beef heifers were fed a diet of 70% barley straw (78.0 ± 3.89 neutral detergent fiber [NDF]) and 30% supplement (36.6 ± 0.76 CP, 37.6 ± 1.41 NDF) on a dry matter (DM) basis. Cattle were inoculated with bison rumen contents twice, 2 wk apart. Intact bison rumens were obtained from an abattoir and transported in insulated containers in a heated truck. Rumens were opened and contents mixed in a heated tub under CO_2. Rumen contents were removed from the cattle, weighed and approximately 72% of the contents (DM basis) were replaced by mixed bison rumen contents in each transfer. The in situ technique was used to measure ruminal degradation of canola straw, barley straw, timothy hay, and alfalfa hay before inoculation and 11 d after the second inoculation. Duplicate bags (10 × 20 cm; 6 g DM/bag) were incubated in the rumen of each heifer for 0, 4, 8, 12, 24, 48, 96, 120 h. The percentage NDF disappearance (NDFD) from the bags was analyzed as: $NDFD = A + B(1-e^{-k_{d(time-lag)}})$, where A = soluble fraction, b = slowly digestible fraction, K_d = rate of digestion of fraction b, and lag = time before digestion began; and effective ruminal degradability (ERD) = A+B(kd/(kd+kp)) where kp = rate of passage (measured for each animal). Transfer of rumen contents decreased ($P < 0.05$) the potentially digestible fraction (A+B) in barley straw, but increased it in alfalfa hay ($P < 0.05$) (Table 1). No effect of inoculation on ERD were observed, suggesting fiber utilization by cattle was not substantially improved by introducing

Table 0481.



Feed	Variable	Pre-inoculation Mean	Pre-inoculation STD	Post-inoculation Mean	Post-inoculation STD	*P* value
Canola straw	ERD	21.9	2.59	22.0	1.56	0.92
	A+B	37.4	1.31	36.3	2.20	0.12
Barley straw	ERD	38.5	3.87	37.5	2.55	0.21
	A+B	60.1	1.14	58.5	1.29	0.002
Timothy hay	ERD	45.0	3.87	44.4	3.46	0.50
	A+B	69.2	1.60	68.6	1.45	0.14
Alfalfa hay	ERD	40.8	2.76	40.1	2.64	0.49
	A+B	52.2	0.87	54.1	1.29	<0.001

A+B = % total digestible NDF fraction, ERD = % effective ruminal degradability of NDF; STD = standard deviation

microbes from bison rumen contents.

Key Words: bison, effective ruminal degradability, microbiome

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0482 CNCPS fractions 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.

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Carinata meal, new co-product from bio-fuel processing, is ready to be used as animal feed nowadays. Canola meal has high levels of methionine and cysteine, but limiting in lysine. Pulse products contain high starch, also have high levels of lysine and tryptophan. There is little information available on chemical profile, as well as its nutritive value 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 MIXED procedure of SAS 9.3 with significance declared at $P < 0.05$. The results from CNCPS 6.5 system indicated all canola based pellet products 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), BPP7 (high level of canola meal, low level of peas and no lignosulfonate) and BPP8 (high level of canola meal, low level of peas and lignosulfonate) showed higher levels of indigestible protein (PC, $P < 0.05$) and higher soluble true protein (PA2, $P < 0.05$). All carinata based pellet products showed the higher fiber bound protein (PB2, $P < 0.05$). 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), BPP7 and BPP8 had the higher levels of water-soluble carbohydrates (CA4, $P < 0.05$); 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) and BPP6 showed the higher levels of starch (CB1, $P < 0.05$), while BPP1, BPP3 and BPP4 had higher digestible fiber (CB3, $P < 0.05$). In conclusion, carinata meal can be used as a potential feed ingredient for ruminants.

Key Words: canola, carinata, lignosulfonate

0483 Comparison of barley silage with varying digestible fiber content to corn silage on rumen fermentation characteristics and microbial protein synthesis using RUSITEC technique.

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The effect of barley silage with enhanced in vitro fiber digestibility on rumen fermentation characteristics and microbial protein synthesis has not been well investigated in barley grown in western Canada. The objective of this study was to evaluate the effects of barely silage with varying in vitro NDF digestibility (IVNDFD) in comparison to corn silage on rumen fermentation characteristics and microbial protein synthesis using rumen simulation technique (RUSITEC). The experiment was a completely randomized design with four treatments. The experimental diet 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: T1 = P7213R corn silage, T2 = CDC Cowboy barley silage, T3 = CDC Copeland barley silage, and T4 = Xena barley silage. The experiment consisted of 10 d of adaptation and 6 d of data collection. Statistical analyses were performed using the PROC MIXED procedure of SAS 9.4 with significance declared at $P < 0.05$. The 30 h IVNDFD of corn silage, CDC Cowboy, CDC Copeland and Xena varieties were 27, 37, 31, and 29%, respectively. Barley silage T2, with the highest IVNDFD, had no effect on rumen fermentation characteristics ($P > 0.10$) when compared with T3 and T4 barley silage. However, corn silage vs. the average of T2, T3 and T4 barley silage ($P < 0.05$) had lower ruminal pH (6.65 vs. 6.73), greater molar proportion of propionate (28 vs. 23%) and lower C2/C3 acid ratio (1.8 vs. 2.2). Nutrients disappearance of total mixed ration (DM and CP) were not affected by the treatments. On the other hand, corn silage in T1 had the highest DMD compared with the average DMD of barley silages in T2, T3 and T4 (69.1 vs. 64.8%, $P < 0.05$). There was no significant effect of higher digestible fiber content in T2 on bacterial protein production compared with T3 and T4 (averaged 49.5 mg/d) while T1 diet had a higher bacterial protein

production than the average of T2, T3 and T4 (53.5 vs. 49.5 mg/d, $P < 0.05$). These results imply that higher in vitro NDF digestibility of barley silage might not necessarily correspond with greater impact on rumen fermentation and microbial protein synthesis. However, feeding the corn silage had a higher microbial protein produced in the rumen and may enhance the dairy cattle performance compared with the barley silages.

Key Words: bacterial N production, rumen fermentation, RUSITEC

0484 Phosphorus utilization on dairy farms in Manitoba.

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A survey was performed on 19 dairy farms in Manitoba representing a range of sizes, feeding, housing and management systems to identify factors that affect the utilization of dietary phosphorus (P) by lactating dairy cows. Each farm was visited once to collect milk, blood, feed and feces samples as well as production data from 10 early/peak, 10 mid-lactation, and 10 late lactation cows. Phosphorus content of feed (FEED P), feces (FECAL P), milk (MILK P), blood (BLOOD P) and calcium content of feed (Ca) were determined. Pearson correlation analysis among the various measures was conducted using SAS 9.4 software. The average P contents (DM basis) of FEED P, FECAL P, MILK P, and BLOOD P was 0.41% (0.34 and 0.53%), 0.76% (0.30 and 1.35%), 0.09% (0.05 and 0.12%) and 2.04 mmol/L (1.34 to 3.04 mmol/L), respectively. The output of P in milk (P OUT) which is obtained by multiplying MILK P with daily milk yield (MY), was positively correlated with the MILK P, FEED P, MY, Parity, Ca and negatively correlated with days in milk (DIM). But no correlation was observed with the BLOOD P and FECAL P. FEED P was positively correlated with the MILK P, FECAL P, MY, and negatively correlated with Ca and DIM. BLOOD P was positively correlated with Ca and DIM, but not correlated with any other measures (Table 1). Results show that the P content of diets, and feces vary considerably among cows and among farms, suggesting that the P contents in diets and feces can be reduced. Furthermore, more than 50% of the animals received diets which contain excess P levels than the NRC (2001) recommendations. The P content of blood was not indicative of P output in milk, nor the P contents of the diet or feces. The output of P in milk was highly correlated with the yield and P content of milk, but a 1% increase in the dietary P content lead to a 0.21% increase in P OUT. Better understanding of the dynamics between these dietary and cow factors can help to develop efficient P management strategies to improve P utilization and avoid excess P use.

Key Words: phosphorus, dairy, cow

0485 Effect of variety and level of inclusion of barley grown for silage on performance and carcass characteristics of growing and finishing beef steers.

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This study was designed as a 3 × 2 factorial to evaluate three barley silage varieties when included at two (high and low) inclusion rates on performance and carcass characteristics of beef steers. Barely varieties CDC Cowboy (CB), CDC Copeland (CL) and Xena were chosen based on results of a preliminary study for high (CB, 37.0%), medium (CL, 31.1%) and low (Xena, 28.8%) NDF digestibility (NDFD; % NDF). For the present trial, the three varieties were seeded and managed identically including harvesting at the mid-dough

Table 0484.

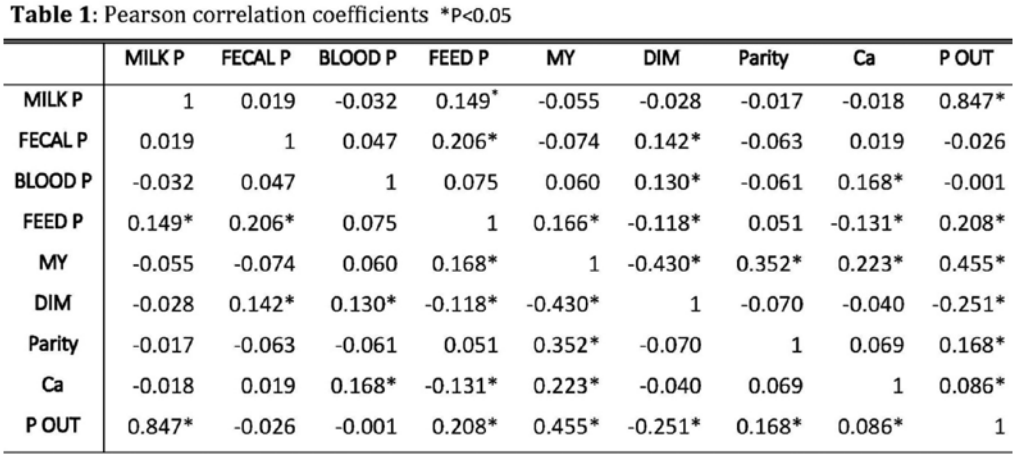

Table 1: Pearson correlation coefficients *P<0.05

	MILK P	FECAL P	BLOOD P	FEED P	MY	DIM	Parity	Ca	P OUT
MILK P	1	0.019	-0.032	0.149*	-0.055	-0.028	-0.017	-0.018	0.847*
FECAL P	0.019	1	0.047	0.206*	-0.074	0.142*	-0.063	0.019	-0.026
BLOOD P	-0.032	0.047	1	0.075	0.060	0.130*	-0.061	0.168*	-0.001
FEED P	0.149*	0.206*	0.075	1	0.166*	-0.118*	0.051	-0.131*	0.208*
MY	-0.055	-0.074	0.060	0.168*	1	-0.430*	0.352*	0.223*	0.455*
DIM	-0.028	0.142*	0.130*	-0.118*	-0.430*	1	-0.070	-0.040	-0.251*
Parity	-0.017	-0.063	-0.061	0.051	0.352*	-0.070	1	0.069	0.168*
Ca	-0.018	0.019	0.168*	-0.131*	0.223*	-0.040	0.069	1	0.086*
P OUT	0.847*	-0.026	-0.001	0.208*	0.455*	-0.251*	0.168*	0.086*	1

stage for ensiling. Crossbred steers ($n = 288$; 320 ± 23 kg) were allotted to one of 24 pens (12 steers/pen) with each pen assigned to one of 6 treatments for a 68-d backgrounding (BK) and 148-d finishing program. Diets with the low inclusion level during BK consisted of 40.1% BS, 9.4% brome grass hay (hay), 40.1% barley grain (BG), 5.6% canola meal (CM) and 4.8% mineral-vitamin supplement (supplement; %DM), while high inclusion diets consisted of 53.5% BS, 9.4% hay, 26.7% BG, 5.6% CM and 4.8% supplement. During finishing, low inclusion diets consisted of 5.0% BS, 87.0% BG, 3.5% CM and 4.5% supplements while high inclusion diets consisted of 15.0% BS, 77.0% BG, 3.5% CM and 4.5% supplement (%DM). Actual NDFD averaged 37.6 ± 3.5, 34.7 ± 3.8 and 36.9 ± 3.0% for CB, CL and Xena, respectively. Data were analyzed as completely randomized design with pen as the experimental unit and treatment as the fixed effect using the mixed model procedure of SAS (9.4). During BK, cattle fed CB exhibited lower ($P < 0.01$) ADG and end of period BW (EBWT) than cattle fed CL or Xena. Low BS inclusion resulted in greater ($P < 0.01$) ADG and EBWT relative to high inclusion diets. The DMI during BK was less ($P < 0.01$) for steers fed CB relative to those fed CL, with Xena being intermediate. Low BS inclusion resulted in greater ($P < 0.01$) DMI than high inclusion. Feed efficiency was greater ($P = 0.02$) for steers fed low, relative to high inclusion diets. During finishing, ADG and DMI were greater ($P < 0.01$) for steers fed high BS inclusion diets. However, over the entire trial, performance and carcass characteristics were not impacted by treatment except for carcass weight where steers fed CL had heavier ($P = 0.04$) carcasses relative to those fed CB or Xena. These results indicate that barley variety and inclusion level will impact performance of growing cattle. Barley variety has a minimal impact on finishing performance.

Key Words: barley silage, cattle, performance

0486 Development of a genetic marker panel for ketosis in dairy cattle.

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During the transition period high-yielding dairy cattle are susceptible to ketosis, a metabolic disease which has negative impacts on the health, fertility and milk production of the cow. Genetic selection of animals resistant to developing ketosis is a potential solution to the economic losses faced by producers, as well as the reduced herd health and welfare associated with this disease. Genetic evaluations for ketosis, a health trait with low heritability, would benefit from the additional information provided by genetic markers. The objective of this study is to identify novel single nucleotide polymorphisms (SNP) within candidate genes for ketosis to be incorporated into a custom marker panel. Investigating candidate genes provides the opportunity to discover SNP with a functional role that are not currently included on commercially-available marker panels. A list of 123 candidate genes, selected based on biological relevance, were selected for in silico investigation; this includes genes which encode key enzymes and regulatory factors involved in metabolic pathways, genes that have been shown to be differentially expressed in ketotic animals, and genes that have been proposed by genome-wide association studies (GWAS). A preliminary GWAS from our group identified 462 SNP from high-density genotypes that are associated with de-regressed estimated breeding values for ketosis. These SNP were mapped to genes involved in pathways that were expected to be involved in ketosis (i.e., PPAR signaling pathway, CoA biosynthesis), as well as unexpected (i.e., T and B cell receptor signaling, apoptosis). Within the candidate genes, putative SNP were identified by aligning sequence data from online cDNA libraries with the gene reference sequence. The variant calling program, Sequencher 4.9, was used to identify SNP and their corresponding amino acid substitutions. SNP were prioritized for inclusion in the panel based on their Sorting Intolerant From Tolerant prediction score, to select polymorphisms which would most likely alter the function of the encoded protein. A set of 1081 SNP were incorporated onto a custom low-density panel. To our knowledge, this is the first custom panel composed of markers found in candidate genes that are specific to ketosis. The second phase of this project will use this panel to genotype several thousand cows from herds originating from Quebec, Canada; these data to be collected spring 2016.

Key Words: ketosis, SNP, candidate gene

0487 Taxonomic assessment of the rumen microbiome of bulls under backgrounding and finishing diets.

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To examine the effect of backgrounding and finishing diets on the rumen microbial community in beef cattle, 16 healthy beef bulls were blocked by BW and randomly assigned to 1 of 2 dietary regimes: a backgrounding diet (BCK: 45% grain) or a high-grain finishing diet (FIN: 80% grain). Initiation of both diets was staggered such that both groups received their final diets for 30 d. At the end of the treatment period, bulls were

slaughtered and samples of mixed ruminal digesta were collected for microbial analysis. A 454 pyrosequencing was performed on DNA amplicons, targeting the bacterial/archaeal partial 16S rRNA genes and protozoal partial 18S rRNA gene. Taxonomy was assigned using QIIME, with only those OTUs represented at > 0.05% in more than 4 bulls/treatment considered for downstream analysis. As a whole, the bacterial community of BCK was more diverse than FIN ($P < 0.01$). The bacterial phyla *Firmicutes, Bacteroidetes,* and *Proteobacteria* dominated regardless of treatment, with *Spirochaetes* (0.83% vs. 0.29% total bacteria) and *Fibrobacteres* (2.36% v 0.09%) higher in BCK ($P < 0.05$). *Choloroflexi* (0.44%; $P < 0.05$) was only found in in the BCK group. Twenty-four genera were affected by treatment, with *Ruminococcus* (6.92% vs. 2.13%) and *Fibrobacter* (2.36% vs. 0.09%) greater in abundance in BCK ($P < 0.05$) than FIN. *Succinivibrio* was among the genera that increased in FIN (2.12% vs. 0.025%; $P < 0.05$) relative to BCK, and *Megasphera* appeared exclusively in FIN (1.45%). Archaeal composition was not affected, with the *Methanobrevibacter gottschalkii* clade predominating in both groups. However, the methanogen community for BCK was more diverse ($P < 0.01$) than for FIN. The protozoal genus *Epidinium* predominated under both treatments (74–77% abundance), and the genus *Eudiplodinium* appeared exclusively in FIN bulls (6.42%, $P < 0.05$). Our results revealed that the responses to treatment differed across the three microbial groups, suggesting that future studies are needed to define their respective roles in rumen function during diet change.

Key Words: rumen microbiome, backgrounding diet, finishing diet

0488 The transition cow: May the odds be ever in her favor.

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Longevity is a key component of sustainable dairy farming. High-yielding dairy cows often suffer from ovarian dysfunction and infertility leading to reduced reproductive and productive longevity. Infertility has been attributed to the metabolic stress during the transition period. However, potential metabolic alterations that may dysregulate ovarian functions have not been completely cataloged. Our objective was to characterize metabolic parameters of dairy cows during the transition period. In the first experiment, we examined the metabolic profiles in circulation to pinpoint time-points of major changes. We collected weekly blood samples from Holstein cows ($N = 15$) from 3 wk before until 12 wk after calving. As expected, glucose levels reduced during pre-calving weeks to reach a nadir at 3 wk post-calving ($P < 0.05$) and the first increase in glucose concentration occurred at 10 wk post-calving ($P < 0.05$). Also, β-hydroxybutyric acid levels increased from calving until wk 3 of lactation ($P < 0.05$) and subsequently returned to baseline. Levels of triglycerides decreased during pre-calving weeks, while significant increase occurred at 5 wk post-calving ($P < 0.05$). Total cholesterol concentrations increased from the third to seventh week post-calving ($P < 0.05$). Total bile acid levels increased from 3 wk to 2 wk before calving and stayed elevated throughout the transition period ($P < 0.05$). Oxidative stress indicator, glutathione, decreased to reach a nadir by 7 wk in lactation ($P < 0.05$), while the ferric reducing ability of plasma remained constant ($P > 0.05$). Thus, post-calving wk 3 to 7 are associated with major changes in metabolic indicators in circulation. In the second experiment, we evaluated changes in liver mRNA levels and circulating metabolic indicators during the periods of major metabolic changes above. We collected blood and liver biopsy samples from Holstein dairy cows at 3 wk pre-partum, during the calving week and 7 wk post-partum ($N = 13$). Quantitative PCR analyses ($N = 4$) did not reveal any changes in the hepatic mRNA abundance of genes indicative of liver functions including acyl-CoA:cholesterol acyltransferase 1 (*ACAT1*), Paraoxonase-1 (*PON1*) and sterol regulatory element-binding factor-1 (*SREBF1*) during wk 6–7 post-calving compared with peri-calving period. Taken together, transition period in dairy cows features increasing cholesterol, triglycerides, total bile acids and decreasing glucose and glutathione compared with pre-calving period. However, these changes appear to be independent of alterations in mRNA levels in the liver. Further studies, including liver function assays, are required to thoroughly investigate the relationship between liver health and alterations in circulating metabolic indicators during transition period in dairy cows.

Key Words: cow, liver, infertility

0489 Effect of dietary wheat bran inclusion on nutrient digestibility in weaned pigs.

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Wheat bran (WB) as a source of insoluble fiber has been shown to confer gut health benefits in weaned piglets. However, there is limited data on the influence of WB inclusion in weaner pig diets on digestibility. Thus, the aim of this study was to assess the effect of a 4% dietary inclusion of coarsely milled (1088 μ of particle size) WB on nutrient digestibility in weaned pigs. Six barrows (7.3 ± 0.1kg BW) fitted with a T-cannula at the distal ileum were fed one of two test diets consisting of: (1) a barley-wheat-corn-soybean meal-based diet (Control) and (2) a WB diet with 4% coarsely milled WB. Diets were assigned according to a 2x2 Latin square design repeated three times. At the end of the second period, all pigs were fed a 5% casein-corn starch-based diet to estimate basal endogenous amino acid (AA) losses. Each period lasted 9 d consisting of

5 d for adaptation followed by 2 d for fecal collection and 2 d for ileal digesta collection (12 h/d). All pigs were fed diets mixed with 0.3% titanium dioxide as an indigestible marker to calculate apparent total tract digestibility (ATTD), apparent ileal digestibility (AID) and standardized ileal digestibility (SID) of nutrients. Treatment means were compared using the Student *t* test procedure of SAS (SAS Inst. Inc., Cary, NC). Piglets fed the WB diet had lower ATTD of organic matter and AID of dry matter (DM) compared with those fed the control diet (89.4 vs. 88.3% and 60.8 vs. 66.4%; $P < 0.05$). However, piglets fed the WB diet had higher ATTD of fat compared with those fed the control diet (70.4 vs. 62.6%; $P < 0.05$). There were no differences in the AID and SID of nitrogen (N) and AA between the two diets ($P > 0.10$). Average AID values (%) were 66.3, 80.5, 41.5, 79.9, 80.4, 80.9, 87.2, 81.3, 71.6, and 76.0 for N, Arg, His, Ile, Leu, Met, Phe, Thr, and valine, respectively. Respective average SID values (%) were 79.7, 88.9, 66.4, 86.3, 84.5, 85.2, 90.3, 84.8, 80.2, and 82.7. In conclusion, results indicated that dietary inclusion of WB increased ATTD of fat and reduced ATTD of OM and AID of DM in weaned piglets. Further research is warranted to evaluate effects of WB, especially on growth and health performance, gut microbiota and fecal and/or ileal digesta volatile fatty acids production.

Key Words: digestibility, piglets, wheat bran

0490 Effect of steam flaking and seed type on carbohydrate molecular structure features associated with nutrient availability of legume seed in ruminants.

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The objectives of this study were to evaluate the effect of steam flaking processing and different seed type on carbohydrate spectroscopic features in relation to degradation kinetics. Six different sources of peas from Duck Lake and COOP were processed at Canadian Feed Research Center (CFRC, University of Saskatchewan, North Battleford, Canada). The carbohydrate molecular structure makeup was detected using attenuated total reflectance-Fourier transform infrared spectroscopy instrument at molecular spectroscopy lab, Department of Animal and Poultry Science, University of Saskatchewan. Three rumen-cannulated lactating Holstein cows were used to determine the in situ rumen degradation kinetics of DM and starch at Rayner Dairy Teaching and Research Facility (RDTRF). Statistical analyses were performed using the PROC MIXED procedure of SAS 9.3. The Tukey method was used for multi-treatment comparison. Difference was declared at $P < 0.05$. The results of univariate molecular spectral analyses showed that the whole pea seed had a significantly higher ratio of structural carbohydrate to total carbohydrate area than split pea seed (0.313 vs. 0.307; $P < 0.05$). The spectral ratio of cellulosic compound to structure carbohydrate area was significantly affected by steam flaking treatment, which was higher in flaking pea seed than the control (0.153 vs. 0.135; $P < 0.05$). Additionally, steam flaking treated pea seed also had a significant higher spectral ratio of cellulosic compound to total carbohydrate area than control untreated pea seed as a control (0.047 vs. 0.042; $P < 0.05$). In conclusion, steam flaking affected the inner molecular makeup of pea seed, which may be highly associated with the nutrient utilization.

Key Words: flaking, pea seed type, molecular structure

0491 Dynamics of progesterone concentrations and insemination outcomes in dairy cows.

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The objective was to evaluate the association between milk progesterone (P4) concentrations and its dynamics with insemination outcomes. In-line milk P4 records (Herd Navigator, DeLaval Inc.) relating to 605 inseminations (AI) were assessed from two dairy farms. Only cows that had confirmed luteolysis (P4 declined to < 5ng/mL) and ovulation (P4 increased to > 5 ng/mL) were included. The day of luteolysis was considered d 2 and AI occurred on d0. Progesterone at d 2, 5, 10, 14, and maximum P4 (Peak) within d 21 were considered, in addition to the rate of increase in P4 (e.g., d 2 to d 5). Insemination outcomes were defined as open (P4 > 5 ng/mL for < 20 d; $n = 357$), pregnant (P4 > 5 ng/mL for > 45d; $n = 170$) or pregnancy loss (P4 > 5 ng/mL for > 20 to ≤ 45 d, $n = 78$). Progesterone concentrations were modeled against outcomes of AI and parity, while herd and AI (first or second) were considered random variables, and data analyzed using MIXED procedure of SAS. Milk P4 at d 2 tended to be lower ($P = 0.10$) in pregnant (3.33) than in open (3.44) or cows that suffered pregnancy loss (3.44). Pregnant cows had greater P4 ($P < 0.01$) than open cows at d 10, 14 and at Peak (9.6, 18.3 and 23.4 vs. 8.3, 16.7 and 20.3, respectively). Rate of P4 increase (ng/mL/d) was also greater ($P < 0.01$) in pregnant than in open cows from d 2 to 14, d 2 to Peak, d 5 to 10, d 5 to 14 and d 5 to Peak (0.9, 1.0, 1.1, 1.6 and 1.5 vs. 0.8, 0.9, 0.9, 1.4 and 1.3, respectively). However, the aforesaid dynamics of P4 did not differ among cows that remained pregnant or suffered pregnancy loss. Primiparous cows had higher P4 ($P < 0.03$) than multiparous cows at d 2, 5, 10, 14 and at Peak (3.5, 4.8, 10.8, 19.7 and 23.6 vs. 3.3, 3.0, 7.7, 16.0 and 21.2 ng/mL, respectively). Furthermore, primiparous cows had a greater rate of P4 increase ($P \leq 0.05$) than

multiparous from d 2 to 5, d 2 to 14, d 2 to Peak, d 5 to 10, d 5 to 14, d 5 to Peak and d 10 to 14 (0.2, 1.0, 1.0, 1.2, 1.6, 1.4 and 2.2 vs. −0.1, 0.8, 0.9, 0.9, 1.4, 1.3 and 2.0, respectively). Cows that conceived, regardless of whether or not they suffered pregnancy loss, had greater P4 concentrations (except on d 2) and a greater rate of P4 increase than open cows. Also, primiparous cows consistently had greater P4 concentrations and rate of increase than multiparous cows.

Key Words: in-line milk progesterone,
estrous cycle, fertility

CSAS SYMPOSIUM: REDUCING THE USE OF ANTIBIOTICS IN LIVESTOCK PRODUCTION

0492 Alternatives to antibiotics in swine and poultry.

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To reduce the risk for the spread of antibiotic resistant bacteria from livestock to humans, the European Union banned the use of antibiotics as growth promoters in animal feeds for pigs and poultry since January 2006. As a result, the use of veterinary prescribed antibiotics increased in a sort of compensation phenomenon. In intensive husbandry systems, veterinary prescribed antibiotics are mainly used around birth and in newborn animals.

To study the effects of antibiotic usage during early life stages, we performed several experiments in piglets and poultry. We analyzed both the short-time and long-term effects at the level of intestinal microbiota and intestinal mucosal functions. To this end, we applied metagenomics, transcriptomic and immunologic analytical approaches on intestinal tissues and luminal contents, taken at different intestinal locations and at different time-points after treatment. These studies clearly demonstrated both short-term and long-term effect on the expression of immune related genes. We hypothesized that that these long-lasting effects are due to differences in the programming of the gut immune system as induced by the temporary early life perturbation of the gut microbiota.

To search for alternatives for antibiotic growth promoters, a large variety of farming approaches are proposed, including organic acids, probiotics and prebiotics, enzyme, clays and minerals, trace elements, and botanicals. In this presentation, we will show the effect of the administration of fructooligosaccharides (FOS) to suckling piglets on intestinal microbiota and gene expression. Twelve days of intervention with FOS resulted in a bifidogenic effect in the colon of treated piglets. Furthermore, after 23 d of intervention with FOS, decreased expression in immune related gene sets was observed in treated piglets.

In this context, it is also important to identify major intrinsic and extrinsic factors that (co)determine the early life gut microbial colonization of livestock species. From literature it is already known that several extrinsic factors are important, including the sow/mother-hen and the environment. Here we show data that indicate that also the genetic make-up of host is an important factor in the early life microbial colonization of the gut and consequently for immune system development.

In conclusion, during early life, the interplay between the host (genetics), environment (nutrition and/or management), in association with the microbiota modulate bacterial colonization, drives gut development and immune maturation. The use of antibiotics during early life stages perturbs this interplay significantly with serious consequences for the functionality of the host immune system.

0493 Management of dairy cows to improve resistance to infectious diseases.

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The incidence of infectious diseases varies greatly during the lactation cycle. Most new cases of clinical mastitis appear at the beginning of lactation (transition period), and the incidence increases with the level of milk production. In addition to mastitis, the majority of other infectious diseases becomes clinically apparent during the first 2 wk of lactation. During this time, cows are in negative energy balance and they must mobilize body reserves to balance the deficit between food energy intake and energy required for milk production. Cows undergoing energy deficit have a weakened immune system, which increases their susceptibility to infections. Therefore, we evaluated the effects on blood metabolite concentrations and immune functions of limiting milk production in early lactation to reduce the negative energy balance. In a first experiment, multiparous Holstein cows were milked either once a day or twice a day for the first postpartum week. In a second experiment, the amount of milk harvested was limited by milking cows incompletely (about one-third of expected milk production was collected) twice a day until d 5 after calving. In a third experiment, first-wk milk production was limited by administering a prolactin secretion inhibitor, quinagolide, during the first days of lactation. Globally, the results of these studies indicate that reducing the amount of milk harvested postpartum while maintaining milking stimuli reduces metabolic stress and immunosuppression without compromising productivity of high-yielding dairy cows. The second period that has the highest incidence of new intramammary infections