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0712 A comparison between propylene glycol and a multiple component drench on energetic variables in early lactating Holstein cows.

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Gluconeogenic precursors are therapeutically administered to treat ketosis in early lactation dairy cows and frequently provided as a standard management practice on all fresh cows. Study objectives were to compare and contrast a multiple component drench (MCD) containing glycerol, propylene glycol, calcium propionate, and water to propylene glycol (PG) on circulating glucose, insulin, NEFA, and β-HBA. Lactating Holstein dairy cows (n = 24, 11.6 ± 1 DIM; parity 1 to 7) were utilized in a replicated experimental design. Cows were randomly assigned to receive one of four treatments: 1) control (300 mL water), 2) 300 mL of PG (Propylene Glycol USP/EP, Dow Chemical Company, Midland MI), 3) 300 mL (M-MCD; TechMix, Stewart MN), and 4) 360 mL (H-MCD; TechMix, Stewart MN). The PG and H-MCD treatments were designed to provide a similar amount of gluconeogenic precursors. Cows were fasted for 4 h and then received a rumen drench of their respective treatment at 0800 h. All products were administered using an orogastric tube to assure successful rumen delivery and chased with 100 mL of warm water. Blood samples were collected via a jugular catheter at -15, 0, 15, 30, 60, 90, 120, and 150 min relative to treatment administration. Metabolite and hormone responses were calculated as area under the curve (AUC) by linear trapezoidal summation between time coordinates after subtracting their respective baseline values. Compared to controls, PG, M-MCD, and H-MCD all increased ($P < 0.01$) circulating glucose following the drench, but the glucose AUC did not differ between treatments. The insulin response peaked at +30 min in the PG, M-MCD, and H-MCD; the overall response was similar amongst treatments. Compared to controls, PG, M-MCD, and H-MCD all markedly decreased ($P < 0.05$) NEFA (42% at +120 min) and NEFA nadir occurred 60 min following treatment administration. Compared to controls, all three treatments decreased β-HBA, but PG tended ($P < 0.09$) to decrease ketones more than M-MCD and H-MCD. In summary, although variable, all three gluconeogenic precursor treatments influenced energetic variables, and thus the MCD product appears to be a viable strategy to manage energetic deficits in early lactation.

Key Words: dairy cow, propylene glycol, multiple component drench

0713 A comparative analysis of metabolomics and transcriptomics from prepartal liver of cows developing ketosis postpartum and healthy cows supplemented with Smartamine M and MetaSmart during the transition period.

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Cows overfed energy during the dry period are most susceptible to developing ketosis postpartum. Supplementation with Smartamine M (SM) and MetaSmart (MS) during the transition period improves postpartal dry matter intake and resulted in fewer cases of clinical ketosis postpartum. Metabolomics (GC–MS, LC-MS; Metabolon Inc.) and transcriptomics (45K-whole-transcriptome microarray; Agilent) analyses were performed in liver tissue harvested at -10 d relative to parturition from cows that were healthy on 7 d postpartum or were diagnosed with clinical ketosis (K, n = 8). From -21 d to calving all cows consumed a higher-energy diet without (developed K) or with SM (n = 8) and MS (n = 8) (clinically healthy). From 313 identified biochemical compounds, metabolomics analysis ($P \leq 0.10$) revealed 34 or 33 affected in the comparison of K vs. SM or K vs. MS. Comparing profiles in K vs. SM revealed 13 compounds up-regulated and 21 downregulated. Among the up-regulated compounds most belong to bile acid, fatty acid, branched-chain amino acid, and arginine and proline metabolism. Among the downregulated compounds, there were several lysolipids and di-carboxylic acids along with components of pentose, purine, and sphingolipid metabolism. Citrate was markedly lower in liver of K vs. SM. In the comparison of K vs. MS, seven compounds were up-regulated and 26 were downregulated. The up-regulated compounds are intermediates of glycolysis/gluconeogenesis/pyruvate, histidine, glycine/serine/threonine, and fatty acid metabolism. Among downregulated compounds, seven were lysolipids, but also citrate, squalene, several pentoses, and purines were affected. Analysis of transcriptomics data resulted in 834 or 1261 differentially expressed genes (DEG, $P \leq 0.05$) in K vs. SM or K vs. MS. Bioinformatics analysis using the Dynamic Impact Approach (DIA) revealed a strong activation in K vs. MS of Notch, Hedgehog, and TGF-β signaling pathways along with "steroid biogenesis." In contrast, "synthesis and degradation of ketone bodies" was markedly inhibited. The pathway response in K vs. SM was less pronounced in part due to the fewer number of DEG. For example, the Hedgehog signaling pathway was highly impacted but moderately activated; whereas, the "renin-angiotensin system" was the most impacted and markedly inhibited. Preliminary data analysis suggests that supplemental MS and SM elicit distinct metabolomics and transcriptomics responses in liver before calving. Cows developing K postpartum also had a distinct molecular phenotype compared with those supplemented with methionine. The functional relevance of these differences remains to be determined.

Key Words: ketosis, transition cows, metabolomics

0714 The effect of subacute ruminal acidosis on milk fat synthesis and relative expression of key lipogenic enzyme genes in liver tissue in dairy cows. Y. Guo[*1,2], S. L. Li[1], Z. J. Cao[1], X. Xu[1], and Y. Zou[1], [1]*State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing,* [2]*Shijiazhuang Academy of Agriculture and Forestry Science, Shijiazhuang, China.*

The aims of this study were to: 1) determine the variation of performance and relative expression of lipid anabolism related genes in liver tissue triggered by induced subacute ruminal acidosis (SARA), and 2) evaluate the ability of pelleted beet pulp (BP) as a substitute for ground corn to alleviate SARA. Eight mid-lactation Holstein cows were fed four diets during four successive 17-d periods: 1) total mixed ration (TMR) containing 0% finely ground wheat (FGW) (W0), 2) TMR containing 10% FGW (W10), 3) TMR containing 20% FGW (W20), and 4) TMR containing 10% BP as a replacement for 10% ground corn (BP10). The SARA induction protocol reduced the mean ruminal pH from 6.37 to 5.94 ($P < 0.01$), and the minimum ruminal pH decreased from 5.99 to 5.41 from baseline to challenge period. Mean ruminal pH increased from 5.94 to 6.05, and minimum pH increased from 5.41 to 5.63, when BP was substituted for corn. Dry matter intake and milk yield were not affected by the dietary treatments; however, milk fat percentage and yield were reduced ($P < 0.01$) in the W20 and BP10 treatments than the W0 treatment. Cows fed the W20 diet had a lower ($P < 0.01$) plasma concentration of triglyceride and total cholesterol, and a higher ($P < 0.01$) plasma concentration of glucose and insulin than cows fed the W0 diet. Liver tissue relative expression of acetyl-CoA carboxylase α (ACACA) ($P = 0.03$), FA synthase (FASN) ($P = 0.05$), sterol-response element binding protein 1 (SREBF1) ($P < 0.01$) was increased in cows fed the W20 diet, but there were no significant differences among the W10, W20, and BP10 diets. Our results indicate that the SARA could decrease of milk fat synthesis and increase of relative expression of lipid synthesis key genes in liver tissue. The substitution of pelleted BP for ground corn in a high-concentrate diet could reduce the risk of SARA in dairy cows.

Key Words: subacute ruminal acidosis, milk fat, key lipogenic enzyme

0715 Effect of 2-hydroxy-4-(methylthio)butanoate (HMTBa) on risk of diet-induced milk fat depression. M. Baldin[*1], J. Y. Ying[1], G. I. Zanton[2], and K. J. Harvatine[1], [1]*Penn State University, University Park,* [2]*Novus International, Inc., St. Charles, MO.*

Dietary polyunsaturated fatty acids (FA) and diet fermentability are key risk factors for diet-induced milk fat depression (MFD). A role for HMTBa in increased milk fat yield has been proposed, but the interaction of HMTBa and dietary risk factors for MFD have not been investigated. The objective was to evaluate the effect of HMTBa (ALIMET feed supplement, Novus International, Inc., St. Charles, MO) on milk fat synthesis when feeding diets with increasing risk for MFD. Thirty multiparous Holstein cows [227 ± 88 DIM, producing 38 ± 17 kg milk/d (Mean ± SD)] were used in a randomized block design. Treatments were control (corn carrier) and HMTBa (HMTBa fed at 0.1% of the diet DM provided with a corn carrier). The experiment was 70 d and included a 14-d covariate period followed by three phases that fed diets with increasing risk of MFD. During the low-risk phase (28 d) the base diet was balanced to 33.5% NDF and had no exogenous oil, during the moderate-risk phase (14 d) the diet was balanced to 31% NDF and contained 0.75% soybean oil, and during the high-risk phase (14 d) the diet was balanced to 28.5% NDF and contained 1.5% soybean oil. Milk yield, DMI, and BW were measured daily. Milk was sampled every 7 d and analyzed for fat and protein concentration. Data were analyzed using PROC MIXED with repeated measures and the effect of treatment was tested at each time point. There was no overall effect of treatment or treatment by time interaction for DMI, BW, milk yield, and milk protein concentration and yield. A treatment by time interaction was observed for milk fat concentration ($P = 0.02$) and yield ($P = 0.01$). HMTBa increased milk fat percent during the high-risk phase on d 63 (2.83 vs. 3.55, $P < 0.0001$) and d 70 (2.91 vs. 3.43%, $P = 0.005$) and increased milk fat yield on d 63 (821 vs. 1093 g/d, $P = 0.002$) and d 70 (771 vs. 951 g/d, $P = 0.018$). In conclusion, HMTBa increased milk fat yield when cows were fed a diet with a high risk of diet-induced MFD.

Key Words: HMTBa, milk fat depression

0716 Time-course of changes in select ruminal microbes during induction and recovery from diet-induced milk fat depression in dairy cows. D. E. Rico*, S. H. Preston, and K. J. Harvatine, *Penn State University, University Park.*

Diet-induced milk fat depression (MFD) results from bioactive fatty acids produced in the rumen during altered biohydrogenation, and changes in the rumen microbial population are commonly proposed as a key factor in development of the condition. An experiment was conducted to characterize the changes in select rumen microbes during induction and recovery from diet-induced MFD. Eight ruminally cannulated cows were used in repeated design and fed a low fiber, high PUFA diet (Induction; 29.5% NDF and 3.7% PUFA; DM basis) for a period of 21 d, and then switched to a high fiber, low PUFA diet (Recovery; 36.9% NDF and 1.1% PUFA) for 21 d. The control was the high fiber, low PUFA diet. We have previously reported decreased milk fat yield by d 7 and near maximal MFD by d 13 during induction, and a progressive increase in milk fat yield with full recovery by d 15. Ruminal digesta samples were collected 8 h after feeding on Days 0, 4,

8, 12, and 20, and select ruminal microbes were quantified by Real-time PCR. Data were analyzed by PROC MIXED with the repeated statement and treatments compared at each time point. Treatment by time interactions were observed for most taxa ($P < 0.05$). *Megasphaera eldesnii* and *S. ruminantium* (lactate using bacteria) increased progressively > 170% until d 12 of induction and decreased progressively during recovery. *Streptococcus bovis* (amilolytic bacteria) peaked at 350% higher than control on d 4 of induction ($P < 0.01$) and rapidly decreased during recovery. *Prevotella bryantii* (amilolytic bacteria) decreased 66% from d 8 to 20 of induction compared with the control and increased to control levels by d 12 of recovery. *Ruminococcus albus* (fibrolytic bacteria) and *P. ruminicola* (fibrolytic bacteria) were nearly constant during induction and recovery. However, *F. succinogenes* (fibrolytic bacteria) decreased 97% compared to control by d 4 of induction and increased progressively to an equal extent during recovery. The *Butyrivibrio/Pseudobutyrivibrio* group (*t*11–18:1 producer) decreased progressively during induction and increased during recovery, whereas the *Butyrivibrio hungatei* group (*t*11–18:1 producer) was not affected by treatment. Both ciliate protozoa and total fungi decreased progressively by > 90% during induction and increased during recovery. Rapid adaptation of most of the observed microbes occurred during both induction and recovery from diet-induced MFD, and the time-course of adaptation matches the time-course of changes in biohydrogenation intermediates and inhibition of milk fat.

Key Words: dairy cows, milk fat depression, ruminal microbes.

0717 The effect of length of adaptation to a high-grain diet and acidosis challenge and recovery on rumen papillae mRNA expression of genes relating to barrier function, inflammation, and short-chain fatty acid transport in beef heifers.

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Ruminal acidosis induced by high-grain diets can have serious negative effects on animal health and performance. The objective of this study was to investigate if the duration that ruminally cannulated beef heifers were fed a high-grain diet influences mRNA expression of genes relating to barrier function, immune response and short-chain fatty acid (SCFA) absorption in rumen papillae. Heifers were assigned to one of four blocks and randomly allocated to be long adapted (LA; 34 d; $n = 8$) or short adapted (SA; 8 d; $n = 8$) from a backgrounding diet to a high-grain (81% barley) finishing diet before inducing ruminal acidosis. Ruminal acidosis was induced by restricting DMI to 50% for 24 h followed by an intra-ruminal dose of barley grain (10% of DMI). Rumen papillae from the ventral sac were collected and stored in RNA later during the baseline period (BASE; 6 d of before challenge), 24 h after challenge (Recovery1; REC1), and 8 d after challenge (REC2). Total mRNA was isolated from papillae using TriZol and quantitative real-time PCR was conducted to quantify relative expression of genes relating to gut barrier function (zonula occluden 1, claudin 1, and occuldin), immune response (TNF-α, Toll-like receptor 4;TLR4), and intracellular pH regulation and SCFA metabolism (Na^+/H^+ exchanger 1 and 3, monocarboxylate transporter 1 and 4; MCT1 and 4 respectively, and 3-hydroxy-3-methylglutaryl-CoA synthase 1 and 2; HMGS 1 and 2 respectively). Expression of mRNA were normalized for expression of GAPDH and β-actin and expressed as normalized relative fold-change. Data were analyzed using PROC MIXED in SAS and mean separation conducted using Tukey post-hoc separation test. Dietary treatment ($P \geq 0.19$) and the treatment × period interaction ($P \geq 0.06$) did not influence mRNA expression of genes of interest. Total mRNA expression was affected by period ($P \leq 0.03$) for TLR4, ZO1, claudin, occludin, MCT1 and MCT4. In general, REC1 showed least expression and expression during REC2 returned to values similar (TLR4, claudin 1, and occludin) or intermediate (ZO1, MCT1, and MCT4) to BASE. These results indicate that length of dietary adaptation used in our study was not sufficient to differentially influence the expression of mRNA for key genes influencing barrier function, immune response and SCFA transport following an acidosis challenge. However exposure to ruminal acidosis generally reduced mRNA expression with values returning to baseline conditions within 8 d.

Key Words: barrier function, cattle, immune response, rumen acidosis, short-chain fatty acids

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0718 Induction of subacute ruminal acidosis affects the rumen microbiome.

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Subacute ruminal acidosis (SARA) negatively impacts the dairy industry by decreasing milk production, efficiency of milk production, and increasing culling rate and death loss. Six lactating Holstein cows were used in a replicated 2 × 2 Latin square design to determine the effects of SARA induction on the rumen microbiome. Experimental periods were 10 d with d 1 through 3 for ad libitum intake of control diet, followed by 50% feed restriction on d 4, and ad libitum access on d 5 of the control diet (control) or control diet + 4.6 kg of a 50:50 wheat/barley pellet (challenge). Ruminal samples were collected on d 1 and 6 of each period before morning feeding and separated into liquid and solid fractions. Bacterial DNA was extracted from the solid fraction after physical homogenization. Real-time quantitative PCR was used to determine SARA challenge effects on culturable bacterial species. *Butyrivibrio proteoclasticus* was observed in the greatest rela-

tive abundance of the evaluated species (0.4 to 0.2%) with a treatment × day effect ($P < 0.01$). For the control treatment, *Butyrivibrio proteoclasticus* increased ($P = 0.04$) from d 1 to d 6, but there was a tendency to decrease ($P = 0.08$) for the challenge treatment from d 1 to d 6. *Anaerovibrio lipolytica* remained stable during the challenge treatment; however, relative abundance increased ($P < 0.01$) decidedly on control d 6. A primary cellulolytic species, *Fibrobacter succinogenes*, was decreased ($P < 0.02$) from d 1 to d 6 of the control and challenge treatment. While *Selenomonas ruminantium* and *Eubacterium ruminantium* decreased ($P \leq 0.03$) from d 1 to d 6 of the challenge treatment, both species were unaffected by control treatment. Relative abundance of *Prevotella bryantii* increased ($P < 0.01$) on d 6 of the challenge treatment, but no effects of the control treatment were observed. Similarly, the lactate-utilizing species, *Megasphaera elsdenii*, had a tendency to increase ($P < 0.06$) on d 6 of the challenge treatment, yet populations remained stable during the control treatment. Overall, results indicate the challenge treatment caused greater shifts within the rumen microbiome and are likely linked to the onset of SARA.

Key Words: acidosis, SARA, microbiome

0719 Effects of feeding a negative DCAD diet prepartum for varied lengths of time on serum metabolites and performance.

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Forty-five multiparous Holstein cows and 15 springing heifers were used in a completely randomized design trial to determine the effect of length of feeding a negative DCAD diet prepartum on serum metabolites, DMI, milk yield and composition. After training to eat through Calan doors, cows within parity were assigned randomly to negative DCAD diets for 3 (3WPC), 4 (4WPC) or 6 wk (WPC) before predicted calving. Actual days cows were fed negative DCAD diets were 19.2 ± 4.1, 27.9 ± 3.1, and 41.5 ± 4.1d for 3WPC, 4WPC, and 6WPC, respectively. All cows were fed a diet formulated for late gestation (14.6% CP, 42.3% NDF, 20.5% starch, 7.1% ash, and 0.97% Ca) supplemented with Animate (Prince Agri Products, Inc., Quincy, IL) with a resulting DCAD (Na + K– Cl–S) of -21.02 mEq/100 g DM. After calving, cows were fed a diet formulated for early lactation (18.0% CP, 36.4% NDF, 24.2% starch, 8.1% ash, and 0.94% Ca) for the following 6 wk with a DCAD of 20.55 mEq/100 g DM. Urine pH was not different ($P > 0.10$) among treatments before calving and averaged 6.36. No differences ($P > 0.10$) were observed in prepartum DMI which averaged 11.4, 11.5 and 11.7 kg/d for 3WPC, 4WPC, and 6WPC, respectively. Prepartum serum total protein ($P = 0.03$), albumin ($P = 0.01$), Ca ($P = 0.02$), and anion gap ($P < 0.01$) were within normal limits, but decreased linearly with the increasing time cows were fed a negative DCAD diet. No differences were observed in serum metabolite concentrations on the day of calving. After calving, serum total protein ($P = 0.04$) and globulin ($P = 0.02$) increased linearly with the increasing time cows were fed a negative DCAD diet. No differences were observed in postpartum DMI, milk yield, or concentration of fat or protein among treatments: 19.1, 40.6, 4.30, and 2.80; 19.6, 41.5, 4.50, and 2.90; and 18.6 kg/d, 41.0 kg/d, 4.30% and 2.73% for 3WPC, 4WPC, and 6WPC, respectively. Results of this trial indicate that extending the length of time cows are fed a negative DCAD diet does not negatively affect serum metabolites or resulting performance.

Key Words: DCAD, serum metabolites, milk yield, milk composition

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0720 Effect of pre-calving dietary cation anion difference on milk production: A meta-analysis.

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The effects of dietary cation anion difference (DCAD) of pre-calving diets on milk production. A total of 15 studies and 34 comparisons were identified and analyzed (Stata 13.0 Statacorp, Texas) using a random effects model. A weighted mean difference between treated and control was also calculated. Meta-regression analysis evaluated whether parity of the cattle, difference in DCAD between treatment and the control diet and estimated energy density, crude protein, crude fat, neutral detergent fiber, non-fiber carbohydrates, DCAD, calcium, magnesium, phosphorus, potassium, and content of the control diet influenced responses. The average ± SE days of exposure to transition diets was 29 ± 3, and the DCAD of controls and treated cows was 232 ± 37 and -27 ± 33 meq/Kg, respectively. Only the parity of the cow ($P = 0.003$) and NDF of the control diet ($P = 0.02$) influenced responses with milk production increased in cows ($P = 0.0001$) and lowered in heifers ($P = 0.027$). The effect size (ES) for milk production of studies in cows was positive (0.629 95% CI 0.292 to 0.965). Estimated responses in milk or fat corrected milk over 65 ± 14 d of lactation were 1.153 (95% CI 0.335 to 1.971) L per day. In heifers, milk production responses were ES of -1.211 (95% CI -2.288 to -0.135) and the weighted mean difference was -1.482 (95% confidence interval -1.872 to -1.093) L per day. The I^2 was 77.1 for cows and 87.2 for heifers, indicating very considerable variability in responses. The effect size response was lower with higher NDF diets. The lower response to DCAD in high NDF studies may indicate a role for ruminal outputs to influence acid-base status. Critically, other sources of variation, as indicated by the high I^2, were not identified, despite the large number of covariates tested. Reference: Lean IJ, DeGaris PJ, McNeil DM, Block

E (2006) Hypocalcemia in dairy cows: Meta-analysis and dietary cation anion difference theory revisited. *Journal of Dairy Science*. 89: 669–684.

Key Words: dietary cation anion difference, pre-calving diet, meta-analysis

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0721 Evaluation of choline metabolites in milk as potential biomarkers for choline absorption in the lactating dairy cow. V. M. Artegoitia*[1], C. L. Girard[2], H. Lapierre[2], S. R. Campagna[1], F. Harte[1], and M. J. de Veth[1,3], *[1]University of Tennessee, Knoxville, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, [3]Balchem Corporation, New Hampton, NY.*

Choline is an essential nutrient for growth and performance of production animals, and an established symptom of choline deficiency in periparturient cattle is fatty liver. Dietary choline is extensively degraded in the rumen, and although rumen-protected choline (RPC) has been found to reduce the extent of hepatic fat infiltration, no biomarkers have been established to assess the efficacy of RPC supplements in dairy cows. Secretion of total choline in milk could be a potential biomarker; however, choline is secreted in milk in many metabolic forms and some specific metabolites in milk may be more closely associated with choline absorption than total choline secretion. The objective of this study was to evaluate secretion of choline metabolites in milk as potential biomarkers of choline absorption. Five lactating Holstein cows (237 ± 17 DIM) were used in a 5 × 5 Latin square design, with 5-d treatment periods and a 2-d interval between periods. Treatments were 1) control (0 g/d choline), 2) RPC- low dose (RPC-L), 3) RPC-high dose (RPC-H), 4) abomasal infusion (ABO)– low dose (ABO-L), 5) ABO– high dose (ABO-H). The low and high doses of RPC (Reashure, Balchem Corp.) and ABO each supplied 12.5 and 25 g choline/d, respectively. Milk samples from d 5 were analyzed for acetylcholine (AC), betaine (Bet), free choline (Cho), glycerophosphocholine, lysophosphocholine, phosphatidylcholine, phosphocholine (PC), and sphingomyelin, using liquid chromatography-tandem mass spectrometry. Although total choline secretion in milk was not affected by ABO, Cho and Bet secretion increased ($P < 0.01$) in a dose dependent manner with ABO by 74% and 171%, respectively, with ABO-L and 146% and 278%, respectively, with ABO-H. The amounts of Cho and Bet secreted in milk increased from 0.54 to 0.94 and 1.33 g/d and from 0.14 to 0.38 and 0.53 g/d, respectively for the low and high doses. Increases in the yields of AC and PC were also observed ($P = 0.04$), although only with ABO-H. The other metabolites were not changed by ABO ($P > 0.12$), nor were any changes observed in secretion of individual choline metabolites with RPC. Multiple regression indicated the changes in milk PC and Bet secretion could be explained to a large degree by the ABO dose of choline ($P = 0.01$; $R^2 = 0.72$). The results of this study suggest that some choline metabolites may be more sensitive biomarkers than total choline for absorption of supplemental choline.

Key Words: choline, bioavailability, dairy cow

0722 Association of plasma ghrelin concentrations with feed intake in beef cattle. A. P. Foote*, K. E. Hales, C. A. Lents, and H. C. Freetly, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Active ghrelin is an acylated peptide produced in the gastrointestinal tract of animals that is thought to stimulate appetite. Cattle used in this experiment were sired by bulls representing five breeds in the United States, including Hereford, Angus, Limousin, Charolais, and Gelbvieh. Steers ($n = 128$) and heifers ($n = 133$) were fed a finishing diet and individual intake was recorded for 84 d. Blood samples were collected via jugular puncture at 113 d on feed. Active ghrelin was protected by acidifying the blood plasma and adding a protease inhibitor. Active ghrelin was quantified using a commercial RIA specific for the acylated form of ghrelin. The mixed model procedure of SAS was utilized to determine factors influencing active ghrelin levels. Fixed effects included sex, sire breed, dam breed, total dry matter intake (TDMI), and BW at time of blood collection. Sire nested within sire breed was included as a random effect. A mixed model was also used to determine if concentrations of active ghrelin could be used to predict TDMI. Fixed effects included concentrations of active ghrelin, sire breed, dam breed, sex, BW, and sire nested within sire breed was included as a random effect. Concentrations of active ghrelin were positively associated with TDMI ($P = 0.012$) when sex and breed effects were accounted for in the model. Regardless of breed, heifers had lower TDMI than steers ($P = 0.012$) but tended to have greater concentrations of active ghrelin ($P = 0.099$). Gelbvieh-sired cattle had the greatest concentrations of active ghrelin and Angus, Limousin, and Charolais had the lowest concentrations while concentrations of ghrelin in Hereford-sired cattle were intermediate ($P = 0.003$). Angus-sired cattle had the highest TDMI, while Limousin-, Charolais-, and Gelbvieh-sired cattle had the lowest TDMI with Hereford cattle intermediate ($P < 0.001$). Modeling the data showed that active ghrelin concentrations had a positive association with TDMI; however, both the sex and sire breed effects indicate that cattle with lower intakes (e.g., heifers and Gelbvieh-sired cattle) tend to have greater concentrations of active ghrelin than cattle with higher intakes. Data indicate there is a genetic effect on active ghrelin levels that may affect the association with intake. *USDA is an equal opportunity provider and employer.* *Funded in part by NIFA Grant 2011–68004–30214 through the National Program for Genetic Improvement of Feed Efficiency in Beef Cattle.*

Key Words: breed differences, feedlot cattle, gut peptides

0723 Effects of ruminal dose of sucrose, lactose, and starch on ruminal fermentation and expression of genes in ruminal epithelial cells. M. Oba*, J. Mewis, and Z. Zhu, *University of Alberta, Edmonton, Canada.*

The objective was to evaluate effects of ruminal dose of sucrose (SUC), lactose (LAC) and cornstarch (STA) on ruminal fermentation and expression of genes in ruminal epithelial cells. Six ruminally cannulated non-lactating non-pregnant Holstein cows (BW = 725 ± 69.6 kg) were fed a diet containing whole crop barley silage and dry ground corn (dietary NDF and CP contents: 41.8 and 13.2% at DM basis, respectively), and assigned to treatments in a 3 × 3 Latin square design with 7-d periods; 1 d for data and sample collection followed by a 6-d washout period. Treatment was a pulse-dose of SUC, LAC, and STA (3.0, 3.0, and 2.85 kg DM, respectively, to provide similar amount of hexose across the treatments) through the rumen cannulas. All treatments were given with alfalfa silage (1.75 kg DM) to prevent acute rumen acidosis. Rumen pH was continuously monitored, and rumen fluid was sampled at 0, 30, 60, 90, 120, 150, and 180 min after the dose. In addition, ruminal papillae were sampled from the ventral sac at 180 min after the dose. Ruminal dose of SUC and LAC, compared with STA, increased ($P < 0.05$) ruminal total VFA concentration and molar proportion of butyrate since 60 min after the dose, and expression of genes for sodium hydrogen exchanger 1 and 2, and ATPase-1 in ruminal epithelial cells. Ruminal dose of SUC, compared with LAC and STA, decreased ($P < 0.05$) rumen pH since 120 min after the dose and molar proportion of acetate in ruminal fluid from 60 to 150 min after the dose, and increased ($P < 0.05$) molar proportion of propionate in ruminal fluid from 60 to 150 min, and expression of genes involved in butyrate metabolism (3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1) and anion exchange across ruminal apical cell membrane (putative anion transporter 1). These results suggest that replacing dietary starch with sugar may affect ruminal fermentation, and metabolism regulating intracellular pH and fermentation acid absorption in ruminal epithelial cells, and that these effects can be greater for SUC than LAC.

Key Words: sucrose, lactose, starch