121 had greater NDF (*P*=0.07) and lower starch (*P*=0.01) and TP (*P*=0.01) contents than DK39T, DK61T and DK68T. In addition, OMD was similar across corn and sorghum hybrids before ensiling. In experiment 1, inoculation did not affect fermentation, chemical composition, DMR or OMD of M369 silage. Reductions in silage DM contents were observed with 4x4 inoculation of DK780S silage (*P*=0.06) and SA inoculation of DK790S silage (*P*=0.07). Both inoculants increased 6h OMD in DK780S silage (*P*=0.02) and NDF (*P*=0.08) content and 72h OMD (*P*=0.07) in SIL-3 silage. In experiment 2, microbial inoculation did not affect fermentation, chemical composition, DMR or OMD of DK39T and DK61T silages. Inoculation with 4x4 increased total N (*P*=0.06) and CP (*P*=0.06) content in DK68T silage. Inoculation with SA increased TP (*P*=0.02) content in DK68T silage and reduced NDF (*P*=0.09) content in SX-121 silage. We conclude that the beneficial effects of microbial inoculation of corn and sorghum silages depend on the particular hybrid and inoculant used.

Key Words: Silage, Corn, Sorghum

W221 Fermentation characteristics and microbial succession of silage from organic residues of orange (*Citrus sinensis*) and pineapple (*Ananas comosus*) processing plants. S. Pagán*, A. Rodríguez, and E. Valencia, *University of Puerto Rico*, *Mayagüez, Puerto Rico*.

Two experiments were conducted to evaluate the microbial succession and fermentation end-products of organic residues from orange (*Citrus sinensis*, **CS**) and pineapple (*Ananas comosus*, **PS**) fruit processing plants. Residues composed of pulp, skins and seeds were fermented in PVC micro-silos for 0, 4, 7, 11, 29 and 65 days. Triplicate samples from each residue and fermentation period (d) were analyzed for pH, microbial succession (coliforms, **C**; lactic acid-producing bacteria, **LAPB**; molds and yeast, **MY**), and fermentation end-products (organic acids). Data within each fermented residue were analyzed as a completely randomized design using the General Linear Model. Bonferroni test was used for means separations. Final pH was 3.32 and 3.21 for **CS** and **PS**, respectively. During the whole fermentation and, for both silages, **C** populations were not detected, while **LAPB** and **MY** had a typical microbial growth. After 65 d of fermentation lactic acid was the main end product associated with the fermentation process, (0.90 and 1.02% for **CS** and **PS** respectively), low percentages of acetic acid were also detected (0.19% **CS** and 0.98% **PS**). Butyric acid was not detected on both fruit residues silages. These results indicate that silage production is an alternative for the disposal of organic residues from orange and pineapple fruit processing plants. Inclusion of these fruit silages on farm animal's diets must be evaluated.

Key Words: Organic Residues, Silage, Fermentation

W222 Silages carbohydrate fractions and degradation rates estimated by gas production technique. E. S. Pereira*[1], A. M. V. Arruda[1], and I. Y. Mizubuti[2], [1]*Universidade Estadual do Oeste do Paraná, Marechal Cândido Rondon, Paraná, Brasil*, [2]*Universidade Estadual de Londrina*, *Londrina, Paraná, Brasil.*

The objective of this work was to determine the total carbohydrates composed fractions, and to estimate the digestion rate of the non fiber carbohydrate (NFC) and neutral detergent insoluble fractions of five silages prepared with Tifton 85 grass forage using the gas production technique. Silages were: 1-exclusive Tifton 85, 2-Tifton 85 silage with 16.5% of corn industrial residue added, 3-Tifton 85 silage with 16.5% corn meal added, 4-Tifton 85 silage inoculated with lactobacillus (1 g for each 3 liters of water for ton of fresh material) and 5-beforehand dry Tifton 85 silage, with the drying time of 90 minutes. The total carbohydrate fraction and C, B2 and NFC fractions were determined by laboratory methods (Cornell system). The statistical analyses performed including general variation analyses and comparative means by tukey test in five percent probability. The in vitro gas production from dry matter (DM), neutral detergent fiber (NDF) and NFC in the silages were determined by laboratory anaerobic incubations. The Tifton 85 silage with corn industrial residue and Tifton 85 silage with corn meal additive, showed highest potential digestible content of NFC and B2 carbohydrate fractions. The Tifton 85 silage dry presented lower gas production. The beforehand dry Tifton 85 silage with corn industrial residue and Tifton 85 silage with corn meal additive showed highest gas production from NFC carbohydrate fraction. The rate of digestion to the NFC and NDF carbohydrate fraction in the Tifton 85 silages in this work showed a range of 0.0652 to 0.2273%/hour and a range of 0.0315 to 0.0552%/hour, respectively. More studies with the by-products used in this work as additives for silage were necessary for knowing your influence on the nutritional quality and future recommendations.

Acknowledgements: Fundação Araucária, Paraná - Brasil

Key Words: Carbohydrate Fractions, Gas Production Technique, Silages

Ruminant Nutrition: Protein and Amino Acids

W223 Use of Synchrotron FTIR microspectroscopy to determine the effect of heat treatment on protein secondary structures of brown and golden flaxseeds at a cellular level in relation to nutritive value of protein: A novel approach. P. Yu*[1], J. J. McKinnon[1], H. W. Soita[1], C. R. Christensen[2], and D. A. Christensen[1], [1]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Canadian Light Source*, *Saskatoon, SK, Canada*.

An understanding of the structure of the whole protein is often vital to understanding its digestive behavior and nutritive value in animals. Protein secondary structures include α-helix and β-sheet. The percentage of these two structures influences protein nutritive value and quality. High percentage of β-sheet structure may cause low access to gastrointestinal digestive enzymes, which results in a low protein value. The objective was to use the synchrotron FTIR microspectroscopy (S-FTIR) to reveal chemical features of protein secondary structures of flaxseed tissues affected by varieties and heating in relation to protein nutritive value. The results showed that with the S-FTIR, the structural-chemical makeup and nutritive characteristics of the flaxseed tissues could be revealed. The protein secondary structure differed between the golden and the brown seed coat types. The golden contained higher percentage of α-helix (47.1±3.2 vs. 36.9±4.7%, n=20), lower percentage of β-sheet (37.2±3.4 vs. 46.3±4.0%, n=20) and higher ratio of α-helix to β-sheet (1.3 vs. 0.8) ($P < 0.05$), indicating higher protein nutritive value and availability in the golden. The effects of roasting on protein secondary structures depended on the variety. The roasting reduced percentage of α-helix (47.1 to 36.1%), increased percentage of β-sheet (37.2 to 49.8%) and reduced α-helix to β-sheet ratio (1.3 to 0.7) of the golden variety ($P < 0.05$). However, roasting did not affect protein secondary structures of the brown. These results indicated that: 1) different sensitivities of protein secondary structure to the heat processing between the varieties; 2) roasting affected protein value and availability in the golden but not in the brown. The results demonstrate the potential of highly spatially resolved S-FTIR to reveal protein secondary structures. Further study is needed to quantify the relationship between protein secondary structures and protein nutrient availability in animal models.

Key Words: Synchrotron FTIR, Protein Secondary Structures, Nutritive Value

W224 The role of protein matrix in the digestion of corn grain: Assessment by scanning electron microscopy. Y. Wang*[1], D. Sapienza[2], V. J. H. Sewalt[3], Z. Xu[1], and T.A. McAllister[1], [1]*Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada*, [2]*Sapienza Analytica, LLC*, *Johnston, IA*, [3]*Kemin AgriFoods North America*, *Des Moines, IA*.

Corn grains (Pioneer Hi-Bred International, Inc.) harvested at maturities for silage (SIL) and for grain (black layer, GRN) were halved longitudinally and ruminally incubated for up to 48 h in nylon bags in a non-lactating cow fed a corn grain/corn silage diet, and then for 8 h in artificial post-ruminal digestion solution (ANKOM Daisy II). Grains retrieved after 4, 24, and 48 h in the rumen (4R, 24R, 48R), and after 24 h in the rumen plus 8 h post-ruminal incubation (24R8P), were processed for viewing on a Hitachi S-570 scanning electron microsope (accelerating voltage 7-10 kV). The grains were examined extensively in the vitreous (V), horny starch (H) and floury starch (F) areas of the endosperm. Disappearance of starch granules was consistently more rapid (4R to 48R) or extensive (24R8P) than that of protein matrix, in both SIL and GRN. In all regions of the endosperm, bacterial colonization of starch granules was the first microbial activity observed upon exposure of sectioned grains to the ruminal environment. Extensive bacterial colonization and digestion of protein matrix was evident at 48R but not at 4R. Compared with 24R, the primary effect of 24R8P was an increased disappearance of starch granules from exposed areas. The proportion of protein matrix was highest, and its association with starch granules was tightest, in area V, followed by H and then F, but the order of bacterial colonization and disappearance of protein matrix was reversed (F>H>V). Trends in bacterial colonization and digestion of protein matrix, as compared with starch granules, were similar between SIL and GRN, although overall disappearance of endosperm was greater with SIL than with GRN, suggesting greater vulnerability of protein matrix in SIL as compared with GRN. In corn cut for silage and for corn, the protein matrix regulates the rate and extent of digestion of exposed endosperm.

Key Words: Corn Grain, Maturity, SEM

W225 Development of an *in vitro* technique to monitor the fate of true proteins of feedstuffs in the rumen. A. A. Sadeghi*[1] and P. Shawrang[2], [1]*Islamic Azad University*, *Tehran, Iran*, [2]*Tehran University*, *Karaj, Iran*.

An integrated artificial rumen (AR) and electrophoretic technique were used to develop an *in vitro* technique to monitor the fate of true proteins of feedstuffs in the rumen. The objective was to adapt an *in vitro* procedure to obtain simulated rumen fluid and many residue at different incubation times that could be analyzed for true protein patterns by using SDS-PAGE technique. Duplicate nylon bags containing two grams of soybean meal and canola meal were suspended into the rumen (R) of three 450 kg Holstein steers and artificial rumen from 0 to 24 h. A 50 µl aliqout of rumen and artificial rumen fluid samples, also twelve mg of well-ground feed sample and bag residues from *in situ* and artificial rumen incubation were placed into 750 µl SDS-PAGE sample buffer. After 30 min of thorough mixing, samples were immersed at 90°C for 3 min, and then centrifuged at 10000 × g for 1 min. A 30 µl aliqout of each protein sample was then loaded into the sample well. Samples were fractionated by a SDS-PAGE discontinuous system. The sub-units of the gel were monitored by densitometric scanning at 580 nm. In soybean meal two major proteins (glycinin with acidic and basic subunits, and β-conglycinin with α', α and β subunits) and in canola meal (napin with two subunits and cruciferin with four subunits) were observed. In rumen fluid collected from steers consuming two test feeds, no protein bands were found after 5-h incubation, but in artificial rumen fluid, there were some small bands after 6-h incubation. In AR, there were some bands between original protein bands of two test feeds at shorter incubation times. These bands were related to small polypeptides produced from larger ones. Densitometrical scanning data for R and AR fluid samples were not correlated (P>0.10). SDS-PAGE patterns of bag residues of R and AR were similar. Densitometrical scanning data for bag residues of R and AR were highly correlated (r = 0.92; P<0.05). These results indicate that the integrated artificial rumen and electrophoretic technique could be used to monitor the fate of true proteins of feedstuffs in the rumen.

Key Words: Artificial Rumen, Electrophoresis, True Protein

W226 Degradability characteristics of crude protein of some feedstuffs in ruminants using in vitro technique. A. Taghizadeh*[1], H. Abdoli[1], A. Tahmasbi[1], and R. Noori[2], [1]*Tabriz University*, *Tabriz, East Azarbayjan, Iran*, [2]*Ekrami Highschool, Training and Education Ministry*, *Tabriz, East Azarbayjan, Iran*.

The degradability characteristics containing fractional rates of digestion, soluble fraction and degradable fraction were determined using in vitro technique. The feeds were barley grain (BG), soybean meal (SBM), and wheat bran (WB). The in vitro studies were conducted consecutively over a period of two weeks using rumen fluid obtained pre-feeding from two sheep (38±4kg, fed a diet containing (as fed) 600 g kg^{-1} concentrate and 400 g kg^{-1} forage containing DE (3.35 Mcal/kg DM) and CP (160 g/kg DM) and used as ruminal fluid donors for the preparation of inoculums. Crude protein degradation (CPD) was estimated 0, 2, 12, 24 and 48 h of incubation. The results were analyzed using completely randomized design (CRD) in each incubation time with Duncan's multiple range test used for the comparison of means. Feeds were the only sources of variation considered. Degradabilities data in triplicate were fitted to an equation of p=a+b ($1-e^{-ct}$); where (p) is CP degradability at time, t, (a) is intercept and ideally reflects the soluble fraction, (b) is the degradable of insoluble (but with time fermentable) fraction, (c) is the fractional rate at which b is fermented per hour. The CP soluble fraction (a) for BG, SBM and WB was (%) 31.7, 36.7 and 50.0, respectively. The insoluble (but with time fermentable) fraction (b) was (%) 66.0, 62.0 and 37.0, respectively. The fractional rate of fermentation (c) was (%/h) 0.04, 0.02 and 0.06, respectively. The results showed that the soluble fraction (a) and fractional rate (c) in WB were more than the other feedstuffs (P<0.05), while CP insoluble fraction in BG was more than the other test feeds (P<0.05). This variability in CP fermentation parameters can be resulted from the differences among CP fractions and type of CP in feeds.

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Key Words: Degradability, In Vitro, Crude Protein

W227 Effects of adaptation time of a specific blend of essential oils on rumen nitrogen metabolism and fermentation profile in sheep. L. Castillejos[1], S. Calsamiglia*[1], A. Ferret[1], and R. Losa[2], [1]*Universitat Autonoma de Barcelona*, *Bellaterra, Spain*, [2]*AKZO NOBEL/CRINA SA*, *Gland, Switzerland*.

Eight sheep (average body weight of 57 kg) were used to study the effects of long term adaptation of rumen fluid to a specific blend of essential oils (BEO, Crina® for ruminants) on rumen fermentation. Animals received 1.3 kg of a 50:50 forage:concentrate diet (16% CP and 38% NDF). Four sheep were assigned at random to the control (CTR, without BEO) and four sheep were adapted to BEO (110 mg/d) for four weeks (ADBEO). After four weeks samples of ruminal fluid were obtained at 0 and 3 h after the morning feeding and in two consecutive days using an oro-ruminal probe. Samples were analyzed for peptide, amino acid and ammonia N concentrations, total and individual VFA, and pH. Differences between means were declared at P < 0.05. Total VFA and ammonia N concentrate were higher, and the acetate:propionate ratio was lower at 3 than at 0 h. Treatment ADBEO tended (P < 0.10) to increase the proportion of acetate and decrease the proportion of valerate compared with CTR. Treatment ADBEO had no effect on N metabolism and pH, but ADBEO sheep had a 16% numerical decrease in ammonia N concentration. Ruminal fluid collected from each of CTR and ADBEO sheep was used to study in vitro fermentation profile of soybean meal, corn meal, alfalfa hay and ryegrass hay. Treatments were: control fluid (CTR, without BEO), CTR fluid plus a single dose of BEO (11 mg/l; CTR+BEO) and ADBEO fluid plus a single dose of BEO (11 mg/l; ADBEO+BEO). The proportion of acetate and acetate to propionate ratio was higher, and the proportion of propionate and isovalerate, and branch-chained VFA and ammonia N (-14%) concentration were lower in ADBEO+BEO fluid compared with CTR fluid. However, treatment CTR+BEO had no effect on ammonia N concentration and VFA profile compared with CTR. A four weeks adaptation period of rumen microorganisms appear necessary to observe the effects of BEO on VFA and ammonia N concentration.

Key Words: Essential Oil, Nitrogen Metabolism, Rumen Fermentation

W228 Exogenous proteolytic enzymes improve in vitro degradation of alfalfa hay but not alfalfa silage. J.-S. Eun* and K. A. Beauchemin, *Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada.*

An enzyme product containing only protease activity was shown previously to increase in vitro and in vivo fiber digestibility of alfalfa hay and TMR. An in vitro experiment was therefore conducted to evaluate the efficacy of this exogenous proteolytic enzyme (EPE) product (Protex 6L®, Genencor Int., Rochester, NY) using a 2 × 2 factorial design for improving the degradation of alfalfa silage. Fresh, milled alfalfa silage or alfalfa hay (0.5 g DM) was weighed into fermentation bottles. The amount of enzyme added to substrate was the same as in previous experiments (1.25 µL/g DM). Anaerobic buffer medium (20 mL) adjusted to pH 6.5 and strained ruminal fluid (5 mL) were inoculated into culture bottles and incubated for 24 h. Headspace gas production (GP) was measured at 2, 6, 12, and 24 h of inoculation. At the end of the 24 h-incubation, contents of the incubation bottles were centrifuged, and 5 mL of the supernatant was added to 1 mL of 25% meta-phosphoric acid for VFA determination. After discarding the supernatant, the bottle and its contents were dried at 55°C for 48 h. Degradation of DM, NDF, and ADF was sequentially determined. Data were analyzed using the Proc Mixed procedure of SAS. Adding EPE increased ($P < 0.01$) GP from only alfalfa hay throughout the fermentation, resulting in an interaction between substrate and EPE starting at 6 h of incubation. In addition, adding EPE increased degradability of DM ($P = 0.04$), NDF ($P = 0.05$), and ADF ($P = 0.05$) for alfalfa hay. Total VFA production was not affected by EPE. However, EPE addition decreased molar proportion of acetate (A) for alfalfa hay and increased molar proportion of propionate (P) for both alfalfa silage and alfalfa hay, resulting in decreased A:P ratio for only alfalfa hay ($P < 0.01$). Adding EPE to alfalfa silage had minimal effects on ruminal fermentation, and it had no effect on in vitro GP or degradability. In summary, adding EPE improved in vitro degradation of alfalfa hay, but not alfalfa silage, highlighting the importance of enzyme and substrate specificity.

Key Words: Exogenous Proteolytic Enzyme, Alfalfa Silage, Alfalfa Hay

W229 Amino acid content of residues from *in vitro* and *S. griseus* incubations. D. A. Ross* and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY.*

The degradability of ruminant feed proteins has been measured using *in vitro* (IV) and protease procedures but without comparative amino acid (AA) contents of the residues. The objective of this study was to evaluate the AA contents of the residues following a 24-hr IV fermentation and a comparative *S. griseus* (SG) incubation (1 EU/ml; Licitra et. al., 1998) at time points designed to correspond to the protein degradation observed in the IV fermentation for twelve feeds (four alfalfa forages, four corn silages and four soy products). The incubation times for the protease were predetermined to be 0.5 and 1 hr for the forages and 9 and 10 hr for the soy products. Only the time point that represents the value closest to the 24-hr IV nitrogen (N) degradation is presented. Parallel IV and SG incubations without feed were run and analyzed for AA content which were subtracted from the respective incubations in an attempt to correct for the microbial and protease contributions, respectively. The N content (g/g DM; mean ± SD) of the feeds were: alfalfa, 0.036 ± 0.003; corn silages, 0.013 ± 0.001; soy products, 0.080 ± 0.004. Residues from these incubations were analyzed for AA content using HPLC after acid hydrolysis or preoxidation followed by acid hydrolysis for sulfur AA. Significant differences were obtained when IV and SG incubations were performed on the same samples, even with the variation within feeds (Table 1). Apparently protease cleaves the N specifically without degrading the cell wall and was most prominent in the corn silages in which the protease degraded 58.7 % of the N but only 17.7 % of the DM while the IV significantly degraded more DM than N.

Table 1. The mean values for degraded DM, N and selected AA contents following IV and SG incubations (n= 4 samples per type).

Feed	trt	Degraded—>		Met	Lys	Leu	His
		% DM	% N	—mg	AA per	100 g	CP—-
Alfalfa	IV	53.6[a]	48.5[a]	9.2[a]	11.2[a]	15.0[a]	2.9[a]
	SG	37.1[b]	54.5[b]	4.9[b]	6.7[b]	10.9[b]	2.3[b]
Corn	IV	59.1[a]	14.1[a]	14.0[a]	19.1[a]	27.1[a]	5.8[a]
	SG	17.7[b]	58.6[b]	3.1[b]	5.6[b]	9.0[b]	2.5[a]
Soy	IV	68.9[a]	68.3[a]	11.7[a]	14.5[a]	20.2[a]	3.3[a]
	SG	56.1[b]	64.9[b]	5.8[b]	2.6[b]	10.7[b]	1.2[b]

[ab]Means within feed in same column with different letters are significant ($P < 0.05$).

Key Words: Amino Acids, *In Vitro*, *S. Griseus*

W230 Estimation of duodenal microbial N flow: Level of agreement between two methods of analysis. R. Martineau*[1], H. Lapierre[2], D. R. Ouellet[2], D. Pellerin[1], and R. Berthiaume[2], [1]*Université Laval*, *Québec, Canada*, [2]*Dairy and Swine R&D Centre, AAFC*, *Lennoxville, Québec, Canada*.

The concordance correlation coefficient (**CCC**) and the error of prediction (in central tendency, **ECT**; due to regression, **ER**; or due to disturbances, **ED**) were used to compare the level of agreement between 2 methods of estimation of duodenal microbial N flow. Either urinary purine derivatives (method 1) or duodenal purine flow and purine:N ratio from duodenal bacteria as microbial markers (method 2) were used. Duodenal DM flow was estimated using chromium oxide as an indigestible marker. Samples were collected during an experiment (replicated 3 x 3 Latin square design) evaluating the effects of three modes of conservation of timothy: 1) hay (**H**), 2) restrictively- (**F**; formic acid), or 3) extensively-fermented silage (**I**; inoculant). Diets were tested in 6 duodenally-cannulated Holstein cows (DIM = 162 ± 135 at start of experiment) fed 12 equal daily meals. Each period had a 14-d adaptation to the diet, followed by a 6-d total collection of feces and urine (method 1) and by a 2-d collection of digesta 14 d later (method 2). Duodenal digesta samples were collected at 0900, 1100, 1300 and 1500 on day 34, and at 0800, 1000, 1200 and 1400 on day 35. The DMI averaged 15.3 kg/d (SEM = 1.15; $P = 0.79$) during sampling in method 1, and 14.7 kg/d (SEM = 1.14; $P = 0.86$) during sampling in method 2. Three cow-period data were missing (2 for **H** and 1 for **F**). Duodenal microbial N flows were 195, 235 and 224 g/d (SEM = 31.4; $P = 0.18$) for method 1, and 248, 239 and 246 g/d (SEM = 24.5; $P = 0.83$) for method 2 in **H**, **F**, and **I**, respectively. The **CCC** over all treatments was 0.38, and was 0.44, 0.63 and 0.22 for **H**, **F**, and **I**, respectively. The **ECT** over all treatments was 11%, and was 81, <1 and 7% for **H**, **F**, and **I**, respectively. The **ER** over all treatments was 60%, and was 6, 60 and 72% for **H**, **F**, and **I**, respectively. The **ED** over all treatments was 29%, and was 13, 40 and 21% for **H**, **F**, and **I**, respectively. Present findings show a poor level of agreement between the 2 methods even though the correlation was high for **H** and average values were similar for **F** and **I**.

Key Words: Urinary PD, Purine, Microbial N

W231 Efficiency of microbial N supply (EMNS) and digestibility of N in dairy cows fed timothy conserved as restrictively- or extensively-fermented silage or as hay. R. Martineau*[1], H. Lapierre[2], D. R. Ouellet[2], D. Pellerin[1], and R. Berthiaume[2], [1]*Université Laval*, *Québec, Canada*, [2]*Dairy and Swine R&D Centre, AAFC*, *Lennoxville, Québec, Canada*.

The effects of three modes of conservation of timothy (*Phleum pratense L.*) on EMNS and N digestibility were investigated in a replicated 3 x 3 Latin square design with 35-d periods. Timothy was conserved as: 1) hay (**H**), 2) restrictively- (**F**; formic acid), or 3) extensively-fermented silage (**I**; inoculant). Diets (forage-to-concentrate ratio of 60:40) were tested in 6 ruminally- and intesti-

nally-cannulated Holstein cows (DIM = 162 ± 135) fed 12 equal daily meals. On days 34 and 35, 8 digesta samples (duodenal, ileal and fecal) were collected (ileal sampling on 3 cows only). Chromium oxide was used as an indigestible marker. Microbial N flow was estimated from the purine flow and the purine:N ratio of duodenal bacteria. The DMI averaged 14.7 kg/d (SEM = 1.14; P = 0.86). The EMNS was not affected by treatments. Duodenal N flux averaged 385 g/d and was similar (SEM = 31.0; P = 0.96) among treatments despite a lower N intake for cows on the hay diet. Cows receiving the hay diet had a higher preduodenal N recycling than cows receiving the silage diets. Total tract digestibility of N was not affected by treatments (P = 0.55) but intestinal digestibility of N was 3% higher (P = 0.01) in cows receiving the hay diet. Intestinal digestibility of non-microbial N was not affected by treatments (P = 0.43) whereas that of microbial N was 4% higher (P = 0.04) in cows receiving the hay diet compared to cows receiving the silage diets. Digestibility of microbial N in the small intestine was 10% greater (P = 0.06) for cows receiving the hay compared to the silage diets. Extent of silage fermentation did not affect any of the measured parameters. In conclusion, expected benefits on EMNS associated with feeding a forage with a low protein solubility and a high water soluble carbohydrate content were not observed in this experiment.

	Treatments				Contrasts (P)	
	H	**F**	**I**	SEM	**H** vs **F+I**	**F** vs **I**
EMNS[a]						
- g MN/kg OMADR	49.2	46.2	50.1	9.70	0.83	0.42
- g MN/kg OMTDR	29.5	28.3	29.3	3.35	0.71	0.61
N intake, g/d	275	310	317	24.7	< 0.01	0.43
Preduodenal N recycling, g/d	109	73	66	26.5	0.03	0.65
Non-microbial N, g/d						
- duodenal	135	146	137	16.7	0.37	0.22
- ileal	57	60	67	12.4	0.60	0.53
- fecal	63	64	65	13.0	0.75	0.93
Microbial N, g/d						
- duodenal	248	239	246	24.5	0.71	0.62
- ileal	50	78	71	7.4	0.15	0.41
- fecal	37	45	46	8.1	0.07	0.71

[a]OMADR and OMTDR: OM apparently and truly digested in the rumen

Key Words: Microbial Synthesis, Restrictively-Fermented Silage, Extensively-Fermented Silage

W232 Endogenous nitrogen (EN) flows: Effects of methods of conservation of timothy in lactating dairy cows. D. R. Ouellet*[1], R. Berthiaume[1], G. Holtrop[2], G. E. Lobley[3], R. Martineau[4], and H. Lapierre[1], [1]*Agriculture and Agri-Food Canada*, *Lennoxville, Canada*, [2]*BIOSS*, *Aberdeen, UK*, [3]*Rowett Research Institute*, *Aberdeen, UK*, [4]*Department of Animal Science, U. Laval*, *Quebec, Canada*.

The current NRC model (2001) estimates EN at the duodenum as 1.9 g per d per kg DMI, with no allowance for differences in diet quality. The current study used 4 lactating cows in a replicated incomplete 4x3 Latin square to study the effect of 3 methods of conservation of timothy (*Phleum pratense* L.) on EN flows. Treatments were: 1) sun-cured hay (**H**), 2) formic acid-treated silage (**F**) or 3) inoculated silage with *L. plantarum* and *P. cerevisiae* (**I**). Diets (60% forage) were fed every 2h. From d 27 to 35, cows were infused into a jugular vein with ^{15}N-leucine (0.45 mmol/h). On d 34 and 35, intestinal wall, duodenal digesta and feces were sampled (4 samples/day) to determine enrichment of ^{15}N. Contributions of EN flows were calculated as described (Ouellet et al., 2002; JDS 85:3013). Nitrogen intake and total N flow at the duodenum were similar between treatments but the contribution of free EN was greater for cows when fed H, both in absolute terms (P=0.06) or related to DMI (P=0.04; 3.0, 1.8, and 1.8 ± 0.36% of DMI for H, F and I). Total EN at the duodenum, however, was not affected by diets (84, 72, 75 ± 6.1 g/d for H, F and I). The EN loss in feces did not vary with treatments but real intestinal N digestibility was higher (P=0.06) for cows when fed H compared with F or I (77.5, 74.3, and 73.7 ± 0.75%). Overall, total EN represented 20% of total N at the duodenum and tended to vary (P=0.09) with diets (5.9, 4.5, 4.6 ± 0.54% of DMI for H, F and I), with a greater contribution than adopted by NRC (2001).

	Treatment				P	
Parameter (g N/d)	H	F	I	SEM	H vs. F, I	F vs. I
Intake	263	302	302	19.4	0.14	0.99
Duodenal digesta	399	398	381	23.1	0.74	0.54
-Undigested feed	126	130	114	12.5	0.79	0.32
-Free EN	43	29	30	4.5	0.06	0.91
-Bacterial	231	239	237	9.4	0.52	0.86
— From feed	155	158	156	8.8	0.90	0.86
— From EN	42	43	45	2.1	0.46	0.48
— From urea-N	34	39	37	2.0	0.13	0.42
Feces	97	111	111	5.2	0.07	0.91
-EN from duodenal EN	19	18	20	1.3	0.96	0.47
-EN from SI[a] secretions	8	9	10	3.4	0.60	0.83

[a]SI: small intestine

Key Words: Endogenous, Gastrointestinal Tract, Forage Conservation

W233 Effects of glutamate on microbial efficiency and metabolism in continuous culture of ruminal contents and on performance of mid-lactation dairy cows. H. M. Dann*[1], C. S. Ballard[1], R. J. Grant[1], K. W. Cotanch[1], M. P. Carter[1], and M. Suekawa[2], [1]*W.H. Miner Agricultural Research Institute*, *Chazy, NY*, [2]*Zen-Noh National Federation of Agricultural Co-operative Associations*, *Tokyo, Japan*.

Three experiments were conducted to determine 1) the dose of glutamate (Glu) needed to alter fermentation and N partitioning in a continuous culture system, 2) the effect of supplemental Glu in diets varying in rumen-undegradable protein (RUP) on fermentation and N partitioning in a continuous culture system, and 3) the effect of dietary supplemental Glu on the performance of lactating Holstein cows, total tract nutrient digestibility, and microbial N synthesis. All experiments added Glu in the form of monosodium L-glutamate. In Experiment 1, 0, 40, or 80 g Glu·cow^{-1}·d^{-1} was added to a basal diet and evaluated in a continuous culture system using a completely randomized design. Glu linearly decreased crude protein (CP) digestion (72, 67, 62%; P=0.03) and microbial N (2.1, 1.9, 1.7 g/d; P=0.02) and linearly increased non-ammonia, non-microbial N (NANMN; 0.8, 1.0, 1.2 g/d; P=0.03). Glu did not affect (P>0.05) carbohydrate digestion, volatile fatty acid (VFA) production, or fermenter pH. In Experiment 2, diets were formulated to have high RUP [HRUP; 6.8% of dry matter (DM)], low RUP (LRUP; 6.2% of DM), and low RUP plus 80 g Glu·cow^{-1}·d^{-1} (LRUP+G). Diets were evaluated in a continuous culture system using a completely randomized design. Digestion of CP and carbohydrate, microbial N, and NANMN were similar (P>0.05) among diets. LRUP+G had lower VFA production (376 vs 412 mmoles/d; P=0.04) and higher fermenter pH (6.3 vs 6.1; P=0.04) than LRUP. In Experiment 3, 40 lactating cows were utilized in a crossover study to test the effect of 2 dietary treatments: 0 or 80 g of supplemental Glu·cow^{-1}·d^{-1}. Glu did not affect (P>0.05) milk yield (0 vs 80 g Glu; 34.8 vs 34.2 kg/d), microbial N (254 vs 257 g/d), or total tract nutrient digestion. Based on the results from these in vitro and in vivo experiments, the addition of Glu to lactating cow diets is not recommended.

Key Words: Glutamate, Dairy Cow, Rumen

W234 Metabolic and production responses of dairy cows to glutamine (Gln) supplementation. L. Doepel*[1], J. F. Bernier[2], G. E. Lobley[3], P. Dubreuil[4], M. Lessard[5], and H. Lapierre[5], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Universite Laval*, *QC, Canada*, [3]*Rowett Research Institute*, *Aberdeen, UK*, [4]*Coll. Vet. Med., U. Montreal*, *St. Hyacinthe, QC, Canada*, [5]*Agriculture & Agri-Food Canada*, *Lennoxville, QC, Canada*.

This study examined the effect of supplemental Gln on the plasma metabolic profile and milk production of lactating dairy cows. Seven multiparous Holstein cows received abomasal infusions immediately after calving of either 300 g/d Gln (85 mmol/h) delivered in 10 L of water, or water alone in a crossover design with 21 d periods. Cows were fed a TMR twice daily except during d18-21 when they were fed 12x daily. Jugular blood samples were obtained on d4, 11, and 18 of each period. Dry matter intake was higher for the control cows than the Gln treated cows (18.9 vs. 18.0 ± 0.24 kg/d, P = 0.04) during d12-17. Both milk (39.4 vs. 41.2 ± 0.72 kg/d, P = 0.14) and milk protein (1197 vs. 1291 ± 57.0 g/d, P = 0.30) yields were unaffected by Gln treatment. Gln supplementation increased plasma Gln concentrations by 45% (225 vs. 326 ± 10.7 μM, P = 0.001). Total essential AA concentrations tended to be lower in Gln cows (900 vs. 756 ± 50.1 μM, P = 0.10). Glucose, lactate, NEFA, and BHBA concentrations were not affected by treatment, while urea-N increased with Gln supplementation (Table). These data suggest that decreased concentrations of Gln observed in early lactation do not limit milk protein secretion although an effect on AA metabolism cannot be excluded.

Plasma metabolite concentrations

	Ctrl	Gln	SEM	P
BHBA, mM	1.6	0.9	0.25	0.12
Glucose, mM	3.2	3.3	0.09	0.20
Lactate, mM	0.6	0.8	0.17	0.43
NEFA, mM	932	913	62.9	0.84
Urea, mM	8.3	11.2	0.19	0.01
Ala, mM	182	181	13.0	0.96
Glu, mM	41	42	1.2	0.36
Gly, mM	440	385	18.1	0.08
His, mM	48	51	2.0	0.35
Leu, mM	179	147	10.5	0.08
Lys, mM	75	63	5.1	0.14
Met, mM	29	23	1.4	0.04
Tyr, mM	42	36	2.0	0.08
Val, mM	267	213	15.9	0.06

Acknowledgements: Thanks to Ajinomoto for supplying the glutamine.

Key Words: Glutamine, Metabolic Response, Dairy

W235 Effect of glutamine (Gln) supplementation on splanchnic flux in lactating dairy cows. L. Doepel*[1], J. F. Bernier[2], G. E. Lobley[3], P. Dubreuil[4], M. Lessard[5], and H. Lapierre[5], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Universite Laval*, *Quebec, Canada*, [3]*Rowett Research Institute*, *Aberdeen, UK*, [4]*Coll. Vet. Med., U. Montreal*, *St. Hyacinthe, QC, Canada*, [5]*Agriculture & Agri-Food Canada*, *Lennoxville, QC, Canada*.

Seven multicatheterized Holstein cows were used to determine if Gln affected net splanchnic flux of N and energy metabolites. Cows received abomasal infusions of water (10L) or 300 g/d Gln (85 mmol/h) in a cross-over with 21-d periods starting 1 d after calving. Cows were fed a TMR every 2 h during the last 4 d of each period. On d 21, six blood samples were collected simultaneously from arterial, portal and hepatic vessels at 45 min intervals. Para-amino hippurate was infused to determine blood flows. Together, the increment in Gln plus Glu portal absorption accounted for 77% of the Gln infused. Despite increased Gln absorption, the increment in hepatic removal resulted in no effect on splanchnic net release of Gln (13 vs 2 ± 5.4 mmol/h: P = 0.22). Although there was no effect on individual amino acids (AA), Gln tended to decrease absorption of the total AA-N measured (sum of Ala, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Tyr & Val; excludes Gln). Splanchnic net flux of total AA-N also decreased with Gln (362 vs 253 ± 34.0 mmol/h; P = 0.08). Increased hepatic removal of total AA and Gln was accompanied by elevated ureagenesis. Net portal flux of glucose was unaffected by Gln, indicating no sparing of glucose utilization by the gut. Despite reports that Gln impacts on intestinal metabolism *in-vitro*, supplementation to cause a major increase in Gln net absorption does not appear to improve either energy (glucose and lactate) or protein (AA) metabolism across the gut of lactating dairy cows.

Effect of Gln infusion on net splanchnic flux of N and energy metabolites (mmol/h)

	portal Ctrl	portal Gln	SEM	P	liver Ctrl	liver Gln	SEM	P
Gln	8	69	5.7	0.01	6	-67	7.0	0.01
Glu	10	13	0.9	0.03	31	28	1.5	0.22
Ala	84	88	5.1	0.62	-63	-77	8.7	0.30
Total AA-N[1]	502	461	19.7	0.19	-140	-208	47.5	0.34
Urea-N	-478	-469	55.0	0.91	1120	1378	109.6	0.16
Ammonia	446	480	32.3	0.49	-428	-470	30.0	0.37
Glucose	33	23	17.9	0.71	692	666	57.9	0.76
Lactate	164	176	6.3	0.22	-291	-293	23.4	0.94

[1]Excludes Gln

Acknowledgements: Thanks to Ajinomoto for supplying the glutamine

Key Words: Glutamine, Splanchnic, Dairy

W236 Determination of the first-limiting amino acid for milk production in dairy cows consuming a high concentrate diet containing corn and soybean meal. H. S. Kim[1], J. M. Yeo*[1], K. S. Ki[1], and C. -H. Kim[2], [1]*Dairy Science Division, National Livestock Research Institute, Rural Development Administration*, *South Korea*, [2]*Department of Animal Life and Resources, Hankyong National University*, *South Korea*.

Four lactating Holstein cows consuming a high concentrate diet were used in a 4 x 4 Latin square with 10-d periods to determine the first-limiting amino acid (AA) for milk production. The four intravenous infusion treatments were no infusion (control); a mixture of 6 g/d methionine, 19.1 g/d lysine, 13.8 g/d isoleucine and 15.4 g/d valine (4AA); the mixture without methionine (-Met); and the mixture without lysine (-Lys). Cows were given a basal diet of alfalfa hay (1 kg/d), corn silage (10 kg/d) and a concentrate mixture (14 kg/d; 63.0 % dry ground corn, 20.0 % soybean meal, 9.4 % cotton seed meal, 6.0 % sugar beet pulp and 1.6 % mineral and vitamin mixture on a fresh weight basis) and *ad libitum* access to timothy hay. The four AA were expected as limiting AA, which would be deficient for milk production from the basal diet according to NRC (2001). Alfalfa hay, corn silage and the concentrate mixture were completely consumed on all treatments. Relative to control, the 4AA treatment significantly (P < 0.05) increased the yield (913 vs. 997 g/d) and concentration (2.93 vs. 3.08 %) of milk protein and this response was not diminished by omission of lysine. However, excluding of methionine showed no response over control, suggesting that methionine was the first limiting AA. No significant differences were found in timothy hay DM intake and milk yield between treatments. The 4AA treatment numerically increased the concentrations of the infused AA in plasma compared with control. The results of the present experiment indicate that secretion of milk protein was limited only by methionine deficiency in cows fed a high concentrate diet containing primarily corn and soybean meal although it was calculated that lysine, isoleucine and valine would seem to be also deficient.

Key Words: Amino Acids, Milk Protein, Dairy Cow

W237 Effect of supplementing rumen-protected methionine at two levels of dietary crude protein in lactating dairy cows. G. A. Broderick*[1], M. J. Stevenson[2], R. A. Patton[3], N. E. Lobos[4], and J. J. Olmos Colmenero[4], [1]*U.S. Dairy Forage Research Center*, *Madison, WI.*, [2]*Degussa Corp.*, *Kennesaw, GA*, [3]*Nittany Dairy Nutrition, Inc.*, *Mifflinburg, PA*, [4]*University of Wisconsin*, *Madison*.

Leonardi et al. (J. Dairy Sci. 86:4033, 2003) reported that supplementing rumen-protected Met (RPM) increased milk protein concentration at both 16.1 and 18.8% crude protein (CP), with no interaction. This would be unexpected if Met were the first-limiting metabolizable AA. Cows in their study were calculated to be in positive energy balance. A 4x4 Latin square lactation trial was conducted with a 2x2 arrangement of diets: 17.3 or 16.1% CP, with or without supplementation of about 15 g/d of RPM (as Mepron®). Diets were fed as TMR and contained (DM basis) 21% alfalfa silage, 28% corn silage, 4.5% roasted soybeans, 5.8% soyhulls, 0.6% sodium bicarbonate, 0.5% vitamins and minerals, and 27% NDF. Dietary CP was lowered by replacing solvent soybean meal with high moisture shelled corn. Thirty-two multiparous Holstein cows averaging 604 kg BW were blocked by DIM into 8 groups and randomly assigned to the 4x4 Latin square sequences. Periods were 4-wk long and production data were collected from the last 2-wk. The statistical model included square, period, cow(square), CP, RPM, and CP*RPM; least square means are reported. All treatments were calculated to be in negative energy balance due to lower than expected DMI. There were no effects of RPM supplementation on any production trait. However, higher CP increased ($P \leq 0.03$) yield of milk, protein, and SNF by 1.0, 0.04, and 0.11 kg/d; there were trends ($P \leq 0.09$) for increased DM intake and lactose yield at higher CP. A trend ($P = 0.08$) for an interaction suggested that protein yield increased when RPM was fed at higher CP but decreased when RPM was fed at lower CP. However, apparent N efficiency (milk N/N-intake) was greater ($P < 0.01$), and MUN lower ($P < 0.01$), on lower CP diets and both were unaffected by RPM feeding. Under the conditions of this trial, reducing dietary CP from 17.3 to 16.1% reduced yield of milk, protein and SNF and this reduction was not reversed by supplementing with RPM.

Item	CP, %	17.3	17.3	16.1	16.1	Contrasts (P > F)		
RPM g/d	0	15.4	0	14.6	SE	CP	RPM	CP*RPM
DMI, kg/d	21.6	21.8	21.6	20.9	0.3	0.09	0.44	0.14
Milk, kg/d	39.8	40.1	39.2	38.7	0.4	0.01	0.87	0.34
Fat, %	3.57	3.59	3.65	3.62	0.09	0.55	0.94	0.81
Fat, kg/d	1.40	1.43	1.42	1.38	0.04	0.71	0.94	0.81
Protein, %	3.08	3.09	3.07	3.06	0.02	0.37	0.98	0.67
Protein, kg/d	1.21	1.23	1.19	1.17	0.01	0.01	0.94	0.08
SNF, %	8.85	8.85	8.83	8.83	0.02	0.24	0.79	0.99
SNF, kg/d	3.47	3.57	3.44	3.38	0.05	0.03	0.67	0.10
MUN, mg/dl	12.4	12.1	10.2	10.2	0.2	< 0.01	0.38	0.45
Milk N/N-intake	0.32	0.32	0.34	0.35	0.01	< 0.01	0.37	0.91

Key Words: Mepron, Rumen-Protected Methionine, Milk Yield

W238 Effects of supplemental DL-methionine and L-lysine-HCl on ruminal fermentation and ruminal and total tract digestibility in non-lactating Holstein cows. H. G. Bateman, II*, T. W. Braud, C. C. Williams, D. T. Gantt, C. F. Hutchison, J. D. Ward, P. G. Hoyt, and G. A. Sod, *Louisiana State University*, *Baton Rouge*.

Four non-lactating Holstein cows (average 642 kg body weight) were used in a replicated switchback design experiment to evaluate the use of supplemental DL-methionine and L-Lysine-HCl on ruminal fermentation and apparent ruminal and total tract digestibility. The base diet consisted of (DM basis) 45% corn silage, 20% cottonseed hulls, 15% ground corn, 15% soybean meal, and 5% vitamin and mineral premix. Treatments were either the base diet or the base diet top dressed with 190 g L-lysine-HCl and 20g DL-methionine. To insure that cows would consume all feed, as offered feed intake was restricted to approximately 12 kg/d prior to the addition of the amino acids. Periods were 7 d in length with an abrupt switch of treatments at the beginning of each period. Flow of digesta was estimated using Cr_2O_3 (10 g/d) as an external marker. Samples were collected every 4 h over the last 3 d of each period moving the collection time forward 2 h each day. Addition of amino acids tended ($P < 0.1$) to increase DMI but had no effect of apparent ruminal or total tract dry matter digestibility. Apparent total tract N digestibility was not affected by treatment. Ruminal pH averaged 6.4 and was not affected by addition of amino acids. Addition of amino acids did not alter the proportions of VFA or total VFA concentrations in ruminal fluid. Ruminal ammonia N averaged 2.9 mg/dl but was not affected by treatment. Results indicate that supplemental methionine and lysine were not effective in stimulating ruminal fermentation and altering ruminal or total tract digestibility in non-lactating cows.

Key Words: Rumen, Methionine, Lysine

W239 The effects of Alimet feed supplement and Sequent feed supplement on rumen digestibility, protein synthesis and ruminal disappearance. M. Vazquez-Anon*, *Novus International, Inc*, *St. Louis, MO*.

A dual effluent continuous culture system was used to investigate the effect of inclusion of Alimet (2 hydroxy 4 [methylthio] butanoic acid (HMTBA),source Novus International, Inc.) and Sequent (2-propyl ester of HMBTA (HMTBi), source Novus International, Inc) in the diet on nutrient digestibility, bacterial protein synthesis and ruminal disappearance. Twelve fermenters were fed a basal diet two times a day that consisted of 52% grain mixture and 48% forage for 9 days. In experiment one, 0, 0.1% of HMTBA, and 0.1% HMTBi were added to the diet and fed to the fermenters. In experiment two, 0.1% HMTBA was added to the diet in the presence and absence of active yeast (10^{12} cfu/kg diet), and in experiment three, 0.1% HMTBA + 65 ppm Agrado® feed supplement were added to a diet that contained 1.9% rumen protected fat or 1.9% of a blend of corn, linseed, and menhaden fish oils. In experiment one, HMTBA significantly improved and HMTBi significantly ($P < 0.05$) reduced microbial protein synthesis and efficiency. The by-pass of HMTBA and HMTBi were 63% and 75%, respectively. In experiment two, HMTBA improved CP digestibility, microbial protein synthesis and efficiency, and yeast improved CP and ADF digestibility. In experiment three, addition of HMTBA + Agrado restored the microbial protein synthesis depression observed in diets with unprotected fat. It can be concluded that a fraction of HMTBA survived rumen degradation and therefore provides a rumen protected form of methionine at the same time as it improves bacterial protein synthesis and efficiency in the presence and absence of yeast and unprotected fat. It is also concluded that a fraction of HMTBi escapes rumen degradation but has limited ruminal effect.

Acknowledgements: ALIMET and AGRADO are trademarks of Novus International, Inc. and are registered in the United States and other countries SEQUENT is a trademark of Novus International, Inc.

Key Words: HMTBA, Yeast, Fat

W240 Effects of corn source with or without supplementation of lysine and methionine on milk production in dairy cows. C.-H. Kim*[1], H. S. Kim[2], and J. M. Yeo[2], [1]*Hankyong National University*, *Ansung, Gyeonggi, Korea*, [2]*Dairy Science Division, National Livestock Research Institute, Rural Development Administration*, *Cheonan, Chungbuk, Korean*.

Four lactating Holstein cows were used in a 4 x 4 Latin square with four 10-day periods and a 2 x 2 factorial arrangement of treatments to examine the effect of intravenous infusions of lysine (19.1 g/d) and methionine (6 g/d) (IVLM) in diets containing dry ground (GC) or steam flaked corn (SFC) on milk production. The treatments were as follows: GC diet, GC diet plus IVLM, SFC diet and SFC diet plus IVLM. Cows were given a fixed amount of alfalfa hay (1 kg/d), corn silage (10 kg/d) and a concentrate mixture (14 kg/d) containing primarily GC or SFC (410 g/l) and *ad libitum* access to timothy hay. There were no interactions between the amino acids infusion and corn source. Alfalfa hay and corn silage and the concentrate mixture were completely consumed on all treat-

ments. Timothy hay DM intake (10.4, 10.1, 8.7 and 8.5 kg/d, respectively) was significantly lower for the SFC diet than for the GC diet ($P < 0.01$) but the amino acids infusion did not affect it. No significant differences were found in milk yield (36.3, 35.8, 36.8 and 36.6 kg/d) between treatments. Therefore, the SFC diet significantly increased feed efficiency (4 % fat corrected milk/DM intake) compared with the GC diet (1.38, 1.33, 1.53 and 1.54; $P < 0.001$). There were no significant differences in the concentrations and the yields of milk composition between treatments with the exception that the SFC diet significantly increased milk protein yield (1087, 1103, 1143 and 1135 g/d; $P < 0.01$) compared with the GC diet. Allantoin/creatinine ratio in spot urine and the concentrations of glucose and urea-N in plasma were not affected by treatments. The results of the present experiment show that the diet itself was sufficient to meet the requirement of methionine and lysine for milk production and that the yield of milk protein could be modulated by changes in corn source.

Key Words: Corn Source, Amino Acids, Dairy Cow

W241 Effect on milk protein of reducing crude protein intake while maintaining methionine and lysine: A field study. L. E. Armentano[1], R. A. Patton*[2], and M. J. Christians[3], [1]*University of Wisconsin*, *Madison*, [2]*Nittany Dairy Nutrition*, *Mifflinburg, PA*, [3]*Degussa Corporation*, *Kennesaw, GA*.

The objective of the study was to increase the ratio of methionine and lysine as % of metabolizable protein by maintaining the supply of methionine and lysine as predicted by the Mepron 2.6 program, while reducing the amount of CP in the diets of dairy cows. Treatments consisted of a Control which was the normal herd ration and an AA Balanced ration which was balanced for the same g of MET and LYS but lower in CP. Predicted LYS g were maintained with soybean products and blood meal and MET g with corn gluten meal, fishmeal or Mepron®. The experiment was conducted over 6 wk, consisting of 2 periods of 3 wk. Nineteen herds in central Wisconsin participated with half the herds starting the experiment on the control diet and half on the AA Bal diet. At the end of 3 wk diets were abruptly switched. Once each period milk was weighed and sampled for milk components. Statistical analysis was by Proc Mixed of SAS and included terms for diet, sequence, period and herd, where herd was the observational unit. Data from pre-peak cows or cows that left the herd prior to period 2 sampling were excluded. The AA bal diets were only slightly lower in CP (17.2%) compared to the control (17.9%). This resulted in slight, but significant differences in AA % MP (2.10 vs 2.18 for MET and 7.11 vs 7.17 for LYS, both P<.01) and LYS:MET (3.39 vs 3.29) for control relative to AA Bal rations. Production variables were unaffected by diet. We conclude there is potential to reduce the amount of CP in dairy diets. If MET and LYS as MP affect milk protein percent, differences would need to be larger than those in this study.

Item	Control Mean	AA Bal Mean	SEM	Diet P Values	Sequence P Values	Period P Values
Milk kg/d	34.6	34.5	0.53	0.89	0.55	0.01
Protein %	3.19	3.23	0.03	0.18	0.10	0.44
Protein kg/d	1.10	1.11	0.08	0.71	0.85	0.02
Fat %	3.69	3.63	0.08	0.45	0.73	0.50
Fat kg/d	1.27	1.25	0.12	0.42	0.33	0.04

Key Words: Methionine, Lysine, Metabolizable Protein

W242 Postruminal protein infusion increases leucine use by the gastrointestinal tract of sheep while glucose utilization remains unchanged. S. El-Kadi*[1], R. Baldwin, VI[2], N. Sunny[1], S. Owens[1], and B. Bequette[1], [1]*University of Maryland*, *College Park*, [2]*USDA-ARS*, *Beltsville, MD*.

To date, the metabolism of amino acids (AA) and glucose by the gastrointestinal tract (GIT) of ruminants in response to increments of postruminal protein supply has not been studied. Our aim was to determine if leucine and glucose metabolism by the mesenteric (MDV; small intestine) and portal (PDV; whole gut) drained viscera represents a fixed amount or a fixed fraction of intestinal supplies in sheep fed a low protein diet with duodenal casein infusion. Wethers (n=4, 33 ± 2.0 kg) were fitted with catheters for casein infusion and for measurements of PDV and MDV leucine and glucose metabolism. Animals were fed a forage-based diet (9.5 % CP) to 1.4 × maintenance and given 5-d duodenal casein (0, 35, 70 and 105 g/d) infusions in a 4 × 4 Latin square design. On day 5 of each period, jugular [1-^{13}C]leucine and [6-$^{2}H_2$]glucose and duodenal [$^{2}H_3$]leucine tracers and a blood flow marker were infused for 8 h. Blood was continuously withdrawn over 1-h intervals during the last 4-h period of tracers infusion. Postruminal protein supplementation increased whole body leucine irreversible loss ($P < 0.05$). Leucine arterial sequestration by the MDV was not affected, however, arterial sequestration by the PDV increased linearly ($P < 0.05$) in response to casein infusion. Leucine removal by the GIT represented a fixed proportion of leucine irreversible loss (MDV = .16; PDV = .33) for all levels of casein. Despite the increase in glucose entry rate with casein infusion ($P < 0.05$) and the significant increase in blood glucose concentration, GIT arterial removal did not change. Our data show that casein infusion could have stimulated hepatic gluconeogenesis possibly from AA. It also appears that the GIT is opportunistic in its use of AA from arterial and/or luminal sources, whereas the fixed glucose utilization could reflect an obligatory GIT requirement.

Key Words: Leucine, Glucose, Gastrointestinal Tract

W243 Appearance of free and peptide-bound AA in blood from the rumen, abomasum, and intestines and in lymph from the intestine of sheep. L. A. Sullivan and K. E. Webb, Jr.*, *Virginia Tech*, *Blacksburg*.

Appearances of free (FAA) and peptide-bound AA (PBAA) in blood from the rumen, abomasum, and intestines and in lymph from the intestine were quantified. Six ewe lambs (avg. wt. = 28.2 kg) were anesthetized with pentobarbital 2 hr postprandial, the abdominal cavity was opened and a catheter was placed in a mesenteric lymph duct and lymph was collected on ice for 30 min. Blood was collected via syringe and needle from a mesenteric artery and from ruminal, abomasal, and mesenteric veins midway through lymph collection and plasma was separated immediately by centrifugation. Lymph and plasma were combined with two volumes of methanol and allowed to stand at 2°C overnight and then were centrifuged (27,000 x g, 2°C, 30 min) and the supernatants were filtered using Centricon-3-microconcentrator 3,000 MW cut-off filters. Individual AA concentrations were determined on the filtrate for FAA and the filtrate following hydrolysis (vaporized HCl at 112°C for 24 h) for total AA. Concentrations of PBAA were calculated as the difference between total and FAA. There was a net appearance of total FAA and PBAA in blood draining the intestines and rumen as indicated by positive veno-arterial differences. There was a net appearance of total PBAA in and a net disappearance of total FAA from blood draining the abomasum as indicated by positive and negative, respectively, veno-arterial differences. Concentrations of individual FAA were greater ($P < 0.04$ to 0.001) than PBAA in lymph from the intestine and were reflected in a greater ($P < 0.001$) total FAA than PBAA concentration (274.6 and 122.2 mg/L, respectively). As observed previously, the results of the present study confirm that both FAA and PBAA enter the blood from the rumen and the intestine. The novel observations from the present study are that peptides may be absorbed from the abomasum and that both FAA and PBAA leave the intestine via the lymph. Accounting for the contributions of all of these pools will result in the most accurate estimate of absorbed AA.

Key Words: Amino Acid, Peptides

W244 Digestibility and N flux in steers fed diets with differing sources of supplemental protein. J. Eisemann*, G. Huntington, and M. Poore, *North Carolina State University*, *Raleigh*.

The objective was to determine the nutritional value of duckweed (DW, *Lemma gibba*, 391g CP/kg DM) in diets of cattle. The DW used was harvested locally and dried until DM reached 90%. The experimental design was a 4 X 4 Latin square with four Holstein steers (326 kg BW). Steers were fed diets containing no supplemental protein (Basal), a positive control with supplemental protein from soybean meal (SBM), a diet with 2/3 of the supplemental protein from corn gluten meal (CGM) and a diet with 2/3 of the supplemental protein from

DW. The basal diet included (g/kg DM) wheat hay (440), soybean hulls (255), ground corn grain (250), minerals (12.5) and molasses (42.5). Diets were fed at 2.8 kg/d per 100 kg BW. Each period was 2 wk of dietary adaptation followed by a 5-d total urine and feces collection. Beginning 4 d before and during the balance trial steers were fed equal-weight meals every 6 h. A 60 min infusion (i.v.) of ^{15}N-glycine (2.6 mg/kg BW) was begun on d2 of the balance trial. Total urine was collected at 5, 11, 17, 23, 35, 47 and 71 h following glycine infusion. Concentration and ^{15}N-enrichment of urinary urea were determined for calculation of N flux. N excreted was subtracted from N flux to estimate N used to synthesize protein (PS). Individual treatment values were compared where protein sources differed (P<0.10). Data are listed for Basal, SBM, CGM and DW treatments, respectively. N digestibility was greater (P<0.01) for supplemented diets and greater (P=0.06) for DW than SBM. Values (%) were 46.2, 55.0, 58.3 and 60.4. N intake, N retained, and N retained/N digested values were greater (P<0.01) for supplemented diets. N retained/digested was greater (P<0.05) for CGM than DW. Values for N intake (g/d) were 135.1, 172.2, 173.1, and 176.5; for N retained (g/d) were 35.2, 52.2, 62.5, and 56.2; and for N retained as % of digested were 56.4, 54.9, 63.1 and 51.9. N flux toward PS was greater (P<0.01) for supplemented diets and greater (P<0.05) for SBM than DW. Values (g/d) were 249, 335, 314, and 290. Steers readily consumed the DW. Post-absorptive use of N from DW was less efficient than from CGM.

Key Words: Steers, Protein Supplements, Protein Turnover

W245 Effect of RDP source on production and ruminal metabolism of lactating dairy cows. S. M. Reynal*[1] and G. A. Broderick[2], [1]*University of Wisconsin*, *Madison*, [2]*US Dairy Forage Research Center*, *Madison, WI*.

Twenty-eight lactating dairy cows (8 with ruminal cannulas) averaging 137 DIM were used in a 4 x 4 Latin square design with 28-d periods to study the effect of dietary RDP source on production and ruminal metabolism. Diets contained (DM basis) 15% alfalfa silage, 40% corn silage, 29 to 27% high-moisture corn, and 16 to 18% concentrate mix. Proportions of ingredients (DM basis) in the four concentrate mixes in diets A to D were changed in equal increments to replace RDP from solvent soybean meal (SSBM) with RDP from urea as follows: ground shelled corn, from 0 to 6.3%; SSBM, from 13.7 to 2.7%; lignosulfonate-treated SBM, from 0 to 6.0%, and urea, from 0 to 1.0%. Diets contained on a DM basis 16.3% CP, 26% NDF, and 14% ADF. Estimated (NRC, 2001) dietary concentrations of NEl, NFC, RDP, and RUP were constant across diets and were, respectively, 1.60 Mcal/kg and 50, 10.6, and 5.7% of diet DM. Data were analyzed as a Latin square design using the Proc Mixed procedure of SAS. Linear effects (tested using contrasts) of replacing SSBM with urea from diets A to D were negative for DMI (23.6 to 22.3 kg/d; P < 0.01), body weight gain (BWG; 0.57 to 0.34 kg/d; P = 0.04), and yields of milk (39.3 to 36.0 kg/d; P < 0.01), 3.5% FCM (36.7 to 34.2; P < 0.01), milk protein (1.27 to 1.17 kg/d; P < 0.01), milk fat (1.20 to 1.11 kg/d; P = 0.02), and SNF (3.59 to 3.32 kg/d; P < 0.01). Concentrations of fat, protein, and SNF in milk and ruminal pH were not significantly affected by RDP source and averaged, respectively, 3.05, 3.19, and 9.04%, and 6.53 across diets. Replacing non-urea N with urea N in the RDP resulted in linear increases in the concentrations of urea-N in milk (from 6.8 to 9.1 mg/dl; P < 0.01) and blood (from 8.9 to 12.8 mg/dl; P < 0.01) and of ammonia-N in the rumen (from 8.4 to 10.8 mg/dl; P < 0.01). Replacing SSBM with urea in the RDP negatively affected milk production and BWG (mainly through an effect on DMI) and N utilization in lactating dairy cows.

Key Words: RDP Source, Performance, Dairy Cows

W246 Effects of protein source on ruminal and total tract nutrient digestibility in non-lactating Holstein cows. T. W. Braud*, H. G. Bateman, II, C. C. Williams, C. C. Stanley, D. T. Gantt, C. F. Hutchison, J. D. Ward, P. G. Hoyt, and G. A. Sod, *Louisiana State University*, *Baton Rouge*.

Six non-lactating Holstein cows with ruminal and duodenal cannulas were used in a replicated 3x3 Latin square design experiment to investigate the effects of supplemental protein source on ruminal and total tract digestibilities. Supplemental protein was provided from soybean meal (SBM), expeller processed soybean meal (EXP), or menhaden fish meal (FISH). Basal diets consisted of (DM basis) 33% corn silage, 20% bermudagrass hay, 27% ground corn, and 2% minerals and vitamins. Supplemental protein was provided as (DM % of total diet) 18% soybean meal (SOY), 17% soybean meal and 1% fish meal (FISH), or 12% soybean meal and 6% expeller processed soybean meal (EXP). Period length was 14 d. Flow of digesta was estimated using Cr_2O_3 (20g/d) as an external marker. Dry matter intake averaged 9.5 kg/d and was not affected by treatment. Apparent ruminal dry matter digestibility was not affected by source of supplemental protein. Source of supplemental protein did not affect apparent total tract dry matter digestibility. Feeding low ruminal degradable protein to non-lactating cows resulted in no appreciable impact on feed intake or apparent diet digestibility.

Key Words: Rumen, Protein, Degradability

W247 Influence of slow-release urea on N balance and nutrient absorption of steers. C. C. Taylor*[1], N. A. Elam[1], S. E. Kitts[1], K. R. McLeod[1], D. E. Axe[2], and D. L. Harmon[1], [1]*University of Kentucky*, *Lexington*, [2]*Mosaic*, *Riverview, FL.*

Effects of urea or slow-release urea (SRU) on N balance and nutrient absorption were investigated. Four Holstein steers (236 ± 43 kg BW) and six Angus steers (367 ± 46 kg BW) were surgically prepared with hepatic portal, hepatic venous, mesenteric venous, and mesenteric arterial catheters. Catheterized steers were utilized in a crossover design with 21 d periods. Treatments were either urea or SRU at 1.6% of diet DM combined as a total mixed ration with 88.4% corn silage and 10% ground corn-based supplement on a DM basis. Diets were offered twice daily (12 h apart) at 2.0% of BW. Total fecal and urine output were measured on d 15 to 19. Nutrient absorption across the portal drained viscera (PDV) was determined on d 21 of each period by continuous infusion of p-aminohippuric acid into the mesenteric venous catheter. Simultaneous arterial, portal and hepatic blood samples were obtained 0, 2, 4, 6, 8, and 10 h relative to feeding. Mean DMI was 6.25 kg/d and did not differ among treatments. Mean N intake (124.9 g/d), urinary N excretion (total and as a percent of N intake) did not differ among treatments. SRU increased fecal N as a percent of intake N (34.4 vs. 38.5%; P < 0.05) by numerically increasing fecal N (43.7 vs. 47.4 g/d; P < 0.11). N balance was 41.0 g/d and 47.4 g/d for animals fed SRU and urea, respectively (P < 0.16), but did not differ as a percent of N intake (P < 0.30). Both treatments increased arterial urea concentrations from 2 to 6 h after feeding but SRU consistently reduced mean arterial urea N concentration (trt×time P < 0.01). SRU increased mean portal plasma flow (P < 0.05). Portal venous-arterial urea N difference did not differ but mean net portal urea flux was -52 and -64 mmol/h for urea and SRU, respectively (P < 0.06), indicating SRU increases net transfer of urea to the PDV. These results show SRU reduces plasma urea concentrations but increases net recycling of urea to the PDV; however, greater fecal N may suggest limited availability or timing of urea availability for utilization.

Key Words: Urea, N Balance, N Recycling

W248 Encapsulated slow release urea in lactating dairy cow diets impacts microbial efficiency and metabolism in continuous culture. J. Garrett*[1], T. Miller-Webster[2], W. Hoover[2], C. Sniffen[3], and D. Putnam[1], [1]*Balchem Encapsulates*, *New Hampton, NY*, [2]*West Virginia University*, *Morgantown*, [3]*Fencrest, LLC*, *Holderness, NH*.

The objectives were to compare the effectiveness of encapsulated, slow release urea (SRU), containing 89% urea, (Nitroshure™; Balchem, New Hampton, NY) relative to urea (U) or soybean meal 48 (SBM) in lactating dairy cow diets. Diets were formulated for a cow producing 45 kg/d, eating 24.5 kg of DM/d, and tested in a continuous culture fermentation system (Rumen Profiling Lab., West Virginia University, Morgantown, WV). The six diets tested were: T0, (0 SRU, 0.16 kg U), T1 (0.11 kg SRU, 0.05 kg U, T2 (0.16 kg SRU, 0 U,) T3 (0.07 kg SRU, replaced 0.36 kg SBM), T4 (0.17 kg SRU, replaced 0.9 kg SBM), T5 (0.27 kg SRU, replaced 1.46 kg SBM). For diets T0, T1 and T2, SBM was held constant at 12.3% of DM. For T3, T4, and T5, a mix of 18.9% SRU, 12.1% molasses, and 69% corn replaced SBM on an equal DM basis, while U was held

at 0.14 kg/d. Culture conditions were: liquid dilution rate, 13.0 %/h, solids dilution rate 4.5%/h, solids retention time 22.0 h, feeding frequency, 25 g DM, every 6 h. Each diet was tested in triplicate 9 d fermentations with effluent samples composited for analysis from the last 3 d of each fermentation. Data were analyzed using the GLM procedure of SAS®, with Duncan's Multiple Range Test used to compare individual treatment means. Results are shown in Table 1 below. The response to SRU appeared to be optimized at 0.16 kg per day and, for most parameters, T4 was the optimum treatment.

Table 1. Changes in rumen metabolism.

Item	T0	T1	T2	T3	T4	T4
DMD[1],%	60.0[a,b,c]	58.6[b,c]	56.6[c]	57.7[b,c]	65.6[a]	63.1[a,b]
NAN, g/d	2.88[a,b]	2.94[a]	2.93[a]	2.91[a,b]	2.87[a,b]	2.82[b]
NANMN[1], g/d	0.69[a,b]	0.86[a]	0.60[a,b]	0.67[a,b]	0.48[b]	0.44[b]
MN[1], g/d	2.18	2.08	2.33	2.23	2.39	2.37
MN g/kg DMD	36.3[b]	35.5[b]	41.3[a]	38.8[a,b]	36.5[b]	37.5[b]
TVFA[1] mol/kg MN	189[a,b]	194[a]	172[a,b]	174[a,b]	169[a,b]	162[b]

[a,b,c] Means differ, P<.05. [1] DMD = DM digested, NDFD = NDF digested, NANMN = non-ammonia non-microbial N, MN = microbial N, TVFA = total VFA

Key Words: Slow Release Urea, Encapsulated, Ruminal

W249 Ruminal degradation of crude protein of cull chickpeas using nylon bag technique in bovines. R. Barajas*, L. R. Flores, and J. J. Lomeli, *FMVZ-Universidad Autonoma de Sinaloa*, *Culiacan, Sinaloa, Mexico*.

The nylon bag technique was used to determine the ruminal degradation of crude protein of cull chickpeas in bovines. Four bovines (Simbrah; female, BW = 280 kg) were fitted with T cannulas in rumen. The animals were fed a diet containing sudan grass hay 30%, corn grain 33.5%, cull chickpeas 20%, soybean meal 3.5%, sugar cane molasses 10%, urea 0.4%, and mineral premix 2.6% (13% CP and 2.78 Mcal ME/kg). Pairs of nylon bags (12 X 18 cm) containing five grams of ground chickpeas (CHP) or soybean meal (SBM) were placed in rumen, and incubated for 3, 6, 9, 12, 15, 18, 21, and 24 h. After removal from the rumen, residual CP content were determined. Solubility was obtained placing the bags in a 0.15 N NaCl solution. Kinetic parameters A, B, and C were calculated for CHP and SBM. Rate of passage of small protein particles (K) was estimated as 0.02 to calculate the effective degradability of CP in rumen. Residual CP values of CHP at 0, 12 and 24 h incubation were used to obtain the rumen undegradable crude protein (UCP), taking as reference the value of 20% for SBM. Chickpeas CP was 80% more soluble (P < 0.05) than SBM-CP (46.51 vs 25.77%). The CP disapearance from nylon bags was higher (P < 0.05) for CHP than SBM during the 3, 6, 12, 15, and 21 hours of incubation. CP degradability at 24 hours was similar (P > 0.10) for CHP and SBM (98.98 vs 98.19%). The degradation rate of CHP-CP was 0.194 %/h (r = 0.95). The effective CP degradation in rumen for CHP was estimated to be 93.9%. The calculated rumen UCP content of chickpeas was 5.16%. It is concluded, that CP of chickpeas is extensively degraded in rumen of bovine.

Key Words: Chickpeas, Degradabilty, Bovine

W250 Utilization of different protein sources as supplements to whey treated straw silage. F. T. Sleiman*, M. N. Afram, M. G. Uwayjan, M. T. Farran, S. K. Hamadeh, and M. R. Darwish, *American University of Beirut*, *Beirut, Lebanon*.

Feed consumption, apparent digestibility and fermentation characteristics of whey treated barley straw silage (WBSS) supplemented with urea (U), cottonseed meal (CSM), soybean meal (SBM) and safflower seed meal (SFM) were studied using 12 Awassi ram lambs averaging 42 kg BW. The study consisted of a 5-wk trial and a 1-wk collection period using the following treatments: I) 49% straw (S) + 50% liquid whey (W)+1% U, II) 41% S + 50% W + 9% CSM, III) 44% S + 50%W + 6% SBM and IV) 36% S +50% W + 14% SFM. Each lamb received 1 kg/d concentrate (14% CP on DM basis), in addition to ad libitum feeding of the experimental silages. Changes in fermentation parameters, temperature and pH, recorded at 3d interval for 21d were not significantly different (P>0.05) among the treatments. The temperature averages were 29.8, 29.2, 29.4 and 29.8 C and the pH averages were 4.8, 4.6, 4.7 and 4.4 for the respective treatments. All lambs had positive but non significant (P>0.05) body weight gains (BWG) at the end of the trial with the highest BWG recorded for treatment III compared to I, II and IV (178 vs 170, 114 and 159g/d, respectively). Silage DMI was not significantly different (P>0.05) among treatments and averaged 451, 411, 373 and 368g/d for treatments I, II, III and IV, respectively. Digestibility of DM, CP, NFE, NDF and ADF was not significantly different (P>0.05) among treatments. Treatment II had significantly higher (P<0.05) EE digestibility than treatments III and IV (85.9 vs 81.5 and 79.1%, respectively) and also had significantly higher (P<0.05) CF digestibility than treatment IV (53.4 vs 43.1%). Results of this study indicate that the protein sources as used resulted in positive response on animal performance, apparent digestibility and fermentation characteristics of the WBSS.

Key Words: Liquid Whey, Protein Supplements, Barley Straw

W251 Effects of dietary crude protein level on growth performance and blood parameters of Holstein heifers and steers. M. A. Bal*, H. Yarar, and M. Sahin, *Kahramanmaras Sutcu Imam University, Department of Animal Science*, *Kahramanmaras, Turkey*.

The objectives of this study were to compare two different levels of dietary CP on growth performance, feed efficiency and blood parameters of Holstein heifers and steers. Experimental diets consisted of 16 (HIGH) and 12% (LOW) CP with 2.7 Mcal/kg of ME (DM basis). Ratios of CP:ME were 61, 60, 46, and 45 gr/Mcal for high heifer (HIH), steer (HIS), low heifer (LOH) and steer (LOS) diets, respectively. Eight animals were assigned to each experimental diet in a 2x2 factorial arrangement of Randomized Block Design for 8 wk period. Diets containing 50% forage (corn silage and alfalfa hay) and 50% shelled corn:barley:cotton seed meal based concentrate (DM basis) were fed twice daily in a TMR. There was no significant difference (p> 0.1) for DMI (9.05 vs 9.64 kg/d) and protein intake (1.27 vs 1.35) between heifers and steers. However DMI was higher (P< 0.05) for 12% CP diet (10.97 kg/d) compared to 16% CP diet (7.71 kg/d) across the groups. As a percent of body weight, DMI was higher (p= 0.07) for LOS (3.62%) and LOH (2.81%) compared to HIH (2.39%) and HIS (2.04%). No significant difference was observed for ADG between heifers (1.18 kg/d) and steers (1.28 kg/d) as well as CP levels (1.21 kg/d for LO and 1.25 kg/d for HI). Feed efficiency was higher (p< 0.05) for HI diet (0.17 and 0.16 for HIS and HIH, respectively) compared to LO diet (0.11 for both LOS and LOH, respectively). There was no significant blood urea N (averaging 8.58 mg/dL)and creatinine (averaging 1.1 mg/dL) difference between treatment groups. Data indicates that heifers responded to 12% dietary CP level better than 16% based on desirable ADG (1.12 kg/d) and low serum urea N concentration (8.3 mg/dL) at 16 mo age. Although DMI was higher for LOH compared to HIH group, these animals performed a compensatory growth pattern for an optimum body weight (366 kg) for breeding. Growth pattern of steers was more efficient in 16% ditary CP level compared to 12%. Similar ADG and lower DMI but higher finishing body weight resulted a higher feed efficiency in this experimental group.

Key Words: Crude Protein, Growth, Urea N

W252 Feed conversion and efficiency of NPK utilization in lactating dairy cows. A. R. Castillo*[1], J. E. P. Santos[2], and J. H. Kirk[2], [1]*University of California*, *Merced*, [2]*University of California*, *Tulare*.

A survey on 51 totally random selected dairy farms was carried out in the Central Valley of California. The aim of this study was to estimate the efficiency of NPK utilization in lactating dairy cows on commercial dairy farms. NRC (2001)

was used for nutrient balances. Silages and hays were based on NRC nutrient composition. Concentrate feeds and mineral mixes samples were taken in each farm and analyzed for DM, N, P and K. A multiple regression analysis was carried out to study the main dietary variables related to N metabolism that can explain efficiency of N utilization (ENU). The model included ENU=Feed Conversion (FC), CP%, and required, supplied and balance (supplied - required) of CP, RDP, RUP, and MP. Dietary contents (averages±SD) of CP (N*6.25), P and K were: 17.0%±1.19; 0.44%±0.07, and 1.53%±0.25, respectively. Results are presented in Table 1. ENU was significantly correlated (P<0.001) with CP balance (R2=0.649) and FC (R2=0.645). Compared to RDP, RUP and MP variables, CP explained better ENU variations

Table 1

		Average/farm	SD	Min	Max
FCM3.5%†	kg/cow/d	30.9	5.31	18.9	45.1
FC	kgFCM3.5%/kgDMI‡	1.41	0.17	1.10	1.88
ENU	kgNmilk/kgDMI	0.26	0.03	0.20	0.34
N excretion d	g/cow/d	447	71.9	261	600
P excretion g	g/cow/d	46	15.8	15	89
K excretion g	g/cow/d	136	52.0	-63	334

(†)Fat Corrected Milk 3.5%; (‡)DMI=Dry Matter Intake; (d)N Excretion=090*N intake-89; (g)Excretion=Total Dietary Supply-Total Absorbed Required

Key Words: Dairy Cows, Nutrient Balances, Feed Conversion

W253 Manure production of heifers fed diets varying in forage, grain, and byproduct content. S. R. Hill*, K. F. Knowlton, R. E. James, R. E. Pearson, G. Bethard, K. P. Pence, and S. W. Wilson, *Virginia Polytechnic Institute and State Univeristy*, *Blacksburg*.

The objectives of this study were to evaluate the effect of varying feed intake and proportions of forage, grain, and byproducts on growth and excretion of urine, feces, and nitrogen in growing heifers. Holstein heifers (n=18) confirmed pregnant were grouped by due date and fed one of three diets for the last 16 weeks of pregnancy. Diets were high forage, fed ad libitum (HF); byproduct-based, fed ad libitum (BP); or low forage, fed at 75% of ad libitum (LF). Diets were designed to supply the same quantities of phosphorus, nitrogen, and metabolizable energy. Total collection of feces and urine was conducted in weeks 4, 8, 12 and 16. The HF ration was 85% forage, 13.7% CP, and contained orchardgrass hay, corn silage, corn grain, soybean meal, and a vitamin-mineral pre-mix. The BP diet was 60% forage and 14.0% CP, with 50% of the grain mix replaced with soybean hulls and cottonseed hulls. The LF ration was 60% forage, 17.8% CP, and fed at 75% of ad libitum. All data was analyzed using the PROC MIXED procedure of SAS with repeated measures (collection week). As intended, heifers fed HF and BP had greater DMI than the heifers limit-fed LF and there was no effect of diet on average daily gain or BW. Intake and digestibility of N was lower in heifers fed HF and BP than heifers fed LF. Fecal N excretion was higher in heifers fed HF and BP compared to those fed LF. Mean feces excretion on both wet and dry basis were highest in heifers fed HF, but heifers fed LF excreted more urine than those fed HF or BP. Despite differences in urine output, diet had no effect on urea N excretion. Heifers fed the LF ration excreted more total manure and urine per kg of BW compared to heifers fed BP and HF. Observed manure and urine excretion from heifers fed LF was greater than current ASAE values, while heifers fed HF excreted less manure and urine than predicted. Heifers achieving similar rates of gain from diets differing in forage, grain and byproduct content excreted widely varying quantities of manure.

Key Words: Manure Excretion

Women & Minority Issues in Animal Agriculture

W254 Heritability and permanent environmental effect for fleece quality assessed by an ancient Tzotzil indigenous evaluation system. H. Castro-Gámez[1], G. Campos[1], R. López[1], R. Perezgrovas[2], and H. Castillo-Juárez*[3], [1]*Universidad Nacional Autónoma de México*, *Ciudad Universitaria, México*, [2]*Universidad Autónoma de Chiapas*, *Chiapas, México*, [3]*Universidad Autónoma Metropolitana-Xochimilco*, *Calzada del Hueso, México D.F.*

The Tzotzil indigenous population living in the mountains of Chiapas (Mexico) obtains up to 36 % of its income from sheep-derived activities. In 1991 a breeding program, where the selection of sheep includes an ancient indigenous criteria for fleece quality, was introduced. This breeding program is supervised by the Teopisca Sheep Center from the Autonomous University of Chiapas. It uses empirical criteria from Tzotzil shepherdesses and formal quantitative fleece-quality and -production traits. The aim of this study was to estimate the heritability (h^2) and the permanent environmental effect (c^2) of fleece quality based on the indigenous grading system (FQ) where FQ depends on the visual and tactile evaluation of fleece volume, staple length, and the amount of coarse-long fibers within the double-coated fleece. This evaluation results in a quantitative discrete measure for FQ ranging from 1 to 4. The percentage of inbred animals within the flock, and the mean inbreeding coefficient of inbred sheep were established. We used 2255 FQ records from 886 animals from the three color varieties of the wool sheep locally named Chiapas Blanco, Raza Café, and Chamula Negro. Feeding of the animals is based on an extensive grazing system in the highlands covered by native vegetation, and a supplement of corn fodder during the winter. Shearing is made twice a year. Fleece gradings were made from February of 1998 to February 2004. Heritability and c^2 were estimated using an animal model that included shearing number, year-season of shearing, sex, and fleece color as fixed effects. The pedigree file included 935 sheep. Heritability (s.e.) for FQ was 0.31 (0.05) and c^2 (s.e) was 0.11 (0.04). A likelihood ratio test showed that the permanent environmental effect was statistically significant ($P < 0.05$). The breeding values for FQ ranged from -0.79 to 0.61. The percentage of inbred animals was 1.82, these with an inbreeding mean of 13.97 %. It is concluded that the empirical fleece-quality grading system shows a moderate genetic variation and hence it may be successfully included in the breeding programs.

Key Words: Fleece Quality, Genetic Parameters, Indigenous Women