Table 1. Cow urination frequency and location for the 2x4, 1x8 and control treatments

	2x4[#]	1x8	Control	sed
Urinations/cow/day	13.82	12.73	14.28	6.02
Captured (pad + parlour)	0.35[a]	0.38[a]	0.10[b]	0.07
Uncaptured (pasture + race)	0.65[a]	0.62[a]	0.90[b]	0.07
Pasture	0.45[a]	0.51[a]	0.82[b]	0.06
Bark pad	0.13	0.23		0.08
Race	0.20[a]	0.11[ab]	0.07[b]	0.04
Milking parlour	0.22[a]	0.15[b]	0.10[b]	0.02
Milk urea (ng/mL)	7.76	8.20	7.29	0.61

[#]Different superscripts indicate significantly different means (P<0.05)

Key Words: pasture, urine capture, dairy

Ruminant Nutrition: Dairy 1

116 Production of angiopoietin-like protein 4 in ruminal tissue is decreased with increasing dietary fermentability. L. K. Mamedova*[1], G. B. Penner[2], K. A. Beauchemin[3], M. Oba[2], and B. J. Bradford[1], [1]*Kansas State University, Manhattan*, [2]*University of Alberta, Edmonton*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, Canada*.

Angiopoietin-like protein 4 (ANGPTL4, also known as FIAF) is a secreted protein that functions as a lipoprotein lipase inhibitor and a modulator of angiogenesis. Although it is produced by multiple tissues, gut secretion of ANGPTL4 has been implicated in host/microbe interactions, making the ruminal epithelium a site of interest. Ruminal tissues from 2 studies were used to assess effects of dietary fermentability on ANGPTL4 expression. In the first study, 12 mature, non-lactating, non-gestating Holstein cows were randomly assigned to low-concentrate (8% of dietary DM) or high-concentrate (64% of dietary DM) diets for a minimum of 28 d. Ruminal pH was monitored continuously for 3 d and ruminal fluid samples were collected for VFA analysis, then animals were euthanized and ruminal tissue was collected. In the second study, 8 beef heifers (700 kg final BW) were fed a finishing diet (90% concentrate, DM basis) for 140 d and then either left on the finishing diet or assigned to a backgrounding diet (60% concentrate, DM basis) for another 75 d. Ruminal pH was monitored continuously for 6 d prior to euthanization and ruminal tissue collection. Abundance of ANGPTL4 mRNA was measured by quantitative real-time PCR and protein by Western blotting. Diet effects were analyzed by ANOVA and correlations with rumen parameters were assessed by regression analysis. In the first study, the low-concentrate diet tended to increase ANGPTL4 mRNA by 120% ($P = 0.08$), although no effect on protein abundance was detected. Transcript abundance tended to correlate with mean ruminal pH ($P = 0.07$) and was inversely correlated with total VFA concentration ($P = 0.03$). In the second study, the backgrounding diet increased ANGPTL4 protein abundance ($P < 0.001$), and a positive relationship with ruminal pH was also observed ($P < 0.01$). These findings suggest that increased ruminal fermentation results in decreased expression of ANGPTL4 in ruminal tissue.

Key Words: rumen, epithelium, fermentability

117 Mammary transcriptomics response to milk fat-depressing or milk fat-enhancing diets in lactating dairy cows. G. Invernizzi*[1,2], B. J. Thering[1], D. E. Graugnard[1], P. Piantoni[1], M. A. McGuire[3], G. Savoini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana*, [2]*University of Milan, Milan, Italy*, [3]*University of Idaho, Moscow*.

Gene networks regulating lipid metabolism were studied in mammary tissue biopsied at 0, 7, and 21 d of feeding mid-lactation cows (n = 5-6/diet) a milk fat-depressing (MFD, fish/soybean oil (1:2) at 3.5% of DM) or a milk fat-enhancing (MFE, EnergyBooster100, 3.5% of DM) diet for 28 d. Quantitative PCR was used for transcript profiling of 28 genes. Milk yield was not affected ($P > 0.05$) by diets (29 kg/d), but milk fat % (FP) decreased ($P < 0.05$) gradually (3.7% to ≈2.5%) with MFD and reached a nadir essentially by d 13 of feeding. MFE did not increase FP above controls and averaged 3.7%. MFE increased (interaction effect) genes associated with fatty acid (FA) import into cells (LPL, CD36), FA activation (ACSL1), intracellular transport (FABP3), and triacylglycerol synthesis (GPAM, LPIN1) mRNA at 7 and 21 d; whereas, MFD increased CD36, FABP3, GPAM, and ACSL1 mRNA only by 21 d. In addition, MFE increased mRNA expression of genes associated with fatty acid synthesis (ACSS2, ACACA, FASN) and synthesis of 20:5n3 (FADS1) during the treatment period. SCD abundance increased linearly through 21 d with MFE, whereas feeding MDF resulted in marked increase by 7 d followed by a return to basal expression by 21 d. ACACA was not affected by MFD and FASN increased by 21 d. Genes associated with lipid droplet formation and fat secretion (XDH, ADFP) in mammary tissue increased over time only with MFE. Among transcription regulators, MFE increased SREBF1 and INSIG1 throughout the study. MFD, however, resulted in higher expression of INSIG1 by d 7 and lower SREBF1 by d 21 vs. 0. Stearic, oleic, and palmitic acid molar yield was markedly lower by 7 through 21 d with MFD vs. MFE. Overall gene expression profiles with MFE agreed with production of milk fat and major fatty acids. Data also suggested a role for endogenous synthesis of oleic acid via SCD as well as INSIG1 in milk fat synthesis regulation.

Key Words: genomics, lipid nutrition, fatty acids

118 Mammary glucose metabolism in response to energy and/or protein supply in lactating dairy cows. S. Lemosquet*[1,2], F. Bardey[1,2], H. Rulquin[1,2], H. Lapierre[3], and J. Guinard-Flament[2,1], [1]*INRA, Rennes, France*, [2]*Agrocampus ouest, Rennes, France*, [3]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*.

Milk yield usually increases in response to increased supply of energy (E) and protein (P), alone or in combination, in cows fed under require-

ments. Does this increment occur through a similar mechanism: a higher mammary glucose (GLC) uptake leading to an increased lactose yield? Four multiparous dairy cows received 4 diets providing 70% (LP: 1324 g PDI/d) or 125% (HP: 2247 g PDI/d) of protein requirements and 70% (LE: 22.8 Mcal NE_L /d) or 100% (HE: 30.9 Mcal NE_L /d) of energy requirements, in a Latin Square design with 14-d periods. Requirements (INRA, 1989) were determined based on milk yield predicted at mid experiment using a milk persistency of 98%. Cows were fitted with an ultrasonic flow probe to measure blood flow on half udder and with two catheters to determine arterio venous differences in concentrations on d 12 of each period (with samples collected every 2 h between the 12h milking interval). Milk yield increased from 25.3 to 29.7 kg/d with P supply (P<0.01) and from 25.9 to 29.1 kg/d with E supply (P<0.01), with no interaction between E and P. Lactose yield on half udder (d 12) increased (P<0.01) by 17% and 15% with P and E, respectively. Mammary GLC uptake increased by 7% with P (from 222 to 238 mmol/h; P = 0.05) and by 19% (from 210 to 250 mmol/h; P<0.01) with E, with no interaction. The increment observed with E was mainly due to an increased mammary plasma flow. The ratio of lactose yield to GLC uptake averaged 62%, 63%, 56% and 64% in LELP, LEHP, HELP, HEHP, respectively, and tended to be lower in HELP (P×E interaction, P = 0.09). These results suggest different mammary regulations of glucose metabolism with P and E. Increased P supply could improve lactose yield with a concomitant higher GLC uptake and a more efficient lactose synthesis whereas E supply could improve it through a higher GLC uptake, even associated with a less efficient conversion of GLC towards lactose when P supply remained low.

Key Words: dairy cow, glucose, mammary gland

119 Regulation of adipose tissue metabolism in dairy cattle as affected by genetic merit and dietary efficiency. S. Rocco, A. M. Youngquist, G. Duncan, C. Schachtschneider, J. Miller, J. L. Vierck, A. Hutjens, J. P. McNamara*, and A. Lowe, *Washington State University*, *Pullman*.

To continue to define mechanisms of control of energy metabolism in the most efficient dairy cattle, 48 cows were allotted to High Genetic (sire PTAM = 870 kg), or Low Genetic (PTAM = 378); and half of each group was fed either to energy requirements (HE) or to 90% of requirements (LE), other components fed to requirements, from 21 d prepartum to 56 DIM. Samples of adipose tissue were taken at -21, -7, 7, and 28 days around parturition and lipolysis, lipogenesis and expression of key genes that control these pathways were measured. Feed intake in the dry period (-21 to -1 d prepartum) was 13.6 and 12.7 kg DMI/d for HE and LE (SE = 1.5); during lactation (1 to 56 DIM) it was 21.2 and 17.4 kg/d (SE = 1.4). Milk yield was 36.1 and 33. 3 kg/d for HG and LG for 27-56 DIM (P<0.05) across diets and parities. Milk yield was 28.6, 26.0 for HG in parity 1 and 2; and 38.1 and 38.0 (SE 1.2) kg/d for LG in parity 1 and 2. The genetic dietary interaction for the LGHE, HGHE, LGLE and HGLE groups was 33.7, 32.8, 31.7, 31.5 kg/d. Thus HG was slightly more protective of milk production when challenged with LE. Loss of BW, BCS and body fat were greater (P<0.05) on LE diet and in parity 2. Rates of lipolysis in adipose tissue increased in early lactation and were greater on the LE diet. Lipogenesis was similar in the dry period on LE and HE, but on the LE was less than (P < 0.05) 50% of that on the HE diet. In HG animals, lipogenesis was faster in the dry period and first week of lactation, but was lower at 28 DIM. Expression of genes that control lipolysis was similar to higher in lactation, those that control lipogenesis decreased in early lactation and were highly related (P <0.05) to rates of lipogenesis. Animal of greater genetic merit (sire PTAM) peaked with greater milk production on the same amount of energy, and protected milk production and body energy stores better than those from sires with lesser PTAM.

Key Words: lactation, adipose tissue, genetic merit

120 Changes in deposition of visceral adipose tissues and expression of lipogenesis-related genes induced by diets with different energy levels in non-lactating cows. P. Ji*, J. J. Loor, A. Nikkhah, M. Bionaz, N. A. Janovick, and J. K. Drackley, *Department of Animal Science, University of Illinois*, *Urbana*.

Over-accumulation of adipose lipid prepartum increases susceptibility to metabolic disorders postpartum. Effects of moderate excess (M) or low dietary energy (L) on visceral adipose tissue deposition and expression of lipogenic genes were assessed in 18 non-pregnant dry cows. Cows were blocked by BCS and randomly assigned to either an M (NEL = 1.61 Mcal/kg) or L (NEL = 1.37 Mcal/kg) diet. The M diet contained 74.5% (DM basis) forage without straw, while the L diet contained 84.6% forage including 41.9% wheat straw. Cows were euthanized after 8 wk of feeding. Visceral adipose tissues were weighed and sub-samples from subcutaneous (Su), mesenteric (Me), and omental (Om) adipose were snap-frozen in liquid-N. Cows fed M had greater (P < 0.05) DMI than L (15.7 vs. 10.9 ± 0.6 kg), as well as greater Om (28.07 vs. 17.49 ± 1.31 kg) and Me weights (21.99 vs. 12.1 ± 2.35, kg). BCS did not differ between groups (3.62 vs. 3.55 ± 0.11 for M and L). Thirty genes with roles in insulin resistance, inflammation, and/or lipogenesis were chosen for quantitative PCR. Among 6 lipogenic genes studied initially, abundance of thyroid hormone responsive SPOT 14 (THRSP) and stearoyl-CoA desaturase (SCD) was greater for M than L. Abundance of SCD (Su, Me, and Om = 3.86, 2.92, and 3.32 ± 0.25), acyl-CoA synthetase long-chain family member 1 (ACSL1) (Su, Me and Om = 3.71, 4.15 and 3.82 ± 0.15) and adipose differentiation related protein (ADFP) (Su, Me and Om = 4.21, 4.04 and 3.77 ± 0.09) varied among tissue sites. No treatment or tissue source effects were detected for mRNA abundance of acetyl-coenzyme A carboxylase alpha (ACACA) or peroxisome proliferator-activated receptor gamma (PPARG). A moderate excess of dietary energy increased visceral lipid deposition which was undetectable by BCS. Transcriptomics revealed that lipogenic genes across adipose sites differ in sensitivity to altered dietary energy intake.

Key Words: visceral adipose tissue, dry period, gene expression

121 Contribution of changes in gene transcription in dairy cattle adipose tissue to control of metabolic pathways dictating increased overall efficiency. J. M. Sumner, C. Shachtschneider, A. Hutchins, A. M. Youngquist, G. Duncan, S. Rocco, J. Miller, J. L. Vierck, J. P. McNamara*, and A. Lowe, *Washington State University*, *Pullman*.

Metabolic adaptations in adipose tissue contribute to establishment and maintenance of lactation. Previous work determined that several enzymes and pathways are controlled by gene transcription for enzyme synthesis, and hormonal and neurocrine regulation of enzyme activity. Our objective was to evaluate the mechanisms of gene transcriptome changes underlying the adipose response to lactation. We tested the hypothesis that genes encoding for proteins that regulate metabolism would change expression in adipose tissue of dairy cattle in early lactation. Animals (n = 24) from two different experiments were used and ranged from 8.8 to 52.2 kg/d milk production, and from 8 to 32

kg/d DMI. They lost a range of +9.1 to -113.6 kg BW, from 0 to -1.0 BCS units. Subcutaneous adipose tissue biopsies were obtained at -30 adn 30 DIM, tissue extracted RNA, and hybridized to the Affymetrix Genechip® Bovine Genome Array. Genes that control anabolic pathways decreased from 30 d prepartum to 30 DIM ($P < 0.05$), including (mean (% change), (SEM)): SREBP, -25.1, (6.2); GLUT1, - 57.3 (14.1); THRSP14, -30.8 (7.4); LPL, -48.4 (7.7) and AcCoA Carboxylase, -60.6 (13.0), ribosomal S2 expression did not change. These genes were all highly correlated ($r > .80$, $P < 0.05$) with in vitro rates of lipogenesis from acetate, and regression of transcript change on milk production was 0.18 for AcCoA carb and 0.26 for ATP-CL ($P < 0.05$). Expression of genes directing lipolytic pathways were much more varied, including Ca channel subunit 338% (203); B2AR 52.0 (8.8); PKC receptor 10.1 (2.6) and HSL mRNA 23.0 (17.9). The regression of transcript change on milk was 0.30 and 0.25 for B2AR and HSL mRNA. We have confirmed and extended earlier observations that reductions in lipogenesis are primarily due to a systematic reduction in enzyme synthesis, while increases in lipolysis are a combination of increases in transcription and metabolic flux. Both are directly related to milk productive ability and efficiency and can help to identify the mechanisms that direct the most efficient milk production.

Key Words: gene transcription, efficiency, lactation

122 Nitrogen recycling in lactating dairy cows consuming diets predicted by CPM Dairy to be deficient in either ruminal N or metabolizable protein. E. B. Recktenwald*, D. A. Ross, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

Twelve ruminally fistulated, lactating dairy cows (155 DIM ± 13d, 609 kg BW ± 32 kg) were assigned to three diets in a randomized complete block to observe the effects of nitrogen (N) source and quantity consumed on urea N recycling. Diets consisted of approximately 45% corn silage, 2% wheat straw, and 53% concentrates and were as follows: 16% CP and balanced for ruminal N and MP (Diet P), 14% CP and deficient in MP (Diet N), 14% CP and deficient in ruminal N (Diet T). Cows were infused in the jugular vein with 15N15N urea (0.0208 g urea/h) in saline for 72 hr, after which samples of feces, urine, plasma, milk, rumen fluid and total rumen contents were collected. Protozoa, liquid associated bacteria, and solid associated bacteria were isolated based on several published methods. Microbial and fecal samples were analyzed for 15N enrichment by IRMS. Urinary urea was isolated by fractionation on a AG 50W-X8 Dowex column and analyzed by IRMS. Urea kinetics were determined by fecal 15N and urinary 14N15N and 15N15N-urea enrichments using the model of Lobley et al. (2000). Due to total collection problems, urinary urea excretion was estimated according to Nennich et al. 2006 and CPM Dairy v3.0. Nitrogen intake was lower ($P<0.05$) for cows fed Diet T (443 g N/d) compared with cows fed Diets P (620 g N/d) and N (546 g N/d). Urea entry rate followed N intake with 208, 293, and 222 g urea-N/d, but were not different ($P > 0.05$) among diets. Urea entry to the GIT and urea-N return to the ornithine cycle averaged 98 and 69 g urea-N/d, respectively, with no differences ($P > 0.05$) among treatment. The portion of urea production excreted in the urine or contributing to anabolic use averaged 0.65 and 0.27, with no differences ($P > 0.05$) among treatment. The atom percent excess (APE) of liquid associated bacteria (9.4, 6.1, and 6.2 APE, Diets T, P, and N, respectively) and protozoa (7.8, 5.3, and 5.1 APE) were higher for cows on the T diet, but were significant only for the protozoa. Solid bacterial APE averaged 5.1 APE, and were not different ($P > 0.05$) among diets.

Key Words: urea recycling, metabolizable protein, ruminal nitrogen

123 Effect of metabolizable methionine (MET) and lysine (LYS) concentrations on milk production and N utilization in lactating dairy cows. Z. H. Chen*[1], G. A. Broderick[2], N. D. Luchini[3], B. K. Sloan[3], and E. Devillard[4], [1]*University of Wisconsin*, *Madison*, [2]*U. S. Dairy Forage Research Center*, *Madison, WI*, [3]*Adisseo USA Inc.*, *Alpharetta, GA*, [4]*Adisseo, France S.A.S.*, *Commentry, France*.

The amino acids methionine and lysine are considered the two most limiting AA in high producing dairy cows. Balancing rations for MET and LYS according to NRC 2001 may allow lower levels of MP and CP to be fed, without compromising yield of milk components, reducing urinary N excretion and improving feed efficiency. Different commercial sources of methionine are proposed as effective sources of MET. The isopropyl ester of HMB (HMBi) appears to be partly absorbed across the rumen wall with the balance being ruminally metabolized. Seventy cows were blocked by parity and DIM into 14 blocks and randomly assigned within blocks to diets based on alfalfa and corn silage with (DM basis) 28% NDF: 1 diet with 16.9% CP, 6.17 LYS and 1.85 MET as % of MP (positive control; PC), 1 diet with 15.7% CP, 6.60 LYS and 1.84 MET as a % of MP (negative control; NC); the 3 supplements added to NC were 0.16% MetaSmart (0.57 HMBi), 0.06% Smartamine M (SM) + 0.1% HMB (Rhodimet AT 88), or 0.06% Smartamine M; all were estimated to improve the LYS to MET ratio from 3.6 to 3.0. After a 2-wk covariate on the same diet, cows were fed test diets continuously for 12 wk. Data will be analyzed as a randomized complete block using Mixed Model of SAS with covariate production and repeated measures in the model. Diet did not affect DMI, milk yield, or Milk N/N intake. However, adding HMBi to the NC increased yield of energy corrected milk (ECM), milk protein and SNF contents. Moreover, there were trends for effects on milk fat content, fat and protein yield. Feeding the PC elevated MUN without improving production. Results with the different Met sources were similar, suggesting that using HMBi with an assumed rumen absorption of 50% is equivalent to using Smartamine M with an assumed MET contribution of 0.6g/g.

Table 1.

Item	NC	HMBi	HMB+SM	SM	PC	SEM	P > F
DMI, kg/d	24.9	25.7	25.1	24.6	24.7	0.4	0.44
Milk, kg/d	41.8	42.1	41.7	41.7	41.2	0.9	0.98
ECM, kg/d	37.9^{b}	41.0^{a}	39.0^{ab}	40.2^{ab}	39.4^{ab}	0.95	0.02
ECM/DMI	1.54^{b}	1.59^{ab}	1.57^{ab}	1.63^{a}	1.61^{ab}	0.04	0.04
Fat, %	3.52	3.93	3.66	3.77	3.85	0.11	0.08
Fat, kg/d	1.42	1.60	1.54	1.62	1.61	0.06	0.07
Protein, %	3.03^{c}	3.19^{a}	3.17^{a}	3.15^{ab}	3.05^{bc}	0.04	0.01
Protein, kg/d	1.24	1.30	1.33	1.33	1.25	0.03	0.09
SNF, %	8.73^{b}	8.94^{a}	8.92^{a}	8.84^{ab}	8.73^{b}	0.05	0.01
Milk N/N Intake, %	32.7	32.7	33.2	34.1	30.9	0.92	0.14
MUN, mg/dl	10.0^{c}	10.2^{c}	10.8^{bc}	11.2^{b}	13.2^{a}	0.33	<0.01

Key Words: methionine, HMB, HMBi

124 Effects of jugular infused branched-chain amino acid supplementation on milk protein synthesis in high producing dairy cows. J. A. D. R. N. Appuhamy*[1], J. R. Knapp[2], C. A. Umberger[1], and M. D. Hanigan[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Fox Hollow Consulting, LLC*, *Colombus, OH*.

In addition to lysine (Lys) and methionine (Met), current ration balancing programs suggest that branched chain amino acid (BCAA) supply

may also be limiting in dairy cows. The objective of this study was to investigate whether BCAA become limiting for milk protein synthesis when Met and Lys supply were not limiting. Nine multiparous Holstein cows with average milk production of 53.5 ± 7.11 kg/day were randomly assigned to 7 d continuous jugular infusion treatments of saline (CTL), Met and Lys (ML; 12 g and 18 g /d respectively), and ML plus leucine, isoleucine, and valine (ML+BCAA; 35 g, 15 g, and 15 g/d respectively) in 3 x 3 Latin square design with three infusion periods separated by 7 d non-infusion periods. The basal diet consisted of 40% corn silage, 14% alfalfa hay, and a concentrate mix. During the last 3 d of each infusion period, milk and feed samples were collected for composition analysis. Daily feed intake and milk production of individual cows were recorded. Infusion treatments had non-significant effects on dry matter intake, milk yield, fat percentage and fat yield. Protein yield (kg/d) and protein percentage (%) were not significantly different between ML (1.56 ± 0.10 and 2.88 ± 0.03 respectively) and ML+BCAA (1.52 ± 0.11 and 2.81 ± 0.03 respectively), but they were significantly greater than that of CTL (1.41 ± 0.11 and 2.71 ± 0.03 respectively). Protein efficiency, expressed as milk protein yield divided by total crude protein intake (feed plus infusate), was not significantly different between ML (0.41 ± 0.02) and ML+BCAA (0.38 ± 0.03) but that of CTL (0.37± 0.02) was significantly less than that of ML. While high producing cows responded positively to Met and Lys supplementation, there were no apparent benefits of BCAA supplementation.

Key Words: milk protein synthesis, branched chain amino acids, methionine

125 Effect of carbohydrate source on rumen fuid pH and in vitro gas production (GP) in heifers fed pasture silage. A. Britos*[1], A. Mendoza[2], M. Claramunt[1], M. Karlen[1], G. Kelly[1], L. Magallanes[1], S. Ramírez[1], A. Zunini[1], J. L. Repetto[2], and C. Cajarville[1], [1]*Department of Animal Nutrition, Faculty of Veterinary, UdelaR, Montevideo, Uruguay*, [2]*Department of Bovines, Faculty of Veterinary, UdelaR, Montevideo, Uruguay*.

Hereford heifers (n=24; mean BW=224kg; SEM=4) were randomly assigned to four treatments: no supplement (N), soybean hulls (S), corn grain (C) and barley grain (B), to test if carbohydrate source affects the pH and GP of rumen fluid. Heifers were housed in metabolic cages and supplements were offered at 1% of BW in one meal at 0700h. Pasture silage was offered ad libitum from 0700 to 2000h. In supplemented heifers forage was immediately offered after the supplements were consumed. After 21d of adaptation, rumen fluid samples were collected from each heifer through tubes inserted in rumen every hour for 24 hours (hour 0=0700h), and pH was measured with a digital pH-meter. Inoculum for GP was collected and mixed within groups. Pasture silage, S, C, B, wheat straw, oats and lotus were weighed (0.5g DM) in triplicate for each inoculum into 125mL flasks and 38.5mL of media was added before injection of 10mL of inoculum. GP was measured at 2, 4, 6, 8, 10, 12, 18, 24, 48, 72 and 96h. Data were fitted to V=Vf/{1+exp[2+4*Rf*(T-L)]}+Vs/{1+exp[2+4*Rs*(T-L)]}: V=total GP volume (mL/g DM), Vf=fast pool volume (mL/g DM), Vs=slow pool volume (mL/g DM), Rf and Rs=rates (h^{-1}) of fast and slow pools respectively, T=time, L=lag (h). pH and GP data were analyzed by a mixed or general linear model, respectively. Mean (SEM=0.05) and minimum (SEM=0.11) pH values were 6.82 and 6.55, 6.45 and 6.14, 6.48 and 6.16, 6.48 and 6.10 for treatment N, S, C and B, respectively, and were lower for supplemented heifers (P<0.01) but did not differ between carbohydrate sources. pH decreased after the start of the meal until a nadir of 6.27 (SEM=0.05). GP parameters were affected by inoculum, substrate and interaction. Vf decreased according to inoculum as B>S>C>N. *Funded by PEDECIBA; PDT 78/12; ANII.*

Table 1. Effect of inoculum source on in vitro gas production parameters

Inoculum	V	Vf	Rf	Vs	Rs	L
N	210.3^{b}	82.5^{d}	0.138^{a}	127.9^{a}	0.022^{a}	6.2^{a}
S	213.3^{ab}	112.6^{b}	0.114^{b}	100.7^{c}	0.022^{a}	4.3^{bc}
B	216.5^{ab}	118.1^{a}	0.112^{b}	98.4^{c}	0.019^{b}	3.6^{c}
C	220.5^{a}	104.9^{c}	0.130^{a}	115.6^{b}	0.022^{a}	4.7^{b}
SEM	2.793	1.902	0.004	2.451	0.0004	0.348
P(inoculum)	0.080	<.001	<.001	<.001	<.001	<.001
P(substrate)	<.001	<.001	<.001	<.001	<.001	<.001
P(inoculum*substrate)	<.001	<.001	<.001	<.001	<.001	0.048

^{abcd}Superscripts within column differ (P<0.05)

Key Words: carbohydrate source, in vitro gas production, rumen pH

126 TMR particles breakdown through ingestive mastication of dairy cows. I. Schadt*[1], J. D. Ferguson[2], G. Azzaro[1], C. Guardiano[1], R. Petriglieri[1], and G. Licitra[1,3], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*University of Pennsylvania, School of Veterinary Medicine, Kennett Square*, [3]*D.A.C.P.A. University of Catania, Italy*.

The study of feed particle breakdown through mastication might help to understand the formation and characteristics of the ruminal mat, and in consequence might help to explain how feed particle size can affect animal health and productivity. In the present study we examined particle breakdown of TMR samples differing in composition and distribution on the Penn State Particle Separator (PSPS). In particular, TMR and fecal samples from 10 farms were collected. The TMR samples were shaken through the PSPS with an additional sieve of 0.25 cm openings added between the middle and the lower screen to obtain the following treatments 1-6: unprocessed TMR, and TMR components retained on screens of 1.91, 0.79, 0.25, and 0.13 cm, and bottom pan, respectively. Three nonlactating, rumen fistulated cows had rumens evacuated and were offered 1 kg of each treatment in a randomized sequence. Swallowed boli were manually retrieved from the reticulo-rumen at the esophagal orifice. All samples were horizontally, wet sieved through a 0.16 cm screen and proportional dry residues (RES1.6) were determined. Residues of unprocessed TMRs, their respective boli and fecal samples were further analyzed through image analysis for particle distribution and mean size. Mean sizes of the unprocessed TMRs ranged from 1.49 to 2.06 cm (mean = 1.71 ± 0.17 cm). Contents of dry matter (DM), NDF, and crude protein ranged from 49 to 64% (mean = 55 ± 5.5%), from 26 to 35% DM (mean = 31 ± 2.8% DM), and from 15 to 25% DM (mean = 19 ± 3.4% DM), respectively. TMR mean size was positively related to fecal mean size (r = 0.63, P < 0.05, n =10). There was a positive linear response of boli RES1.6 to their respective treatments RES1.6, Y = 0.79X + 0.03 (r = 0.98, P < 0.01, n = 58). Boli RES1.6 differed between cows (P < 0.01).

Key Words: TMR particles, bolus particles, dairy cattle