ADSA PRODUCTION DIVISION GRADUATE STUDENT POSTER COMPETITION: PHD

0750 Elevation of circulating serotonin prepartum decreases β-hydroxybutyrate concentrations and improves energy status postpartum in multiparous dairy cows.

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Peripheral serotonin is known to mediate energy homeostasis in late-lactation dairy cows. However, the majority of energy-related disorders occur primarily during the transition period. To establish if serotonin mediates energy homeostasis during the transition period, we intravenously infused multiparous Holstein ($n = 12$) and Jersey ($n = 12$) cows daily with either 1 L of saline (CON; $n = 6$ for Holstein and Jersey) or 1 mg/kg BW of 5-hydroxytryptophan in 1 L of saline (5-HTP; $n = 6$ for Holstein and Jersey). Holsteins were infused for an average of 5.67 ± 0.78 d and Jersey cows for 8.67 ± 1.53 d prepartum, until parturition. On infusion days, blood was collected before, after, and at 2, 4, and 8 h after infusion. Blood was also collected for 14 d postpartum and on Day 30 postpartum and assayed for glucose, β-hydroxybutyrate (BHBA), and NEFA. Milk yield and feed intake were monitored throughout. All data were analyzed using a two-way ANOVA in SAS for treatment, breed, and day effect and the interaction. Holsteins treated with 5-HTP had elevated circulating serotonin for 6 d before parturition and on Day 0 and Day 1 of lactation ($P < 0.05$). The5-HTP Jerseys treated with 5-HTP had elevated serotonin concentrations 2 d prepartum and on the day of parturition ($P < 0.003$). Treatment did not affect milk yield ($P > 0.05$). There was no treatment effect on feed intake for either breed ($P > 0.05$). The CON Holsteins had higher circulating glucose than CON Jerseys from Day 8 to Day 15 postpartum ($P < 0.05$) and this effect was mediated by 5-HTP treatment. There was no treatment effect in either breed on circulating glucose levels ($P > 0.05$). β-Hydroxybutyrate concentrations tended to be lower on Days 7 and 10 in Holstein 5-HTP compared with Holstein CON ($P = 0.09$) and were significantly lower on Day 7 in Jersey 5-HTP compared with Jersey CON ($P = 0.02$). The CON Jerseys had the highest BHBA concentrations on Days 6 to 10 postpartum. There was no effect of BHBA prepartum in either breed. Nonesterified fatty acids were not affected either pre- or postpartum ($P > 0.05$), although they were elevated in both breeds within an infusion day ($P < 0.05$). Taken together, these data demonstrate that serotonin administration prepartum may have a positive effect on mediating energy status postpartum. Specifically, decreased BHBA concentrations on Days 6 to 10 postpartum demonstrate serotonin's potential to mediate ketosis incidence.

Key Words: energy, serotonin, transition cow

0751 Temporal effects of ruminal propionate infusion on feeding behavior of Holstein cows in the postpartum period.

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Suppression of appetite during the postpartum (PP) period is likely caused by a signal related to hepatic energy status from oxidation of fuels. Propionic acid (PA) is likely the most important fuel stimulating hepatic oxidation within meals in ruminants. However, PA production rate in the rumen varies greatly among starch sources and the temporal pattern of propionate supply to the liver might affect satiety within meals. The objective of this study was to determine the temporal effect of intraruminal propionic acid infusion at initiation of meals on feeding behavior of PP cows. We hypothesized that a faster rate of PA infusion would decrease meal size by stimulating satiety sooner within a meal. Six ruminally cannulated, multiparous Holstein cows in the PP period were used in a duplicated 3 × 3 Latin square design experiment balanced for carryover effects. Cows were blocked by parturition date and randomly assigned to treatment sequence within square. Treatments included a control (no infusion) or infusion of 1.25 mol of propionic acid over 5 (FAST) or 15 min (SLOW) at each meal. Infusions were initiated at the beginning of the conditioned meal (1200 h) and were triggered at each spontaneous meal for 22 h. Feeding behavior was monitored by a computerized data acquisition system. A 24-h recovery period was included between infusion days to reduce potential carryover effects of treatment. In contrast to our hypothesis, FAST increased meal size 55% (1.30 vs. 0.84 kg DM; $P < 0.02$) compared with SLOW. FAST also increased intermeal interval 67% compared with SLOW (149.7 vs. 89.8 min; $P < 0.05$) while decreasing meal frequency 29% (8.0 vs. 11.2 meals/d; $P = 0.01$). Although both PA treatments decreased DMI 48% compared with the control, DMI was not affected by infusion rate. FAST PA supply to the liver at the initiation of meals might have resulted in a saturation of propionate metabolic pathways in the liver, resulting in greater bypass for FAST compared with SLOW. Increased intermeal interval and reduced meal frequency for FAST compared with SLOW might have been caused by extended anapleurosis and hepatic oxidation of acetyl CoA over a longer time after meals, delaying hunger. These results indicate that the depression in feed intake by more fermentable starch sources might be more related to the amount of PA produced rather than its rate of production within meals.

Key Words: feeding behavior, meal size, hepatic oxidation

0752 Forage yield, nutrient composition, and grain yield of corn and soybeans when intercropped at different seeding rates grown under organic conditions.

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Previous research has demonstrated that feeding of forage blends produced through intercropping of corn and soybean could be beneficial for livestock. A field plot study was laid out using a randomized complete block design having three replicates to evaluate an organic corn hybrid, MC 5300 (C), with an organic soybean, Viking 2265 (N) or Vining soybean (V), at five different seeding rates to create nine different treatments (100:0:0 [T1], 0:100:0 [T2], 0:0:100 [T3], 50:50:0 [T4], 67:33:0 [T5], 33:67:0 [T6], 50:0:50 [T7], 67:0:33 [T8], and 33:0:67 [T9] of C with N and V) to determine the optimal intercropping seeding rates. Forages were hand harvested 110 d after planting, inoculated, packed into buckets, weighed, and ensiled for 90 d. Buckets were then reweighed and opened, and forage samples were collected and analyzed for nutrient composition. Fresh biomass yield was higher ($P < 0.01$) for T8 compared with remaining treatments (88.37, 31.34, 17.34, 85.07, 101.49, 68.06, 85.78, 107.00, and 74.86 T/ha for T1, T2, T3, T4, T5, T6, T7, T8, and T9, respectively). Dry matter yield was higher ($P < 0.01$) for T8 compared with others (10.60, 5.93, 27.10, 24.44, 29.31, 36.55, and 25.41 T/ha for T2, T3, T4, T6, T7, T8, and T9, respectively). Nitrogen accumulation by treatments forage was lower ($P = 0.01$) in T3 (0.20 T/ha) compared with the others (0.38 T/ha). Corn grain yield was higher ($P < 0.01$) for T5 and T8 compared with T4, T6, T7, and T9 (11.84, 15.44, 8.84, 11.89, 16.66, and 9.68 T/ha for T4, T5, T6, T7, T8, and T9, respectively). Soybean grain yield was higher ($P < 0.01$) in T4 and T6 compared with T5, T7, T8, and T9 (3.06, 1.80, 3.38, 1.90, 0.53, and 2.36 T/ha for T4, T5, T6, T7, T8, and T9, respectively). Land equivalent ratio was higher ($P < 0.01$) for T4 (1.32) and T5 (1.31) compared with T7 (1.15), T8 (1.16), and T9 (1.11). Crude protein content was higher ($P < 0.01$) for T6 (9.64%) compared with T4 (8.96%), T5 (8.22%), T7 (8.20%), and T8 (7.94%). Starch content was higher for T4 (29.18%) compared with T9 (26.03%). Thirty-hour NDF digestibility was higher ($P < 0.01$) for T4 (45.81%), T6 (47.41%), and T9 (46.19%) compared with T5 (43.86%) and T8 (43.38%). The production of forage blends through intercropping of corn and soybeans has the potential to yield greater quantities of digestible nutrients.

Key Words: corn, silage soybean

0753 Refinement of the *DST* locus associated with bovine respiratory disease complex in Holstein calves.

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Despite best management practices including vaccination and treatment programs, bovine respiratory disease complex (BRDC) continues to be a major cause of morbidity and mortality in cattle. An additional approach to reduce BRDC is to select animals that are less susceptible to respiratory disease. A previous genomewide association analysis identified a 10-kb QTL region on chromosome 23 (BTA23) that included the dystonin (*DST*) gene that plays a major role in herpes virus infections in cattle. The objective of this study was to determine if there were additional variants on BTA23 with a greater association with BRDC that could be used in the selection of cattle with enhanced BRDC resistance. An analysis was conducted using genotypes imputed to whole genome sequence (WGS) for preweaned Holstein calves from California that consisted of 996 controls and 982 cases as defined by the McGuirk health scoring system. Illumina BovineHD genotypes on BTA23 were imputed to WGS using Run 5 data from the 1000 Bull Genomes Project and accuracy was checked by using the WGS of 30 Holstein calves included in the study. Imputation was conducted using Fimpute and errors were corrected by using Beagle 4.1 software. Single nucleotide polymorphisms were filtered for low minor allele frequency (<1%) and low call rate (<90%), resulting in 2,196 biallelic markers being used for analysis in a 1-Mb region surrounding *DST*. Analyses were performed using an allelic model and an additive model with efficient mixed model association expedited (EMMAX) that included age and sex as covariates. A 2.5-kb region including intron 57 (ENSEMBL) of *DST* contained 19 SNP that were associated with BRDC with both allelic ($P = 6.72 \times 10^{-7}$ to $P = 5.07 \times 10^{-5}$) and additive models ($P = 3.82 \times 10^{-6}$ to $P = 6.88 \times 10^{-5}$). Many of the 19 SNP were highly conserved across species, suggesting that they may have a functional or regulatory role in gene expression. These SNP will be used to confirm the BRDC association in independent cattle populations to determine their value for inclusion in a genomic PTA for BRDC. This project was supported by Agriculture and Food Research Initiative Competitive Grant number 2011-68004-30367 from the USDA National Institute of Food and Agriculture.

Key Words: bovine respiratory disease complex, dairy, calves, imputation, loci

0754 Meta-analysis of factors influencing new intramammary infection rate in natural exposure teat dip efficacy trials.

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Teat dips are used to reduce the incidence of new intramammary infection (IMI) on dairies. Although it is widely acknowledged that many factors affect teat dip efficacy and that all teat dips should be confirmed efficacious before commercial circulation, the studies evaluating teat dip efficacy differ in experimental design, pathogen profiles at the herd level, and teat dips tested, among other factors. The objective of the present study was to conduct a meta-analysis of data from peer-reviewed teat dip efficacy trials that used a natural exposure study design to identify factors influencing the new IMI rate. A data set of 16 studies (256 observations) was created, and the new IMI rate, based on percentage of new quarter infections per month (PNQI/mo), was calculated for each observation in the data set. The new IMI rate (PNQI/mo) was used as the dependent variable for model derivation. A linear, mixed-effects model with a random study effect, weighted for the SE of the measurement, was derived in a stepwise manner where parameters were sequentially eliminated for nonsignificance. The final mixed model included the terms of study design ($n = 2$, $P = 0.03$), mastitis pathogen group ($n = 6$, $P < 0.01$), postmilking treatment ($n = 6$, $P = 0.06$), and the two-way interaction between mastitis pathogen group and postmilking treatment ($P < 0.01$). Overall, *Corynebacterium* spp. had the highest new IMI rate, 0.0139 ± 0.0018 PNQI/mo, which was greater than that of the environmental streptococci and Gram-negative species, 0.0023 ± 0.0022 PNQI/mo, both having the lowest new IMI rate ($P < 0.05$). The new IMI rates for *Staphylococcus aureus*, *Streptococcus agalactiae*, and the coagulase negative staphylococci were 0.0046 ± 0.0017, 0.0054 ± 0.0043, and 0.0094 ± 0.0017 PNQI/mo, respectively. The new IMI rate of mastitis pathogen groups was influenced by different postmilking treatments ($P < 0.01$). Studies using a split herd study design had a greater new IMI rate, 0.0089 ± 0.0017 PNQI/mo, than studies using a split udder study design, 0.0046 ± 0.0017 PNQI/mo ($P = 0.03$). The results of this study indicate that mastitis pathogens vary in sensitivity to different postmilking teat dips and suggest that changing the postmilking teat dip used at the farm to a teat dip containing a different active ingredient may increase efficacy against specific pathogens.

Key Words: teat disinfectant, study design, mastitis

0755 Diet starch content and fermentability affects feed intake and milk yield of cows in the postpartum period.

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The objective of this study was to evaluate the effects of diet starch content and fermentability fed during the postpartum (PP) period on DMI, yields of milk (MY) and milk components, and body reserves. Fifty-two multiparous Holstein cows were used in a randomized block design with a 2 × 2 factorial arrangement of treatments. Diets were formulated to 22 (LS) or 28% (HS) starch with dry ground corn (DGC) or high-moisture corn (HMC) as the primary starch source. Treatments were fed from 1 to 23 d PP and then switched to a common diet until 72 d PP to measure carryover (CO) effects. Treatment period (TP) diets were formulated for 22% forage NDF and 17% CP, and starch concentration was adjusted by substitution of corn grain for soyhulls. The diet for the CO period was formulated to 20% forage NDF, 17% CP, and 30% starch. Throughout the experiment, both DMI and MY were measured daily, and milk components, BCS, and back fat thickness (BFT) were measured weekly. During TP, DGC increased DMI by 2.2 kg/d compared with HMC ($P < 0.01$) but tended to increase DMI more with HS (3.4 kg/d) than with LS (1 kg/d; interaction, $P = 0.12$). Treatments also interacted over time; DGC increased DMI throughout the TP for HS but only after the first week for LS compared with the HMC treatments ($P < 0.01$). There was no main effect of starch content on DMI. The effect of corn source diminished over time during the CO period ($P = 0.03$) with no main effects of treatment on DMI. Dry ground corn increased yields of milk by 2.6 kg/d ($P = 0.12$), 3.5% fat-corrected milk (FCM) by 4.3 kg/d ($P = 0.02$), fat by 165 g/d ($P = 0.03$), and protein by 165 g/d ($P = 0.01$) compared with HMC with no effect of starch content throughout the TP. Starch source and content interacted ($P < 0.05$) to affect yields of fat and FCM during the CO period, which were greater for DGC-HS and HMC-LS (1.78 and 52.1 kg/d, respectively) than for DGC-LS and HMC-HS (1.62 and 48.6 kg/d, respectively). Dry ground corn tended to decrease BCS loss until the third week of TP ($P < 0.15$) compared with HMC but had no effect overall. No effects of treatment were detected for BFT during TP but HMC increased BFT 0.1 mm ($P = 0.04$) during the CO period. Ruminal fermentability of starch is an important consideration for diets of cows in the PP period.

Key Words: high-moisture corn, dry corn, fresh cows

0756 Meta-analysis of postruminal microbial nitrogen flows in dairy cattle.

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The objective of this study was to summarize the literature and derive equations that relate the chemical composition of diet and rumen characteristics to the intestinal supply of microbial nitrogen (MicN; g/d), efficiency of microbial protein synthesis (EMPS; g MicN/kg OM truly degraded in the rumen), and flow of nonammonia nonmicrobial N (NANMN; g/d). In this study, 619 weighted treatment means were screened from 183 studies using dairy cattle that were sampled from the duodenum or omasum (sample location [SMPLoc]). Backward elimination multiple regression was used to derive equations to estimate flow of nitrogenous components over a large range of dietary nutrients (% of DM) or ruminal pH, NH_3–N (mg/dL), or individual branched-chain VFA (BCVFA; mol/100 mol). An intercept shift indicated greater MicN flow for omasal sampling relative to duodenal sampling in all MicN models, but sample location did not interact with any other variables tested. Microbial nitrogen was associated with DMI and dietary starch percentage: MicN = −18.4 g/d + 109 g/d more (if SMPLoc = omasal) + 10.8(DMI) + 5.31(starch) − 0.0839(starch × starch). Ruminal pH and NH_3–N were negatively related to MicN flow, with a positive association with ruminal isovalerate. The EMPS = 4.71(isovalerate) + 0.260(NH_3–N) − 0.257(NH_3–N × isovalerate). A similar equation with a parallel role for isobutyrate confirms the importance of BCVFA to increase growth rate and, therefore, assimilation of NH_3–N into microbial protein. The flow of NANMN = −37.5 (if SMPLoc = omasal) + 8.70(DMI) + 9.98(NDF) −1.42(NDF×NDF) + 6.08(CP). Because NANMN is calculated by subtracting MicN, omasal sampling underestimated NANMN relative to duodenal sampling. This equation is probably associated with neutral detergent isoluble N contamination of NDF in certain rumen-undegradable protein sources. As in the MicN equation, sampling location did not interact with any other variables tested for NANMN. Equations derived from dietary nutrient composition are robust across dietary conditions and could be used for prediction in protein supply-requirement models.

Key Words: nitrogen, microbial, flow

0757 Milk yield genotype affects hepatic expression of innate immune genes when challenged with lipopolysaccharide.

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Objectives were to determine effects of milk yield genotype on hepatic expression of genes related to innate immune response during a lipopolysaccharide (LPS) challenge. Multiparous cows (*n* = 12/genotype) from unselected (stable milk yield since 1964; UH) and contemporary (CH) Holsteins that differed by more than 4,500 kg milk/305 d were housed together and fed the same diet ad lib for more than 4 mo before being blocked (2/genotype) by DIM and randomly assigned within genotype to receive saline or 0.25 μg/kg BW of LPS (*Escherichia coli* 055:B5). Cows were synchronized to be at Day 8 of their estrous cycle for the first challenge (C1) at 70 to 84 DIM. Liver biopsies were collected at 0, 4, and 24 h relative to treatment. Acute innate immune responses were assessed in C1. A second identical challenge (C2) and sampling was conducted 4 d later to assess the impact of a repeated challenge. Expression of 44 genes associated with immunity was determined by digital multiplexed analysis (nanoString nCounter). Expression was normalized to the positive control and the geometric mean of 4 internal control genes. Data were transformed (square root) and analyzed by repeated measures using PROC MIXED (SAS) with time as the repeated effect. Means differed when $P < 0.05$. There were time × treatment interactions for 37 genes due to changes in expression after LPS. At 4 h, LPS increased expression of 15 genes and reduced expression of FASLG in UH relative to CH. The 15 genes included TLR4, CD14, ICAM-1, IRF-1, MYD88, IL-6, and TNF. During C2, expression of these genes was less than in C1 and was not affected by genotype. There was a genotype × treatment × challenge interaction for CCL20 as its expression at 4 h in C2 was greater in CH than UH. IL-10 increased at 4 h for both genotypes, but expression during C2 was less than during C1. TGFB1 increased more in UH than CH at 4 h in both challenges. During the acute phase (C1), UH cows had a more robust expression of genes related with immune cell activation, cytokine production, and chemoattractant production and activation than CH. Responses during C2 were diminished in both genotypes, which indicates that compensatory mechanisms invoked by C1 were still affecting the response to LPS. Results indicate milk yield genotype impacts the response to LPS and contributes to a less robust response in the contemporary cow.

Key Words: gene expression, immunity, bovine genotype, lipopolysaccharide

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0758 Effects of feeding different forms of polyunsaturated fatty acids on performance, plasma metabolites, and milk fatty acid composition of dairy cows.

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Objectives were to determine the effects of feeding different types of PUFA on performance and yield of fatty acids in Holstein cows. Eight ruminally cannulated primiparous cows were randomly assigned to a replicated 4 × 4 Latin square design

(28 d; 19 d adaptation, 7 d collection, and 2 d rumen evacuation). Diets were identical except for the type of fatty acid supplements that were incorporated at 2.1% of dietary DM. Supplements were Ca salts (CaS) of palm oil (CaSP), oil (O; a blend of 45% palm and 55% soybean oils), CaS of O in a granular form (CaSOG), and CaS of O in a pelleted form (CaSOP). Intake and yield and composition of milk were averaged from d 20 to 26. The fatty acid profile of milk fat was analyzed in samples collected from d 24 to 26. Blood was sampled at 0, 3, 6, 9, and 12 h relative to feeding on d 26 and analyzed for hormones and metabolites. Ruminal pH was measured for 72 h in each period. Data were analyzed by ANOVA with the MIXED procedure of SAS for a replicated 4 × 4 Latin square. Results of cow performance are presented in Table 1. Results in the text are presented in the following sequence: CaSP, O, CaSOG, and CaSOP. Feeding O increased ($P \leq 0.05$) rumen fluid pH compared with CaSP or CaSOG (6.22, 6.31, 6.20, and 6.26 ± 0.07). Plasma concentration of glucose increased ($P \leq 0.05$) in O compared with CaSP and CaSOG and tended ($P = 0.08$) to be greater than CaSOP (64.8, 66.3, 64.7, and 64.9 ± 0.55 mg/dL). Glucagon concentration in plasma tended ($P = 0.06$) to be greater in CaSP compared with CaSOP (156.4, 152.6, 149.4, and 144.8 ± 8.0 pg/mL). There were no treatment effects on plasma insulin, NEFA, and urea N concentrations. Milk linoleic (3.29, 3.22, 4.88, and 4.71 ± 0.16 g/100 g of fatty acid) and linolenic acids (0.43, 0.46, 0.61, and 0.53 ± 0.02) and total *n*-3 (0.46, 0.48, 0.64, and 0.56 ± 0.02) and *n*-6 fatty acid yields (3.78, 3.64, 5.37, and 5.19 ± 0.17) increased ($P < 0.01$) in cows fed CaSOG and CaSOP compared with cows fed CaSP or O. Conjugated linoleic acids *trans*-10 *cis*-12 and *trans*-9 *cis*-11 were reduced ($P < 0.01$) in cows fed CaSP compared with cows fed other treatments (0.004, 0.013, 0.019, and 0.019 ± 0.003). Source of fatty acids did not affect DMI or milk yield, but feeding O as CaS in a pelleted form improved milk fat content. Feeding CaS of O either as granular or pelleted increased content of PUFA in milk fat.

Key Words: fatty acid, rumen biohydrogenation, performance

Table 0758.

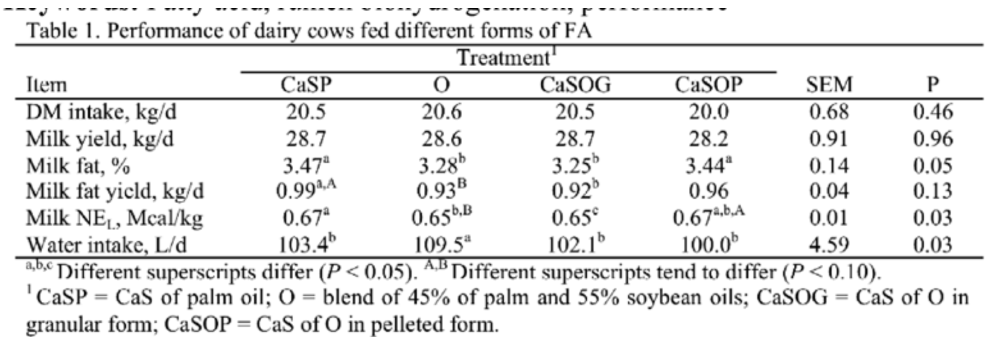

Table 1. Performance of dairy cows fed different forms of FA

Item	Treatment[1]				SEM	P
	CaSP	O	CaSOG	CaSOP		
DM intake, kg/d	20.5	20.6	20.5	20.0	0.68	0.46
Milk yield, kg/d	28.7	28.6	28.7	28.2	0.91	0.96
Milk fat, %	3.47^{a}	3.28^{b}	3.25^{b}	3.44^{a}	0.14	0.05
Milk fat yield, kg/d	$0.99^{a,A}$	0.93^{B}	0.92^{b}	0.96	0.04	0.13
Milk NE_L, Mcal/kg	0.67^{a}	$0.65^{b,B}$	0.65^{c}	$0.67^{a,b,A}$	0.01	0.03
Water intake, L/d	103.4^{b}	109.5^{a}	102.1^{b}	100.0^{b}	4.59	0.03

^{a,b,c} Different superscripts differ ($P < 0.05$). ^{A,B} Different superscripts tend to differ ($P < 0.10$).

[1] CaSP = CaS of palm oil; O = blend of 45% of palm and 55% soybean oils; CaSOG = CaS of O in granular form; CaSOP = CaS of O in pelleted form.

0759 Rumen-protected methyl donors during the transition period: Circulating plasma amino acids in response to supplemental rumen-protected methionine or choline.

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The objective of this study was to profile plasma AA and downstream products of their metabolism during the peripartal period in response to supplemental rumen-protected methionine (MET) and choline (CHO). Forty multiparous Holstein cows were used in a randomized complete block design with 2 × 2 factorial arrangement of MET and CHO level (with or without). Treatments were control (CON), no MET or CHO; CON+MET (SMA); CON+CHO (REA); and CON+MET+CHO (MIX). From −21 (close-up) to 30 d after calving, cows received the same diet (1.52 Mcal NE_L/kg DM) from close-up to calving. From calving to 30 d, cows were on the same diet (1.71 Mcal NE_L/kg DM) and continued to receive the same treatments through 30 d. MET supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow per day. Blood samples were taken at −30, −10, 4, 14, and 28 d relative to calving. Data were analyzed as a factorial design with repeated measures using PROC MIXED in SAS. Previous results from this experiment revealed that both pre- and postpartum DMI was greater with MET ($P = 0.01$) but did not change with CHO ($P > 0.05$). As expected, MET supplementation led to greater ($P < 0.01$) plasma methionine concentration compared with other treatments. Similarly, sulfur-containing AA derivatives (homocystine, cystathionine, and cystine) and taurine (an antioxidant) also were greater in MET-supplemented cows, suggesting an enriched sulfur pool. In addition to plasma methionine concentration, lysine ($P = 0.01$), arginine ($P = 0.02$), tryptophan ($P < 0.01$), and threonine ($P = 0.07$) also were greater in MET-supplemented cows, all of which contributed to the strong tendency ($P = 0.06$) for greater essential AA (EAA) in response to MET. An overall greater ($P = 0.02$) total plasma AA concentration was observed in MET cows due to greater ($P < 0.05$) proline, asparagine, alanine, and citrulline compared with other treatments. In contrast, CHO supplementation had no effect ($P > 0.05$) on overall EAA and total AA, as only tryptophan ($P = 0.02$) and cystine ($P < 0.01$) were greater with this treatment. Plasma concentration of 3-methyl-histidine was lower ($P < 0.05$) in response to CHO, suggesting less protein mobilization in these cows. Overall, data from the present study indicate that peripartal supplementation of rumen protected methionine has positive effects on plasma AA status.

Key Words: amino acid, choline, methionine, transition cow

ADSA–SOUTHERN SECTION GRADUATE STUDENT ORAL COMPETITION

0760 The nutritional quality of winter crops for silage in monoculture or with legumes.

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The objectives of this study were to determine the nutritional quality of different winter crops for silage within various regions of Virginia and to determine the impact of the various winter crops on the succeeding productivity of corn and sorghum. Experimental plots were planted with 15 different winter crop treatments at 3 locations in Virginia. At each site, 4 plots of each treatment were planted in a randomized complete block design. The 15 treatments included 5 winter annual grasses (barley, wheat, rye, ryegrass, and triticale) in monoculture [NO] or with one of two winter annual legumes (crimson clover [CC] and hairy vetch [VE]). The nutritional composition (DM, ash, CP, NDF, ADF, ADL, starch, and sugars) was determined for the fresh samples. Additionally, 200

Table 0760.

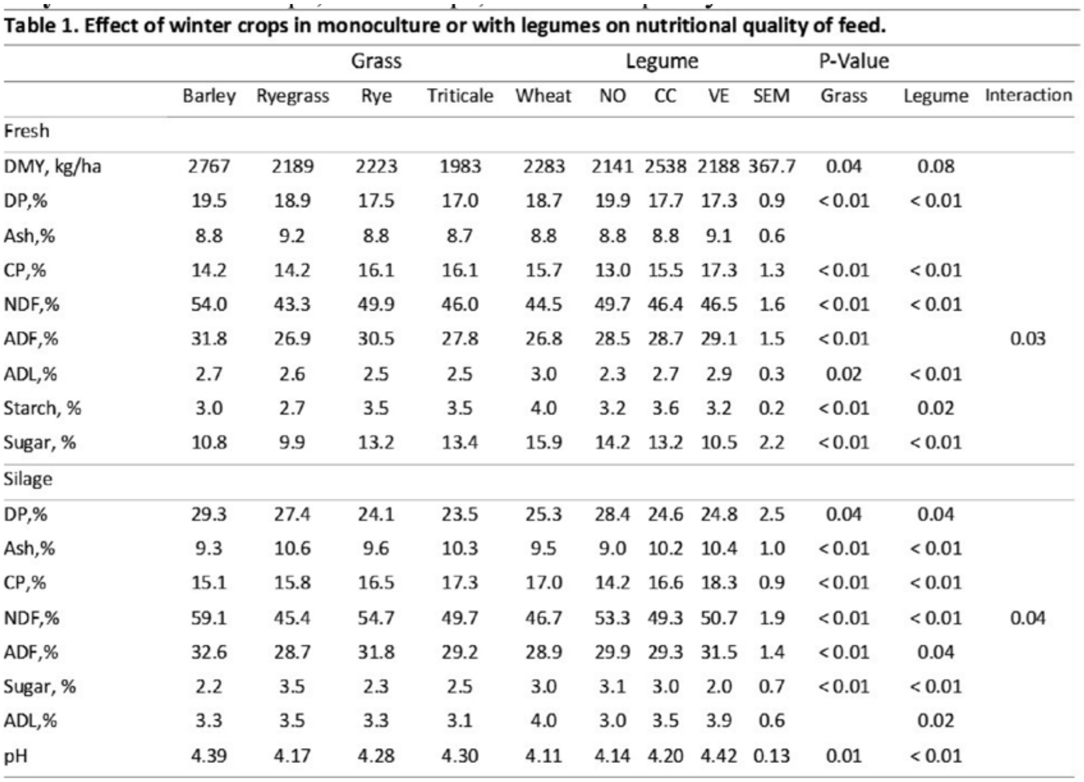

Table 1. Effect of winter crops in monoculture or with legumes on nutritional quality of feed.

	Grass					Legume				P-Value		
	Barley	Ryegrass	Rye	Triticale	Wheat	NO	CC	VE	SEM	Grass	Legume	Interaction
Fresh												
DMY, kg/ha	2767	2189	2223	1983	2283	2141	2538	2188	367.7	0.04	0.08	
DP,%	19.5	18.9	17.5	17.0	18.7	19.9	17.7	17.3	0.9	< 0.01	< 0.01	
Ash,%	8.8	9.2	8.8	8.7	8.8	8.8	8.8	9.1	0.6			
CP,%	14.2	14.2	16.1	16.1	15.7	13.0	15.5	17.3	1.3	< 0.01	< 0.01	
NDF,%	54.0	43.3	49.9	46.0	44.5	49.7	46.4	46.5	1.6	< 0.01	< 0.01	
ADF,%	31.8	26.9	30.5	27.8	26.8	28.5	28.7	29.1	1.5	< 0.01		0.03
ADL,%	2.7	2.6	2.5	2.5	3.0	2.3	2.7	2.9	0.3	0.02	< 0.01	
Starch, %	3.0	2.7	3.5	3.5	4.0	3.2	3.6	3.2	0.2	< 0.01	0.02	
Sugar, %	10.8	9.9	13.2	13.4	15.9	14.2	13.2	10.5	2.2	< 0.01	< 0.01	
Silage												
DP,%	29.3	27.4	24.1	23.5	25.3	28.4	24.6	24.8	2.5	0.04	0.04	
Ash,%	9.3	10.6	9.6	10.3	9.5	9.0	10.2	10.4	1.0	< 0.01	< 0.01	
CP,%	15.1	15.8	16.5	17.3	17.0	14.2	16.6	18.3	0.9	< 0.01	< 0.01	
NDF,%	59.1	45.4	54.7	49.7	46.7	53.3	49.3	50.7	1.9	< 0.01	< 0.01	0.04
ADF,%	32.6	28.7	31.8	29.2	28.9	29.9	29.3	31.5	1.4	< 0.01	0.04	
Sugar, %	2.2	3.5	2.3	2.5	3.0	3.1	3.0	2.0	0.7	< 0.01	< 0.01	
ADL,%	3.3	3.5	3.3	3.1	4.0	3.0	3.5	3.9	0.6		0.02	
pH	4.39	4.17	4.28	4.30	4.11	4.14	4.20	4.42	0.13	0.01	< 0.01	