

that milk E2 concentrations were lower than plasma concentrations in early pregnancy, but were higher than plasma E2 concentrations in late pregnancy. Limited literature is available on enzymes with the ability to convert estrone (E1) to E2 in the mammary gland. The objective of this study was to determine if somatic cells obtained from milk generate 17 $\beta$ -hydroxysteroid dehydrogenase (17 $\beta$ -HSD) mRNA. Production of  $\beta$ -casein ( $\beta$ -CN) mRNA was used to verify presence of mammary epithelial cells (MEC) in somatic cell samples. Primers specific for bovine  $\beta$ -CN, 17 $\beta$ -HSD 7 and 17 $\beta$ -HSD 12 were designed from known and predicted sequences in the NCBI database. Milk was collected from 9 Holstein cows: 3 from each trimester of pregnancy. Milk was centrifuged, fat removed, and the supernatant decanted. The cellular pellet containing somatic cells was washed with PBS and resuspended in Trizol reagent (Invitrogen). RNA was extracted and RT-PCR utilized to determine presence of transcripts for  $\beta$ -CN, 17 $\beta$ -HSD 7, and 17 $\beta$ -HSD 12. The PCR conditions were as follows: 95C for 5 min, 40 cycles of 95C for 30 s, 64C for 30 s, and 68C for 45 s, a final extension step at 68C for 10 min, followed by agarose gel electrophoresis. Milk somatic cells from all 9 cows expressed  $\beta$ -CN, indicating a MEC population. In addition, 17 $\beta$ -HSD 7 and 17 $\beta$ -HSD 12 sequences were detected in cells of cows from all trimesters of pregnancy. The PCR products were cloned, sequenced, and verified against the NCBI database. These data are consistent with the hypothesis that cells within the mammary gland are capable of converting E1 to E2. Additional experiments are needed to determine which cell type(s) express 17 $\beta$ -HSD transcripts from milk-derived somatic cells.

**Key Words:** Estradiol, Mammary Gland, Steroidogenesis

**M187 Estimation of heritability, repeatability and genetic trend for milk yield of Iranian buffalo in Khuzestan province of Iran using a univariate repeatability animal model.** H. Farhangfar<sup>\*1</sup>, B. Zinvand<sup>2</sup>, and F. Amirlou Abolfathi<sup>3</sup>, <sup>1</sup>University of Birjand, Birjand, Iran, <sup>2</sup>Azad University of Shooshtar, Shooshtar, Iran, <sup>3</sup>Jihade Agriculture of Khuzestan, Iran.

In order to estimate heritability, repeatability and genetic trend for milk yield (adjusted to 305,2x) a total of 1214 records from lactation 1 through 5 of 795 Iranian buffaloes calving from 1993 to 2003 and distributed in 189 herds in Khuzestan province was used. A univariate repeatability animal model was applied to analyze the records. In the model, fixed environmental factors were herd-year-month of calving (contemporary group), lactation order and age linear covariate nested in the lactation. Additive genetic and permanent environmental random effects were also included in the model. Additive genetic relationship among animals was partially complete due to major lack of sire or dam identification. Restricted maximum likelihood estimates of variance components were obtained (via Average Information algorithm) using WOMBAT software. The results obtained in the present study showed that heritability and repeatability of milk yield were 0.071 and 0.075 respectively. This indicates that there was not only low additive genetic but also low permanent environmental variation among animals over the first 5 lactations suggesting that temporary environmental variation made up a large proportion of total phenotypic variance. Based upon regression of average predicted breeding value of animals with records on year of first calving it was also revealed that there was no statistically significant genetic trend over the period of time.

**Key Words:** Genetic Parameters, Milk, Iranian Buffalo

## National ADSA Production Division Graduate Poster Competition

**M188 Effect of feeding two forages at two levels with and without Rumensin to high producing Holstein cows on animal performance.** C. M. Martinez\*, Y. H. Chung, T. W. Cassidy, V. Ishler, K. S. Heyler, and G. A. Varga, *The Pennsylvania State University, University Park.*

Two studies were conducted to evaluate the effects of feeding corn silage (study I) or grass silage (Study II) based diets at two levels with and without Rumensin on DMI, milk production and composition and blood metabolites. In both studies, 8 multiparous high producing Holstein cows were used (BW=698 kg $\pm$ 16 and DIM=194 d $\pm$ 3 for study I; BW=656 kg $\pm$ 16 and DIM=124 d $\pm$ 3 for study II) in a replicated 4x4 Latin square design with a 2x2 factorial treatment arrangement to evaluate the effects of forage level with and without Rumensin supplementation (300 mg/cow/d, top dressed). In study I, diets were formulated to contain 50 or 60% forage (DM basis) in which corn silage comprised 70% and western hay comprised 30% of the total forage in the diet. In study II, diets were formulated to contain 50 or 55% forage (DM basis) in which grass silage comprised 55% and corn silage comprised 45% of the total forage in the diet. The length of each period was 4 wks and samples were collected during the last wk. Results from study I (corn silage based diet) showed that DMI was higher (P <0.01) for the 50% forage diets (29.6 kg/d) compared to the 60% forage diet (28.3 kg/d). In study II, DMI was lower (P <0.05) for cows that were supplemented with Rumensin when compared to cows with no supplementation (25.9 vs. 24.7 kg/d, respectively). Milk total solids% was reduced (P < 0.05) with Rumensin supplementation (11.8%) versus no Rumensin supplementation (12.3%). Milk urea

nitrogen was higher (P <0.059) for cows consuming the 55% forage diet (10.1 mg/dL) than for cows provided the 50% forage diet (8.81 mg/dL). Within each forage source, milk yield and fat corrected milk were not affected by forage level source or Rumensin in the diet (40.9 and 42.4 kg/d, for study I; 41.6 and 41.7 kg/d for study II, respectively). Data from these studies showed that higher forage inclusion in dairy rations can be attained without affecting milk production or major components such as milk fat or protein % for either corn silage or grass silage based diets. Rumensin supplementation may affect milk components and DMI depending on the level and type of forage fed.

**Key Words:** Rumensin, Forage Level, Silage

**M189 Conjugated linoleic acids attenuate lymphocyte proliferation and interleukin-4 production in bovine peripheral blood mononuclear cells challenged with concanavalin-A.** C. Caldari-Torres\*, W. R. Collante, and L. Badinga, *University of Florida, Gainesville.*

During the perinatal period, immune functions such as lymphocyte response to mitogens and production of antibodies are depressed in dairy cows. The objective of this study was to examine the short-term effects of *cis*-9,*trans*-11 and *trans*-10,*cis*-12 isomers of conjugated linoleic acid (CLA) on lymphocyte proliferation, tumor necrosis

factor- $\alpha$  (TNF- $\alpha$ ) and interleukin-4 (IL-4) production by mitogen-stimulated bovine peripheral blood mononuclear cells (PBMCs). In preliminary studies, bovine PBMCs were incubated in the absence (Control) or presence of concanavalin-A (ConA, 10  $\mu$ g/mL), lipopolysaccharide (LPS, 10  $\mu$ g/mL), or phytohemagglutinin A (PHA, 10  $\mu$ g/mL) for 24 or 48 h. Proliferative and cytokine responses were measured using thymidine incorporation and enzyme-linked immunosorbent assays, respectively. Compared to untreated cells, proliferation and cytokine production were maximally stimulated ( $P < 0.05$ ) by ConA within 48 h. Tumor necrosis factor- $\alpha$  (range 53 to 84 pg/mL;  $P < 0.01$ ) and IL-4 (range 16 to 197 pg/mL;  $P < 0.01$ ) concentrations increased linearly between 0 and 15  $\mu$ g/mL of ConA. Co-incubation with linoleic acid (LA) and CLA greatly decreased lymphoproliferative (448 cpm  $>$  239 cpm;  $P < 0.01$ ) and IL-4 (580 pg/mL  $>$  272 pg/mL;  $P < 0.05$ ) responses to ConA in cultured PBMCs. There were no apparent differences in TNF- $\alpha$  response to ConA due to fatty acid treatment (119 pg/mL;  $P = 0.68$ ). These *in vitro* studies provide no evidence for LA or CLA-mediated improvement of immune functions in cattle. Whether these findings reflect the physiological effects of these fatty acids *in vivo* warrants further investigation.

**Key Words:** CLA, Immune Response, Cattle

**M190 Evaluation of *in situ* indigestible neutral detergent fiber as an internal marker to determine digestibility of nutrients.** L. O. Chow\*, C. Silveira, and M. Oba, *University of Alberta, Edmonton, Alberta, Canada.*

The efficacy of *in situ* indigestible neutral detergent fiber (ISIDF) as an internal marker was compared to the external marker ytterbium (Yb) in determining apparent total tract digestibility of nutrients. It was hypothesized that the *in situ* method would provide repeatable indigestible NDF measurements, and would be a reliable marker to estimate digestibility. In the first study, ISIDF concentrations were determined with triplicate samples of concentrate mix, silage, TMR, and feces incubated for 120h in the rumen of 3 lactating and 3 dry cows. The overall intra- and inter-assay CVs for ISIDF measurements were 2.9 and 6.9%, respectively. The inter-assay CV was lower for samples incubated in the rumen of early dry cows as compared to those at peak lactation (3.5 vs. 7.2%), which may be due to lower diurnal variation in ruminal fermentation. In the second study, apparent total tract digestibility using ISIDF was compared with that using Yb as an external marker. Feed and fecal samples were collected from a study evaluating two lots of barley grain cultivars at two dietary grain allocations using 8 cows in a duplicated 4x4 Latin square design with a 2x2 factorial arrangement of treatments. Apparent total tract DM digestibility estimated by Yb was greater than that estimated by ISIDF (65.8 vs. 61.1%;  $p < 0.05$ ), suggesting that nutrient digestibility was either overestimated by the Yb method, underestimated by ISIDF, or both. However, standard errors of means for DM digestibility were smaller when ISIDF was used as a digestibility marker compared with Yb (0.9 vs. 1.3%), suggesting that fecal DM flow was estimated more precisely using an 120h ISIDF as a marker. Though external markers such as Yb are used extensively to estimate flow of duodenal digesta or feces, their use requires extra labor for the frequent dosing of markers. The alternative of using the *in situ* method provides repeatable ISIDF measurements and is a reliable marker to estimate nutrient digestibility.

**Key Words:** *In Situ* Indigestible Neutral Detergent, Internal Marker, Apparent Total Tract Digestibility

**M191 Producer perceptions of feed management software.** B. G. Cox\*, R. E. James, K. F. Knowlton, M. L. McGilliard, and C. C. Stallings, *Virginia Polytechnic Institute and State University, Blacksburg.*

Nine Virginia dairy farmers were surveyed in December 2006 to ascertain satisfaction with feed management software after at least 2 mo of use. Each received a subsidy (20%), installed feed management software (TMR Tracker™, Digi-Star LLC, Fort Atkinson WI), and participated in a 24-question personal interview addressing installation, operation, and satisfaction with the software. Herd size ranged from 135 to 450 lactating cows, averaging 271 lactating cows producing 30 kg/cow/d. Number of TMR mixer operators per farm varied from 1 to 5, with 2 or 3 on 5 farms. Number of feeding groups per farm ranged from 1 to 3; 5 farms feeding 2 groups and 3 farms feeding 1 group. All participants reported that the software met expectations and, if given the choice, they would invest again. Despite satisfaction, 4 of 9 were uncertain or would not purchase the software without the subsidy provided by the project. All but one perceived feed management software as economically beneficial. All farms utilized the software to monitor operator performance and saw no change in quantity of feed purchased. Five producers noted improvements in ration consistency following use. Change made to the feeding program due to TMR Tracker correlated ( $r=0.80$ ) with improvement in ration consistency. More than half (5 of 9) claimed employee training as the most challenging aspect of implementing TMR Tracker. The obstacle to viewing reports was dedication of adequate time. Forty-four percent of respondents attributed most problems to operator error. Overall, producers perceived feed management software as a beneficial subsidized investment with most problems arising from inexperience.

**Key Words:** Feed Management Software, Precision Feeding, Survey

**M192 Out wintering pad design affects woodchip condition.** K. O'Driscoll\*<sup>1,2</sup>, L. Boyle<sup>1</sup>, P. French<sup>1</sup>, B. Meaney<sup>1</sup>, and A. Hanlon<sup>2</sup>, <sup>1</sup>*Moorepark Dairy Production Research Centre, Fermoy, Co. Cork, Ireland,* <sup>2</sup>*University College Dublin, Dublin, Ireland.*

This study evaluated woodchip hygiene in 3 out-wintering pad (OWP) designs for spring calving dairy cows; uncovered [UP] and sheltered [SP] OWP where cows fed grass silage at a concrete feedface, and an OWP where cows self-fed silage on the woodchips [SF]. Cows were accommodated on each treatment in two replicates from Nov 05 until calving (mean=21 Feb 06). Cows on UP and SP had a woodchip space allowance of 12m<sup>2</sup> and on concrete of 2.52 m<sup>2</sup>. The concrete was scraped 6 times per day. SF cows had a woodchip space allowance of 14.52m<sup>2</sup>. OWPs were managed so that each cow had a minimum clean lying area of 2.2 m<sup>2</sup>. OWPs were scored weekly using a visual dirt scale (DS) (1-4; 1=clean, 4=dirty) and composite woodchip samples were taken from the surface. Samples were analysed for dry matter (DM) and pH. Presence of bacteria (staphylococci, streptococci, coliforms) and bacterial load (no. colonies/agar plate) from each sample were determined using selective media. Data were analysed using SAS V9.1. A mixed model was used to analyse DS, DM and pH. Correlations between DS, no. weeks in use, and DM were investigated. Fishers exact test was used to investigate differences in species present and bacterial loads (low= $<$ 40 colonies, medium= $>$ 40,  $<$ 200 colonies, high= $>$ 200 colonies) between treatments. UP and SF had higher DS scores than SP ( $P < 0.01$ ). DS increased with weeks in use ( $P < 0.001$ ). Woodchip DM was lower in UP and SF than in SP ( $P < 0.01$ ) and DM decreased with weeks in use ( $P < 0.001$ ). There was no effect

of treatment on pH, and although the effect of time was significant ( $P < 0.05$ ) there was no discernable pattern over time. There was a positive correlation between DS and weeks in use ( $P < 0.001$ ;  $r = 0.764$ ) and a negative correlation between DS and DM ( $P < 0.001$ ;  $r = -0.633$ ). There was no difference between treatment samples in either presence or load of *Staphylococci* sp or in the number of samples per treatment that contained *Streptococci* spp, but SF had more samples with a high load ( $P < 0.01$ ). More samples from SF contained Coliform spp ( $P < 0.05$ ), due to a higher number of samples with a low and medium bacterial load. It is likely that the higher bacterial presence in SF is due to lack of manure removal at the feedface.

**Key Words:** Dairy, Housing, Hygiene

**M193 Effect of metabolizable protein and energy intake on amino acid metabolism in growing dairy calves.** A. G. Rius<sup>\*1</sup>, J. Cyriac<sup>1</sup>, B. J. Bequette<sup>2</sup>, and M. D. Hanigan<sup>1</sup>, <sup>1</sup>*Virginia Polytechnic Institute and State University, Blacksburg*, <sup>2</sup>*University of Maryland, College Park*.

The objective of this study was to examine the relationship between dietary energy and protein on free amino acids (AA) metabolism. Twenty-four newborn Holstein heifer calves were assigned to each of four treatments: 24/17 (24% CP, 17% fat fed at 350 g/d); 32/17 (32% CP, 17% fat fed at 764 g/d); 31/24 (31% CP, 24% fat fed at 782 g/d);

and 31/24+ (fed at 1177 g/d) in a complete randomized block design. Diets were fed for 63 d. Blood samples were collected at wks 1, 5, and 9. Heifers were sacrificed at the end of the study and analyzed for body composition. Within 5 min of slaughter liver and muscle samples were collected. Plasma, liver and muscle AA concentrations were determined by gas chromatography-mass spectrometry. Data were analyzed using the GLM procedure of SAS. Calves fed 32/17 had the greatest lean gain as compared to the 24/17 and 31/24 diets and also had a higher N as a percent of EBW (reported elsewhere). There were no significant effects of treatment on total essential amino acid concentrations in muscle ( $P = 0.342$ ) or liver ( $P = 0.721$ ). In muscle, there was a tendency for a significant treatment effect for aspartate ( $P = 0.103$ ) 128.3, 79.9, 99.1, 122.1  $\mu\text{mol/L}$  (SEM = 20.1), leucine ( $P = 0.127$ ) 107.8, 131.6, 98.7, 97.6  $\mu\text{mol/L}$  (SEM = 14.7), serine ( $P = 0.106$ ) 369.6, 241.2, 269.1, 290.1  $\mu\text{mol/L}$  (SEM = 51.9), and methionine ( $P = 0.066$ ) 16.8, 35.0, 28.6, 31.5 (SEM = 6.7)  $\mu\text{mol/L}$  for the 24/17, 32/17, 31/24 and 31/24+ treatments, respectively. There was a significant treatment effect for liver alanine ( $P = 0.021$ ) 3330.1, 2463.8, 1848.4, 1901.4  $\mu\text{mol/L}$  (SEM = 485.2) and serine ( $P = 0.003$ ) 1915.7, 1517.6, 1124.2, 1184.2  $\mu\text{mol/L}$  (SEM = 205.2), and a trend for glutamate ( $P = 0.061$ ) 5735.2, 4851.6, 4240.6, 3860.3  $\mu\text{mol/L}$  (SEM = 678.8) and histidine ( $P = 0.082$ ) 436.2, 508.8, 344.3, 388.8 (SEM = 58.8) for the 24/17, 32/17, 31/24 and 31/24+ treatments, respectively. Overall, the 32/17 treatment supported the greatest methionine concentration in muscle whereas treatment 24/17 supported the greatest concentrations of alanine and serine in liver.

**Key Words:** Calf, Amino Acid, Energy

## Nonruminant Nutrition: General Nonruminant Nutrition

**M194 Evaluation of antimicrobial effects on monogastric gut microflora by plant waste products.** S. Stella, D. Tedesco<sup>\*</sup>, C. Barbieri, L. Garavaglia, and D. Cattaneo, *University of Milan, Italy*.

EU is focusing on effective alternatives to antibiotics in order to reduce the incidence of potential pathogenic bacteria in the gastrointestinal tract of monogastrics. The aim of the present study was to evaluate the effects of plants and their post-processing derivative waste products, recognized as safe for human or animal health (SAFEWASTES, EU project n. 513949), on growth and viability of gut intestinal microbiota in weaning piglets. A total of 28 plant by-products have been tested. Five strains of *Escherichia coli*, *Clostridia* and *Lactobacilli* were isolated from faecal samples of healthy piglets (60–70 days of age), by inoculation of specific culture media. Aliquots of 0.1 mL of bacterial suspension of each selected strain ( $10^8$  CFU/mL) were inoculated onto the surface of agar plates containing the specific culture media. The effects of plant extracts on gut bacteria have been studied using the paper disc agar diffusion (Kirby-Bauer) method. Samples were solubilized into deionized water or ethanol (10 mg/mL) and sterilized by filtration. Sterile paper discs were moistened with extract solution and dried before use. A test paper disc moistened with the extract, a positive control (a disc with Ampicillin or Apramycin) and a negative control (a disc moistened with sterile deionized water or ethanol) were placed under aseptic conditions onto the surface of inoculated culture medium. After incubation, plates were observed in order to find the presence of growth inhibition areas. Four of the 28 tested substances showed an inhibitory effect on *E. coli* strains, without influence on *Clostridia* growth. It was not observed any negative effect on commensal microbiota beneficial to the host. None of tested substances showed an inhibitory effect on *Lactobacilli* growth. On the basis of

this preliminary screening, further investigations will be performed in order to confirm the antimicrobial activity of these potential feed additives also in in vivo trials with target species.

**Key Words:** Plant Waste Products, Gut Microflora, Antimicrobial Effects

**M195 Microlocalization of digestion-resistant aromatic lignin and cellulosic compounds in feeds at cellular and subcellular levels with the synchrotron: A novel approach.** P. Yu<sup>\*</sup>, *University of Saskatchewan, Saskatoon, SK, Canada*.

The objective of this study was to micro-localize the distribution of digestion-resistant aromatic lignin and cellulosic compounds in feeds at cellular and subcellular levels using advanced synchrotron-powered FTIR microspectroscopy (SFTIRM) as a novel approach. The SFTIRM is a newly emerging and non-destructive analytical technique and can reveal molecular chemistry (structural-chemical make-up) of biological samples at highly spatial resolutions (3–10  $\mu\text{m}$ ) without destruction of the feed internal structures. The experiment was performed at the National Synchrotron Light Source in Brookhaven National Laboratory (NSLS-BNL, US Department of Energy, New York). The exemplified feeds used for this pilot study were corn (cv. Pioneer) and barley (cv. Harrington). The results show that with SFTIRM, the images of the aromatic lignin and cellulosic compounds could be generated to be able to show the distribution and intensity across the feeds tissues. The digestion-resistant aromatic lignin compound only presented in the pericarp region and no lignin has been found in seed coat, aleurone layer and endosperm. The cellulosic compounds presented most in the