acid (NEFA), beta hydroxyl butyric acid (BHBA), glucose, Aspartate aminotransferase (AST), cholesterol and total protein of plasma (P>0.05). We concluded that rumen protected choline supplement can improve milk production of cows in early lactating cows.

**Key Words:** rumen-protected choline, milk, Holstein cows

**W297 Effectiveness of different levels of dietary vitamin E to prevent milk fat depression in dairy cows fed rich soybean oil diet.** L. Q. Wang, J. Q. Wang*, D. P. Bu, S. J. Liu, G. C. Luan, and L. Wang, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

The present study was to evaluate the effectiveness of different levels of dietary vitamin E to prevent milk fat depression when cows receiving rich soybean oil diet and to examine the effect of dietary vitamin E on the *cis*-9, *trans*-11 CLA concentration. Forty-eight Holstein dairy cows were randomly assigned to 4 treatments. The control diet consisted of 60% forage and 40% concentration (no soybean oil) at dry matter (DM) basis, fed as a total mixed ration (TMR). The concentrate was partially replaced in the treatment groups with 4% of DM soybean oil (SOY), 4% of DM soybean oil plus daily 30 g of Vitamin E (containing 15,000 IU of α-tocopheryl, SOY/VE1), and 4% of DM soybean oil plus daily 40 g of Vitamin E (containing 20,000 IU of α-tocopheryl, SOY/VE2). Experiment lasted for 9 weeks. Measurements were taken during 3-9 wk of the experiment. Feed intake, milk yield, energy-corrected milk yield, and energy-corrected milk produced/kg of feed intake were similar among treatments. Percentage and yield of milk protein were not significantly different among treatments. The milk fat production was reduced by 22% when diets were partial replaced by soybean oil (Control vs. SOY). Diets of SOY/VE1 and SOY/VE2 enhanced the milk fat production by 6 (P>0.05) and 16% (P<0.05) compared with SOY treatment, respectively. There was no significant difference at *cis*-9, *trans*-11 CLA concentration when Vitamin E added to soybean oil diets (4.15, 3.95, and 3.60% of total fatty acids for SOY, SOY/VE1, and SOY/VE2; respectively). It was concluded from the present study that supplementation of Vitamin E (at 20,000 IU of α-tocopheryl in 4% of DM soybean oil) was effective to reduce the depression of milk fat, and no negative effect on concentration of *cis*-9, *trans*-11 CLA.

**Key Words:** vitamin E, soybean oil, milk fat

## Ruminant Nutrition: Experimental Methods

**W298 Water bath method for measuring NDF and ADF.** A. C. Pereira, E. J. Bungenstab, J. C. Lin, and S. P. Schmidt*, *Auburn University*, *Auburn, AL*.

A modified procedure was developed for the sequential analysis of NDF and ADF that allows a high volume of samples to be analyzed in a relatively short period of time. In the modified procedure, 60 forage samples (0.5 to 1.0g) were weighed into individual pre-weighed and identified filter bags (F57, 25 µm, Ankom® Technology Corp.) and then heat sealed. The samples were placed in a water bath with either NDF or ADF detergent solutions (10 L for 60 samples) and maintained at a constant temperature (99°C) with agitation at 60 rpm for 60 min. Filter bags were kept immersed with a metal basket. The fiber bag ANKOM® method served as the control for evaluation of the modified water bath method (WB). The objective was to compare both procedures using different harvests of ryegrass, rye and oats forage samples. A completely randomized design with a replicated 2 (analytical procedures) × 3 (forages) × 2 (harvests) factorial arrangement of treatments was used. Mainly, the only difference between the two procedures was the substitution of the pressurized chamber from the Ankom® fiber analyzer by an inexpensive and simple water bath. There was a harvest and forage effect ($P<0.01$) for NDF and ADF and also a harvest × forage interaction ($P<0.05$ for NDF and $P<0.01$ for ADF), but there were no differences between the methods ($P> 0.05$) for either NDF (31.93% WB vs. 31.33% ANKOM®) or ADF (15.54% WB vs. 15.96% ANKOM®). The inter-assay coefficients of variation (CV) were low for NDF (100% of samples with CVs below 2.8%) and for ADF (83% of samples with CVs below 5% with the highest CV at 5.9%). The difference in the NDF value between methods and the mean was 0.3 percentage unit, which is just 0.95% of the mean. For ADF, the value of the difference was 0.21 percentage unit, which is 1.3% of the mean. There was a high relationship for both NDF ($R^2 = 0.97$) and ADF ($R^2 = 0.89$) between the methods. The WB analysis method produced repeatable results that were comparable to the ANKOM® method and can be used to process a large number of samples (up to 60 replicate samples) in the same amount of time that 12 replicate samples are processed using the ANKOM® method.

**Key Words:** detergent system, NDF and ADF, fiber analyses

**W299 Analysis of fiber from coarsely ground corn plant components within in situ dacron bags.** L. J. Nuzback, W. M. Rutherford, and F. N. Owens*, *Pioneer Hi-Bred International*, *Johnston, IA*.

Analysis of fiber within in situ bags would simplify measurement of NDF digestion by avoiding transfer and regrinding of samples and also could increase statistical precision. Automated aNDF analysis employs finely ground (1 mm) samples in stiff Dacron (F-57) bags. In contrast, the Dacron bags used for in situ measurement typically have a larger pore size and the test samples preferably are ground more coarsely. To determine if a modified NDF (CNDF) procedure would give estimates of fiber that match commercially measured aNDF values, 288 samples (whole plant and seven different corn plant parts from 3 hybrids harvested on 3 dates from 4 plots) were assayed. For CNDF analysis, 16 replicate 0.5 g coarsely ground (6 mm Wiley mill) sub-samples were placed in 5X5 cm 50 micron Dacron bags and heat sealed. Standard extraction procedures (Ankom Technology, Macedon, NY) were followed, but because the in situ bags slipped through holes in trays within the automated NDF extractor, screens were developed to guard the bag suspender holes. Following amylase treatment and extraction, residue weights closely matched aNDF (CNDF = 1.089 ± 0.19 aNDF – 5.77 ± 1.17; root MSE 4.0) with the difference being dependent on sample source. CNDF exceeded aNDF for cobs by an average of 4.4%. But CNDF averaged 3.6% less than aNDF for whole plant samples, with this difference being negatively ($R^2 = 0.86$) related to hemicellulose content of samples. Because assays agreed closely for all of the plant parts devoid of starch, increased weight loss by the CNDF procedure may reflect incomplete filtration of starch-rich samples by commercial aNDF procedures. Reliability of CNDF analysis for other sample types and its in vivo applicability remain to be determined. This CNDF procedure could markedly simplify and speed in situ fiber digestibility measurements.

**Key Words:** NDF digestion, analysis, fiber

**W300 Utilization of lignin extracted from different plant sources as standards in the spectrophotometric acetyl bromide lignin method.** R. S. Fukushima*[1] and M. S. Kerley[2], [1]*Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brazil*, [2]*University of Missouri, Columbia*.

A non-gravimetric acetyl bromide lignin (ABL) method has been utilized to quantify lignin content in a variety of plant materials. Lignin is extracted with acidic dioxane and a standard curve built for use in this spectrophotometric procedure. Then, lignin concentration of an unknown sample is determined utilizing cell wall preparation. Because frequently there are several plant species being studied, lignin extraction from all samples leads to a procedural complexity which imposes restrictions for use in routine laboratory analyses. One possible solution to simplify this method could be the utilization of only one lignin extract and a single standard curve used to determine lignin concentration in any vegetable sample, no matter if it is a wood, forage, bamboo or an agricultural byproduct. This would require that all lignins responded in a similar fashion at UV light (280 nm), irrespectively of their botanical origin. This work extracted and isolated lignin from a range of diverse plants (14 plants + 3 commercial lignins) and compared curves among them (Table 1). Similarity of curves, both intercept and slope, lead to similar extinction coefficients (EC), which allowed the adoption of an average EC value of 23.077. The ABL method is faster than other analytical methods and more samples can be handled at same time. A practical implication that may allow utilization of this procedure in routine laboratory analysis: provided that a lignin extract is available, an analyst would not need to extract lignin, only draw a standard curve. If the above EC is adopted, this simplifies the method even further.

**Table 1. Lignin composition (%) and slopes**

| Lignin | Sugars | Uronics | Protein | Ash | Slopes |
|---|---|---|---|---|---|
| Pine | 2.14 | 0.06 | 0.56 | 0 | 23.833 |
| Pau-brasil | 3.53 | 0.98 | 1.37 | 0 | 22.606 |
| Aspen | 4.72 | 1.36 | 1.69 | 0 | 22.861 |
| Bamboo 2 | 4.61 | 1.12 | 1.81 | 0 | 22.711 |
| Bamboo 4 | 4.39 | 1.02 | 1.31 | 0.56 | 23.733 |
| Alfalfa | 3.56 | 1.06 | 5.19 | 0 | 22.667 |
| Red clover | 3.93 | 0.8 | 4.37 | 0.47 | 23.444 |
| Lespedeza | 4.59 | 0.91 | 4.06 | 0 | 22.994 |
| Napier | 4.83 | 1.05 | 2.25 | 0.26 | 22.956 |
| Caucasian blue stem | 2.88 | 0.27 | 3.44 | 0.81 | 23.683 |
| Annual ryegrass | 2.46 | 0.35 | 3.31 | 0 | 22.483 |
| Tall fescue | 3.9 | 0.58 | 2.69 | 0.42 | 23.217 |
| Corn | 3.42 | 1.08 | 1.75 | 0.91 | 22.444 |
| Sugarcane bagasse | 5.0 | 1.32 | 1.69 | 0.46 | 22.510 |

**Key Words:** dioxane, grass, legume

**W301 Degradation kinetics of N in rumen fluid determined with the gas production technique.** J. W. Cone*[1], P. M. Becker[2], and M. A. M. Rodrigues[3], [1]*Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands*, [2]*Animal Sciences Group of WUR, Lelystad, the Netherlands*, [3]*CECAV-UTAD, Vila Real, Portugal*.

With the gas production technique (GPT), fermentation kinetics of organic matter in rumen fluid can be determined. Because there is a need for fast and cheap techniques to determine fermentation kinetics of N (crude protein) for diverse feedstuffs in the rumen, the GPT was adapted to investigate the fermentation kinetics of N. Rumen fluid was obtained from 2 non-lactating Holstein Friesian cows. To determine N fermentation kinetics with the GPT, N has to be the limiting factor for fermentation. The buffer was without N and rumen fluid was diluted 20 times with buffer to minimize N from the rumen fluid. To bind all available N, an excess of glucose, xylose and soluble starch was added to the buffered rumen fluid and incubated until gas production ceased. After 4 h, feed samples containing 15 mg N were added and gas productions were recorded in duplicate. Fermentation characteristics of N of 19 concentrate feed ingredients were compared with data obtained with the nylon bag technique. Nylon bags were incubated in triplicate in three lactating Holstein Friesian cows each, for 0, 3, 8, 16, 48 and 336 h. The washout (W), undegradable and degradable fractions of N were determined. The rate of degradation of N (kd, 1/h) and amount of rumen escape protein (REP) were calculated. Gas production profiles showed that there were large differences between the samples in rate and extent of gas production. Comparing GPT results with nylon bag data showed that there was a moderate relationship between gas production after 5 h and W (r2 = 0.63) and between gas production after 25 h and kd (r2 = 0.52). There was a rather good relationship between gas production after 12 to 20 h and the amount of REP (r2 = 0.83). It can be concluded that the adapted GPT can be used as a rapid screening technique to determine differences in N availability between samples.

**Key Words:** gas production technique, nylon bag, protein fermentation

**W302 Effect of pH and nonforage fiber sources on microbial fermentation and nutrient flow from a dual-flow continuous culture system.** M. Sari, A. Ferret*, S. Calsamiglia, M. Blanch, and M. C. Fuentes, *Universitat Autonoma de Barcelona, Bellaterra, Spain*.

In some conditions, straw may become an expensive ingredient in the diet. Previous research suggested that the amount of straw in beef diets could be further reduced if additional non-forage fiber sources were incorporated in the diet. Eight dual-flow, continuous culture fermenters (1320 mL) were used in 3 periods (5 d adaptation, 3 d sampling) to study the effect of pH and different sources of non-forage fiber in a high-concentrate beef-type diet on rumen microbial fermentation. Temperature (39°C), and solid (5%/h) and liquid (10%/h) dilution rates were maintained constant. Fermenters were fed 97 g of DM/d in 3 equal portions. Treatments were arranged in a 2 x 4 factorial design, being main factors the pH (5.5 and 6.2) and the major fiber source in the diet (straw (CON), beet pulp (BP), soyhull (SH) and full fat cottonseed (CS)). Diets were formulated to have similar crude protein (15% DM), metabolizable energy (2.95 Mcal/kg of DM) and NFC level (55% DM). Data were analyzed using PROC MIXED of SAS and differences declared at $P < 0.05$. Low pH (5.5) reduced apparent OM, NDF and ADF digestion, total and branched chained volatile fatty acid concentrations, and acetate proportion; and increased propionate proportions. Replacement of straw with BP and SH increased OM, NDF and ADF digestion. An interaction between diet and pH was observed for NDF and ADF digestion because of lower digestion with BP and SH at low pH. Low pH decreased NH3-N concentration (2.24 vs 4.10 mg/100 mL and increased non-ammonia N flow (2.77 vs 2.70 g/d) compared with high pH. Total VFA concentration was lower in CON than in BP, SH and CS (112.99 vs 126.18, 129.24 and 124.50 mmol/dL for CON, BP, SH and CS, respectively) and acetate proportion was lower in BP compared with CS (50.28 vs 44.39 mol/100mol). Results indicated that low pH reduced nutrient digestion. However, replacing straw with non-forage fiber sources in high concentrate diets had minimal effect on fermentation.

**Key Words:** wheat straw, byproduct fiber, beef

**W303 In vivo and in vitro measurements of ruminal redox potential: A comparative study.** C. Julien*[1], A. Troegeler-Meynadier[1], J. P. Marden[1,2], F. Enjalbert[1], and C. Bayourthe[1], [1]*Université de Toulouse, INRA, Castanet-Tolosan, France*, [2]*Lesaffre Feed Additives, Marquette-Lez-Lille, France*.

This experiment compared ruminal *in vivo* and *in vitro* conditions in which redox potential ($E_h$) and fermentative parameters were measured during 3 consecutive days. A rumen fistulated dry dairy cow was adapted during 13 days to a hay-based diet supplemented with 43% of concentrates. Ruminal pH and $E_h$ were measured *in vivo* from feeding (0h) to 6 hours (6h) at 15 min interval on d1 and d2. On d3, ruminal fluid was sucked out and divided in 10 flasks for *in vitro* use. In each flask, substrates (starch, hay and urea) and a buffer solution (pH 7) were added and flasks were kept from light and air at 39°C in a waterbath rotary shaker. The pH and $E_h$ were recorded at the start of incubation (0h) to 6 hours (6h) every 15 min. For both methods, VFA and DL-lactate contents were determined at 0h and 6h. At 0h, *in vivo* $E_h$ (– 217 mV) differed ($P = 0.003$) from *in vitro* value (– 123 mV) probably because of ruminal fluid contact with air outside the rumen. After 45 min, $E_h$ measured in rumen (– 227 mV) were not different from $E_h$ recorded in incubated milieu (– 183 mV). After 2 h, both methods yielded similar $E_h$ values. At 0h, total VFA and DL-lactate contents were significantly different between *in vivo* (60.1 and 0.03 m*M*, respectively) and *in vitro* (36.9 and 0.62 m*M*, respectively) methodologies, owing to the transfer of rumen fluid and the dilution by buffer for incubation purposes. At 6h, no more significant difference was observed, suggesting therefore that *in vitro* reflected *in vivo* conditions. At 6h, contents of individual VFA did not differ (49.1 m*M* of acetate, 10.4 m*M* of propionate and 9.16 m*M* of butyrate, on average). In conclusion, during a 6-h incubation, our *in vitro* experimental method offered a fermentative and reducing environment close to the rumen. Moreover, the present study put forward the capacity of ruminal microbiota to restore reducing conditions *in vitro* after an exogenous perturbation.

**Key Words:** redox potential, in vivo, in vitro

**W304 Isolation and identification of urease from dairy rumen content by new culture-independent strategy.** S. G. Zhao, J. Q. Wang*, D. P. Bu, K. L. Liu, H. Y. Wei, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

To isolate urease active protein from cow rumen, rumen contents were collected from three Holstein dairy cows via fistula. Microbial cells were collected by certification and filtration. After lysis by ultrasound, the intracellular proteins were concentrated by ultrafiltration membrane (50 kDa), and then applied to a HiTrap Capto Q ion exchange columns (1ml) pre-equilibrated with 20 mM Tris-HCl (pH 8.0). Gradient elution were used to separate urease protein by 20 mM Tris-HCl (pH 8.0, containing 1 M NaCl) from 0% to 100% with the flow rate of 1 ml/min. The fractions with urease activities were pooled, and concentrated by lyophilization. The enzyme obtained by this procedure was separated by native-PAGE, and one urease containing strap was identified by activity staining. The urease strap was excised from the gels, digested by trypsin and then analyzed by LC-MS. Searches of the peptide mass fingerprint data against databases were performed with the MASCOT. Different kinds of urease were obtained from *Streptococcus thermophilus* , *Streptococcus salivarius* and *Bacillus halodurans*. These results demonstrate the feasibility of direct isolate urease protein from rumen mixture without microorganism cultivation and this strategy could be expected to facilitate the research of uncultured microorganisms.

**Key Words:** urease, isolation, culture-independent

**W305 Cloning of a bifunctional xylanolytic enzyme gene from *Neocallimastix patriciarum*.** J.-R. Liu*[1,2], C.-K. Pai[3], Y.-F. Zeng[1], C.-H. Duan[4], and M.-L. Li[3], [1]*Institute of Biotechnology, National Taiwan University, Taipei, Taiwan, Republic of China*, [2]*Department of Animal Science and Technology, National Taiwan University, Taipei, Taiwan, Republic of China*, [3]*Department of Life Science, National Taiwan Normal University, Taipei, Taiwan, Republic of China*, [4]*Institute of BioAgricultural Sciences, Academia Sinicac, Taipei, Taiwan, Republic of China*.

Rumen fungi are able to degrade the most-resistant plant cell-wall polymers, thus, the rumen fungal population represents a rich and underutilized source of fibrolytic enzymes with tremendous potential for industrial and agricultural applications. To the best of our knowledge, from a thorough search of the literature, there would not appear to be available any published studies pertaining to clone bifunctional acetylxylan esterase/xylanase enzyme gene from rumen fungi. In this study, a gene encoding a bifunctional acetylxylan esterase/xylanase, named *xynS20E*, was cloned from the ruminal fungus *Neocallimastix patriciarum*. The DNA sequence of *xynS20E* revealed that the gene contained a complete open reading frame (ORF) of 2,016 bp with 5' and 3' untranslated regions of 162 and 243 bp, respectively. Translation of the open reading frame of *xynS20E* revealed a protein of 671 amino acids with a predicted molecular weight of 72.4 kDa. According to the sequence-based classification, a putative conserved domain of carbohydrate esterase (CE) family 1 was observed at the N-terminus of XynS20 and a putative conserved domain of glycosyl hydrolase (GH) family 11 was detected at the C-terminus of XynS20E. Two putative conserved dockerin domains were found between the N-terminal CE family 1 catalytic domain and the C-terminal GH family 11catalytic domain of XynS20E. To examine the activity of the gene product, *xynS20E* gene was cloned into the pET-29a expression vector and expressed in *E. coli* as a recombinant His6 fusion protein. A purified XynS20E-His6 fusion protein was obtained after purification by immobilized metal ion-affinity chromatography. Response surface modeling (RSM), with central composite design (CCD), and regression analysis were applied to determine the optimal temperature and pH conditions of the purified XynS20E. The optimal conditions for the highest xylanolytic activity of XynS20E were observed at 40°C and pH 8.0. To the author's knowledge, this is the first report of bifunctional xylanolytic enzyme with acetylxylan esterase and xylanase activities from rumen fungus.

**Key Words:** *Neocallimastix patriciarum*, xylanase, acetylxylan esterase

**W306 Validation of a system for monitoring rumination in dairy cows.** K. Schirmann*[1,2], M. A. G. von Keyserlingk[1], D. M. Veira[3], D. M. Weary[1], and W. Heuwieser[1,2], [1]*Animal Welfare Program, Faculty of Land and Food Systems, The University of British Columbia, Vancouver, BC, Canada*, [2]*Clinic for Animal Reproduction, Faculty of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany*, [3]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada*.

Increased rumination time in dairy cattle has been linked to increased saliva production and improved rumen health. Up until recently the majority of rumination activity measurements have been obtained using visual observations that are labor intensive. An electronic system has been designed that allows for passive monitoring of rumination behavior of individual cows housed in a free stall barn. The objective of this study was to validate the data generated by this Hi-Tag rumination monitoring system. As direct human observations served as the reference method inter-investigator repeatability was first evaluated. Assessments of 2

independent observers were highly correlated (n=23,r=0.99, P<0.001). Measures from the Hi-Tag system were validated by comparing these values with those from the human observer for 51 2-h observations from 27 Holstein dairy cows. Rumination times from the Hi-Tag system were highly correlated with those from direct observation (n=51, r=0.93, P<0.001), indicating that the electronic system is an accurate tool for monitoring rumination time in adult dairy cattle.

**Key Words:** rumination, feeding behavior, dairy cow

**W307 The accuracy and precision of the hand-held Precision Xtra™ meter for measuring β-hydroxybutyrate in whole blood from dairy cows.** T. M. Kaiser, S. E. Stebulis*, and R. R. Grummer, *University of Wisconsin*, *Madison*.

The objective was to determine if the Precision Xtra™ human blood glucose and β-hydroxybutyrate meter is precise and accurate enough to be used in place of a BHBA assay (Gibbard and Watkins, 1968) for analysis of whole blood from dairy cattle. Four late-lactation Holstein cows were used in a 21 d study with 16 d for adaptation to a diet and 5 d for data collection. Cows were allowed to consume feed ad libitum once daily during d 1 through 17 and then restricted to 33% of ad libitum feed intake from d 18 through 21. During the data collection period (d 17 through 21), blood was collected from the coxygeal artery or vein at 4 and 12 hr post feeding. An aliquot of whole blood was analyzed immediately using the Precision Xtra™ meter. The remaining blood was centrifuged and plasma was stored frozen until analysis (Gibbard and Watkins, 1968). The precision of the meters was also tested by analyzing one blood sample with 5 individual meters on d 17 and 21 at 4 and 12 hr post feeding. Meter range was tested using blood samples spiked with various levels of BHBA, some with higher concentrations than the upper limit recommended by the manufacturer (80.3 mg/dL). The coefficient of variation for the five-meters was 9.63%. Results from unspiked samples indicated the hand-held meter did not correlate with laboratory assay results, ($R^2 = 0.414$; $P < 0.0001$). Values obtained from the meter were consistently lower than those obtained by the lab assay. Additionally, the meter failed to produce an error reading at BHBA levels over 80.3 mg/dL as suggested in the instruction manual. Results indicate that Precision Xtra™ is not effective in accurately measuring BHBA concentrations in whole blood, particularly at high BHBA conentrations, and the meter lacks sufficient precision for research use.

**Key Words:** BHBA, meter, ketone

**W308 Re–evaluating the technique of estimating total internal fat using real–time ultrasound and carcass measurements in beef cattle.** F. R. B. Ribeiro*[1], L. O. Tedeschi[2], J. R. Stouffer[3], and G. E. Carstens[2], [1]*Texas A&M University*, *Commerce*, [2]*Texas A&M University*, *College Station*, [3]*Cornell University*, *Ithaca, NY*.

The objective of this study was to re–evaluate our previously published technique of estimating total separable internal fat (IFAT) in beef cattle using real–time ultrasound (RTU) and carcass measurements from live animals. We expanded the original database and performed additional analyses. The database was gathered from 4 studies and contained 110 animals (16 bulls, 16 heifers, and 78 steers). Ultrasound measurements were obtained 7 d prior to slaughter, including the 12 to 13th rib fat thickness (uBF) and ultrasound kidney fat depth (uKFd). The uKFd was measured in a cross–sectional image collected between the first lumbar and 13th rib as previously published. Carcass data were collected 48 h post–mortem and consisted of backfat thickness (cBF), kidney fat depth (cKFd), live BW and hot carcass weight. Total separable internal fat was highly correlated to KPH weight (0.88) and cKFd (0.81), and moderately correlated to uKFd (0.71). Prediction equations were developed for estimating IFAT, KPH weight, and cKFd with the PROC REG of SAS using the stepwise statement to identify the best predictors of IFAT. The best predictors of IFAT were KPH weight or cKFd and cBF ($r^2$ = 0.84 and 0.83 and root mean square error (RMSE) of 4.23 and 4.33 kg, respectively). Ultrasound measurements of uKFd and uBF had an $r^2$ of 0.65 and RMSE of 6.07 kg when used to predict IFAT. These results were consistent with previously published evaluation of this technique. These findings demonstrate that this RTU technique allows the measurement of IFAT in a non-invasive way that may improve our ability to estimate IFAT in beef cattle, be used to more accurately formulate rations, and be applied in sorting cattle at feedyard.

**Key Words:** internal fat technique, ultrasound, carcass

**W309 Determination of ruminal protein degradation kinetics of Soy Best® with and without soy gums using dynamic modeling and a single point in situ protein disappearance and simulations with the CPM Dairy nutrition model.** L. O. Tedeschi[1], G. A. Holub[1], W. Chalupa[2], and C. A. Macgregor*[3], [1]*Texas A&M University*, *College Station*, [2]*University of Pennsylvania*, *Kennett Square*, [3]*Grain States Soya Inc.*, *West Point, NE*.

Technology has been developed to increase ruminally-undegraded protein (RUP) of mechanical-extracted soybean meal (MESBM) using soy gums (MESBM_G). Information of protein fermentation kinetics of feeds is important to determine RUP. The kinetics of ruminal protein degradation can be assessed using an in situ technique, but this requires multiple point measures, thus becoming expensive and time consuming. The objective of this study was to determine if computer modeling and a single point measurement of in situ protein disappearance can be used to determine protein degradation dynamics. A dynamic model containing 3 differential equations was developed to determine the fractional fermentation rates (kd) of MESBM and MESBM_G. Protein fractions (PA, PB, and PC) were consistent with the CPM Dairy. PA, PB, and PC were assumed to be 4.9, 93.5, and 1.6% of CP, respectively; and RUP was assumed to be PC + undegraded PB. A sensitivity analysis was conducted with CPM Dairy to formulate least-cost rations typical for Texas dairies, assuming 31.8, 36.3, and 40.8 kg/d of milk with corn silage and alfalfa hay as forages. Formulation constraints included at least 50% of metabolizable protein from bacteria, 3.1:1 ratio of Lys to Met, and 38 to 39.5% of non-fiber carbohydrate. Preliminary studies indicated the incubation of MESBM_G in situ for 16 h yielded greater RUP than MESBM (73.3 and 62.1 vs 58%, respectively). Because the in situ RUP was obtained using Dacron bags, kp was set to 0 and only PB kd was changed until observed RUP matched the predicted RUP after 16 h of simulation. The simulated PB kd for MESBM_G was 1.66 and 2.69%/h for 73.3 and 62.1% RUP, respectively; and 3.16%/h for MESBM (58% RUP). Based on these simulations, the kd for protein B2 fraction of MESBM_G was assumed to be 2%/h. CPM Dairy simulations indicated MESBM_G enriched with Met and Lys (< 30%) had better income over cost of feed than MESBM. We conclude that modeling and a single point in situ RUP can be used to estimate kd of feeds used in models such as CPM Dairy.

**Key Words:** Lys, Met, simulation modeling

**W310 Assessing the ability of the Cornell Net Carbohydrate and Protein System to predict fecal and urinary nitrogen excretion in lactating dairy cows.** R. J. Higgs*, L. E. Chase, and M. E. Van Amburgh, *Cornell University, Ithaca, NY*.

Herd level manure nitrogen (N) excretion can be predicted using the Cornell Net Carbohydrate and Protein System (CNCPS). Partitioning of urinary and fecal N is important, especially for predicting air emissions. The objective of this study was to compare CNCPS predictions for fecal N (FN) and urinary N (UN) with published data. Studies (n=24) were selected that measured FN and UN by total collection, presented adequate dietary information, and accounted for >85% of the N intake (NI). Individual diets were dropped if the unaccounted N was > 0.5 SD from the mean. Diets in the resulting data set (n=68) accounted for 94%±3% (mean±SD) of the NI. Crude protein content, dry matter intake and milk production ranged from 12.6-21%DM, 14-27.2kg/cow/day and 18.1-46.1kg/cow/day, respectively. Data was analyzed using a mixed model in JMP where study was included as a random variable. Additional assessments of model accuracy and precision were completed for FN and UN (CCC, MSPE; Table 1). Observed and model predicted NI or Milk N (MN) were not different (P > 0.05). The CNCPS calculates UN by subtracting MN and FN from NI. Both, NI and MN are easily quantifiable making the prediction of FN crucial in establishing the correct partitioning of manure N. In this evaluation, FN was predicted with high precision ($r^2$=0.94, b=0.01), but lacked accuracy (CCC=0.75, a=0.22). The lack of model accuracy was exaggerated by studies accounting for less than 100% of the NI. However, high precision, but poor accuracy suggests a calibration problem where FN is being over predicted (10%).

**Table 1. Precision and accuracy statistics for CNCPS predictions**

| | Linear regression | | | | | | MSPE partitioning[b] | | |
|---|---|---|---|---|---|---|---|---|---|
| | Intercept | Slope | $r^2$ | MSE | CCC[a] | MSPE | a | b | c |
| Intake N | -0.91 | 1.00 | 1.00 | 0.72 | - | - | - | - | - |
| Milk N | -0.46 | 1.00 | 1.00 | 1.55 | - | - | - | - | - |
| Fecal N | 26.81 | 0.79 | 0.94 | 186.69 | 0.73 | 1029.70 | 0.22 | 0.01 | .077 |
| Urinary N | 56.28 | 0.64 | 0.95 | 215.47 | 0.75 | 2151.67 | 0.42 | 0.20 | 0.38 |

[a] CCC=Concordance correlation coefficient; [b] Mean square prediction error partitioned into a = mean bias, b = systematic bias, and c = random variation.

**Key Words:** CNCPS, nitrogen, modeling

## Small Ruminant: Growth, Carcass Traits, Meat Quality, Nutrition

**W311 Behavioral aspects and body weight loss in the pre-slaughter management of ewes in distinct physiological stages and meat quality.** R. S. B. Pinheiro, A. M. Jorge*, H. B. A. Souza, and J. P. F. da Silveira, *São Paulo State University, Botucatu, SP, Brazil*.

The objective of this study was to know the behavior of Santa Inês ewes in different physiological stages during the pre-slaughter management, as well as their body weight loss, blood hematocrit values and meat quality. 21 cull ewes were used, with mean age of 6 yr, arranged into the following treatments: T1 = ewes which remained in lactation for 60 d with their respective lambs and slaughtered 1 d after weaning; T2 = ewes which remained in lactation for 60 d with their respective lambs and one more period of approximately 30 d without the lambs, aiming to recover lost body weight during nursing and, afterwards, slaughtered; and T3 = ewes which remained in confinement for 60 d and did not give birth during the year. The analysis of variance was carried out according to procedures of SAS, considering the significance level of 5%. The weight of ewes after transportation (journey of 296 km for 4 h 45 min) was lower for T1 in comparison with T2; T3 was not different from the other experimental treatments. Weight loss in kg and percentage of body weight of ewes during transportation was not influenced by the experimental treatments, with mean values of 2.28 kg and 5.15%, respectively. Weight loss of ewes during the period in which they remained in fast in the waiting pen for approximately 16 h before slaughter was proximate between experimental treatments, with mean values of 1.96 kg and 4.56% of body weight, respectively. Blood hematocrit values of ewes before and after transportation and after fast in the waiting pen were not different among themselves, with mean value of 58.5%. At the property and after transportation, hematocrit value was lower than at the moment of bloodletting of animals. Temperature and pH of the Longissimus lumborum muscle 24 h after slaughter were not influenced by the experimental treatments, with mean values of 6.89°C and 5.52, respectively. Meat luminosity of T1 was higher than T3 24 h after slaughter. Red and yellow values of the Longissimus lumborum muscle were not influenced by the treatments studied in this research.

**Key Words:** animal stress, meat pH, road transportation

**W312 Effects of small ruminant species and origin in Ethiopia (Highland vs. Lowland areas) and lengths of rest and feeding on harvest measures.** G. Abebe[1], G. Kannan[2], and A. L. Goetsch*[3], [1]*Ethiopia Sheep and Goat Productivity Program, Addis Ababa, Ethiopia*, [2]*Agricultural Experiment Station, Fort Valley State University, Fort Valley, GA*, [3]*American Institute for Goat Research, Langston University, Langston, OK*.

Yearling goats (G) and sheep (S) from Highland (H) and Lowland (L) areas of Ethiopia were used to determine effects of species and origin and lengths of rest and feeding on harvest measures, particularly carcass surface lightness. The H goat used was Arsi-Bale, and the L goat was Somali. The fat-tail indigenous H sheep is thought to be an Arsi-Bale genotype, and the fat-rump indigenous L sheep genotype was the Black Head Ogaden. There were two experiments (each a 2 x 2 x 3 factorial), one with rest for 0, 1, and 2 d before slaughter (R0, R2, and R3, respectively) and the second with feeding 0, 2, and 4 wk (0 wk = 2 d rest; 0F, 2F, and 4F, respectively). There were 10 animals per treatment. In the rest experiment, pH of the *longissimus* muscle 1 d post-slaughter (PS) was 5.91, 6.29, 5.82, and 5.98 (SEM = 0.039) for G-H, G-L, S-H, and S-L, respectively. The instrumental color measure L* (indicating lightness) for the hind leg surface 3 d PS was lower (P < 0.05) for H than for L (34.8, 36.3, 37.4, and 38.9 for G-H, G-L, S-H, and S-L, respectively; SEM = 0.45). Surface L* on d 3 was increased (P < 0.05) by 1 and 2 d of rest compared with 0 d for goats regardless of origin, but was not affected for sheep (33.2, 36.3, 37.2, 38.5, 37.8, and 38.2 for G-R0, G-R1, G-R2, S-R0, S-R1, and S-R2, respectively; SEM = 0.56). In the feeding experiment, *longissimus* muscle pH on d 1 PS was 5.93, 5.97, 5.85, and 5.74 for G-H, G-L, S-H, and S-L, respectively (SEM = 0.036). Surface L* on d 3 was lower (P < 0.05) for H vs. L (36.5, 39.0, 36.2, and 39.8 for G-H, G-L, S-H, and S-L, respectively; SEM = 0.46). Feeding 4 wk increased (P < 0.05) surface L* on d 3 regardless of species and origin (37.7, 36.8, and 39.2 for F0, F2, and F4, respectively; SEM = 0.40). In summary, goat and sheep carcasses from Highland areas of Ethiopia may darken more quickly compared with Lowland areas, and 1 or 2 d of rest before slaughter can increase lightness of the surface of goat carcasses.

**Key Words:** goat, sheep, carcass