ADSA Graduate Student (PhD) Production Oral Competition

140 Effects of camelina cake supplementation at two dietary fat levels on ruminal fermentation and nutrient flow in a dual-flow continuous culture system. V. L.-N. Brandao*, X. Dai, L.G. Silva, E.M. Paula, T. Shenkoro, and A. Faciola, University of Nevada, Reno, NV.

This study aimed to assess whether camelina cake (CC) could partially replace canola meal at 2 dietary fat levels and its effects on ruminal fermentation and nutrient flow in a dual-flow continuous culture system. Diets were randomly assigned to 8 fermenters in a double 4x4 Latin square design with four 10-d experimental periods consisted of 7 d for diet adaptation and 3 d for sample collection. Treatments were as follows: CC5: 7.7% CC inclusion at 5% ether extract (EE); NCC5: no CC at 5% EE; CC8: 17.7% CC at 8% EE; and NCC8: no CC at 8% EE. Diets contained 55% of forage, and fermenters were fed 72 g of DM/d twice daily. During sampling days, effluent samples were collected for analyses of digestibility, VFA, NH3-N, N-balance, microbial growth, and amino acids (AA) and fatty acids (FA) flow. Statistical analysis was performed using the MIXED procedure of SAS. Partial data are presented in Table 1. Ruminal pH, total VFA, bacterial-N, RUP and RDP were not affected by treatments. Diet NCC8 had the greatest molar proportion of acetate while CC5 and CC8 had greatest molar proportion of propionate. Ruminal digestibility of OM and CP were not affected, but CC8 diet had the lowest NDF and ADF digestibility. Concentrations of isomers from C18:1, C18:2, C18:3 were affected by treatments, overall CC diets had greater ruminal outflow of isomers cis and lowest of trans. Inclusion of CC decreased biohydrogenation. The increased outflow of important FA and reduction in biohydrogenation observed on CC5 and CC8 diets may be nutritional advantageous; however, NCC8 diet had deleterious effect on AA flow.

Table 1 (abstract 140)

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Key Words: amino acids, canola meal, fatty acids

141 Temporal changes of milk odd- and branched-chain fatty acids in response to acidogenic diets fed to dairy cows. E. Baumann*, PY Chouinard, AR Alfonso-Avila, and R. Gervais, Université Laval, Quebec, QC, Canada.

The milk profile of odd- and branched-chain fatty acids (OBCFA) is generating interest as a non-invasive method for evaluating rumen function. Synthesis by rumen microorganisms is the primary source of milk OBCFA and different groups of rumen bacteria synthesize distinct categories of OBCFA. Sub-acute ruminal acidosis (SARA) is a highly prevalent and costly disease that engenders modifications in rumen bacterial populations, which could be identified by tracking changes in milk OBCFA and how they relate to rumen bacterial groups. The increase of DCAD may alleviate the effects of acidogenic diets, whereas the supplementation of soybean oil (SBO) in the diet may exacerbate them. This trial aimed to determine the length of time required for milk OBCFA to respond to the consumption of an acidogenic diet and to evaluate the effects of DCAD, adjusted using dietary K2CO3, and SBO supplementation on the evolution of the milk OBCFA profile. Twenty-eight early lactation Holstein dairy cows (39 ± 9 DIM) were used in a randomized complete block design with a 2 × 2 factorial arrangement of treatments. Cows were fed a high-risk SARA diet of 40% forage (58% corn silage) and 60% concentrate, with 0 or 1.5% K2CO3 (DM basis), and 0 or 2% SBO. Collection period lasted 3 weeks, and samples were taken on d 1, 4, 7, 10, 14, and 17. Effects of time (repeated measures), K2CO3, SBO, and their interactions were evaluated and contrasts declared significant at P < 0.05. Milk iso 13:0 and iso 17:0 concentrations increased linearly after cows began receiving the acidogenic diets. Similarly, milk concentrations of 5:0, 7:0, 9:0, 11:0, 13:0, and 15:0 increased linearly over time. A 3-way interaction was also significant for 15:0. In contrast, concentrations of iso 14:0, iso 16:0, and iso 18:0 in milk decreased linearly over time. No time or treatment effects were observed for anteiso fatty acids. The common temporal pattern of changes within groups of OBCFA, and the differences between groups indicate distinct origins of OBCFA. Overall, the results show that milk OBCFA respond to the consumption of an acidogenic diet within 3 weeks.

Key Words: rumen acidosis, diagnostic tool, milk fat


The objective of this longitudinal cohort study was to discover whether the milk microbiome of healthy bovine mammary glands differs from that of inflamed mammary glands during the first 150 d in milk (DIM). Aseptic milk samples were collected from each mammary quarter (n = 649) of cows in the UW-Madison dairy herd immediately before dryoff and twice within the first 14 DIM. Samples were cultured for bacterial growth and SCC was measured. Mammary quarters (n = 107) were enrolled to 4 cohorts based on microbiological status and somatic cell count (SCC) at dryoff and early lactation milk samples: LowNeg quarters (n = 81) had a SCC <100,000 cells/mL and no bacterial growth at all 3 samples; HighNegPre quarters (n = 17) had a SCC ≥150,000 cells/mL and no bacterial growth at the dryoff and first calving samples with a variable second calving sample; HighNegPost quarters (n = 6) had a SCC <100,000 cells/mL at the dryoff sample with a SCC ≥150,000 cells/mL at both calving samples and no bacterial growth at any of the 3 samples; HighPos quarters (n = 3) had bacterial growth and a SCC ≥150,000 cells/mL at all 3 samples. Milk samples were collected from all enrolled quarters weekly for SCC and an aseptic milk sample was collected every 28 d until 150 DIM for microbiological analysis. DNA was extracted from aseptic milk samples and PCR was performed with barcoded primers to the V4 region of the 16S rRNA gene; amplified PCR
products were run on a gel, extracted, and sequenced on an Illumina MiSeq platform. Overall bacterial DNA load in our milk samples was low, as evidenced by only approximately 50% of milk samples that had visible DNA bands after PCR. Sequence data were analyzed in mothur. In samples that could be sequenced, *Halomonas* spp. were the most common operational taxonomic unit (OTU) at dryoff, calving, and through the first 150 DIM. Bacterial richness was similar among cohorts across time while Shannon diversity was greatest in LowNeg samples (mean = 2.93; *P* = 0.02). Differing microbial diversity in inflamed and uninflamed mammary quarters suggests that the milk microbiome may be associated with health status and change during lactation.

**Key Words:** microbiome, mammary inflammation

### 143 An on-farm algorithm to guide selective dry-cow therapy.

A. K. Vasquez*1, C. Foditsch1, M. Wieland1, R. A. Lynch2, P. D. Virkler1, S. Eicker3, and D. V. Nydam1, 1Cornell University College of Veterinary Medicine, Ithaca, NY, 2Department of Animal Science, Cornell University, Ithaca, NY, 3Valley Ag. Software, Tulare, CA.

A selective-dry-cow therapy algorithm was evaluated for microbial cure risk, new infection risk, culling and occurrence of clinical mastitis before 30 DIM, and 1st-test milk yield and linear score (LS) in a randomized on-farm clinical trial including 612 dairy cows. An algorithm using DC305 and test-day data was used to identify cows as “low risk” (cows that likely will not benefit from dry cow antibiotics) or “high risk” (cows that will benefit). Low risk cows were those that had all of: <200k SCC at last test, an average SCC <200k on the last 3 tests, no signs of mastitis at dry-off, and have not had more than 1 clinical mastitis event in the current lactation. Low risk cows were randomly assigned to receive either intramammary antibiotics and external teat sealant (DCT) or teat sealant only (TS). Quarter milk samples were obtained from cows at dry-off and 1–7 DIM to determine cure and new infection at the quarter level. Samples from high risk cows were used to determine positive and negative predictive values (PPV, NPV) of the algorithm. Mastitis events, milk production, LS, and culling data were retrieved from DC305. Data analysis was performed in SAS 9.4: categorical outcomes were analyzed using Fisher’s exact tests while continuous outcomes were compared with *t*-tests. PPV and NPV were each 70%. Of cultures eligible for cure analysis (n = 157), 91% of DCT cured, while 83% of TS did (RR of non-cure TS:DCT = 1.9; 95%CI: 0.8–4.6). Positive cultures for coagulase negative staphylococcus (CNS) at dry-off accounted for 95% of the non-cures (n = 19/20). Risk ratio for new infection was 1.4 for TS:DCT (95%CI: 1.0–2.0), CNS accounted for 50% of new infections (n = 46/135). There were no statistical effects of treatment group on culling (DCT n = 14; TS n = 18), clinical mastitis (DCT n = 5; TS n = 3), milk (kg) (DCT = 38.9; TS = 39.8), or LS (DCT = 2.4; TS = 2.5). The impact of CNS to increased new infection risk and decreased bacteriological cure needs to be further investigated. These results suggest that the employed algorithm decreased dry cow antibiotic use by 64% without adversely impacting production outcomes.

**Key Words:** selective dry-cow therapy

### 144 Advancement of Dairying in Austria (ADDA): Conventional dairy farm management with respect to mastitis prevention and detection.

C. L. Firth*1, C. Schleicher2, A. Käsbohrer3, and W. Obritzhauser1, 1University of Veterinary Medicine, Institute of Veterinary Public Health, Vienna, Austria, 2Austrian Agency for Health and Food Safety (AGES), Integrated Risk Assessment, Data and Statistics, Graz, Styria, Austria.

The ADDA project is based on a partnership between academia, farmers’ associations, veterinary organizations and the Austrian government. This was an observational study and farmers were invited to participate by their local veterinarian (respondent-driven sampling). It was hypothesized that a variety of farm management practices would influence mastitis incidence. A total of 251 Austrian dairy farmers enrolled in the study and 211 responded to the farm management survey. Of these, 165 (78%) farmers farmed conventionally. National milk recorders provided details of milking technique via a separate survey. Descriptive statistics determined that these conventional herds were small, with a mean size of 29 cows (range 8–94). The majority (55%) of farms used milking parlors, with 34% having vacuum milking-line systems in the barn, 9% operating a bucket milking unit and 7% using automated milking systems. Teats were dry-wiped on 38% of farms before milking and 60% of milkers wore gloves. Postmilking teat dipping was carried out on 65% of farms, with 11% spraying teats and 24% reporting not using dip. The California Mastitis Test (CMT) was regularly used to check all cows for high somatic cell counts on just 17% of farms, while its use was more common for symptomatic animals (79%). In animals observed to have symptoms of mastitis, a bacteriological culture was routinely ordered on 56% of farms. Discard milk was frequently (64%) fed to calves. Preliminary analysis determined a significant association in the study population between different types of milking machine and milkers wearing gloves (χ² = 12.73, *P* < 0.001), however, this correlation was less significant for teat dipping (χ² = 5.41, *P* = 0.02). No significant correlation was found between either milking machine or barn type, with respect to premilking teat cleaning method. As a multifactorial disease, mastitis requires a whole-farm solution. A preliminary analysis of management factors has determined a small number of significant correlations and it is hoped that the GLMM analysis of farm management factors and their influence on mastitis incidence rates will shed new light on methods to prevent udder disease.

**Key Words:** mastitis, bacteriology, farm management

### 145 Effects of oral administration of acetylsalicylic acid after parturition on milk yield and milk components in lactating dairy cows under certified organic management.

A. A. Barragan*1, L. M. Bauman2, L. da Costa3, J. Veléz3, J. D. Rozo Gonzalez3, G. M. Schuenemann1, and S. Bas1, 1Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, 2Department of Animal Sciences, The Ohio State University, Columbus, OH, 3Aurora Organic Farms, Boulder, CO.

A proper transition from gestation to lactation is critical to optimize health and milk production in the subsequent lactation. While some studies have suggested that the administration of nonsteroidal anti-inflammatory drugs after parturition resulted in increased milk production of lactating dairy cows in conventional dairy herds, others failed to show an effect. The objective of this study was to assess the effects of oral administration of acetylsalicylic acid after calving on milk yield, milk protein, milk fat and somatic cell count (SCC) in lactating dairy cows under organic management. This study was performed in 3 organic dairy herds. Cows were block by parity and calving ease (eutocia; dystocia) at parturition, and were randomly allocated to 2 treatment groups: 1) ASP (n = 278); within 12 h after parturition cows received 4 consecutive treatments every 12 h with acetylsalicylic acid (100 mg/kg; 2 boluses); or 2) placebo (PLC, n = 285); within 12 h after parturition cows received 4 treatments every 12 h with gelatin capsules (2 capsules) filled with water. Data from the first 3 DHIA tests after parturition were recorded. In addition, daily milk yields were collected for the first 30 DIM from a subset of cows (ASP = 110; PLA = 122). The data were analyzed.
using ANOVA by the MIXED procedure of SAS as a randomized block design with repeated measures. Cows in the ASP group had higher ($P = 0.048$) daily milk yield ($26 \pm 0.88$ kg/d) when compared with cows in the PLC group ($24 \pm 0.79$ kg/d) during the first 30 DIM. Similarly, cows in the ASP group had higher milk production on the first 5 DHIA tests compared with PLC cows ($P < 0.05$; ASP $= 31 \pm 0.43$ kg/d; PLC $= 30 \pm 0.43$ kg/d). Additionally, ASP cows had lower SCC ($P < 0.05$; ASP $= 153 \pm 241 \times 10^3$ cells/mL; PLC $= 207 \pm 324 \times 10^3$ cells/mL) during the first 5 DHIA test compared with PLC cows. No difference was found in the percentage of milk fat and protein between groups. The results from this study suggest that treatment with ASP after calving may improve milk yields and decrease SCC during the first 5 DHIA tests. Further research aimed to evaluate strategies to improve the transition from gestation to lactation are required.

**Key Words:** parturition, acetylsalicylic acid, milk yield

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**146 Energy intake and balance of cows in the early postpartum period is affected by diet starch content and fermentability.**

R. Albornoz* and M. Allen, Michigan State University, Lansing, MI.

Our objective was to evaluate effects of diet starch content and fermentability on energy intake and balance during the early postpartum (PP) period. Fifty-two multiparous Holstein cows were used in a randomized block design experiment with a 2x2 factorial arrangement of treatments. Treatment rations were formulated to 22% (LS) or 28% (HS) starch content with dry ground corn (DGC) or high moisture corn (HMC) as the primary starch source. Rations were formulated for 22% forage NDF and 17% CP and fed from 1 to 23 d PP. Starch content was adjusted by substitution of corn grain for soylouths.DMI and milk yield were measured daily, and milk components, BCS, and BW were measured weekly. Feeds and refusals, and fecal samples were collected once a week for 3 weeks. Data were analyzed using a mixed model with block and cow as random effects and day or week PP as continuous measures. DGC increased net energy (NEI) intake compared with HMC (2.4 Mcal/d; $P = 0.01$) by increasing DMI (2.2 kg/d; $P < 0.01$), with a greater effect on NEI intake for HS than LS (4.2 vs. 0.6 Mcal/d; interaction $P = 0.06$). In addition, HS decreased total-tract NDF digestibility compared with LS ($P < 0.01$), with a greater reduction (18%) for HMC compared with DGC (7.1%, interaction $P = 0.09$). DGC increased milk NEI compared with HMC (31 vs. 28.2 Mcal/d; $P = 0.02$) by increasing yields of milk (2.6 kg/d; $P = 0.08$), milk fat (165 g/d; $P = 0.03$) and protein (165 g/d; $P = 0.01$). Compared with HMC, DGC reduced BW loss (−33.4 vs. −64.7 kg; $P < 0.01$) and tended to reduce BCS loss (−0.23 vs. −0.34; $P = 0.08$). HS tended to improve energy balance compared with LS (−15.3 vs. −17.1 Mcal/d; $P = 0.07$), which was greater for DGC than HMC treatments during the first week PP, but lower thereafter (interaction $P = 0.08$). Efficiency of utilization of digestible energy intake for milk production was highest for LS-DGC (67.8%), followed by LS-HMC (61.1%) and HS-DGC (59.8%; interaction $P = 0.09$). Feeding DGC improved energy intake and milk yield but had little effect on energy balance during the early PP period.

**Key Words:** starch fermentability, energy balance, early lactation

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**147 Feeding increasing amounts of ruminally-protected choline (RPC) increasingly reduced fatty liver of Holstein cows.**


Objective was to determine the optimal feeding amount of choline to reduce the triacylglycerol (TAG) concentration of liver and to increase absorption of TAG from the small intestine of dairy cows. Pregnant, nonlactating multiparous Holstein cows ($n = 77$) were enrolled at 64 ± 10 d before calculated calving date. Dietary treatments were 0, 30, 60, 90, and 120 g/d of ReaShure (RPC; Balchem Corp., New Hampton, NY). Experimental periods were 14 d during which cows ate ad libitum (AL) amounts of feed for 5 d and were restricted (R) to consume 36% of their energy/protein requirement for pregnancy and maintenance for 9 d to simulate lactating cows in negative energy balance. Methionine intake was similar during the AL and R periods due to methionine supplementation. Liver was biopsied on d 5 and 14. A saturated fatty acid (454 g of Energy Booster Mag, Milk Specialties, Eden Prairie, MN) was fed after biopsy on d 14 and blood plasma measured for TAG for 19 h post feeding. Data were analyzed using Proc Mixed procedures of SAS. Birth weight of the calves and number of days before calving at the time of enrollment were used as covariates. Significance was declared at $P < 0.05$. Dry matter intake and energy balance decreased from 9.5 to 3.3 kg/d and from 3.6 to −8.2 Mcal NE/d during the AL and feed R periods, respectively. Concentration of liver TAG was not affected by RPC during the period of AL feed intake (2.3% of liver DM) but decreased linearly with increasing intake of RPC from 17.5 to 11.1% during the period of feed R. With increasing intake of RPC, concentration of liver glycerogen increased linearly during the period of AL feed intake and tended to increase quadratically during the period of R feed intake, being greater in liver of cows fed RPC compared with that of control cows. Mean plasma concentration of TAG (0, 5, 7, 9, 11, 13, 15, 17, and 19 h after fat consumption) increased quadratically with increasing intake of RPC (13.6, 17.4, 16.9, 15.9, and 15.7 mg/100 mL). Supplemening RPC from 0 to 120 g/d improved liver status and fat absorption of feed-restricted pregnant, nonlactating multiparous Holstein cows.

**Key Words:** choline, fatty liver

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**148 Ethyl-cellulose rumen-protected methionine supply during late gestation enhances nutrient transporter expression in bovine placentome and calf birth weight.**

F. Batistel*1, A. S. M. Altharbi1, B. Saremii2, C. Parys2, and J. J. Loor1. 1University of Illinois at Urbana-Champaign, Urbana, IL, 2Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany.

Essential AA can activate mTOR signaling and elicit effects on cellular mechanisms controlling protein and lipid metabolism. During gestation the fetus relies almost exclusively on nutrients from the dam, hence, we hypothesized that increasing Met supply to the cow during late-pregnancy alters expression of nutrient transporters and mTOR signaling genes in the placentome leading to differences in calf birth weight. Multiparous cows were fed during the last 28 d of pregnancy with a control or Met-supplemented (Mepron, Evonik Nutrition & Care GmbH, Germany) diet. Mepron was supplied at a rate of 0.09% of DM to ensure a ratio of Lys to Met close to 2:8:1 in the metabolizable protein. Placentome samples were collected from 15 cows per treatment and mRNA expression of 41 genes analyzed using qPCR. Calves from Met-supplemented cows had greater body weight at birth ($P = 0.04$). mTOR and rPS6KB1 (ribosomal protein S6 kinase β-1) were upregulated ($P \leq 0.07$) in Met-fed cows. Met-fed cows also had upregulated 5 neutral AA transporters ($P \leq 0.09$; SLC3A2, SLC7A5, SLC38A1, SLC38A2, and SLC38A10), while it downregulated ($P = 0.05$ SLC43A2. Among the facilitated glucose transporters, Met upregulated ($P \leq 0.07$) the expression of SLC2A1, SLC2A3, and SLC2A4, and downregulated SLC2A8 ($P = 0.07$). In Met-supplemented cows the long-chain
fatty acid transporter SLC27A1 and the betaine transporter SLC6A12 were downregulated (P = 0.06), while the multivitamin cotransporter SLC35A6 was upregulated (P = 0.09). Other genes analyzed related to transport of AA (SLC1A1, SLC1A5, SLC6A6, SLC7A8, SLC38A6, SLC38A7), glucose (SLC2A5, SLC2A6, SLC2A9, SLC2A10, SLC2A11, SLC2A12, SLC2A13, SLC5A11), fatty acid (SLC27A2, SLC27A3), vitamin (SLC19A2, SLC19A3, SLC44A1, SLC44A3), and mTOR signaling (AKT1, EIF4EBP1, EIF4EBP2, EEF1A1, EEF1A2, IRS1) were not affected by Met supply. Overall, our findings indicate that Met supply during late-gestation could enhance utero-placental transport of essential and non-essential AA, glucose and vitamins. As such, differences in body weight at birth in calves from Met-supplemented cows is, at least in part, a result of upregulation of nutrient transporters some of which are controlled by mTOR signaling.

Key Words: amino acid, mTOR, transporter


The ability of diet to affect rumen morphological development in calves has been known for many years. Underlying mechanisms remain unknown but are linked to ruminal VFA production and absorption. VFA production from a given diet is greatly influenced by diet composition, which may lead to differences in development of the rumen. The objective of this pilot-scale study was to determine the effect of diet composition on: calf BW and stature, rumen pH, VFA, lactate, and 3 measurements of rumen morphology. Eight neonatal Holstein bull calves were randomly assigned to one of 2 dietary treatments: high starch:low NDF pelleted starter (HS; n = 4; 4.9% CP, 26.7% starch, 23.6% NDF DM basis) or high NDF:low starch pelleted starter (HN; n = 4; 20.9% CP, 9.5% starch, 36.5% NDF DM basis). Starter grain and water were offered freechoice from birth and milk replacer (22.0% CP, 20.0% fat as-fed basis; 566 g DM/d) was fed twice daily at 13% solids. Calves were individually housed; feed intake was recorded daily. Calf BW, stature measurements, and orosomately-obtained rumen content samples were collected from each calf weekly. All calves were euthanized at 7 wk of age to collect rumen morphology measurements. Data were analyzed by ANOVA using the MIXED procedure in SAS. There were no differences in BW, stature, or DMI measurements between treatments. Mean rumen pH throughout the 7 wk trial was lower for HS compared with HN calves (P = 0.006; 5.37 ± 0.08 and 5.81 ± 0.07, respectively). Mean acetate, propionate, butyrate, with HN calves (P = 0.006; 5.37 ± 0.08 and 5.81 ± 0.07, respectively). Mean rumen pH throughout the 7 wk trial was lower for HS compared with HN calves (P = 0.006; 5.37 ± 0.08 and 5.81 ± 0.07, respectively). Mean acetate, propionate, butyrate, and lactate, and D-lactate throughout the 7 wk trial were not affected by treatment (59.60 ± 3.42 mM, 37.15 ± 3.04 mM, 14.48 ± 3.97 mM, 6.02 ± 1.22 mM, and 5.27 ± 1.00, respectively). Treatment did not affect full or empty rumen mass (6.20 ± 0.39 kg and 1.12 ± 0.13 kg, respectively), ratio of absorptive surface to muscle (2.68 ± 0.39), or 2-dimensional surface area of papillae (4.56 ± 0.70 mm²). Feeding calf starters of 2 drastically different compositions did not affect overall calf or rumen growth. These findings support the idea that composition of diet may not influence the necessary changes in rumen fermentation that would alter rumen growth in calves.

Key Words: growth, nutrition, dairy

150 Ruminal pH in Holstein dairy bull calves from pre-weaning to post-weaning. J. K. van Niekerk*, M. Middeldorp, and M. A. Steele, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.

The goal of this research was to characterize ruminal pH changes that occur pre- and post-weaning (until wk 12 of life) in calves fed an elevated plane of nutrition pre- and post-weaning. Six Holstein dairy bull calves (45 ± 1.5 kg birth weight) were fed milk replacer (MR; 150 g/L) at 15% of body weight in 2 equal volumes per day. Milk volumes were adjusted weekly according to body weight. Calves were weaned using a 1 step-down weaning method; therefore, at the end of wk 5 MR was decreased to 50% and at the end of wk 6 calves were weaned. All 6 calves were fitted with ruminal cannulas in the second week of life. Calf starter, chopped straw and water were offered ad libitum and recorded daily while body weight was recorded weekly. Ruminal pH was measured continuously every 5 min from wk 5 to 12 with a ruminal pH bolus. Data were analyzed using MIXED procedure of SAS. The model included week as a fixed effect and calf as a random effect. Body weight increased from 45 ± 1.5 kg at birth to 109 ± 3.0 kg in 12 weeks, while body weight was maintained at 79 ± 1.5 kg and 77 ± 2.7 kg during step-down (wk 6) and the week after weaning (wk 7) respectively. During step-down, starter intake increased significantly (P < 0.01) from 130 ± 26.7 g/d (wk 5) to 385 ± 41.8 g/d (wk 6) and kept increasing as calves aged (2824 ± 66.9 g/d; wk 12). Pre-weaning the average daily pH was low (5.6 ± 0.09), implying ruminal acidosis. The pH reached its lowest levels during the week after weaning (wk 7) with a mean of 5.5 ± 0.11 and did not increase before wk 11. Furthermore, ruminal pH was below 5.5 and 5.2 for approximately 745 ± 187 and 220 ± 78 min daily during wk 7 and 8, respectively. The pH increased significantly in wk 11 and 12 (P < 0.01), with a mean of 6.1 ± 0.12. In conclusion, our results show that even before step-down weaning, ruminal pH is depressed although starter intake is low. Furthermore, it demonstrates that dietary rumen adaptation post-weaning can take several weeks because of prolonged ruminal pH depression in calves fed an elevated plane of nutrient post-weaning. The prolonged depressed ruminal pH might impact gut development as well as gut health.

Key Words: cannulated calves, elevated plane of nutrition, ruminal pH

151 Alteration of intrinsic molecular structure by steam flaking process improved gastrointestinal digestion of carbohydrate in dairy cows. N. Xu1,2, J. Liu1, and P. Yu1, 1Institute of Dairy Science, MoE Key Laboratory of Molecular Animal Nutrition, College of Animal Sciences, Zhejiang University, Hangzhou, China, 2Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada.

This study was aimed to investigate effects of steam flaking on rumen and intestinal digestibility of corn carbohydrate (CHO) on a molecular basis. Duplicates of 2 corns (Corn1, Corn2) and the corresponding steam-flaked corns (SFCorn1, SFCorn2) were collected from 2 commercial plants. Attenuated total reflectance Fourier-transform vibrational molecular spectroscopy was used to collect CHO molecular spectra (ca. 1188–950 cm⁻¹) with 3 major spectral peaks: 1st (ca. 1188–1132 cm⁻¹), 2nd (ca. 1132–1066 cm⁻¹) and 3rd Peaks (ca. 1066–950 cm⁻¹). Starch rumen and intestinal digestion characteristics were evaluated by conventional in situ procedure. PROC MIXED program of SAS 9.4 was used to analyze molecular spectral peak intensity and starch digestibility based on 2 factory design; and multivariate analyses (Statistica 8.0) were applied to CHO spectral absorption intensity data to distinguish CHO intrinsic molecular difference between raw and steam flaked types of corn. Truly digestible non-fiber carbohydrate was greater in steam flaked corn than their corresponding raw corn (P < 0.01). Rate constant of starch digestion increased (P < 0.01) after steam flaking. Rumen bypass starch of SFCorn1 was lower (P < 0.01) than that of Corn1, but
no difference was found between SFCorn2 and Corn2. Steam flaking process increased effective rumen degradability of starch ($P < 0.01$), but had no effects on intestinally digestible bypass starch and total digestible starch ($P > 0.05$). Steam flaking process increased spectral peak area intensities of total CHO and CHO 3rd Peak ($P < 0.01$). For CHO 1st and 2nd Peaks, molecular spectral peak area intensities increased in SFCorn1 ($P < 0.01$) compared with Corn1, but this was not the case for Corn2. Molecular spectral peak height of CHO 2nd Peak was greater ($P < 0.01$) in SFCorn1 than in Corn1. Multivariate analysis demonstrated that steam flaked corn could be apparently distinguished from their raw corn in carbohydrate molecular spectral region. In summary, steam flaking process altered carbohydrate molecular spectral structure, and improved carbohydrate gastrointestinal digestion.

**Key Words:** steam flaking, carbohydrate molecular spectra, corn digestibility