Ruminant Nutrition: Dairy I

M272 Utilizing dietary nutrients to predict nitrogen efficiency in lactating dairy cattle. N. Swanepoel* and P. H. Robinson, *University of California, Davis.*

Proactive approaches, such as monitoring dietary nutrient profiles, are methods for dairy farmers to improve efficiency of nitrogen (N) utilization (NEF) of their dairy cows and prevent excretion of excess N which can be environmentally harmful. On farm NEF (i.e., milk N/feed N) are often 20–33%, but could theoretically reach 38–40% with optimal nutrition of the total mixed rations (TMR) fed to the cows. Commercial practice suggests that formulating rations to balance essential amino acids (EAA) in metabolizable protein (MP) may further improve NEF. Our objective was to determine if analyzable dietary nutrients of 'high group' lactation TMR could be used to predict NEF, and if AA profiles of MP as predicted by 2 metabolic models (i.e., 'CPM Dairy' & 'Shield') would improve that predictability. Nutrient profiles of 16 commercial dairy cow rations were determined and then model evaluated to estimate AA profiles of MP. Correlation analysis was used to determine the predictability of NEF from single analyte levels in the TMR. The most predictive TMR nutrients were starch (ST; $P = 0.07$), crude protein (CP; $P = 0.07$) and potentially digestible CP (DCP; $P = 0.08$). Soluble CP, fat and neutral detergent fiber were non-predictive (i.e., $P > 0.35$). Multiple correlation analysis of all TMR nutrients resulted in the best fitting model being: NEF (%) = 65.7 – 1.60*(CP, %DM) – 0.48*(ST, %DM) [$r^2 = 0.49$]. That most of the predictive power from CP appeared to be from DCP suggests that it may be the EAA profile of MP that influences NEF. Thus model predicted EAA/MP ratios were added to CP and ST as potential predictors in a stepwise procedure. The final multiple prediction equations differed by model. For 'CPM Dairy': NEF(%) = 49.84 – 1.91*(CP, %DM) – 0.59*(ST, %DM) – 21.90*(Met, %MP) + 13.24*(Ile, %MP) [$r^2 = 0.65$] while for 'SHIELD' no EAA were added to the analyte based model (above). Group milk yields were a poor predictor (i.e., $r^2 = 0.05$) of NEF. This evaluation of commercial dairy rations suggests that analyzable components of TMR only predict a low amount of the variation in NEF of dairy cows but that, dependent upon model, addition of predicted EAA/MP ratios may improve it.

Key Words: amino acid, metabolic model

M273 Effects of water iron concentration, valence and source on drinking water preference of lactating cows. O. N. Genther* and D. K. Beede, *Michigan State University, East Lansing.*

Drinking water can contain high concentrations of Fe, mainly of the ferrous (Fe^{2+}) valence. Current recommended upper tolerable concentration of Fe in drinking water for cattle (0.3 mg/L) comes from guidelines for human palatability, but cattle may be able to tolerate greater concentrations. Our objective was to determine the effects of varying concentrations of ferrous (Fe^{2+}) or ferric (Fe^{3+}) iron and Fe-salt source on lactating Holstein cows' preferences for drinking water offered as choices ad libitum. In 4 separate experiments, cows were offered pairs of water treatments for 22-h periods and water intake and drinking behavior were recorded. Data were analyzed by ANOVA. In Experiment 1 treatments were: 0, 4, or 8 mg of Fe/L from ferrous lactate [$Fe(C_3H_5O_3)_2$]. Cows exhibited no preference between water with 0 or 4 mg Fe/L, but water intake tended to be less with 8 compared with 0 or 4 mg Fe/L ($P < 0.10$). Also, cows spent less time drinking water containing 8 mg Fe/L ($P = 0.01$). Total drinking duration ($r = 0.62$) and frequency ($r = 0.55$) correlated positively with water intake ($P < 0.05$) when pooled across treatments. In Experiment 2, treatments were: 0 or 8 mg Fe/L from either ferrous sulfate ($FeSO_4$) or ferric sulfate [$Fe_2(SO_4)_3$]. Water intake did not differ among treatments. Treatments in Experiment 3 were: 0 or 8 mg Fe/L from either ferrous chloride ($FeCl_2$) or ferric chloride ($FeCl_3$). Again, cows exhibited no preference among the treatments. Treatments in Experiment 4 were: 0 or 8 mg Fe/L from ferrous lactate, sulfate, or chloride. Cows preferred water without added Fe ($P < 0.05$), but did not exhibit a preference among waters containing the Fe sources with different anionic moieties. Total drinking duration and frequency were less ($P < 0.05$) when offered water containing 8 mg of Fe/L from ferrous chloride compared with ferrous lactate or sulfate. Overall, our results indicate that upon first exposure to drinking water, lactating dairy cows tolerate concentrations of Fe up to 4 mg/L without reducing water intake; however, water intake was reduced with 8 mg Fe/L. Preference was not dependent upon Fe valence or Fe source in our studies

Key Words: dairy cattle, drinking water, iron

M274 Effect of cecum starch infusion on hindgut fermentation and inflammatory response in dairy cattle. S. Li,* H. Khazanehei, E. Khafipour, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

To assess the effect of cecum starch infusion (CSI) on hindgut fermentation and inflammatory response, 4 dry Holstein dairy cows (BW = 610.5 ± 42.7kg) were used in a crossover trial with 2 periods. Each period consisted of 23d of adaptation followed by 3 d of CSI. Dietary treatments were: 100% grass hay diet (HF), or 60% grass hay and 40% concentrate diet (CF) that were delivered ad libitum at 0900 h. On the starch infusion days (d 1 to d 3), cows also received a dose of 600g corn starch suspended in 600mL 0.9% saline via the cecal cannula at 0900. On the day before the first starch infusion (d −1) and 3, blood and fecal samples were collected at 0900 and 1500. DMI was monitored daily. Fecal samples were used to measure pH, VFA, ammonia, and lipopolysaccharide (LPS). Inflammatory markers (serum amyloid-A and haptoglobin) concentrations were measured in peripheral blood. DMI was higher in CF than HF animals and tended to be reduced by CSI. Fecal pH was lower in CF than HF group and was reduced by CSI. Total VFA in the feces was higher in CF than HF animals due to greater molar proportion of butyrate but not that of acetate and propionate. Total VFA and molar proportion of propionate increased but acetate decreased on d 1 after CSI but the effects were disappeared by d 3. Ammonia nitrogen concentration in the feces was similar in both CF and HF animals, and only decreased in the CF group due to CSI. Endotoxin concentrations in the fecal water were similar between treatments, and only increased in CF animals following CSI challenge. Inflammatory markers were not affected by treatment and CSI. Results indicate that the increase in the hindgut

LPS concentration following a CSI challenge is greater when the diet contains more concentrate.

Table 1.

	HF diet		CF diet			*P*-value		
Item	Control	CSI	Control	CSI	SEM	CSI	Diet	CSI× Diet
DMI, kg/d	10.7	9.1	12.8	10.0	1.3	0.07	<0.01	0.49
Fecal pH	6.8	6.3	6.4	6.2	0.1	<0.01	<0.01	0.16
Fecal TVFA, mM	32.5	35.9	49.0	47.5	4.1	0.75	<0.01	0.40
Acetate, % TVFA	75.8	72.8	74.5	72.7	1.0	0.01	0.56	0.48
Propionate, % TVFA	15.0	14.4	15.5	13.9	0.5	0.25	0.90	0.12
Butyrate, % TVFA	4.1	7.4	6.5	10.4	0.9	<0.01	<0.01	0.64
Ammonia, mg/dL	8.9	8.2	10.1	7.6	1.0	0.02	0.82	0.01
Fecal LPS, EU/mL	1,654	2,069	2,705	7,495	1,498	0.05	0.02	0.12

Key Words: dairy cows, hindgut, starch infusion

M275 Hepatic triglyceride concentration and fatty acid profile in early lactation Holstein cows fed saturated medium- or long-chain fatty acids. M. Hollmann*[1], T. H. Herdt[2,3], J. A. Zyskowski[3], and D. K. Beede[1], [1]*Department of Animal Science, Michigan State University, East Lansing,* [2]*Department of Large Animal Clinical Sciences, Michigan State University, East Lansing,* [3]*Diagnostic Center for Population and Animal Health, Michigan State University, East Lansing.*

Partitioning of medium-chain fatty acids (FA) in lactating dairy cows is not well understood. We examined hepatic triglyceride concentration ([TG]) and FA profile of early lactation cows fed 2 sources of saturated FA. Dietary treatments were: no added fat (CTRL); 2.7% of DM as saturated long-chain FA (Energy Booster 100; EB); 2.7% as mostly saturated, medium-chain FA (coconut oil; CNO); or, a 2.7% mixture of EB and CNO (1:1; INT). CNO diet had 47 g C12:0/kg and 30 g C14:0/kg. CTRL diet contained 36% NDF (77% from forage), 41% NFC, and 16.5% CP, DM basis. Multiparous (MP; n = 36) and primiparous (PP; n = 31) Holstein cows 10 to 14 DIM were fed 1 of 4 treatments for 16 wk. Hepatic tissue was biopsied before treatment diets were fed, and then on d 14, 28, and 112. Main effects of treatment, biopsy day (repeated measure), and their interaction were tested separately for MP and PP by least-squares ANOVA. Dietary CNO concentration increased hepatic [TG] linearly (CNO > INT > EB; $P < 0.001$). In MP, [TG] decreased linearly from d 14 to d 28 and 112 ($P < 0.001$). In PP [TG] was similar across time ($P > 0.05$). Increasing hepatic [TG] related positively to concentrations of C14:0, C16:0, C16:1, or C18:1 *cis*-9 in total hepatic FA, but negatively to C18:0, C18:2, or FA longer than 18 C ($P < 0.01$). Cows fed CTRL or EB had less than 0.1% C12:0 of total hepatic FA. In contrast, CNO increased hepatic C12:0 to 0.9% (MP) or 0.5% (PP) regardless of day of experiment. Hepatic C14:0 accumulated over time with CNO. MP cows fed EB or CTRL vs. INT or CNO had greater increase in C16:0, C16:1, and C18:1 cis-9 as hepatic [TG] increased (interaction of [TG] by treatment; $P < 0.02$). In MP, CNO decreased C18:0 concentration ($P < 0.01$). Concentration of C18:2 *trans*-10 *cis*-12 in hepatic FA accumulated in CNO and over time, presumably indicative of ruminal biohydrogenation. Dietary CNO increased hepatic [TG] in early lactation cows. Greater hepatic accumulation of C14:0 vs. C12:0 (opposite of dietary concentrations) indicates different physiological partitioning of these FA.

Key Words: fatty acid oxidation, fatty liver, coconut oil

M276 Production and metabolic response of lactating dairy cows to heat stress while supplemented with a dietary antioxidant. A. L. Kenny*[1], Y. M. Wang[2], N. M. Barkley[1], R. R. Rodrigues[1], K. A. Davison[1], G. I. Zanton[2], and M. R. Waldron[1], [1]*University of Missouri, Columbia,* [2]*Novus International Inc., St. Charles, MO.*

The effect of the antioxidant Agrado Ultra [dry blend of ethoxyquin and propyl gallate] on the production and metabolic response of 24 lactating dairy cows to heat stress was investigated. Holstein cows (153 ± 5 d in milk) were blocked by milk production, body condition and lactation and randomly assigned to 1 of 2 treatments: Control (Soy hulls 6.1 g/cow/day; n = 12) or AOX (Agrado Ultra Dry 6.1 g/cow/day; n = 12). Cows were housed in a free stall barn with access to Calan doors from d −2 to 14 of treatment. Cows were then housed in environmentally controlled rooms for 7 d at thermoneutral temperature (d 15 to 21; Constant at 20°C) and then 14 d of programmed 12 h cyclical heat stress (HS; d 22 to 35; Mean THI range of 72.5 ± 0.1 to 81.3 ± 0.5). Cows were returned to free stalls for 7 d of recovery (d 36 to 43). Plasma and milk were sampled 17 times during the experiment. Rectal temperature was measured daily except during HS (3 times/day). Data were analyzed using SAS by mixed model ANOVA with repeated measures. Pretreatment values were used as covariates if found to be significant. Rectal temperature increased ($P < 0.01$) during HS with a tendency for cows fed AOX to have lower rectal temperatures ($P = 0.09$). Plasma glucose concentration was greater ($P = 0.004$) in the AOX group and also responded to HS differently ($P = 0.02$) than controls. Only changes in time, particularly during HS, were observed for BHBA and NEFA ($P < 0.01$). All milk composition variables decreased during HS except for milk urea nitrogen which increased for 4 d of HS before declining to pre-HS levels by the end of study. Control cows had a greater milk fat yield ($P = 0.02$) and AOX cows had a greater percentage of milk protein ($P = 0.001$). Dry matter intake and milk yield decreased ($P < 0.01$) in both groups during HS. Live weight decreased ($P < 0.01$) by 45 ± 5 kg during the time cows were housed in the environmental rooms. Cows fed an antioxidant had a tendency to respond to HS better with lower rectal temperatures and also had greater plasma glucose concentrations and milk protein concentrations.

Key Words: dairy, antioxidant, heat stress

M277 Effect of supplemental fatty acids on production responses and hepatic fatty acid composition and gene expression of dairy cows fed diets containing low concentrations of fatty acids. L. F. Greco*[1], M. Garcia[1], B. L. Artiaga[1], E. K. Ganda[1], R. S. Bisinotto[1], F. S. Lima[1], N. Martinez[1], E. S. Ribeiro[1], A. L. Lock[2], W. W. Thatcher[1], C. R. Staples[1], and J. E. P. Santos[1], [1]*University of Florida, Gainesville,* [2]*Michigan State University, East Lansing.*

Objectives were to evaluate the effects of supplementing diets containing low amounts of long chain fatty acids (FA, < 1.8% DM) with either mostly saturated free FA (SFA, 35% C16:0, and 52% C18:0) or with Ca salts enriched with essential FA (EFA, 27% C18:2 n-6 and 3.5% C18:3 n-3 of the FA) on production responses and hepatic FA composition and global gene expression of Holstein cows. In study 1, prepartum cows were allocated randomly to 1 of 3 dietary treatments from 60 d before to 90 d after calving. Supplementation with FA (% dietary DM) consisted of 0% (CTL, n = 26), 1.7% SFA (n = 25, Energy Booster100), and 1.9% as Ca salts of EFA (EFA, n = 25, Megalac-R). On d 14 postpartum, liver was biopsied and analyzed for FA and global gene expression. Feeding supplemental fat did not affect ($P = 0.35$) the FA content of the liver, but increased ($P = 0.02$) the content of n-6 FA (15.4, 19.0 and 19.3 g/100 g FA, respectively

for CTL, SFA and EFA). Feeding EFA increased ($P < 0.01$) the content of total conjugated linoleic acid and C18:1 *trans* isomers in liver. Feeding fat upregulated genes related to T cell activation, antigen receptor-mediated signaling pathway and activation of immune response. In study 2, 30 cows at 12 DIM were allocated randomly to the same treatments as in study 1. The DMI, BW, and milk yield and composition were recorded daily for 10 wk. Supplementing the diet of cows with fat increased yields of milk and milk components, and the response was greater for EFA than SFA (Table 1). Milk composition and BW were not influenced by dietary treatment.

Table 1.

	Treatment				*P*-value[1]			
Item	CTL	SFA	EFA	SE	TRT	TRT*P	Fat	FA
DMI, kg/d	20.2	21.4	21.4	0.6	0.23	0.42	0.09	0.93
Milk, kg/d	37.6	40.3	43.6	0.8	< 0.001	0.56	< 0.001	<0.01
FCM, kg/d	38.9	41.4	45.4	0.9	< 0.001	0.89	< 0.001	< 0.01
Milk fat, %	3.52	3.54	3.70	0.07	0.17	0.36	0.30	0.14
Milk protein, %	2.88	2.93	2.92	0.03	0.62	0.55	0.34	0.87
Milk lactose, %	4.89	4.92	4.90	0.02	0.45	0.70	0.32	0.41
BW, kg	558.0	566.3	598.4	14.9	0.15	0.22	0.20	0.14

[1]TRT = treatment; TRT*P = treatment by parity interaction; Fat = CTL vs. EFA + SFA; FA = EFA vs. SFA.

Key Words: dairy cow, linoleic acid, gene expression

M278 Effect of lactation stage on milk production and milk quality in dairy cows in confinement. J. A. de Freitas*[1], J. C. de Souza[3], R. P. Lana[2], A. F. G. Neto[1], V. L. Souza[1], and A. L. dos Santos[1], [1]*Federal University of Parana, Palotina, Parana, Brazil,* [2]*Federal University of Viçosa, Viçosa, Minas Gerais, Brazil,* [3]*Federal University of South of Mato Grosso, Aquidauana, Mato grosso do Sul, Brazil.*

Milk is a rich food of high biological quality that presents important substances with anti-carcinogenic action. Some factors can affect the qualitative characteristics and milk production like animal breed, age, stage of lactation, milk production at peak lactation, health and previous nutrition. The study of factors affecting the production and milk quality were very important in economic aspect. The aim of this study was to analyze the influence of lactation stage on production, milk quality, milk production on lactation peak and period of occurrence of peak of lactation. It were used 8700 data from a commercial herd using Holstein cows in the state of Parana, Brazil. The animals were kept under confinement (free stall) during the lactation. The total ration contained 17% of crude protein in DM and the concentrate: silage proportion was 1:1 in DM. The animals were fed and milked 3 times daily. The dependent variables used were: fat correct milk (FCM), milk fat, protein, lactose and total solids (expressed in %), somatic cells count (x1000), milk production (kg), peak of production (kg) and peak occurrence (in days). The dependent variables were submitted to ANOVA using the GLM (Generalized Linear Model) procedure of SAS (2009) and means were compared using a Tukey's test at 5% probability, considering the effect of lactation stage. The percentage of protein, lactose, total solids and peak occurrence did not vary ($P > 0.05$) according to stage of lactation. However, the lactation stage on % of fat, somatic cells count, fat corrected milk and peak of milk production vary ($P < 0.05$) with stage of lactation (Table 1).

Table 1. Percentage of fat, protein, somatic cell counting, total solids (TS) and fat-corrected milk (FCM) as a function of number of lactation for Holstein cows

Lactation stage	Fat (%)	Protein (%)	SCC (x1000)	TS (%)	FCM
1	3.74[a]	3.17[a]	92.27[a]	12.51[a]	8821.08[a]
2	3.62[a]	3.27[a]	135.79[a]	12.64[a]	9692.93[b]
3	3.56[a]	3.16[a]	151.60[a]	12.89[a]	10603.43[b]
4	3.82[b]	3.12[a]	194.96[a]	12.13[a]	8252.35[a]
5	4.19[b]	3.08[a]	232.15[b]	12.07[a]	7379.20[a]

[ab]Values in the same column followed by same letter do not differ statistically at 5% probability by the F test.

Key Words: dairy cows, lactation number, milk quality

M279 Comparison of growth curves between two genetic compositions of dairy goats using nonlinear mixed models. J. G. L. Regadas Filho*[1], M. T. Rodrigues[1], R. A. M. Vieira[2], L. F. Brito[1], and T. S. Oliveira[1], [1]*Universidade Federal de Viçosa, MG, Brazil,* [2]*Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brazil.*

Studies on the growth curves for animals have been used extensively to examine how body mass and others parameters of interest develop over time and in relation to the environment, genotype, diet management and other factors. The goal of this study was to evaluate which nonlinear model normally used in the literature best describes dairy goat growth, and compare the curve parameters obtained for 2 genetic compositions of dairy goats. Data used in this study were collected from the goat flock of the Universidade Federal de Viçosa, MG, Brazil, 12,573 records were used from 2,476 females collected between 1992 and 2010. Two genetic compositions of dairy goats were assessed: predominantly Alpine (+A; n = 1,458; weighings = 7,335) and predominantly Saanen (+S; n = 1,018; weighings = 5,238). The models evaluated were the Brody, Van Bertalanffy, Richards, Logistic, and Gompertz models. Random effects (μ_1, μ_2, and μ_3 were linked to the β_1 (asymptotic value), β_2 (sigmoidal curve shape parameter), and β_3 (rate of maturing) parameters, respectively. We used dummy variables to estimate curve parameters independently for each genetic composition. Residual variance and the Schwartz Information Criteria were used to evaluate the models. After selecting the model that best describes the growth curves and possesses the variance and covariance matrix previously estimated, we were able to test the equality hypotheses all parameters of the growth curve using the Wald statistic. The Brody model (+A: $\beta_1 = 56.54$; $\beta_2 = 0.9324$; $\beta_3 = 0.00258$; and +S: $\beta_1 = 58.84$; $\beta_2 = 0.9383$; $\beta_3 = 0.00244$) with 2 variance component ($\mu_1 = 23.86$ and $\mu_3 = 4.04\text{E-}07$; $P < 0.001$), provided the best fit to the data. A significant difference was detected between the estimated parameters for the 2 genotypes in selected model ($P < 0.001$). Despite the genotypes have the same origin and are often considered similar in terms of productive animals (only visibly different in their coats), differences have been found in their lactation curves, and now, in this study, in their growth parameters. There are differences in the growth patterns between the 2 genetic compositions.

Key Words: Alpine, Saanen, Wald statistic

M280 Nonlinear mixed models fitted to growth curves of dairy goats. J. G. L. Regadas Filho*[1], M. T. Rodrigues[1], R. A. M. Vieira[2], L. F. Brito[1], and T. S. Oliveira[1], [1]*Universidade Federal de Viçosa, MG, Brazil,* [2]*Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brazil.*

Measurements taken on the same experimental unit (animal) are more closely correlated than those taken in other experiment units, as well as measures taken at closer time intervals. These relationships are inherent in animal growth data, which may disrupt the basic assumptions of statistical analysis, such as independence of errors. However, there is still controversy about which growth curve parameters normally used in the literature should be considered as random. This decision should be based on the biological interpretation of the parameters and significance of the estimated variance components. The goal of this study was to evaluate the nonlinear mixed model methodology for fitting the growth curves of dairy goat. Data used in this study were collected from the goat flock of the Universidade Federal de Viçosa, MG, Brazil, were used 12,573 records from 2,476 females. The models evaluated were the Brody, Van Bertalanffy, Richards, Logistic and Gompertz models. Random effects μ_1, μ_2, and μ_3 were linked to the β_1 (asymptotic value), β_2 (sigmoidal curve shape parameter), and β_3 (rate of maturing) parameters, respectively. In addition to the traditional fixed-effects model, we evaluated 4 combinations of random variables: all parameters linked to random effects (μ_1, μ_2, and μ_3), only the β_1 and β_2 parameters (μ_1 and μ_2), only the β_1 and β_3 parameters (μ_1 and μ_3), and only the β_1 parameter (μ_1). Residual variance and the Schwartz Information Criteria were used to evaluate the models. There was reduced residual variance in all scenarios in which random effects were considered. The Brody (μ_1 and μ_3), Van Bertalanffy (μ_1 and μ_3), and Richards (μ_1) models provided the best fit to the data. Interestingly, all 3 models have in common parameters with biologically significance linked to variance component significant ($P \leq 0.01$). A major advantage of using nonlinear mixed model methodology in fitting animal growth curves is the possibility of including population variation measurements in stochastic models to predict animal performance. Growth curves should be fitted using the nonlinear mixed model methodology, linking biologically parameters to random effects.

Key Words: stochastic, parameters, random effect

M281 Increasing doses of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) and changes in milk fat content and secretion of dairy ewes. M. Baldin[1], R. Dresch[1], D. R. M. Alessio[1], J. Souza[2], M. A. S. Gama[3], M. P. Soares[4], and D. E. Oliveira*[1,5], *[1]Centro de Ciências Agroveterinárias, UDESC, Lages, SC, Brazil, [2]Esalq/USP, Piracicaba, SP, Brazil, [3]Embrapa, CNPGL, Juiz de Fora, MG, Brazil, [4]Instituto Federal Catarinense, Araquari, SC, Brazil, [5]Centro de Educação Superior do Oeste, UDESC, Chapecó, SC, Brazil.*

The aim of this study was to examine the relationship between milk fat depression and increasing levels of t10, c12 CLA fed as a rumen unprotected supplement (UnCLA, 29.9% of t10, c12) to dairy ewes. Twenty-three Lacaune ewes, 40 DIM, were used in a completely randomized design. Treatments were fed during a 14-d experimental period: Control (C): 30g of Megalac-E, n = 5; T1: 20g of Megalac-E plus 10g of UnCLA, n = 6; T2: 10g of Megalac-E plus 20g of UnCLA, n = 5 and T3: 30g of UnCLA; n = 7. The treatments provided 0, 2.99, 5.98 and 8.97 g/d of t10, c12 CLA, respectively. Ewes received after a.m. and p.m. milkings an isoproteic concentrate (1.0 kg/ewe/d) in which the fat supplements were added. Ewes were grazing paddocks of a tropical pasture. Milk samples were taken every 2d and on the last day of the experimental period for fat content and FA profile analyses, respectively. The relationships between milk fat and t10, c12 CLA-related variables were tested by linear regression analysis using the REG procedure of SAS, where Y is the variation observed in milk fat content or yield and X is the t10, c12 CLA in the diet or in milk fat. Outliers were removed from the data set. Milk fat content was decreased by 5.2, 14.1 and 26.5% and milk fat yield by 10.9, 17.9 and 26.8% in response to T1, T2 and T3, respectively. Inclusion of CLA linearly increased t10, c12 CLA content (C = 0.03; T1 = 0.10; T2 = 0.19; T3 = 0.30; $r^2 = 0.92$; $P < 0.001$) and t10, c12 CLA secretion (C = 0.03; T1 = 0.06; T2 = 0.12; T3 = 0.15; $r^2 = 0.95$; $P < 0.001$) in milk fat. Overall, estimated regression models (Table 1) show that the magnitude of milk fat depression increased linearly as t10, c12 CLA increased either in the diet or in milk fat.

Table 1. Estimated regression models

Predictors	Change in fat content (%)	Change in fat yield (%)
Dose of t10, c12 CLA (g/d)	$y = 6.97 - 2.87x$[1]	$y = -11.57 - 1.32x$
	$r^2 = 0.69$, n = 21	$r^2 = 0.44$, n = 18
Milk t10, c12 CLA (g/100g FA)	$y = 7.76 - 80.61x$	$y = -7.56 - 60.73x$
	$r^2 = 0.50$, n = 22	$r^2 = 0.84$, n = 14
Milk t10, c12 CLA (g/d)	$y = 7.46 - 143.13x$	$y = -10.11 - 73.05x$
	$r^2 = 0.43$, n = 23	$r^2 = 0.56$, n = 17

[1]All model coefficients were significantly different from zero ($P < 0.001$).

Key Words: CLA, milk fat

M282 Impacts of fat level and source on production of high producing California dairy cows. J. M. Soderstrom*[1], P. H. Robinson[1], and K. Karges[2], *[1]University of California, Davis, [2]POET Nutrition, Sioux Falls, SD.*

Addition of supplemental fat is common in total mixed rations (TMR) fed to high producing dairy cows, but these fats often have different saturations which influences their maximum dietary inclusion level. Unsaturated fats, especially those high in linoleic and linolenic acids, can affect rumen microbial activity leading to altered rumen biohydrogenation intermediates which can inhibit fat synthesis in the mammary gland. Saturated fats are less likely to affect rumen fermentation due to their high rumen stability. We determined if increasing net energy (NE) of a TMR with fat affects productive performance of high producing cows, and if unsaturated fat can be added at the same level as saturated fat without negatively affecting animal performance. The experiment was a 3 × 3 Youden square with 4 28 d periods and it was completed on a dairy farm using 3 high group pens (i.e., cows not yet confirmed pregnant), each with ~340 early lactation multiparity cows. All TMR were formulated with 75% of dry matter (DM) the same, mainly corn grain, wheat and sorghum silages, alfalfa hay, corn grain, canola meal, almond hulls and cottonseed. The other 15% of each TMR was 9% high crude protein (CP) (i.e., fat extracted) distillers dried grains with solubles (HPDDGS) and 6% beet pulp (BP) (diet LOWFAT); 15% DDGS (high fat diet with unsaturated fats: diet UNSAT); 11.1% HPDDGS, 2% BP and 1.9% rumen inert fat (high fat diet with saturated fat: diet RIFAT). The TMR had the same CP (avg. 17.3% DM), but fat levels were 3.8, 4.8, 5.0%. DM intake was highest for UNSAT ($P < 0.05$). Milk, fat and true protein yields, and milk energy output, were higher ($P < 0.01$) for RIFAT vs. UNSAT and LOWFAT. Milk fat % was lowest ($P < 0.01$) for UNSAT, highest for RIFAT and intermediate for LOWFAT. In contrast, true protein % was lowest ($P < 0.01$) for RIFAT. Change in body condition score was lowest for LOWFAT ($P < 0.01$). Whole tract digestibility of neutral detergent fiber did not differ among diets, but CP was higher for UNSAT vs. RIFAT ($P = 0.05$). Production performance and milk fat % were decreased by feeding unsaturated fat to increase diet NE but were increased by feeding rumen stable saturated fat.

Key Words: milk fat, saturated, unsaturated

M283 Meta-analysis: Impact of grain type and corn harvest and processing practices on digestion and lactation performance by dairy cows. L. F. Ferraretto* and R. D. Shaver, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

A meta-analysis was performed to evaluate the effect of cereal grain type and corn grain harvest and processing practices on intake, digestion and milk production by dairy cows using a data set comprised of 414 treatment means from 100 peer-review articles published 2000 - 2011. Categories for cereal grain type, corn processing and mean particle size (MPS) were: barley, corn and wheat; dry ground, cracked or rolled corn (DRY), high-moisture shelled or ear corn (ENS), and steam-flaked or steam-rolled corn (STM); 500–1000, 1000–1500, 1500–2000, 3000–3500 and 3500–4000 µm for DRY and <2000 or ≥2000 µm for ENS. Data were analyzed using Proc Mixed of SAS with treatments as fixed effects and trial as a random effect. Digestibility of dietary starch was lower for corn than barley ruminally, but not ($P = 0.89$) total tract (TT). The TT digestibilities of dietary DM and OM tended ($P = 0.06$ and$P = 0.09$, respectively) to be greater for corn than barley or wheat. Ruminal and TT dietary NDF digestibilities were similar among the grains ($P = 0.92$ and $P = 0.25$, respectively); actual and fat-corrected milk yields and concentrations of milk fat, protein and urea-nitrogen (MUN) did not differ ($P > 0.10$) either. The TT dietary starch digestibility was reduced ($P = 0.01$) and ruminal starch digestibility tended ($P = 0.08$) to be reduced for DRY compared with ENS or STM. Milk yield was 1.0 kg/d greater ($P = 0.01$) and DMI tended to be 1.3 kg/d lower ($P = 0.08$) for ENS than DRY. Milk fat and protein concentrations were greatest ($P = 0.05$) for DRY and STM, respectively. The TT digestibility of dietary DM, OM and starch were reduced ($P = 0.01$) for both DRY and ENS as MPS increased. The MPS, however, did not affect ($P > 0.10$) DMI or actual and fat-corrected milk yields for either DRY or ENS. Milk fat concentration decreased ($P = 0.01$) with decreasing MPS for ENS, but not ($P = 0.28$) DRY. The MUN concentration tended ($P = 0.08$) to increase with increasing MPS for DRY. Corn ensiling and particle size were major factors influencing dietary nutrient digestibilities in lactating dairy cows.

Key Words: dairy cow, meta-analysis, starch

M284 Finding a proxy for the inhibiting effects of polyunsaturated fatty acids on milk fat in dairy cows. G. Maxin*[1], H. Rulquin[1], and F. Glasser[2], [1]*INRA-Agrocampus Ouest, Rennes, France,* [2]*INRA, Theix, Saint-Gènes-Champanelle, France.*

Diets supplemented with plant lipids, high in polyunsaturated fatty acids (PUFA), often induce milk fat depression (MFD) in dairy cows. Several *trans* FA isomers inhibiting milk fat synthesis have been identified, but cannot fully account for diet-induced MFD. There is still debate on which FA isomers and/or other mechanisms are responsible for diet-induced MFD. The experimental approaches meet several limits (availability of pure FA isomers, simultaneous variations in several FA, and modification of rumen metabolism and other nutrients following dietary lipid supplementation), making it almost impossible to identify the FA that are involved in diet-induced MFD. The aim of this study was to identify, using a modeling approach, a proxy of the inhibiting effects of PUFA on milk fat. A database was compiled from published studies of dietary lipid addition in dairy cow diets. It included 38 responses to lipid addition (differences between a lipid-supplemented diet and a control). From diet composition and intake, using published empirical equations, we predicted the changes in nutrient flows (VFA, glucose and proteins) following lipid addition. Then, the milk fat responses to these changes in nutrient flows were predicted using another set of published empirical equations. We thus got a prediction of the milk fat changes induced by the nutrients other than FA. The prediction bias was computed for each response by difference between this prediction and the response of milk fat reported in the publications, and was assumed to be caused by the inhibiting FA. To identify proxies of the inhibiting effect of PUFA, several variables linked to lipid addition (FA intake, duodenal flows of various FA) were regressed on this bias using GLM model. The 2 best proxies (best regressors on the prediction biases of both milk fat yield and content, based on R^2 and RMSE) were the intake of 18:2+18:3 and the duodenal flow of 18:2. These results have to be confirmed on a larger database, but this modeling approach seems to be a good alternative to complement experimental studies of milk fat inhibition by dietary PUFA, and overcome some of their limits.

Key Words: dairy cow, milk fat, lipids