

Ruminant Nutrition: Dairy: Rumen Metabolism

739 Effects of lauric and myristic acids on ruminal fermentation, production, and milk fatty acid composition in lactating dairy cows. A. N. Hristov*¹, C. Lee¹, T. Cassidy¹, M. Long¹, K. Heyler¹, and B. Corl², ¹Pennsylvania State University, University Park, ²Virginia Tech, Blacksburg.

The objective of this experiment was to investigate the effects of lauric and myristic acids on ruminal fermentation, production, and milk fatty acid (FA) profile in lactating dairy cows. The experiment was conducted as a replicated 3 × 3 Latin square. Six ruminally-cannulated cows (95 ± 26.4 DIM), were subjected to the following treatments: 240 g/cow/d of each, stearic (SA, control), lauric (LA), or myristic (MA) acids. The basal diet contained (DM basis) 15.2% CP and 33.9% NDF. Experimental periods were 28 d and cows were refaunated between periods. LA reduced ($P < 0.001$) protozoal counts in the rumen by 96% (no effect of MA), acetate, total VFA, and ammonia concentrations, and microbial N outflow from the rumen (by 32%; $P = 0.002$), compared with SA. Ruminal methane production was not affected by treatment. DMI was severely depressed ($P < 0.001$) by LA (18.6) compared with SA (26.7) and MA (24.7 kg/d), which decreased ($P = 0.017$) milk yield (35.8 and 43.6 kg/d, LA and SA, respectively). Feed efficiency, however, was the highest ($P = 0.008$) for LA (1.91), followed by MA (1.81), and SA (1.63 kg/kg). Milk fat content was also severely depressed ($P = 0.021$) by LA (2.59) compared with SA (3.42%). Treatment had no effect on milk protein content. Milk N efficiency was greater ($P = 0.022$) for LA (34.9) than SA (30.6%). Concentration of milk FA < C16 was 20% lower ($P = 0.011$) for LA than MA. Concentration of C12:0 was more than doubled ($P < 0.001$) by LA and C14:0 was increased by MA (by 45%; $P < 0.001$), compared with SA. LA resulted in lower ($P = 0.027$) C16, but greater ($P = 0.014$) long-chain FA, compared with SA and MA. Concentrations of trans C18:1 and *cis*-9, *trans*-11 CLA were doubled ($P < 0.01$) by LA compared with SA and MA. In conclusion, LA had profound effects on ruminal fermentation, mediated through inhibited microbial populations, and decreased DMI, milk yield, and milk fat content. Both LA and MA modified significantly milk FA profile.

Key Words: lauric acid, myristic acid, dairy cow

740 Time course of recovery from diet induced milk fat depression in dairy cows. D. E. Rico* and K. J. Harvatine, *The Pennsylvania State University, University Park.*

Nine ruminally cannulated cows were randomly assigned to treatment sequence in a Latin Square designed for analysis of recovery from diet-induced milk fat depression (dMFD). A control diet with 32% NDF was fed during the Control and Recovery periods. A low fiber and high oil diet containing 27% NDF and 3.0% soybean oil was fed during the diet-induced MFD period (dMFD). Treatment periods were 21 d in length. Milk yield and DMI were measured daily. Milk samples were taken every other day and milk was analyzed for fat and true protein. Data was analyzed using the repeated measures statement of Proc Mixed (SAS Institute); the model included period, sequence, and cow nested in sequence as random effects, and treatment, day on diet and the interaction of treatment and day on diet as fixed effects. Day was the repeated variable and the heterogeneous autoregressive covariance structure was used. Denominator degrees of freedom were adjusted by the Kenward Rogers method. DMI progressively decreased when cows were switched to dMFD and was significantly different from control after d 6 ($P < 0.05$). Intake recovered after d 15 of the recovery period. Milk yield was not affected by treatment and averaged 32.5 ± 2.1 kg.

Milk fat percent and yield decreased progressively from d 1 when fed the MFD diet and were significant by d 3 ($P < 0.05$) and 7, respectively ($P < 0.05$). After switched to the recovery diet, milk fat concentration and yield progressively increased from d 1 and were the same as control on d 19 and 11, respectively. Milk protein percent increased progressively when cows were on the MFD diet and was significantly different from control after d 11 ($P < 0.001$ from d 11 to 21), reaching a plateau on d 13. Milk protein percent was 6% higher on average for dMFD vs. control cows between d 11 and 21. Milk protein yield was not affected by treatment. Our data shows that recovery from diet induced milk fat depression occurs progressively with a very short lag when dietary NDF and polyunsaturated fatty acid concentration are corrected.

Key Words: milk fat depression, dairy cows

741 Meta-analysis to calculate volatile fatty acid production in the rumen of cattle. D. Sauvant*¹ and P. Nozière², ¹AGROPARISTECH-INRA MoSAR, Paris, France, ²INRA-URH, 63122 St Genes Champanelle, France.

The estimation of the production of volatile fatty acids (VFA) in the rumen remains a limit for diet evaluation and formulation. To progress on this topic, a meta-analysis of published data where apparently digestible organic matter in the rumen (ADOMr) and VFA profiles were documented was performed. A database was compiled from 237(nexp) experiments (599 treatments, tr), 59% being conducted on lactating cows. Most were focused on the effects of dietary protein (32%), starch (23%), NDF (18%), or particle size (11%). There were large variations of dry matter intake (2.7 ± 0.8% LW), dietary NDF (37.4 ± 12.0% DM) or concentrate (CO, 46.8 ± 22.8% DM). The OM digestibility in the whole tract (OMDt), and intake of ADOMr were 70.3 ± 6.7% and 10.6 ± 3.7 g/kg LW, respectively. The ADOMr represented 61.6 ± 15.4% of OM digested in the whole tract. The molar percentages were 62.9 ± 5.7 for acetate, 21.4 ± 5.0 for propionate, 11.7 ± 2.0 for butyrate, and 3.8 ± 1.6 for minor VFA. ADOMr being considered as the OM recovered as VFA and gas, it was interpreted as C flows, assuming 37 and 45 mmol of C per g of carbohydrate and protein, respectively. Production of VFA was calculated from C flows and VFA profiles assuming 0.33, 0.0, 0.33, 0.15 mol of C as gas per mol of C as acetate, propionate, butyrate and minor VFA, respectively. The calculated production of VFA was 121.2 ± 42.7 mmol/kg LW, i.e. 7.1 ± 1.8 mmol/g OM digested in the whole tract. The % of C as VFA in C from ADOMr was 74.2 ± 1.5. This ratio increased with the % CO (73.0 + 0.02% CO, R² = 0.82, RMSE = 0.8, nexp=43). For 513 of the tr, the true DOMr (TDOMr) was also measured, and the ratio VFA/TDOMr was 8.3 ± 1.2 mmol/g TDOMr. This is close to the value obtained by other approaches. Thus, Nozière et al. (2010, Animal, in press) obtained a ratio of 8.0 ± 0.6 with a database of VFA production measured in vivo with labeled VFA. In conclusion, it is possible to interpret experimental data on ADOMr and VFA profile to calculate realistic values of production of VFA from ADOMr.

Key Words: volatile fatty acid, rumen, meta-analysis

742 Forage physically effective fiber source alters ruminal pH and site of digestion. M. B. Hall*, *U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI.*

The study objective was to evaluate the effects of physically effective fiber source (peNDF) and starch sources with different rates of fermentation (ST). Thirty-two lactating Holstein cows (8 cannulated) were

used in an incomplete Latin square design with 3 21-d periods. Dietary treatments were inclusion of chopped wheat straw (WS) or ensiled corn stover (ES) to provide 10% of diet DM as NDF, and inclusion of dry ground corn (DC) or high moisture shelled corn (HC) as the starch sources. Diets were formulated to contained similar concentrations of starch, N, and NDF. DMI was not affected by treatment. Time per day spent ruminating did not differ by diet, but time spent eating tended to be greater for cows with DC than for HC. At 2 h post-feeding, ruminal digesta DM% was greater with WS than ES. Rumen digesta DM kg did not differ by treatment. Ruminal digesta liquid kg tended to be greater with DC than HC on ES diets, but HC was greater than DC on WS diets. Ruminal pH was lower with WS than ES. In contrast, fecal pH was lower with ES than with WS. Neither pH was affected by ST. Lower ruminal pH and higher fecal pH with WS suggests that WS retained more feed to be digested in the rumen, whereas the reverse response with ES suggests that this peNDF source allowed more fermentable carbohydrate to pass from the rumen to ferment in the hindgut. Forage peNDF source may affect passage of carbohydrate.

Table 1. Effects of physically effective fiber (peNDF) and starch (ST) sources

	Diets					P-values		
	ESHC	ESDC	WSHC	WSDC	SED	peNDF	ST	Int.
DMI, kg	22.3	22.8	22.7	23.4	0.69	0.38	0.18	0.86
Rumination, min/d	485	474	494	486	15	0.34	0.36	0.89
Eating, min/d	232	240	225	239	11	0.58	0.13	0.73
Digesta, DM%	15.9	15.7	16.3	16.8	0.46	0.04	0.66	0.31
Digesta DM, kg	15.5	16.2	15.9	16.2	1.03	0.77	0.47	0.76
Digesta liquid, kg	81.7	86.4	83.7	80.0	3.5	0.42	0.83	0.12
Rumen pH	6.01	5.97	5.90	5.84	0.10	0.02	0.31	0.71
Fecal pH	6.05	5.95	6.30	6.26	0.07	0.01	0.47	0.55

Key Words: forage, fiber, dairy cattle

743 Evaluation of 2-hydroxy-4-(methylthio) butanoic acid isopropyl ester (HMBi) and methionine (Met) supplementation on digestibility and efficiency of bacterial growth in continuous culture. C. M. Fowler¹, S. K. R. Karnati¹, B. J. Bequette², Z. Yu¹, and J. L. Firkins^{*1}, ¹The Ohio State University, Columbus, ²University of Maryland, College Park.

Assuming that HMBi metabolism is slower than dl-Met in the rumen, we hypothesized that HMBi would provide a more continual supply of Met for direct incorporation into protein or for methyl donating reactions or else spare common intermediates for bacterial synthesis of other AA. Four 50% concentrate:50% crushed alfalfa pellet diets were fed to 4 dual flow fermenters every 8 h (100 g/d). Diets were moderately limited in RDP (7.8% of DM) and CP (14.2%) to ensure that preformed AA would limit bacterial growth. The 4 treatments were 1) control (no infusion), 2) dl-Met (0.097% of DM) or isomolar 3) HMBi or 4) a 50:50 mix of HMBi and dl-Met, which were pulse-dosed 3 times daily with the feedings. On d 9, C-13 labeled HMBi or dl-Met replaced a portion of the unlabeled doses for 6 continuous infusions (over 2 d) to analyze isotopic plateau and elimination kinetics. N-15 was dosed 3 d before and during sampling, and enrichment measured in effluent, bacterial, and ammonia N. Neither NDF nor ADF digestibility were affected, but hemicellulose (NDF-ADF) digestibility and total VFA production were linearly decreased ($P < 0.05$) as HMBi replaced Met. Although flow and efficiency of bacterial N production were not affected, ammonia N concentration and flow linearly decreased ($P < 0.08$) and, conversely,

peptide concentration linearly increased ($P < 0.05$) as HMBi replaced Met. Correspondingly, the bacterial N derived from ammonia increased ($P < 0.05$) with increasing HMBi. Preformed Met was transferred extensively into bacterial Met (25% for Met and 48% for the dl-Met/HMBi mix). The HMBi washout from the fermenters [kp/(kd+kp)] averaged 62%, although there likely would be significant absorption from the rumen. HMBi that did not pass out of the fermenters was readily converted to Met, which accumulated in the free Met pool, with only 5% transfer into bacterial Met. Future research is evaluating if HMBi is converted to d-Met, which would accumulate if mixed bacterial cultures lack sufficient racemase activity.

Key Words: HMBi, methionine, bacterial protein synthesis

744 Ruminal degradability of forages and diets in lactating dairy cows fed a hemicellulose extract. K. J. Herrick^{*1}, M. Abdullah², A. R. Hippen¹, D. S. Schingoethe¹, K. F. Kalscheur¹, and R. S. Patton³, ¹South Dakota State University, Brookings, ²University of Veterinary and Animal Sciences, Lahore, Pakistan, ³Temple Inland, Inc.

Inclusion of hemicellulose extract in cattle diets has shown potential for improving fiber digestibility and production efficiency. The objective of this research was to evaluate production and in situ digestibility effects of a hemicellulose extract (Temple Inland Inc.) on mid-lactation cows. Twelve multiparous Holstein cows (142 ± 44 DIM, 685 ± 19 kg BW) including 4 with ruminal fistula were used in a 2 × 2 Latin square with 21-d periods. Cows were fed a control diet containing 55% forage (DM basis, 2/3 corn silage and 1/3 alfalfa hay) or a similar diet where 1.0% of the diet DM forage was replaced with the extract. Dry matter intake averaged 27.1 and 26.9 kg/d for the control and treatment, respectively, and was not affected by treatment. The percentage of protein (3.40 vs. 3.29) in milk was less ($P = 0.03$) and the percentage of fat (3.91 vs. 3.80) tended ($P = 0.06$) to be less for cows fed the treatment diet. Because of numerically greater milk production (38.8 vs. 39.2 kg) for cows fed the treatment diet, there were no differences in component yields other than lactose (1.86 vs. 1.94 kg/d) which tended to be greater ($P = 0.08$) for cows fed the treatment. For in situ determinations, Dacron bags containing corn silage, alfalfa hay, and either the control or treatment TMR were incubated in triplicate in the rumens of the cannulated cows at 0, 3, 6, 9, 12, 24, and 48 h on d 18 of each period. Each TMR was incubated only in cows assigned to the corresponding diet. For corn silage, the rate of disappearance (K_d) of NDF (1.7 vs. 4.3) and ADF (1.8 vs. 4.7%/h) increased ($P < 0.05$) for cows fed the treatment diet. For alfalfa hay, the disappearance of fraction A of DM, NDF, and ADF decreased and fraction B of DM and NDF increased with treatment ($P < 0.05$). The K_d for DM (8.0 vs. 11.0), NDF (6.3 vs. 10.3), and ADF (5.5 vs. 9.2) increased greatly for the alfalfa hay in rumens of treated cows ($P < 0.05$). Results demonstrated that supplementing diets of lactating dairy cows with a hemicellulose extract had a beneficial effect on fiber degradation characteristics and provide opportunities for improving animal performance.

Key Words: hemicellulose extract

745 Effect of replacing canola meal with wheat-based dried distillers grains with solubles on ruminal fermentation, microbial nitrogen supply and milk production in dairy cows. G. E. Chibisa^{*}, D. A. Christensen, and T. Mutsvangwa, University of Saskatchewan, Saskatoon, Canada.

The objective was to determine the effect of replacing canola meal (CM) with wheat-based dried distillers grains with solubles (WDDGS) on ruminal fermentation characteristics, microbial N supply, and animal

performance. Eight lactating dairy cows were used in a replicated 4 × 4 Latin square design with 28-d periods (20 d of dietary adaptation and 8 d of measurements). Four cows in one Latin square were ruminally cannulated for measurement of ruminal fermentation characteristics and total tract nutrient digestion. Cows were fed either a standard barley silage-based TMR containing CM as the major protein supplement (control) or rations formulated to contain 10, 15 and 20% WDDGS (DM basis). Wheat-based DDGS replaced CM. Inclusion of WDDGS linearly increased DMI ($P < 0.01$; 29.5, 31.2, 30.2 and 31.9 kg/d for 0, 10, 15 and 20% WDDGS diets, respectively; $n = 8$). Ruminal VFA concentrations were unaffected, except that the inclusion of 20% WDDGS resulted in a decrease ($P < 0.01$) and a tendency ($P = 0.09$) for a decrease in molar concentrations of isobutyrate and total VFA, respectively. There were no differences ($P > 0.05$) among treatments for ruminal pH and ammonia concentrations, and apparent total tract nutrient digestibilities. Urinary excretion of purine derivatives (PD) was not different ($P = 0.20$) among diets; consequently, microbial N supply, estimated using urinary PD excretion, was not affected ($P = 0.19$). The addition of WDDGS in place of CM resulted in a quadratic change ($P < 0.01$) in milk yield (42.8, 42.2, 43.6 and 40.5 kg/d for 0, 10, 15 and 20% WDDGS diets, respectively; $n = 8$). There were no differences ($P > 0.05$) among treatments for concentrations and yields of milk fat, protein, and lactose. These data indicate that WDDGS can substitute for CM in dairy cow diets without a negative impact on ruminal fermentation characteristics, microbial N supply and animal performance.

Key Words: wheat-based DDGS, nutrient supply, milk production

746 Shifts in fermentation and intermediates of biohydrogenation induced by potassium supplementation into continuous cultures of mixed ruminal microorganisms. T. C. Jenkins^{*1}, E. Block², and J. H. Harrison³, ¹Clemson University, Clemson, SC, ²Arm and Hammer Animal Nutrition, Princeton, NJ, ³Washington State University, Puyallup.

Recent studies have reported increased fat percentages in milk of lactating dairy cattle when diets were supplemented with potassium carbonate. Because milk fat yield has been associated with ruminal production of certain conjugated linoleic acid (CLA) isomers, this study was conducted to determine if increasing K exposure to ruminal microorganisms alters biohydrogenation and CLA production. Five dual-flow continuous fermenters were fed 60 g/d of a 1:1 forage (10% alfalfa hay and 90% corn silage) to concentrate mix in 2 equal portions at 0800 and 1600 h for 10-d periods ($n = 4$). Three of the 5 fermenters were injected just before each feeding with a 10% (w/w) stock potassium carbonate solution to provide the equivalent of 0.6 (K1), 1.2 (K2), and 1.8 (K3) g K/d. One of the remaining fermenters received no injection (K0) and the last fermenter (pHCON) was injected with adequate NaOH stock solution (10%, w/w) to match the pH observed for the K3 treatment. pH and acetate/propionate in fermenters increased ($P \leq 0.05$) linearly for K0 to K3. pH was the same but acetate/propionate was lower ($P \leq 0.05$) for pHCON compared with K3. Losses of oleic, linoleic, and linolenic acids averaged 216, 872, and 125 mg/d, respectively and were not affected by treatment. Stearic acid production changed ($P = 0.14$) from K0 to K3 (397, 449, 562, and 316 mg/d), but K3 and pHCON (206 mg/d) did not differ. Production of *trans*-10 C18:1 declined ($P \leq 0.05$) and *trans*-11 C18:1 increased ($P \leq 0.05$) linearly from K0 to K3, but pHCON and K3 were the same for both C18:1 isomers. The *cis*-9, *trans*-11 and *trans*-9, *trans*-11 isomers increased ($P \leq 0.05$) linearly from K0 to K3, but K3 and pHCON did not differ. There was a numerical decrease in production of *trans*-10, *cis*-12 from K0 to K3 (11.4, 11.5, 7.9, and 8.5 mg/d), but its production remained high (13.2 mg/d) for

pHCON. The results show that increasing K in the diet has effects on shifting fermentation and biohydrogenation pathways, which can only partially be explained by elevation of pH.

Key Words: potassium, biohydrogenation, rumen

747 Methane production, fermentation patterns and protozoa numbers In Vitro as related to source of rumen fluid and feed as substrate from different cattle feeding systems. M. A. Froetschel*, C. L. Ross, S. Buaphan, S. Chinnasamy, and K. C. Das, *The University of Georgia, Athens.*

Rumen fluid, collected by stomach tube, and samples of diet of beef cattle grazing pasture, lactating dairy cattle fed a total mixed ration, and beef cattle fed a feedlot ration were used to determine the influence of substrate and rumen microbial population on In Vitro methane production and fermentation in a 3x3 factorial designed experiment. A modified Tilley and Terry, procedure was used and fermentation gas was collected in sampling bags with septum valves. Dry matter and gross energy digestion and volatile fatty acids and ammonia production and protozoa counts were measured using standard techniques after 24 h incubations. All parameters were corrected with measurements from rumen fluid blank incubations without substrate. Rumen fluid from feedlot and dairy cattle produced 32.8% more methane volume ($P < 0.01$). Dairy and feedlot substrate produced 60% to 116% more methane volume than grazing substrate ($P < 0.01$). Although rumen fluid source from dairy and feedlot cattle increased moles of methane per digestible energy fermented by 70.5% as compare with that from grazing cattle ($P < 0.05$), methane production per energy fermented was not influenced by substrate. Methane production efficiency was positively related to VFA production ($r = 0.98$, $P < 0.01$) and the molar percentages of propionate and butyrate but negatively related to the molar percentage of acetate ($r = 0.92$, $P < 0.02$). Protozoa counts in rumen fluid from feedlot and dairy cattle were several-fold higher than that from grazing cattle but numbers decreased dramatically in vitro after 24 h. These results imply that the methane production is more related to the level of energy fed than the pattern of rumen fermentation.

Key Words: rumen fermentation, methane, digestible energy

748 Time course of changes in ruminal chemistry and bacterial community composition following exchange of ruminal contents between lactating Holstein cows. P. J. Weimer^{*1,2}, D. M. Stevenson¹, H. C. Mantovani³, and S. Man², ¹USDA-ARS, Madison, WI, ²University of Wisconsin, Madison, ³Universidade Federal de Viçosa, Viçosa, MG, Brazil.

The purpose of this study was to examine the stability and host specificity of a cow's ruminal bacterial community following massive challenge with the ruminal microflora from another cow. In each of 2 experiments, one pair of cows was selected on the basis of differences in ruminal bacterial community composition (BCC), determined by automated ribosomal intergenic spacer analysis, a culture-independent "community fingerprinting" technique. Each pair of cows was then subjected to a one-time exchange of > 95% of ruminal contents without changing the composition of a corn silage/alfalfa haylage-based TMR. In experiment 1, the 2 cows differed ($P < 0.01$) in pre-feed ruminal pH (mean = 6.88 vs. 6.14) and pre-feed total VFA concentration (mean = 57 vs. 77 mM), averaged over 3 d. Following exchange of ruminal contents, ruminal pH and total VFA concentration in both cows returned to their pre-exchange values within 24 h. Ruminal BCC also returned to its original profile, but this change required 14 d for one cow and 61 d for the other cow. In experiment 2, the 2 other cows differed ($P < 0.01$) in pre-feed

ruminal pH (mean = 6.69 vs. 6.20) and total VFA concentration (mean = 101 vs. 136 mM). Following exchange of ruminal contents, the first cow returned to its pre-exchange pH and VFA values within 24 h; the second cow's rumen rapidly stabilized to a higher pre-feed pH (mean = 6.47) and lower pre-feed VFA concentration (mean = 120 mM) that was retained over the 62 d test period. Both cows reached somewhat different BCCs than before the exchange. However, the BCC of both cows remained distinct and were ultimately more similar to that of the pre-exchange BCC than of the donor animal BCC. The data indicate that the host animal can quickly re-establish its characteristic ruminal pH and VFA concentration despite dramatic perturbation of its ruminal microbial community, and that ruminal BCC displays substantial host specificity that can re-establish itself when challenged with a microbial community optimally adapted to ruminal conditions of a different host animal.

Key Words: rumen, ruminal bacterial community

749 Acute phase protein response during acute bovine ruminal acidosis. A. M. Danscher^{*1}, M. B. Thoenner¹, P. M. H. Heegaard², C. T. Ekstroem¹, P. H. Andersen¹, and S. Jacobsen¹, ¹University of Copenhagen, Denmark, ²Technical University of Denmark, Copenhagen, Denmark.

The aim was to describe the acute phase protein response during acute oligofructose-induced ruminal acidosis. Two experiments involved oral oligofructose (OF) overload (17g/kg BW) to non pregnant Danish Holstein heifers. Trial 1 included 12 heifers (8 fed grass hay and 4 barley silage) sampling was done in a 3 d control period before overload (baseline) and 9 d after overload. Trial 2 included OF overload in 10 heifers and 6 control heifers receiving tap water. Blood samples (6–48 h intervals) were analyzed for serum amyloid A (SAA), haptoglobin and fibrinogen. Heifers receiving OF generally developed a profound ruminal and systemic acidosis. In Trial 1, SAA concentrations exceeded baseline on all time points from 6 to 216 h ($P < 0.001$). Heifers fed hay had higher SAA levels (max. 290 ± 151 mg/L) than heifers fed silage (max. 225 ± 137 mg/L, $P < 0.001$). In Trial 2, SAA concentrations in OF heifers were higher than controls on all time points from 6 to 72 h (max. 325 ± 149 mg/L, $P < 0.05$). In Trial 1, haptoglobin concentrations in hay fed heifers exceeded baseline on all time points from 36 to 168 h (max. 3449 ± 1702 mg/L, $P < 0.05$). Heifers fed silage had lower haptoglobin concentrations than heifers fed hay at 60, 72 and 120 h (max. 1802 ± 950 mg/L, $P < 0.05$). In Trial 2, haptoglobin concentrations in OF heifers were higher than controls on all time points from 18 to 72 h (max. 4226 ± 924 mg/L, $P < 0.001$). In Trial 2, fibrinogen concentrations in OF heifers were higher than control heifers at all time points from 36 to 72 h (max. 12.2 ± 3.3 g/L, $P < 0.01$).

Acute ruminal acidosis caused by OF overload resulted in a distinct

acute phase protein response in dairy heifers. The magnitude of the response was dependent on the feeding of the animals before overload. This difference might be due to specific adaptation of the ruminal flora and mucosa to the carbohydrate substrate supplied in the feed. Although the acute phase response is nonspecific, measurement of acute phase proteins may be used to monitor the inflammatory reaction occurring in bovine ruminal and systemic acidosis.

Key Words: ruminal acidosis, acute phase proteins, oligofructose overload

750 Redox potential measurement: A new way to explore ruminal metabolism. C. Julien^{*1}, J. P. Marden², R. Moncoulon¹, and C. Bayourthe¹, ¹Université de Toulouse, INRA, UMR 1289 INRA/INPT/ENVT TANDEM, 31326 Toulouse, France, ²Lesaffre Feed Additives, 59520 Marquette-Lez-Lille, France.

Microbial metabolism is thermodynamically driven by numerous biochemical reactions that can be assessed either by free energy (ΔG) calculation or redox potential (E_h) measurement. Recent studies reported that positive E_h values recorded in a buffered sterile rumen fluid, i.e., deprived of any living organism, revealed oxidative conditions (+270 mV). On the contrary, in vivo E_h values ranged generally between -220 and -110 mV which confirmed that ruminal reducing conditions directly originated from microbial activity. Furthermore, considering that the evolution of pH with time around meal reveals ruminal metabolism, the simultaneous E_h evolution seemed to reflect the varying energetic transfers involved. Therefore, ruminal metabolism could be associated to a redox equilibrium also expressed by means of Clark's exponent (rH) which combines both E_h and pH measurements. Several experiments revealed that E_h and rH equilibrium varied with diet composition in lactating dairy cows. For example, ruminal E_h and rH were significantly different in cows receiving a corn silage-based diet complemented with different degradable protein sources: -166 mV and 6.36 for soybean meal and -147 mV and 7.48 for tanned soybean meal, respectively. To go a step further, live yeast used as ruminant feed additive proved to be a potent modulator of E_h and rH equilibrium in rumen. Recent studies showed that live yeast significantly improved ruminal reducing power in dairy cows fed a high concentrate diet: -115 mV and 8.05 for the control diet and -149 mV and 7.31 for the yeast diet. Even if ruminal E_h is not easy to assess in field conditions, it proved to be an endogenous parameter as meaningful as ruminal pH or fermentative profiles, allowing a different focus on rumen metabolism. It should be considered as a precious and interesting tool for future investigations in ruminant feeding.

Key Words: ruminal redox potential, metabolism, microflora