

Teaching

292 Teaching an applied swine nutrition and feeding management course using WebCT. G.C. Shurson*, J.S. Knott, M.J. Spiehs, B.J. Rae, and J.A. Renteria, *University of Minnesota, St. Paul, MN.*

We developed a Web-based applied swine nutrition and feeding management course for undergraduate and graduate students in animal science. The course is managed through WebCT at the University of Minnesota at <http://webct.umn.edu>, and is designed to be completed in fifteen weeks (6 to 8 hrs/wk). Each of the 39 lessons is primarily text-based, but most lessons have illustrations, graphs, data tables, and/or photos that help the student visualize key points. At the end of each lesson, there are several study questions for the student to use in reviewing key points of the lesson. These questions are also helpful for students preparing for each of the five exams. Exams are taken "on-line" during designated times mutually agreed upon by the students and instructor. Along with the exams, there are 14 problem sets related to practical nutritional decisions that can be printed, completed, and resubmitted electronically to the instructor for comments and grading. Students are able to download swine diet formulation software from the course Web

site for use in completing many of the problem sets. The course Web site features a chat room where students can ask questions of the instructor and other students, and the responses can be viewed by all who are enrolled in the course. In addition, students can track their exam and problem set scores, and their current course grade on the Web site. The course is also linked to all of the major feed industry Web sites to allow easy access for students who are interested in learning more about career opportunities in the feed industry. Using a Web-based course offers unique opportunities and challenges for both the instructor and the students compared to using more traditional learning environments. When students were asked if they were satisfied taking this course on the Web, 29% were very dissatisfied, 14% were dissatisfied, 14% were uncertain, and 43% were satisfied. Some of the major reasons for students being dissatisfied with this Web-based learning environment included spending too much time learning to use the technology, inadequate computer skills, and lack of adequate computer hardware and software on their personal computers.

Key Words: Teaching, Web-based, Nutrition

Undergraduate Student Competitive Research Papers

293 Development of a multiplex microsatellite marker panel for whole genome scans in sheep. B. Mote*¹ and B. Freking², ¹*University of Nebraska, Lincoln*, ²*USDA, ARS, U.S. Meat Animal Research Center.*

A primary objective of genome scans is to estimate the location of genes influencing a trait of interest using uniformly spaced informative genetic markers. Initial scans are typically conducted with an intermarker distance of approximately 20 cM. The sheep genome is reported to span 3500 cM for 26 autosomes and 130 cM for the female map of chromosome X. Multiplex amplification reactions decrease costs and time to conduct whole genome scan studies, but panels of markers which amplify together are not readily available for sheep. Microsatellite markers available from published ovine genetic maps were first sorted by annealing temperature and average product size, then arranged into groups of three primer pairs for amplification tests. Markers from chromosome 18 were excluded due to previous extensive mapping efforts associated with callipyge research in the population of interest. A total of 155 multiplex amplification reactions, with 465 unique primer pairs, were tested on sheep genomic DNA resulting in 57 successful duplex and 18 successful triplex marker sets. The current marker sets flank 2865 cM of the sheep genome. Seventeen chromosomes have been sufficiently covered to achieve the initial scan objective. With a targeted goal of 208 uniformly spaced markers, these results have reduced the number of reactions and gel lanes needed per animal from 208 to 115, or 55% of the previous number of marker reactions and gel lanes necessary for complete coverage. Average heterozygosity of the parental generation of the target resource population was 65.2%. It may be necessary to fill in gaps with additional markers where marker informativeness is low. This panel of markers can be a valuable resource for the sheep gene mapping community.

Key Words: Sheep, Microsatellites, Multiplex

294 Flocculation of swine manure: influence of flocculant, rate of addition, and diet. L. Flatow*¹ and W. Powers¹, ¹*Iowa State University.*

Manure was collected from growing pigs fed one of 11 diets varying in total and available phosphorus content. Reduced phosphorus diets were amended with feed additives intended to improve availability of phytate phosphorus. Diets were replicated over three feeding periods resulting in collection of 33 manure samples. During the course of the three feeding periods average pig weight increased from 22 kg to 48 kg. Actual dry matter and phosphorus content of each collected manure sample were determined. Ten g of each collected manure sample was diluted to a final volume of 1 L, producing a solution with average solids content of 0.24% total solids, and poured into Imhoff cones. Five flocculants plus a control were added, at each of three concentrations, to the diluted mixtures and allowed to settle for 10 minutes followed by a second

10-minute settling period. Volume of settled material was recorded following each settling period. At the end of the second settling period (20 min total settling) supernatant was poured off and frozen for future phosphorus analysis, and settled solids were weighed and dried for total solids determination. Mass of solids settled was measured. Mass of phosphorus settled was calculated as the differences between the P content in the 10 g originally added to the Imhoff cone and the g P in the supernatant. Results indicated that $Al_2(SO_4)_3$ and $FeCl_3$ were the most effective flocculants. Little improvement was observed when the flocculant was added at a concentration of 625 mg/L compared to 250 mg/L. Both flocculants recovered over 85% of solids and over 70% of the phosphorus. Addition of $Al_2(SO_4)_3$ at a concentration of 625 mg/L increased phosphorus removal to 90%. Diet and feeding period were significant influences on results. As the pigs aged, manure phosphorus was more soluble, possibly explaining the observation that less phosphorus was settled in feeding period 3 compared to phosphorus settled in feeding periods 1 and 2. Removal efficiency of total solids and phosphorus with flocculation was predicted quite well using developed equations ($r^2 = 0.86$ and 0.84 , respectively). As producers consider nutrient management options, feed-to-field strategies should be implemented.

Key Words: Manure, Flocculation, Phosphorus

295 Effects of manure storage time and filling scheme on odor and headspace analysis using simulated manure storage pits. S. Bastyr* and W. Powers, *Iowa State University.*

Dilute swine manure, approximately 11% dry matter, was stored in constructed 2-L vessels for up to 91 d. Initiation of vessels was staggered to allow for simultaneous evaluation of manure stored for varying time periods. Vessels were filled, in duplicate, under two filling schemes; either filled completely on d 0 (SF) or filled over the course of 10 wk by adding 200 ml per wk (WF). On d 70, 34 vessels were operational. Once weekly, cotton swatches were placed in each vessel cap overnight for evaluation by human panelists using triangular forced-choice methodology. Each panelist assigned an odor score, on a scale of 1-10, to identified swatches ($n=3736$). Headspace contents of each vessel were analyzed, weekly, by gas chromatography (GC-MS) and with a Cyranose 320 32-sensor electronic nose. Vessel contents were sampled for compositional analysis when each vessel was terminated. Results indicate that odor score was affected by days stored ($P=0.002$), increasing until approximately d 42 before leveling off, and filling mode ($P=0.008$). An interaction between filling mode and days stored was significant; swatches from the WF vessels had lower scores than swatches from the SF vessels until approximately d 49. Of the 32 analytes quantified using GC-MS, dimethyl disulfide and 4-methylphenol were best correlated to odor. Correlations were, however, low ($r < 0.30$). A prediction equation from headspace concentrations of analytes produced an r^2 value of 0.18. The odor predictive capability of the electronic nose was similar ($r^2 = 0.20$). Given panelist variation, it is likely that the predictive capability of any

method is limited to an r^2 of 0.50. Therefore, the GC-MS equation and the electronic nose response were moderately effective in mimicking human response. Breakdown of solids and organic matter occurred to a greater extent when the manure was added in a single addition (SF), although odor scores were initially greater in the SF vessels. Nitrogen and ammonia content of the manure, stored for an equivalent period of time, was less in the SF vessels. Results indicate that manure-handling strategies, within the housing facility, may be developed to reduce mal-odor potential. Further work is needed to develop instrumental methods for odor assessment.

Key Words: Manure, Odor, Odorants

296 Selected fractionate digestibility coefficients of an extruded mixture containing whole soybeans and separated slurry solids. P Walker, D Finnigan*, J Dust, and R Knight, ¹Illinois State University, Normal, IL/USA.

Suffolk wethers 8-9 months old and weighing 59.25 ± 4.4 kg were used in a trial to determine the apparent digestible energy and digestibility coefficients of dietary DM, CP, ADF and ether extract (EE) of an extruded mixture containing whole soybeans (WS) and separated swine slurry solids (SS). Solids were separated from co-mingled gestation to finishing swine slurry using a gravity screen-rollerpress Key DollarTM separator. Separated slurry solids were mixed with whole soybeans in a 50:50 ratio (wet wt. basis), passed through a single screw, dry extruder at 146-149 C and dried in a hot air continuous belt dryer. Lambs were randomly allotted to metabolism crates and were fed the mixture at 3.4% of body wt, for 30d with total fecal collection the last 7d. Gross energy was determined on all samples with an adiabatic bomb calorimeter. On a percent basis, SSS contained: $42.46 \pm 6.57\%$ DM, $8.80 \pm 2.33\%$ CP, $4.20 \pm 1.28\%$ EE, $25.14 \pm 2.20\%$ ADF, $13.74 \pm 3.34\%$ CELL, $10.90 \pm 2.35\%$ LIG, $0.50 \pm 0.25\%$ AIA, and $8.03 \pm 3.29\%$ ASH. Apparent digestibility coefficients of the extruded mixture were $52.03 \pm 6.55\%$ DM, $68.46 \pm 8.36\%$ CP, $77.48 \pm 9.71\%$ EE, and $48.94 \pm 8.56\%$ ADF. Crude fat as estimated by EE was more digestible ($P < 0.05$) than other fractionates evaluated. The extruded mixture was found to contain $52.03 \pm 6.55\%$ DM, $21.43 \pm 2.79\%$ CP, $8.43 \pm 1.47\%$ ADF, $11.48 \pm 1.4\%$ EE on a dry matter basis. Apparent digestible energy of the extruded mixture was $2.66 \pm .37$ Mcal:kg. This study suggests extruded mixtures composed of separated slurry solids and whole soybeans can be an acceptable method for including separated slurry solids into livestock diets.

Key Words: Separated Slurry Solids, Extruded, Feed

297 Digestibility of Amino Acids in Soybean Meal with added Soy Hulls. R. Dilger*, J. Sands, D. Ragland, and L. Adeola, Purdue University, West Lafayette, IN.

Soy hulls (SH) were incorporated into four 17%-CP diets at 0, 3, 6, or 9% and fed to 35-kg barrows to determine their effect upon apparent and true digestibilities of amino acids measured at both the terminal ileum and over the total tract. A low protein casein diet was fed to estimate endogenous amino acid losses and two control diets were also administered. Pigs were surgically fitted with simple T-cannula at the terminal ileum and fed the seven-semipurified cornstarch diets according to a 7 X 7 Latin square design. Each period lasted 7 d, with fecal samples collected on d 5 and ileal samples collected for 12-h on both days 6 and 7. Feed was restricted to 90% of metabolic body weight and fed in two equal portions at 0800 and 2000. The apparent ileal digestibilities of dry matter (DM), nitrogen (N), and amino acids (AA) (except tryptophan) decreased with the addition of SH (quadratic effect, $P < 0.05$). DM, energy (E), and most of the AA also showed a linear decrease ($P < 0.05$) in digestibility. Apparent total tract digestibilities of DM, E, N, and AA produced a decreasing quadratic effect ($P < 0.05$), and all of these nutrients except E, N, and tryptophan also exhibited a linear decline in digestibility ($P < 0.05$). True ileal digestibilities of N and AA (except tryptophan) showed a quadratic decrease ($P < 0.05$) from the addition of SH. Arginine, tryptophan, cysteine, serine, aspartate, and glutamate showed a linear decline in true ileal digestibility ($P < 0.05$). All true total tract digestibilities of AA decreased (linear and quadratic effects, $P < 0.05$), except for N and tryptophan (linear effect only, $P < 0.05$). In conclusion, the addition of soy hulls up to the 6% level reduced DM, E, N, and AA digestibilities of soybean meal. The inclusion of 3 or 6% SH reduced the average apparent ileal digestibility of the indispensable AA 7.8 or 15.2 percentage units, respectively, but 9% SH led to a reduction

of only 1.6 percentage units. Similarly, SH led to 5.7 or 11.3 percentage unit decreases for the average true ileal digestibility of the indispensable AA at the 3 or 6% SH levels, respectively, while 9% SH resulted in only a 1.4 percentage unit decrease.

Key Words: Soybean Meal, Amino Acid Digestibility, Swine

298 Mapping of the HMG-I gene family in the pig. N.-T. Nguyen*, K.-S. Kim, Y. Zhang, and Max F. Rothschild, Iowa State University, Ames Iowa.

The HMG-I gene family consists of two genes that encode three proteins (HMG-I, -Y, and -C) associated with chromatin structure and control of transcription. The HMG-I and -Y proteins are products of an alternative spliced RNA of the same gene, but a separate gene encodes for HMG-C. Recent studies indicate the *HMG-I* gene products may be involved in the pathogenesis of several human cancers and the chromosomal regions localized for the human *HMG-I* genes are also known to be involved in several chromosomal abnormalities correlated with many human cancers. This study was designed to map the HMG-I genes to specific pig chromosomes. Primers for PCR amplification of the porcine *HMG1Y* and *HMGIC* were designed from human and rodent sequences. PCR-RFLP tests were developed to genotype the single nucleotide polymorphisms (SNPs) identified in both genes. Two-point and multi-point linkage analyses were performed from the Iowa State University Berkshire and Yorkshire crossed reference families. In addition, both genes were physically mapped using PCR with the pig/rodent somatic cell hybrid panel. The *HMG1Y* gene was assigned to SSC 7 by both linkage and physical methods, which is in agreement with other comparative mapping studies. Interestingly, the pig *HMGIC* fragment (1.2 kb) spanning exon 5 and the 3' UTR was assigned to the SSC 1 by both methods. This result is striking because human *HMGIC* maps to HSA 12q15, so the pig *HMGIC* was expected to map on SSC5, a region corresponding to HSA12q. Previously a 500 bp fragment of 5' UTR of the pig *HMGIC* had been physically mapped on SSC5 (D. Pomp, personal communication). The discrepancy could suggest the presence of a pseudogene. However, it might also be evidence of the possible chromosomal rearrangement (or break) within the pig *HMGIC* gene since *HMG-I* genes have been evolved through gene duplication and exon shuffling events. The human *HMGIC* gene is known to contain chromosomal breakpoints associated with many cancers.

Key Words: Hmg1y, Hmgic, Pig

299 Fish oil, conjugated linoleic acid, and body fat deposition. B. J. Meyer*, K. M. Hargrave, and J. L. Miner, University of Nebraska.

Conjugated linoleic acid (CLA), which causes body fat depletion, can be metabolized in a manner similar to linoleate thereby yielding isomers of arachidonate. Dietary linoleate deficiency enhances sensitivity to CLA. Therefore, we hypothesized that CLA depletes body fat by inhibiting synthesis of arachidonate from linoleate or, alternately, by being metabolized to an arachidonate isomer. If the former is true, reducing arachidonate stores should sensitize mice to dietary CLA. Fish oil diets can decrease the stores of arachidonate. The present objective was to determine if mice fed a diet containing fish oil are more sensitive to the effect of CLA on body fat than mice fed a diet containing soy oil. Eighty, newly-weaned male mice (3 wk of age, 15 g BW) were blocked by weight and genetic background, and allotted to four diets: SOY = 20% soy oil diet for 9 wk; SOY + CLA = SOY for 7 wk then 19.5% soy oil with 0.5% CLA for 2 wk; FISH = 20% fish oil diet for 9 wk; FISH + CLA = FISH for 7 wk then 19.5% fish oil with 0.5% CLA for 2 wk. Feed intake and BW were determined weekly. After 9 wk, the mice were killed and liver and fat pads (epididymal and retroperitoneal) were collected. Body fat and lean weight were determined by Dual Energy X-ray Absorptiometry. Analysis of variance detected no significant interactions with genetic background, therefore mean comparisons were limited to diet effects. Lean weight was not affected by diet. Compared to mice fed SOY, body fat and fat pad weights were reduced ($P < 0.01$) by 19% in mice fed FISH, and by 15% in mice fed SOY + CLA, but were not reduced by FISH + CLA (fat source x CLA interaction; $P < 0.01$). Liver weight was increased ($P < 0.01$) by 10% due to fish oil, but was not affected by CLA. We conclude that sensitivity to CLA is not greater in mice fed fish oil versus soy oil. Our interpretation is that the mechanism by which CLA depletes body fat is independent of arachidonate stores and thus independent of arachidonate production from linoleate.

These results support the alternate hypothesis that CLA metabolism to an arachidonate isomer leads to body fat depletion.

Key Words: Mice, Conjugated Linoleic Acid, Adipose

300 Identification of genes regulated by zinc supplementation of weaned pigs. M.A. Closs*, C.P. Wilkinson, N.E. Raney, G.M. Hill, J.E. Link, M.M. Martinez, K.M. Hargrave, and C.W. Ernst, *Michigan State University, East Lansing.*

Supplementation of weaning pig diets with pharmacological levels of zinc (Zn) as Zn oxide (ZnO) results in increased growth performance. We hypothesize that the positive effects of Zn are, at least in part, the result of gene expression regulation by Zn. The objective of this experiment is to identify differentially expressed genes regulated by dietary Zn supplementation of weaned pigs (approx. 21 d of age) using the differential display reverse transcription polymerase chain reaction (DDRT-PCR) technique. In study 1, liver tissue was obtained from pigs fed either an adequate Zn diet (150 ppm) or a diet containing 2,000 ppm Zn as ZnO (n = 4 per treatment) for 14 d post-weaning. In study 2, liver tissue was obtained from pigs fed either an adequate Zn diet (150 ppm) or a diet containing 1,000 ppm Zn as ZnO (n = 4 per treatment) for 14 d post-weaning. Total RNA was extracted from liver tissue and used in DDRT-PCR analyses. Five primer pairs (1 oligo-dT anchor with 5 arbitrary primers) were used in study 1 and three primer pairs (1 anchor with 3 arbitrary) were used in study 2 to identify putative differentially expressed genes. Thirteen fragments (6 from study 1 and 7 from study 2) that were amplified in all samples of one treatment but were faint or undetectable in all samples of the other treatment were excised, PCR-reamplified and cloned. Clones were sequenced and compared to entries in the GenBank databases using the BLAST software. Sequences for 10 of the 13 clones significantly matched entries in the GenBank non-redundant or expressed sequence tag (EST) databases and the remaining 3 clones did not match any entry in the databases. Three clones shared significant homologies to known genes (alpha-1 acid glycoprotein, nickel specific induction protein and tight junction protein 1) and 7 matched ESTs of unknown identity. These results provide new information concerning Zn regulation of liver gene expression in nursery pigs and could help elucidate the mechanism by which dietary Zn improves pig growth.

Key Words: Nursery Pigs, Zinc, DDRT-PCR

301 Effect of ryanodine, nifedipine, and low sodium on contracture force in isolated muscle bundles from horses with recurrent exertional rhabdomyolysis. G.A. Searls* and G.W. Onan, *University of Wisconsin River Falls, Wisconsin.*

Previous studies have shown that isolated muscle bundles from Thoroughbred horses with an inherited form of Recurrent Exertional Rhabdomyolysis (RER) develop contractures in the presence of either halothane or lower concentrations of caffeine than isolated bundles from normal horses. Therefore contracture tests similar to those used for identification of humans subject to malignant hyperthermia have been developed for early identification of foals carrying the RER gene. The purpose of this study was to determine if any other substances might have a differential effect on *in vitro* contractures of muscle bundles from RER vs. normal horses in order to better refine diagnoses of foals and to further indicate a potential source for the defect in RER muscle. A series of pharmaceuticals known to have effects on calcium channel proteins or calcium transport proteins were investigated. Muscle bundles from RER horses developed significantly stronger contractures in the presence of 0.05 μM and 0.1 μM ryanodine ($P < .05$) than did bundles from normal horses. This is consistent with the reaction of malignant hyperthermia muscle from human and swine subjects, offering further evidence that the RER condition in Thoroughbreds is a related disease and that the defect lies in the calcium buffering ability of the sarcoplasmic reticulum. A further series of studies investigated the effects nifedipine (a dihydropyridine calcium channel blocker) and low extracellular sodium (which affects the sarcolemmal sodium-calcium transporter protein) on the extent of caffeine-induced contractures in RER vs. normal muscle bundles. The presence of 10 μM nifedipine or low (15mM) sodium both caused increased contracture force at 1.0 mM, 2.0 mM, and 5.0 mM caffeine ($P < .05$) in muscle bundles from all horses with no differential effect between types. These results would indicate that sarcolemmal calcium regulating proteins are not important in the etiology of RER onset in affected horses and further substantiate that the defect lies with the

sarcoplasmic reticulum. Furthermore ryanodine may be a useful adjunct in early diagnosis of the disease in foals.

Key Words: Recurrent Exertional Rhabdomyolysis, Ryanodine, Nifedipine

302 Reed-sedge peat as a feed additive for dairy cows. P. W. Clark and G. L. Golombeski*, *U. W.- River Falls.*

The effect of reed-sedge peat as a feed additive (MenefeedR) for dairy cows was investigated with reference to milk yield, milk composition, and somatic cell count (SCC). Thirty-four cows were divided into two groups balanced for parity and milk yield in a crossover design with four three-week periods. The MenefeedR was fed once daily at a rate of 4 ounces per head in a .90 kg mixture of oats, corn, and molasses for the Treatment group. The Control group received the same grain mix without the MenefeedR. Milk samples were taken at the end of every three-week period for eight consecutive milkings and milk weights were recorded. Milk samples were analyzed for fat and protein concentration and SCC. There was no significant difference ($P > .05$) between the Control (34.9 kg/d) and Treatment (34.0 kg/d) groups for energy corrected milk yield. There was also no significant difference between Control (2.88) and Treatment (2.92) groups for mean linear SCC score.

Key Words: Reed-Sedge Peat, Somatic Cell Count

303 A comparison of different particle size analysis techniques. A.L. Baldrige*, T.L. Stainbrook, J.C. Woodworth, M.D. Tokach, J.L. Nelssen, R.D. Goodband, and S.S. Dritz, *Kansas State University, Manhattan.*

Particle size of ground grain is determined in labs using the ASAE approved, 13-sieve method. Because this method is time consuming, a 1-sieve, hand-shaking method has been developed (1s; IFA, Stanly, IA). Questions on the accuracy of the 1-sieve method led us to develop an alternative method to quickly determine particle size with 3 sieves and to compare the various methods. Forty-three samples of ground corn were analyzed by the approved 13-sieve procedure (13s; 3350 μm to 53 μm opening mesh screens) with mean particle size of samples ranging from 1143 to 422 μm . The same samples were analyzed by the 1s method and the developed 3-sieve (3s) method. For 13s, the approved ASAE protocol was followed: 100 g of corn was placed on top of the sieve stack and shaken for 10 min on a Rotap sieve shaker. For 1s, IFA protocol was followed: 280 g of corn was placed on a sieve (1400 μm opening) and shaken by hand until no more sample fell through. For 3s, 50 g of sample was placed on top of a stack (1700, 600, and 300 μm opening) and shaken by hand for 1.5 min. Mean particle size was calculated based on the amount of sample resting on each screen after shaking. For 1s, the IFA procedure also was compared to a new prediction equation ($11.86 \times \text{wt on screen, } g + 435; R=0.74$). For 3s, the prediction equation was $18.89 \times (X1700) + 10.87 \times (X600) + 1.18 \times (X300) \# 150 (R=0.88)$ where X equals the percentage of sample on the respective screens. The different methods were compared by calculating the residual of the predicted particle size from the particle size determined from the 13s method. The residual for 3s (44 μm) was lower ($P < 0.01$) than 1s using both the IFA protocol (133 μm) and the new prediction equation (74 μm). Residual of 1s using the prediction equation also was lower ($P < 0.01$) than 1s using IFA protocol. In conclusion, 3s is a quick method that can be used to predict particle size with less variation than the 1s method commonly used. The 1s method can be improved by using a different prediction equation than that provided by the company.

Key Words: Grain, Particle size, Procedures

304 Effect of ruminal protein degradability and supplementation frequency on intake, diet digestibility, and nitrogen balance in forage-fed lambs. D. E. Carter*, P. A. Ludden, V. Nayigihugu, and B. W. Hess, *University of Wyoming.*

Twenty-four wether lambs (initial BW = 36.8 ± 0.7 kg) were used in a 56 d split block, 2×2 factorial designed experiment to evaluate the effects of ruminal protein degradability (RDP) and supplementation frequency on intake, diet digestibility, and N retention. All lambs were fed chopped (7.6 cm) bromegrass hay (7.4% CP, 61.1% RDP, 59.3% NDF, 33.7% ADF) for ad libitum consumption, and either soybean meal (high RDP) or feather meal (low RDP) daily or on alternate days. Supplements were fed on an isonitrogenous basis (0.28 and 0.20% of BW daily

for the high and low RDP supplements, respectively), with alternate-day supplements fed at twice the level of daily supplementation. Beginning on d 21 and 49 of the trial, two 8-d N balance collections were conducted. No protein degradability \times supplementation frequency interactions ($P \geq 0.24$) were noted in this experiment. No treatment effect was noted for forage DM intake ($P \geq 0.21$), total DM intake ($P \geq 0.08$), N intake ($P \geq 0.79$), or total tract DM digestibility ($P \geq 0.10$). Total tract N digestibility was not affected ($P \geq 0.42$) by protein degradability, but was increased ($P = 0.01$) with alternate day supplementation (57.2 vs 54.6%). A protein degradability \times collection period interaction was observed for N retention (g/d and % of N intake; $P \leq 0.05$), wherein feeding the low RDP supplement produced a greater increase in N retention during the second collection period. Overall, protein degradability did not affect ($P \geq 0.29$) urinary N excretion or N retention; however, alternate day supplementation decreased ($P = 0.02$) urinary N excretion, thereby increasing N retention in g/d (6.57 vs 5.32; $P = 0.01$), as a % of N intake (33.8 vs 27.0; $P = 0.003$) and as a % of digested N (58.8 vs 49.4; $P = 0.01$). Supplementing protein to forage-fed ruminants on alternate days appears to enhance efficiency of N utilization, irrespective of ruminal protein degradability.

Key Words: Ruminal Protein Degradability, Supplementation Frequency, Nitrogen Retention

305 Effects of harvest date and late-summer fertilization rate on dry matter yield and chemical composition of stockpiled bermudagrass forage. A.A. Gelvin*¹, D.L. Lalman¹, C.F. Taliaferro¹, and J. Ball², ¹Oklahoma Agricultural Experiment Station, ²Noble Foundation, Ardmore, OK.

A randomized complete block design with four replications was used to test the effects of N fertilization rate and harvest date on yield and

chemical composition of stockpiled Greenfield bermudagrass at the Eastern Research Station near Haskell, OK. Four N fertilization rates were applied on August 17, 1998 (0, 34, 67, 135 kg/ha) and forage was sampled at five 28-d intervals beginning on November 5. During late April, prior to the experiment, 112 kg N/ha was applied and P & K was applied as indicated by soil test. Hay was harvested from the plots during early June and again during early August. Near infrared reflectance spectroscopy (NIRS) was used to determine chemical composition including CP, soluble protein (SP), neutral detergent insoluble crude protein (NDICP), ADF, NDF, lignin (LIG), non-structural carbohydrate (NSC), fat, and ash. Total digestible nutrients was calculated using the summative approach. Fifteen percent of the samples were analyzed for each component using wet chemistry procedures to calibrate the NIRS equations. Degradable protein concentration (DIP) was determined using the *Streptomyces griseus* enzymatic procedure. Monthly precipitation was 16.1, 21.4, 9.2, 5.9, 6.6, and 5.8 cm for September, October, November, December, January, and February, respectively. Forage dry matter yield, determined on November 5, increased linearly ($P < .01$; $y = 37.454x + 3120$) with increasing N fertilization. Concentration of CP, SP, DIP, NDICP, and TDN increased ($P < .05$) with increasing N fertilization. However, concentration of cell wall constituents and fat decreased ($P < .01$) with increasing N fertilization. Ash and NSC were not affected by N fertilization rate ($P > .2$). As the winter progressed, concentration of CP, SP and NDICP decreased ($P < .01$), although DIP increased ($P < .01$) over time. Later harvest dates were associated with increased ($P < .01$) ADF and NDF concentration and decreased ($P = .01$) NSC, with no change in LIG or TDN ($P > .2$). Increased N fertilization resulted in greater stockpiled bermudagrass yield and nutritive value, although the effects of harvest date were variable.

Key Words: Stockpiled Bermudagrass, Forage Nutritive Value, Protein Fractions