1149 (M132) Effect of feeding diets with different type of carbohydrates on dry matter intake, rumen fermentation, and productivity of lactating dairy cows. X. Gao*, J. Mewis, and M. Oba, *University of Alberta, Edmonton, Canada.*

The objective of this study was to investigate the effect of feeding different types of carbohydrates on DMI, rumen fermentation, and milk production of lactating dairy cows. Our hypotheses were that both high sugar and high starch diets will decrease rumen pH compared to a basal diet, but a high sugar diet has higher DMI and milk fat yield than a high starch diet. Six ruminally cannulated peak-lactating dairy cows (DIM = 75 ± 12.2; BW = 630 ± 59.2 kg) were used in a replicated 3×3 Latin square design with 21-d periods. Cows were fed diets consisting of 35.5% barley silage and 64.5% concentrate mix on a DM basis. Control diet (CON) contained 27% starch, 4% sugar and 28% NDF, high starch diet (STA) supplemented with additional steam-rolled barley grain contained 32% starch, 4% sugar and 26% NDF, while high sugar diet (SUG) supplemented with sucrose contained 27% starch, 9% sugar and 26% NDF. All diets were formulated to contain 17% crude protein. Although DMI was not different among these three diets, mean rumen pH of STA and SUG diets was lower than CON diet (6.29 and 6.23 vs. 6.38; $P < 0.01$). However, there was no significant difference between STA and SUG diets. In addition, duration of rumen pH < 5.8 was not different between STA and SUG diets, but it tended to be longer for SUG diet than CON diet (117 vs. 30.1 min/d; $P = 0.08$). Concentrations of total VFA and NH_3-N in rumen fluid were not different among the treatments. However, compared with CON, STA and SUG diets had lower acetate proportion (62.0 vs. 59.6 and 59.4 mol / 100 mol; $P = 0.01$), but there was no difference between STA and SUG diets. Although DMI, milk yield, milk component yields and milk fat concentration did not differ among the treatments, concentrations of milk CP (3.14 vs. 3.08 and 2.97%; $P < 0.01$) and MUN (16.2 vs. 13.3 and 14.9 mg/dL; $P < 0.01$) were higher for SUG diet compared with STA and CON diets. These results suggested that feeding high sugar and high starch diets to lactating dairy cows might decrease rumen pH without affecting DMI or milk fat yield, but that high sugar diet may increase milk CP content.

Key Words: sugar, starch, milk production

1150 (M133) Propionate is a dominant inducer of bovine cytosolic phosphoenolpyruvate carboxykinase gene expression. Q. Zhang*, S. L. Koser, and S. S. Donkin, *Purdue University, West Lafayette, IN.*

Expression of cytosolic phosphoenolpyruvate carboxykinase (PCK1) is a critical control point for gluconeogenesis. Indirect evidence suggests that increased feed intake after calving and diet modification that increase rumen propionate production, the primary precursor of gluconeogenesis in ruminants, induces PCK1 mRNA. Our objective was to determine the direct effects of propionate on regulation of bovine PCK1 promoter activity and the relationship to hormones known to modulate glucose metabolism. The full length proximal promoter of bovine PCK1 from -1238 to +221 relative to transcription initiation and nested 5' truncation deletions at -815, -409, -281 and -85 to +221 were ligated to pGL3 Firefly Luciferase Reporter Vector and transfected into rat hepatoma H4IIE cells. The pGL3-Basic (*P*romoterless) and pGL3-Promoter (SV40 promoter driven) vectors served as negative and positive controls for the experiment. Renilla Luciferase Reporter Vector was cotransfected to normalize transfection efficiency. At 5 h after transfection, cells were exposed to either 2.5 mM propionate (PRO), 100 nM insulin (INS), 1 mM 8 Br-cAMP (cAMP), 5 µM dexamethasone (DEX), or the double and multiple combinations of PRO, INS, cAMP and DEX for 23 h. Promoter activity was expressed as the ratio of firefly luciferase to renilla luciferase and data were analyzed using the PROC MIXED of SAS 9.3. All bovine PCK1 promoter constructs were capable of driving firefly luciferase expression. Propionate induced ($P < 0.001$) expression of all PCK1 promoter constructs compared with no treatment control. The induction by propionate was greatest for the -1238 to +221 promoter construct (up to 6-fold) and similar for the other four PCK1 promoter constructs (about 3-fold). Activity of the -1238 to +221 PCK1 promoter was not altered by cAMP and DEX alone but was induced (3-fold) by their combination ($P < 0.01$). Induction of the -1238 to +221 PCK1 promoter construct with cAMP and DEX, was repressed by 24% in response to INS and PRO prevented this effect ($P < 0.0001$). The data demonstrate an inductive effect of propionate on bovine PCK1 promoter activity that is dominant to the repressive effect of insulin. Furthermore, the effect of propionate to induce PCK1 appears to be independent of the actions of cAMP and dexamethasone to also induce bovine PCK1 transcription.

Key Words: cytosolic phosphoenolpyruvate carboxykinase, propionate, hormones

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1151 (M134) Slow-release urea, rumen-protected methionine, and histidine: Effects on expression and activation of the mTOR signaling pathway in skeletal muscle of dairy cows receiving a diet deficient in metabolizable protein. F. Giallongo[*1], H. Sadri[2], A. N. Hristov[1], J. Werner[3], C. Parys[4], B. Saremi[4], H. Sauerwein[2], and C. Lang[5], [1]*Dep. of Animal Science, Pennsylvania State University, University Park,* [2]*Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Germany,* [3]*Animal Resource Program, Pennsylvania State University, University Park,* [4]*Evonik Industries AG, Hanau, Germany,* [5]*Dep. of Cellular and Molecular Physiology, Penn State College of Medicine, Hershey.*

The mammalian target of rapamycin (mTOR) signaling pathway is mediated by two functionally distinct multi-protein complexes, mTORC1 and mTORC2. The mTORC1 is a nutrient sensor, in particular of amino acids, activating protein synthesis by phosphorylation of ribosomal protein S6 kinase (S6K1) and eukaryotic initiation factor 4E-binding protein (4E-BP1). The mTORC2 responds to growth factors but is largely nutrient insensitive and phosphorylates protein kinase B (Akt) on Ser473, resulting in activation of cell growth, and survival. We hypothesized that supplementation of diets deficient in metabolizable protein (MP) with slow-release urea or rumen-protected (RP) Met and His will affect the gene expression of key factors of the mTOR pathway, in particular of mTORC1, and will alter their activation by phosphorylation in skeletal muscle of dairy cows in support of protein synthesis. Sixty Holstein cows were blocked based on DIM and milk yield and within block randomly assigned to 1 of 5 diets in a 10-wk experiment (including the first 2 wk as covariate period): MP-adequate diet (AMP); MP-deficient diet [DMP; 5% below MP requirements (NRC, 2001)]; DMP supplemented with slow-release urea as Optigen (Alltech Inc.; DMPO); DMPO supplemented with RPMet (Mepron; Evonik Industries AG; DMPOM); and DMPOM supplemented with RPHis (Balchem Corp.; DMPOMH). Muscle biopsies were collected from *Longissimus dorsi* during the last wk of the experiment. The mRNA abundance of the following target genes was quantified by qPCR: mTOR, S6K1, and 4E-BP1. Western blotting was used to assess total (t)- and phosphorylated (P)-S6K1 (Thr389), t-Akt and p-Akt (Ser473), p-mTOR (Ser2481), and p-S6 (Ser240/244). Data were analyzed by the PROC MIXED of SAS. The mRNA abundance of the target genes was not affected by the treatments; treatment effects were limited to p-mTOR and p-S6: p-mTOR values in DMPO were decreased when compared against DMP ($P = 0.03$) and also tended to be lower ($P = 0.07$) in DMPOMH than in DMPOM. The p-S6 values in DMPOM tended to be greater ($P = 0.07$) than in DMPO. There was also a trend ($P = 0.09$) for decreased p-S6 in DMPO versus DMPOM and DMPOMH. In conclusion, supplementation of the DMP diet with slow-release

urea, or RPMet and RPHis, respectively, altered the phosphorylation status of mTOR-associated signaling proteins in muscle. No such effects were observed when comparing the AMP and DMP diets, thus indicating specific effects of the supplements.

Key Words: rumen-protected amino acid, mTOR, dairy cow

1152 (M135) Attenuation of the integrated cortisol response following administration of oral firocoxib in preweaned calves prior to cautery disbudding. M. L. Stock[*1], R. Gehring[2], S. T. Millman[1], C. Wang[1], L. W. Wulf[3], L. A. Barth[1], and J. F. Coetzee[3], [1]*Iowa State University, Ames,* [2]*Kansas State University, Manhattan,* [3]*Pharmacology Analytical Support Team, Iowa State University College of Veterinary Medicine, Ames.*

Perioperative analgesic effects of oral firocoxib following cautery disbudding were investigated in preweaned calves. Twenty Holstein calves (55.2 ± 5.8 kg) approximately 35 d old were orally administered firocoxib, a non-steroidal anti-inflammatory prostaglandin blocker, using a dose of 0.5 mg/kg ($n = 10$) or whey protein placebo ($n = 10$) in a randomized clinical trial. All animals received a cornual nerve block using a local anesthetic prior to disbudding. Pain biomarkers including ocular temperature determined by infrared thermography, pressure algometry measuring mechanical nociception threshold, and heart rate were evaluated following cautery disbudding at 2, 4, 7, 8, and 24 hr. Blood samples were collected over 96 hr and analyzed for plasma cortisol and substance P concentrations by radioimmune assay. Additionally, ex-vivo prostaglandin E_2 (PGE_2) concentrations were determined over the same 96-hr study period using an enzyme immunoassay. Data were analyzed using a linear mixed effects model with repeated measures. An attenuation of the integrated cortisol response (mean $\pm$ LSM) as calculated as area under the effect curve was greater in placebo treated calves (1611.1 ± 249 nmol.h/L vs. 1114.2 ± 181 nmol.h/L) ($P = 0.058$). A significant decrease in cortisol concentrations (mean $\pm$ LSM) was observed in firocoxib treated animals at approximately 48 hrs after disbudding (11.3 ± 1.9 nmol/L vs. 22.8 ± 2.8 nmol/L) ($P = 0.0013$). Additionally, a significant inhibition ($P < 0.01$) of ex vivo PGE_2 concentration was observed from 12 to 48 hr following disbudding in calves treated with firocoxib. These data support the potential for firocoxib to be used to provide analgesia after cautery disbudding in calves; however, further investigation of its perioperative analgesic effects is warranted.

Key Words: disbudding, welfare, NSAID

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1153 (M136) Effect of storage temperature on the bacterial growth and pH levels of bovine colostrum.

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Storage of colostrum is a convenient practice that ensures supplies are readily available should they be needed, however storage temperature may affect colostrum quality. The objective of this study was to investigate the effect of storage temperature on bacterial growth and pH levels of colostrum. The study took place at Teagasc Moorepark Research Farm, Cork, Ireland. Colostrum from six Holstein-Friesian cows ([3]rd lactation) was collected from March 5 to 12, 2013, at the first scheduled milking post-calving (<9hr post-calving). Immediately after collection samples were separated into 100-ml aliquots, which were replicated and stored in separate temperature-controlled units at one of three temperatures: 4°C, 13°C and 20°C. Aliquots were removed and frozen at 0, 6, 12, 24, 36, 48, 60 and 72 hr post storage. Consequently, they were defrosted at 4°C to determine total bacterial count (TBC) using serial dilution. Dilution rate ranged from 1:10,000 (lowest expected) to 1:10,000,000 (highest expected). Diluted samples (1ml) were incubated at 32°C for 48 hr on 3M petrifilm aerobic count plates. Subsequent recordings were obtained using a 3M Petrifilm Plate Reader. Duplicate TBCs were prepared and an average was calculated. Simultaneously, aliquots were measured for pH using an OHM Delta 2105.2 datalogger (www.lennox.ie). Calibration was carried out before each test period and the probe was cleaned weekly using product guidelines. Data was tested for normality using PROC UNIVARIATE in SAS (v9.3) displaying positively-skewed data, thus a log transformation was performed. Transformed data was analysed using a mixed model (PROC MIXED; SAS v9.3). The model included treatment, time and their interactions. Significant differences between treatments were seen in TBC once colostrum was stored for [3]12 hours. Storage at 20°C had significantly higher TBC from 12 hours than storage at both 13°C and 4°C ($P < 0.001$), while TBC of colostrum kept at 13°C for $\geq$ 24 hours was significantly greater than colostrum kept at 4°C ($P < 0.001$). Additionally, colostral pH was significantly lower from 24 hr in colostrum kept at 20°C compared to 13°C and 4°C ($P < 0.001$). Furthermore, from hour 60 of storage the pH of colostrum stored at 13°C was significantly lower than that kept at 4°C ($P < 0.01$). Analysis revealed that a LogTBC >7.5 cfu/ml resulted in a pH drop to < 6.5. Further research is warranted to determine if this affects passive transfer of immunity in calves. It is clear however that stored colostrum should be refrigerated ($\leq$ 4°C) to minimise bacterial proliferation and maintain pH.

Key Words: colostrum, storage, bacteria

1154 [Withdrawn]

1155 (M138) The effect of prepartum housing on metabolic and reproductive health in dairy cows.

C. L. Miltenburg[*] and S. J. LeBlanc, University of Guelph, ON, Canada.

The determinants of metabolic and reproductive health disorders and the degree to which housing and management can influence health are only partially understood. The objective of this randomized controlled study was to determine if a prepartum housing strategy of providing non-competitive feeding and lying access improves metabolic health and immune function and reduces reproductive disease. Forty-eight Holstein cows of all parities were randomly assigned to a close up treatment group of 6 to 10 cows in 1 pen with either 80% cows to stalls and 90 cm of feeding space/cow or 120% stocking density and 45cm of feeding space/cow for 3 weeks before expected calving. Pen size and bunk space were adjusted to maintain space per cow as animals were removed for calving. Weekly coccygeal blood samples measured non-esterified fatty acids (NEFA), beta-hydroxybutyrate (BHB), calcium, glucose, albumin, aspartate aminotransferase (AST), bilirubin and haptoglobin from 3 weeks before to 5 weeks after calving. Neutrophil phagocytosis and oxidative burst were assessed at -2, -1, 1, 2, 3 and 5 weeks relative to calving. A modified glucose tolerance test to assess insulin resistance was performed 1 week before calving. Liver biopsies were performed at weeks +1 and +3 to assess liver triglyceride content and gene expression. Vaginoscopy was used to identify cows with purulent discharge (PVD) and uterine and cervical cytobrush samples were collected to assess endometritis and cervicitis as well as uterine gene expression at weeks +3 and +5. There were no interactions of treatment with time. Cows in the crowded treatment had significantly lower mean albumin ($P = 0.05$) and bilirubin ($P = 0.01$) but had greater BHB ($P = 0.01$) and NEFA ($P = 0.05$). At 5 weeks postpartum, 7% of cows had PVD and 33% of cows were diagnosed with endometritis based on > 5% neutrophils. There was no significant effect of treatment on endometritis. Cows that had endometritis at week 5 tended ($P < 0.1$) to have lower average glucose and bilirubin and higher albumin concentrations throughout the study period. These results indicate that metabolic and reproductive health is more complex than can be explained solely by exposure to what is understood to be optimal access to feeding and lying space.

Key Words: endometritis, transition, crowding

1156 (M139) Intake, milk production, ruminal, and feed efficiency responses to DCAD in lactating dairy cows. M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park.*

Previous meta-analyses (Hu and Murphy, 2004, J. Dairy Sci. 87:2222) of the effects of dietary cation anion difference (DCAD) in lactating dairy cow diets utilized studies conducted after the development of the DCAD concept. Dietary buffers such as $NaHCO_3$ and K_2CO_3 increase DCAD and have been used in lactating dairy cow diets for several decades. However, most published studies on buffer feeding were conducted prior to the development of the DCAD concept. Our objective was to determine the intake, milk production, ruminal, and feed efficiency responses to DCAD using previous studies with dietary buffer addition and more recent studies that focused on DCAD as dietary treatments. The database consisted of 44 articles that were published between 1965 and 2011. The studies included 196 dietary treatments, and 89 treatment comparisons that varied in DCAD. For studies that lacked analyses of one or more of the dietary cations (Na, K, or Cl), ion percentages were estimated from ingredient composition using the 2001 Dairy NRC Software. Two basic models were used to evaluate DCAD responses using the NLPROC MIXED in SAS 9.2: 1) A simple linear model: $Y = A + B*(DCAD)$ where A = intercept and B = the increment (slope) in performance per unit DCAD (meq/kg diet DM); and 2) a nonlinear model: $Y = A + M(1-e^{(K \times DCAD)})$ where M = maximal increment in performance from DCAD and K = the rate constant. In both models, study was designated as the random effect. DCAD effects best described by the linear model included milk fat percent, fat yield, rumen pH, NDF digestibility, and FCM/DMI where a 100 meq/kg increase in DCAD resulted in respective increases of 0.10% ($P < 0.001$; RMPSE = 0.01), 35 g/d ($P < 0.001$; RMPSE = 5), 0.033 pH units ($P < 0.001$; RMPSE = 0.001), 1.5% NDF digestibility ($P < 0.001$; RMPSE = 0.4), and 0.0013 FCM/DMI units ($P < 0.001$; RMPSE = 0.005). DMI, milk yield, and 3.5% FCM were best described by the nonlinear model where the maximal responses were 3.05, 2.88, and 6.57 kg/d, respectively ($P < 0.001$). The DCAD concentration at which 80% of the maximal response occurred was 456, 207, and 617 for DM intake, milk yield, and 3.5% FCM, respectively. These results suggest that DCAD has significant effects on intake, milk production and composition, digestion, and feed efficiency in lactating dairy cows.

Key Words: DCAD, meta-analysis, dairy cows

1157 (M140) Hepatic metabolomics and transcriptomics in prepartal dairy cows supplemented with Smartamine M and MetaSmart during the transition period. K. Shahzad*[1], J. S. Osorio[2], D. N. Luchini[3], and J. J. Loor[1], *[1]University of Illinois, Urbana-Champaign, Urbana, [2]University of Illinois, Champaign, [3]Adisseo S.A.S., Alpharetta, GA.*

Supplementation with Smartamine M (SM) and MetaSmart (MS) during the transition period improves postpartal dry matter intake, milk production, and blood neutrophil immune function. In the current study we used metabolomics and transcriptomics to provide a more holistic view of the adaptations induced on the liver by dry period nutrition. Liver from cows fed a control high-energy diet without (OVE) or with SM or MS were used. Metabolomics was performed via LC-MS and GC-MS (Metabolon Inc.) and transcriptomics using a whole-transcriptome bovine microarray (Agilent). From a total of 313 biochemical compounds identified, metabolomics analysis ($P \leq 0.10$) revealed a total of 20, 21, and 48 compounds affected by SM vs. OVE, MS vs. OVE, and SM vs. MS, respectively. Comparing profiles in SM vs. OVE revealed that compounds up-regulated belong to the pentose, sterol, inositol, and purine metabolism pathways, while down-regulated compounds belong to secondary bile acid, arginine and proline, purine and pyrimidine, and eicosanoid metabolism pathways. In MS vs. OVE, the compounds up-regulated belong to primary bile acid, pyrimidine, and lysolipid metabolism, while compounds down-regulated were linked with glycolysis, gluconeogenesis, urea cycle, sphingolipid, and pyruvate metabolism. Liver of MS vs. OVE cows had lower hydroxybutyrate and lactate concentration. The transcriptomic analysis of these groups resulted in 922 (SM vs. OVE), 1,573 (MS vs. OVE) and 1,033 (SM vs. MS) differentially expressed genes (DEG, P £0.05). Bioinformatics analysis using the Dynamic Impact Approach (DIA) that SM vs. OVE resulted in a marked impact and activation of 'fatty acid biosynthesis', 'cyanoamino acid metabolism', 'O-glycan biosynthesis', and 'glycosaminoglycan biosynthesis'. In MS vs. OVE, however, among the top-5 most-impacted pathway there was marked inhibition of 'phenylalanine, tyrosine, and tryptophan biosynthesis' and 'phenylalanine' metabolism. 'Cyanoamino acid metabolism' and 'taurine and hypotaurine' metabolism were highly-impacted and activated pathways in MS vs. OVE. Unique responses in SM vs. MS included a marked activation of 'fatty acid biosynthesis', 'glycosphingolipid metabolism', 'valine, leucine, and isoleucine biosynthesis', and 'sulfur metabolism'. Preliminary data interpretation suggests MS and SM induce distinct changes on the metabolome and transcriptome phenotype of the prepartal liver. The functional relevance of such changes remains to be determined.

Key Words: systems biology, metabolic profiling, bovine liver

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1158 (M141) Detection of subclinical milk fever and ketosis in fresh dairy cows using rumination time, lying time, reticulorumen temperature, and neck activity.

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The objective of this study, conducted at the University of Kentucky Coldstream Dairy, was to evaluate changes in rumination time (RU), lying time (LT), reticulorumen temperature (RT), and neck activity (NA) around subclinical hypocalcemia (SHC) and ketosis (SKET) events. Fresh cows (90 Holstein, 19 crossbred, and 11 Jersey cows) were assigned HR Tags (SCR Engineers Ltd., Netanya, Israel), IceQubes (IceRobotics, Edinburgh, Scotland), and DVM boluses (DVM Systems, LLC., Boulder, CO) $\geq$ 14 days pre-partum. The Milpro P4C (Milkline, Gariga di Podenzano, Italy) system measured milk yield (MY). Blood calcium was measured on 3, 7, and 14 DIM to determine SHC ($\leq$ 1.8 mmol/L). Milk KetoTest (Elanco, Greenfield, IN) and blood Precision Xtra (Abbott Laboratories, Abbott Park, IL) beta-hydroxybuterate tests were analyzed on 3, 7, and 14 DIM to determine SKET (both tests $\geq$ 1.2 mmol/L). Mean RU, LT, RT, NA, and MY were recorded and summarized for each cow day for the first 7 DIM. The GLM Procedure of SAS (Cary, NC) was used to evaluate the relationship between SKET or SHC presence and RU, LT, RT, NA, and MY. LSMeans NA was less in cows with SHC than cows without SHC (210.30 ± 6.40 and 253.81 ± 3.93, respectively, $P < 0.01$). LSMeans RT was less for cows with SHC than cows without SHC (38.58 ± 0.05 and 39.01 ± 0.03 °C, respectively, $P < 0.01$). No difference was observed for RU (316.99 ± 8.35 and 299.90 ± 5.12 min/d for SHC and non- SHC cows respectively, $P = 0.08$), MY (48.57 ± 1.64 and 50.83 ± 1.14 kg/d for SHC and non- SHC cows respectively, $P = 0.26$), or LT (10.66 and 9.97 h/d for SHC and non-SHC cows, respectively, $P = 0.03$). LSMeans LT was greater for cows with SKET than cows without SKET (10.26 and 9.58 h/d, respectively, $P = 0.04$). LSMeans NA was greater for cows without SKET compared with cows with SKET (258.86 and 236.73, respectively, $P < 0.01$). No difference was observed for RT (38.91 ± 0.04 and 38.93 ± 0.04 °C, for SKET and non-SKET cows respectively, $P = 0.72$), RU (307.11 ± 4.88 and 295.84 ± 8.14 min/d, for SKET and non-SKET cows respectively, $P = 0.24$), or MY (51.64 ± 1.09 and 49.03 ± 1.65 kg/d for SKET and non-SKET cows respectively, $P = 0.19$). These parameters may be useful for identifying fresh cow diseases.

Key Words: ketosis, hypocalcemia, fresh cow

1159 (M142) Effects of stage of gestation and feeding regime on intake and apparent total tract digestibility in Holstein × Gyr dairy cows.

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Two experiments were conducted to determine the effects of stage of gestation (SG) and feeding regime (FR) on DMI and apparent total tract digestibility (ATTD) in Holstein × Gyr dairy cows. Exp. 1: 20 multiparous Holstein × Gyr cows with average initial BW of 495 ± 10.4 kg and age 5 ± 0.3 of yr were used in this experiment. Cows were individually fed a corn silage-concentrate based diet (93% and 7% DMB, respectively). In order to allow cows ad libitum access to feed, feed delivery was adjusted to allow approximately 5% orts daily. Dry matter intake was evaluated at 122, 150, 178, 206, 234 and 262 d of gestation. Overall, DMI decreased ($P < 0.05$) as days in gestation increased. The decrease in DMI may be associated with reduction in ruminal volume caused by the rapid increase in fetal size during late gestation. Exp. 2: 44 multiparous Holstein × Gyr cows with average initial BW of 480 ± 10.1 kg and age of 5 ± 0.5 of yr were allocated to 1 of 2 FR. Feeding regimes consisted of: 1) ad libitum intake (ADLIB; $n = 20$) and maintenance intake (MAIN; $n = 24$). Maintenance intake was considered as 1.15% of BW. Cows were individually fed a corn silage-concentrate based diet (93% and 7% DMB, respectively) as a total mixed ration, twice a daily. Apparent total tract digestibility was evaluated every 28 d beginning at 122 d of gestation through day 262 by collecting 24 h fecal excretion for the last 5 d of each 28 d period. Within feeding regime, DM digestibility decreased ($P < 0.05$) as days in gestation increased. An interaction ($P < 0.05$) existed for DMI and OM apparent digestibility between FR and SG on days 150 and 178 of gestation. Cows fed at MAIN had greater ($P < 0.05$) DM and OM apparent digestibility than cows fed ADLIB. However, DM and OM apparent digestibility were similar ($P > 0.05$) for FR at 122, 206, 234 and 262 d of gestation. These data indicate that FR and days in gestation can influence ATTD.

Key Words: dairy cattle, digestibility, pregnancy

1160 (M143) Description of high cow premix recipes in California dairies.

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The objective of this study was to describe high cow premix (HCP) recipes prepared in 13 California dairies ranging in size

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from 1,000 to 6,000 cows. Records from a consecutive twelve month period, starting from Jan-June 2012, were extracted from the feeding management software FeedWatch 7.0. The variables included were: date, drop number, recipe, ingredient, loading sequence, target weight, as-fed weight, tolerance level, and mixer wagon capacity. Descriptive statistics were conducted with SAS 9.3. Throughout the study period, HCP recipes were prepared on farm at least 90% of the days ($n = 3$) or less than 70% of the days ($n = 5$). The median number of HCP recipe prepared per day were one ($n = 5$), two ($n = 7$) or four ($n = 1$). The median number of ingredients included daily in the HCP recipe was four to six ($n = 7$) and seven to nine ($n = 6$). The number of ingredients included in HCP recipe varied over time within dairy in three ($n = 3$), two ($n = 5$), one ($n = 4$) or zero ($n = 1$) ingredients. The most commonly used ingredients in HCP recipes were canola meal ($n = 13$), whole cotton seed ($n = 11$), dry distillers grains ($n = 8$), corn gluten meal ($n = 8$), almond hulls ($n = 6$), wheat middlings ($n = 6$), molasses ($n = 5$) and rolled corn ($n = 5$). Forages were also included in the HCP [straw ($n = 5$), alfalfa hay ($n = 1$)]. Other ingredients used less frequently were slow release non-protein nitrogen ($n = 3$), beet pulp ($n = 2$), rice grain ($n = 2$), cotton meal ($n = 2$), safflower ($n = 2$), whey ($n = 2$), soybean meal ($n = 2$), by-pass fat ($n = 1$), ground wheat ($n = 1$), and soyhulls ($n = 1$). All dairies but one added the mineral-vitamin mix in the HCP. The ingredients most frequently added first were straw ($n = 4$), cotton seed ($n = 3$), canola meal ($n = 3$), almond hulls ($n = 1$), mineral-vitamin mix ($n = 1$) and wheat middlings ($n = 1$). The ingredients added most frequently last were molasses ($n = 5$), whey ($n = 2$), mineral-vitamin mix ($n = 4$), beet pulp ($n = 2$), soybean ($n = 1$) or corn gluten meal ($n = 1$). Ingredients with assigned tolerance level >10% of admissible deviation from target were mineral-vitamin mix, molasses, and straw ($n = 1$) and mineral-vitamin mix ($n = 1$). The frequency of HCP recipes prepared over 10% of the mixer wagon capacity (based on weight) was over 90% in four dairies. There is a large variation in HCP ingredients and preparation across dairies in California.

Key Words: dairy cattle, high cow premix, feeding management software