for SI II and SI I respectively. Although the increase in production level for SI II is not as high as for SI I, the increase in tolerance is considerable and might lead to a better survival rate and save costs under African environmental conditions.

**Key Words:** Trypanotolerance, Selection Index, Breeding Objective

**W115 Using the n-alkane technique to estimate the herbage intake of steers grazing *Zoysia japonica* grassland.** Y. Zhang*[1], Y. Togamura[2], and K. Otsuki[2], [1]*China Agricultural University*, *Beijing, PR China*, [2]*National Institute of Livestock and Grassland Science*, *Tochigi, Japan*.

The alkane technique was evaluated for estimating herbage intake of grazing steers in a natural *Zoysia japonica* grassland in Japan. Six steers continuously grazed *Z. japonica* grassland in which species coverage was measured to be 78.8% *Z. japonica*, 13.5% eastern bracken (*Pteridium aquilinum*), 6.2% other plants and 1.5% bare area by point method. The steers were dosed with a controlled release device (CRD) capsule (Captec TM, New Zealand) for the estimation of herbage intake. Fecal samples were collected once daily from the ground immediately after defecation. Over the same period, herbage samples were hand plucked. Steer BW was measured before and after the 15-d experimental period. Herbage and fecal samples were kept at -20°, freeze-dried, and milled through a 1 mm sieve. Concentrations of n-alkanes were determined by gas chromatography. Herbage intake was calculated using both the C{31}/C{32} and the C{33}/C{32} alkane pairs, based on the whole diet and fecal concentrations of these alkanes, and the C{32} release rate from the alkane-CRD. The effects of steers and alkane pairs (C{31}/C{32} or C{33}/C{32}) on intake were tested by Analysis of Variance using a completely random design. Relationships between steer BW changes and intakes were investigated by correlation. Herbage intake calculated by alkane technique was 1.6% to 2.4% of BW. Intake estimates based on either C{31} or C{33} alkanes did not differ ($P > 0.05$). Estimated intake of *Z. japonica* differed significantly between steers ($P < 0.05$), and was related significantly ($P < 0.05$) to the changes of steer BW (r = 0.583 and 0.651 for intake calculated by C{31}/C{32} and C{33}/C{32}, respectively). Herbage intake estimates were reasonable for the explanation for the BW changes according to the Japanese Feeding Standard for Beef Cattle. We conclude that herbage intake of steers grazing (*Zoysia japonica* grassland was estimated successfully with alkane technique.

**Acknowledgements:** The thanks are granted to Dr Elaine Grings from the Fort Keogh LARRL, USDA-ARS who presented his comments on the writing of paper.

**Key Words:** Steers, Intake, Grazing

# Lactation Biology

**W116 Udder morphology and milking characteristics in dairy goats milked once- or twice-daily.** A. A. K. Salama[1], G. Caja*[1], M. Rovai[1], R. Casals[1], and A. Martí[2], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Spain*, [2]*Universidad Miguel Hernández de Elche*, *Orihuela, Spain*.

The effect of once- (**1x**) vs. twice- (**2x**) daily milking on udder morphology and milk emission during machine milking (42 kPa, 90 pulses/min) was studied in multiparous Murciano-Granadina dairy goats. Kids were removed from their mothers at birth and the goats milked 2x until the end of wk 2 when they were assigned to the milking frequency treatments: 1x (0900; n = 8), and 2x (0900 and 1700; n = 8) throughout lactation. Main udder and teat traits were measured 7 h after the a.m. milking at wk 2, 20 and 28 of lactation. Milk emission was recorded for each udder half during the a.m. milking on two consecutive days at wk 14 and 23 of lactation. Compared to 2x, 1x goats tended to have greater udder volume (1.67 vs. 1.53 L; $P < 0.14$) and udder depth (18.3 vs. 17.5 cm; $P < 0.06$). No differences were detected for teat traits. Stage of lactation affected ($P < 0.01$) all morphological traits studied when wk 2 and 28 were compared (udder: volume, 1.86 and 1.28 L; depth, 19.7 and 17.4 cm; teat: angle, 41 and 29°; length, 27 and 30 mm; floor distance, 25.3 and 26.2 cm). Interaction between week of lactation and milking frequency was only detected for teat length, where teats become longer as lactation advanced in 2x. All goats gave milk emission curves with a long plateau indicating a sustained high milk flow during machine milking. Peak (680 ml/min) and average (403 ml/min) milk flow rates did not vary according to milking frequency treatment and stage of lactation (wk 14 and 23). Udder halves of 1x goats yielded a greater volume of machine milk (560 vs. 365 ml; $P < 0.05$) and needed longer milking time (83 vs. 58 s; $P < 0.05$) than 2x goats. Machine milk and milking time decreased as lactation advanced, but differences between wk 14 and 23 were only significant for 2x goats (412 and 317 ml; 65 and 51 s, respectively). Results showed morphological udder changes in order to adapt milk storage capacity to milk yield according to stage of lactation and milking interval. On the contrary, milk flow did not vary according to the amount of milk stored, suggesting that teat sphincter features more than intramammary pressure condition milk flow in goats.

**Key Words:** Milking Frequency, Milk Flow, Udder Traits

**W117 Effects of milking frequency prepartum on postpartum milk production, milk composition and dry matter intake in dairy cows.** R. R. Rastani*[1], N. Silva del Rio[1], T. F. Gressley[1], G. E. Dahl[2], and R. R. Grummer[1], [1]*University of Wisconsin*, *Madison*, [2]*University of Illinois*, *Urbana*.

Forty-eight Holstein cows were utilized in a randomized block design to evaluate different dry period lengths and prepartum milking frequency on subsequent milk production, milk composition and dry matter intake. Lactating cows began the experiment 35 d prior to expected calving date, were milked 2x/d during a 7 d covariate period and were assigned to one of three treatments. Cows were milked 0x/d (0x), 1x/d (1x), and 4x/d (4x) for the last 28 d of gestation. If milk production decreased to less than 0.5 kg/milking or 1 kg/d, milking via machine ceased; however, teat stimulation continued 1x/d or 4x/d according to treatment assignment. All cows were milked 2x/d postpartum (wk 1 to 8). Prepartum DMI tended to be greater for 1x and 4x compared with 0x ($P < 0.10$). Prepartum, cows milked 1x produced 17% less than cows milked 4x (5.9 and 7.1 kg/d, respectively). There were no differences in prepartum and postpartum BCS and BW, and postpartum DMI. There was a parity by treatment interaction for postpartum milk production ($P < 0.05$). Postpartum milk production by multiparous cows through 56 days in milk was greater for 0x/d and 4x/d compared with 1x/d (44.6, 44.6, and 34.6 kg/d, respectively; $P < 0.02$). Postpartum milk production by primiparous cows was significantly decreased with increased milking frequency (39.8, 33.9, and 30.2 kg/d for 0x/d, 1x/d, and 4x/d; $P < 0.01$). Postpartum fat yield was greater for 0x compared with 1x and 4x (1.51 vs. 1.32 and 1.21 kg/d; $P < 0.01$). Postpartum protein yield tended to be greater for 0x compared with 1x and 4x (1.28 vs. 1.17 and 1.13 kg/d; $P < 0.10$). Continuous milking resulted in a loss of milk production in the subsequent early lactation with primiparous cows; however, increasing milking frequency to 4x/d in the last 28 days of gestation eliminated the previously observed loss in milk production associated with continous milking for multiparous cows.

**Key Words:** Dry Period Length, Continuous Milking, Milking Frequency

**W118 Mid term lactational effects of once- versus twice-daily milking in Manchega and Lacaune dairy ewes.** V. Castillo*, X. Such, G. Caja, E. Albanell, and R. Casals, *Universitat Autònoma de Barcelona*, *Bellaterrra, Spain*.

The effects of once- (x1) vs. twice-daily (x2) milking, throughout the milking period (wk 6 to 22) on milk yield, milk composition and somatic cell count

(SCC) were studied in a total of 60 dairy ewes (Manchega, MN; n = 32; and, Lacaune, LC; n = 28). After the weaning of the lambs (wk 5), ewes were assigned to two machine milking treatment: x1 (1830) or x2 (0700 and 1900). Treatments were switched at wk 14 according to a crossover design, but 8 MN and 5 LC ewes continued in group x2 as a control. Recording was individually conducted weekly for milk yield, biweekly for milk composition, and monthly for SCC. Cisternal milk was measured by using an oxytocin receptors blocking agent at wk 7, 12, 16 and 20. Cisternal milk varied according to breed (MN, 63%; and LC, 77%; $P < 0.01$) and milking frequency (x1, 75%; and x2, 66%; $P < 0.01$). According to their cisternal size, once daily milking resulted in a reduction ($P < 0.05$) in milk yield in early- (MN, 33%, and LC, 10%) and in late-lactation (MN, 11%, and LC, 9%), in both breeds. Milking frequency did not affect ($P < 0.001$) percentages of total solids (18.1 and 20.7% in MN; 16.6 and 17.5 % in LC), fat (6.7 and 7.9% in MN; 5.8 and 6.5% in LC) and protein (5.5 and 6.1% in MN; 5.0 and 5.5% in LC) in early- and late-lactation, respectively. In addition, the logSCC did not vary significantly ($P > 0.5$) according to the milking treatment, throughout the milking period. Our results showed that high yielding dairy sheep can be milked once daily throughout lactation. Reduction in milk yield was lowest in the highest milk yield level dairy breed which also had the greatest percentage of cisternal milk. Obtained results showed that genetic selection for milk yield also increased cisternal compartment and milkability of dairy sheep breeds. Moreover, losses in milk yield would be reduced if x1 is done during mid- or late-lactation. Once-daily instead of twice-daily machine milking reduces farmer working time with no negative effects on main milk components for cheese making or on udder health in dairy sheep.

**Acknowledgements:** This research has been supported by CICYT-Spain, Project AGL2002-03472.

**Key Words:** Once Daily Milking, Milk Production, Dairy Ewes

### W119 Incidences of calving related disorders of Holstein cows supplemented with low dose of bST prepartum and during early lactation.

M. S. Gulay*[1], M. Liboni[2], M. J. Hayen[2], and H. H. Head[2], [1]*Akdeniz University, Turkey*, [2]*University of Florida, Gainesville*.

Objective was to evaluate whether supplementing Holstein cows with bST (10.2 mg/d), beginning 21 d (±3 d) before expected calving and continued through 42 d (±3 d) postpartum, affected incidence rates of retained fetal membranes (RFM), metritis (MET), clinical mastitis (MAS), digestive problems (DP), ketosis (KET), milk fever (MF), displaced abomasum (DA) or lameness (LAM) during the first 60 d postpartum. Multiparous cows from two separate trials were combined for analyses. Cows in bST supplemented group (I; n=149) received biweekly injections of POSILAC® in ischiorectal fossa, whereas control cows (II; n=154) were not supplemented. A group of cohorts also was used in the statistical analysis (III; n=84). Disease frequencies were collected from farm records. Across all treatment groups the incidence rates (number of diseased cows divided by the total number of cows) for RFM, MET, MAS, DP, KET, MF, DA and LAM were 9.6, 16.7, 14.4, 4.2, 4.2, 3.2, 3.2 and 6.2%, respectively. Incidence rates of RFM, MET, MAS, DP, KET, MF, DA and LAM for TRT-I, II and III were 10.0, 8.4 and 12.1%; 12.9, 18.2 and 20.2%; 7.9, 17.5 and 19.1%; 1.4, 6.5 and 4.5%; 1.4, 5.2 and 6.7%; 1.0, 4.6 and 4.5%; 1.4, 3.9, and 4.5%; and 7.2, 5.2 and 6.74%, respectively. The proportions of sick cows in each group (number of cows having one or more cases of diseases divided by the total number of cows) were 31.4, 43.5 and 51.7%, respectively. Significant Chi-Square values ($P<0.05$) were detected between TRT-I and II for MAS, DIG, KET and MF, with a greater number of healthy cows in TRT-I than II ($P<0.04$). No differences were detected between TRT-II and III. The results indicated that a low dose of bST supplemented to Holstein cows during prepartum and early postpartum periods did not have a negative effect on postpartum calving disorders compared to control cows. Moreover, cows supplemented with bST were less likely to have calving related disorders than non-supplemented counterparts.

**Key Words:** Transition Cows, bST, Diseases

### W120 Association between dry period length (30 or 60 d) and calving related disorders.

M. S. Gulay*[1], M. J. Hayen[2], and H. H. Head[2], [1]*Akdeniz University, Turkey*, [2]*University of Florida, Gainesville*.

Objective was to evaluate effects of dry period length (60 d vs. 30 d) on incidence of calving related disorders of multiparous Holstein cows (n=84 treated cows and 27 cohorts) during the first 60 d postpartum. Treatments were arranged in a 3x2x2 factorial design that included dry period (60 d dry, 30 d dry, and 30 d dry+ECP), prepartum and postpartum bST supplementation (POSILAC®; 10.2 mg/d), and prepartum anionic or cationic diets. To accelerate mammary involution, estradiol cypionate (ECP; 15 mg) was injected intramuscularly at dry-off. Across all TRT groups [(n=112); cows in TRT-I (60 d dry, n=28), TRT-II (30 d dry, n=28), TRT-III (30 d dry+ECP, n=29), and TRT-IV (cohorts, n=27)] the overall observed incidence rates (number of diseased cows divided by the total number of cows) were: displaced abomasum (DA; 1.8%), retained fetal membranes (RFM; 9.8%), metritis (MET;10.7%), clinical mastitis (MAS; 9.8%), ketosis (KET; 2.7%), and lameness (LAME; 4.5%). Incidence rates of DA, RFM, MET, MAS, KET, and LAME for TRT-I, II, III and IV were 3.6, 0, 0 and 3.7%; 10.7, 3.6, 10.3 and 14.8%; 14.3, 7.1, 6.9, and 14.8%; 3.6, 3.6, 0 and 3.5%; 3.6, 7.1, 3.5, and 3.7%, respectively. The proportions of sick cows in a group (number of cows having one or more cases of diseases divided by the total number of cows) were 39.3, 28.6, 31.0 and 37.0%, respectively. No significant Chi-Square values ($P<0.1$) were detected among the three dry TRT groups and cohorts. Thus, results indicated that shortening dry period length with or without ECP did not increase incidence of calving related disorders.

**Key Words:** Dry Period Length, Transition Period, Diseases

### W121 Assessing changes in mammary gland gene expression using a cDNA microarray in the dairy cow following administration of bovine somatotropin.

J. Kelsey*[1], A. Nudda[1], A. Corato[1], E. Mosley[1], S. Mosley[1], B. Williams[1], J. Grimberg[1], D. Henderson[2], J. Hoying[2], K. Greer[2], and M. McGuire[1], [1]*University of Idaho, Moscow*, [2]*University of Arizona, Tucson*.

To determine gene expression changes in the mammary gland following bovine somatotropin (bST) treatment, four lactating Holstein cows (253±143 DIM) were used. Mammary tissue biopsies were taken on d -5, -2, 1 and 6 relative to a single 500 mg dose of bST (Posilac®, Monsanto, St. Louis, MO). Total RNA was isolated, amplified, converted to cDNA, labeled with Cy3 or Cy5 dye, and hybridized to the NBFGC bovine microarray (Michigan State University). Comparisons were made using a modified loop design with each cow on each day represented once. Milk yield was increased (30%; $P < 0.05$) by d 4 and remained elevated through the end of the study. Milk fat, protein and lactose content were not affected ($P > 0.1$). Microarray data were analyzed by two methods. In the first analysis, raw data were background adjusted using the procedure by Edwards (Bioinformatics 2003, 7:825) and normalized using Loess normalization. An empirical Bayes procedure to estimate individual gene shrunk variances was then used to create moderated t-statistics following an ANOVA model. The model included fixed treatment and dye effects, all second order interactions, as well as random cow and array effects. Treatment contrasts within gene were estimated and p-values adjusted using a false discovery rate procedure. Based on this analysis, two genes changed ($P < 0.05$). The second analysis began with a local background intensity subtraction and linlog transformation followed by Lowess normalization between the two channels of each array and among both channels of all arrays. A gene-by-gene fixed effects ANOVA followed which included array, dye and time terms in the model. P-values were determined using a shrunk variance consisting of a portion of the pooled variance for all genes and the individual gene variances. This analysis yielded a list of 495 genes that changed ($P < 0.05$); however, no false discovery rate procedure was employed and a random cow effect was not included. Statistical analysis of microarray data is a complex and evolving field.

**Acknowledgements:** Supported by USDA-IFAS (2001-52100-11211).

**Key Words:** Microarray, bST, Bioinformatics

### W122 Fatty acid composition of porcine milk throughout lactation and comparison to human and bovine milk.

S. Donovan*[1], S. Taylor[2], and E. DePeters[2], [1]*University of Illinois*, *Urbana*, [2]*University of California*, *Davis*.

Fatty acids (FA) in milk provide an important energy source, influence cell membrane FA composition and regulate neural development of the suckling neonate. Milk FA are derived from de novo mammary synthesis and plasma FA, which is influenced by dietary FA intake and hepatic FA synthesis, and FA synthesis by ruminal microbiota. The FA compositions of bovine and human milks are well characterized. Although the pig is an important production species and biomedical model Less is known of the FA composition of porcine milk. Thus, the FA composition of porcine milk throughout lactation was determined and compared to bovine and human milk. Milk samples were obtained from three sows fed a standard corn/soybean meal diet at farrowing (0 h), 12 h and d 1-4, 7, 14, 18, 21 and 24 postpartum. Human milk samples (n=8) were obtained between 1 and 3 months postpartum and bovine milk (n=3) from cows fed 40% alfalfa/60% concentrate. Fatty acids were determined by capillary gas chromatography and expressed as % of total fatty acids (g/100g). Longitudinal changes in porcine milk FA were analyzed by repeated measures ANOVA using the MIXED model within SAS and data are expressed at means ± SEM. No FA less than C10 and no docosahexaenoic acid (C22:n6) were detected in porcine milk. The predominant FA's in porcine milk, C18:1 cis 9 & 10 (33.7 ± 2%) and C16 (30.5 ± 3%), were unaffected by stage of lactation. Seven FA were affected ($P<0.001$) by stage of lactation. C18:2 decreased ($P<0.001$) from 18.2 ± 0.5% in colostrum to 10.9 ± 0.5% in milk. C17, C18:3, C20:4 and C22:5cis10 also decreased from colostrum to milk, whereas C10 and C12 increased over lactation. Porcine, human and bovine milk FA were compared by 1-way ANOVA. All FA tested differed ($P<0.001$) among the three species, except C22:n5. C4 and C6 were only found in bovine milk and C22:n6 in human milk. Nine (26%) FA were similar in human and bovine, 9 (26%) in human and porcine, and 8% in bovine and porcine. Twelve FA (35%) differed ($p<0.001$) among the species. In summary, the FA profile of porcine milk is influenced by stage of lactation and is more similar to human than bovine milk.

**Key Words:** Milk, Fatty Acid, Pig

### W123 The effect of conjugated linoleic acid (CLA) on transcriptional activation of the Stearoyl-CoA desaturase gene in bovine mammary cells.

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The majority of CLA present in bovine milk is produced by conversion of rumen-produced trans-vaccenic acid to CLA in the mammary gland by the action of the Stearoyl Co-A desaturase gene, however the regulation of this process is poorly understood. In this study, regulation of the Scd gene promoter was examined by creating truncated promoter luciferase reporter constructs and carrying out transient transfection of a bovine mammary cell line, Mac-T. Promoter fragments were designated F1 to F8 and were 212, 380, 416, 760, 996, 1264, 1523 and 1824bps in length respectively. Fragment F4, an area 732bp upstream of the proposed transcriptional start site, was shown to have the highest transcriptional activity of the truncated clones, with fragment F7 also showing high activity. These results also showed that an 35bp area ranging from 354 to 388bp from the proposed transcriptional start site was critical for activation of the Scd promoter (F2 and F3). The effect of CLA isomer treatment on the Scd promoter was also examined. Treatment with CLA isomers caused a marked reduction in the overall activity of the Scd gene promoter with differences in the isomer effect (Table 1).

**Table 1. Effect of CLA isomers on Scd gene promoter.**

| Fragment | F1 | F2 | F3 | F4 |
|---|---|---|---|---|
| NT | 10960 | 12212 | 109806 | 255815 |
| c-9, t-11 CLA | 1192 | 1333 | 5317 | 9804 |
| t-10, c-12 CLA | 1696 | 2910 | 5371 | 12746 |
| F5 | F6 | F7 | F8 | |
| NT | 173800 | 173800 | 209520 | 2481 |
| c-9, t-11 CLA | 3683 | 4875 | 10788 | 290 |
| t-10, c-12 CLA | 771 | 11361 | 8871 | 200 |

Relative Light Units from Scd promoter truncated constructs are shown.

**Acknowledgements:** This work was supported by the Dairy farmers of Canada and the CLA Network.

**Key Words:** Conjugated Linoleic Acid, Promoter Regulation

### W124 Effects of body weight and plane of nutrition on histological development of mammary tissue in Holstein heifers.

K. M. Daniels*[1], M. L. McGilliard[1], P. L. Boyle[1], M. J. Meyer[2], M. E. Van Amburgh[2], A. V. Capuco[3], and R. M. Akers[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Cornell University*, *Ithaca, NY*, [3]*USDA-ARS*, *Beltsville, MD.*

Our objective was to determine effects of rate of gain and body weight (BW) on udder development. Mammary tissue samples were available from heifers (n = 54) reared on one of two dietary treatments (Moderate (M) 650 g/d or High (H) 950 g/d of daily gain), and slaughtered at 150, 200, 250, 300, or 350 kg BW. At slaughter, mammary parenchymal samples were excised, preserved, prepared for histology, and stained with hematoxylin and eosin. Representative digital images of tissue sections were captured for analysis. Tissue areas occupied by interlobular stroma, epithelium, lumen, and intralobular stroma were measured ($\mu m^2$) and the numbers of epithelial and luminal structures per image were tabulated (Image-Pro Plus software, Version 4.5). Mean percentages of mammary parenchyma occupied by interlobular stroma, epithelium, lumen, and intralobular stroma were 28, 20, 7, and 45%, respectively; percentages did not differ by BW or treatment, nor was there an interaction between treatment and BW. Number of epithelial (31 ± 6 vs. 47 ± 5) and luminal (24 ± 5 vs. 38 ± 4) structures per image increased between 150 and 350 kg BW. For heifers slaughtered between 150 and 350 kg of BW, alterations in the rate of gain between 650 and 950 g/d, accomplished by feeding varying amounts of the same diet, had no significant effect on tissue characteristics or the pattern of mammary parenchymal development. Perhaps with other diets, changes in parenchymal tissue composition would be noted. These data support the hypothesis that the length of time between birth and slaughter, not plane of nutrition, plays the predominant role in determining the amount of mammary parenchyma a heifer will have.

**Key Words:** Heifer, Histology, Mammary

### W125 Use of an immortalized bovine mammary epithelial cell line (MAC-T) to measure the mitogenic activity of extracts from heifer mammary tissue: effects of nutrition and body weight.

K. M. Daniels*[1], P. L. Boyle[1], M. L. McGilliard[1], M. J. Meyer[2], M. E. Van Amburgh[2], and R. M. Akers[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Cornell University*, *Ithaca, NY*.

Our objective was to determine effects of rate of gain and body weight (BW) on the mitogenic activity of mammary gland extracts (MGE) prepared from bovine mammary parenchyma. Mammary tissue samples were available from heifers (n = 54) reared on one of two dietary treatments (Moderate (M) 650 g/d or High (H) 950 g/d of daily gain), and slaughtered at 150, 200, 250, 300, or 350 kg BW. Cytosolic MGE were prepared from frozen mammary parenchyma. Proliferation of the bovine cell line MAC-T, as affected by addition of MGE to

culture medium was measured by the incorporation of $^{3}$H-thymidine into DNA. Addition of MGE markedly stimulated cell proliferation (5-fold vs. no addition and 1.5-fold greater than 5% fetal bovine serum). However, heifer BW did not impact response to MGE. Moreover, in contrast to a prior study, but in agreement with in vivo data (bromodeoxyuridine labeling) from a current study, we measured only a modest and generally non-significant effect of diet, irrespective of BW from 150 to 350 kg, on the proliferative response of MAC-T cells, irrespective of how the data were expressed i.e. parenchymal mass basis, protein basis, or DNA basis. Response trends were however similar i.e. greater proliferation with MGE from M heifers. Possible reasons for these differences may be attributable to differences in animal genetics and/or diet composition between past and present studies. Regardless, these data support the hypothesis that the length of time between birth and slaughter, not plane of nutrition, plays the predominant role in determining the amount of mammary parenchyma a heifer will have.

**Key Words:** Heifer, Mammary, Nutrition

### W126 Use of $^{13}$C-mass isotope distribution analysis (MIDA) to define precursors for lactose and amino acid synthesis by bovine mammary explants.

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Despite the fact that mammary uptake of carbon and N substrates balances with milk component outputs, the biochemical organization of substrate fluxes remains ill-defined. Our aim was to determine the contribution of glucose to lactose and to non-essential amino acid (AA) synthesis by the bovine mammary gland. Mammary explants (each 100 mg) from two late-lactation cows were incubated (for 0.5, 1, 2, 3 or 6 h) in Delbecco's Modified Medium (5 mL) containing all essential AA plus [U-$^{13}$C]glucose. For Cow 1, explants were incubated with 0.67, 3.33 or 14.4 mM [U-$^{13}$C]glucose and for Cow 2 incubations contained 1.11, 5.55 or 27.7 mM [U-$^{13}$C]glucose. After incubation, explants were separated from media, and $^{13}$C-MIDA conducted on intracellular free AA. Media lactose was separated from free sugars and lactose hydrolyzed to glucose and galactose for $^{13}$C-MIDA. From 1 h of incubation onwards, parameters were not different. The proportion of galactose derived from glucose increased (3 to 88%; $P<0.001$) with increasing glucose level, whereas all glucose in lactose derived from media glucose. The net contribution of glucose carbon to aspartate (2 to 10%), glutamate (5 to 11%) and glutamine (3 to 11%) synthesis increased ($P<0.05$) only slightly with glucose level. Thus, most of these AA derived carbon skeletons from essential AA catabolism. The proportion (~4%) of acetyl-CoA flux, and thus Krebs cycle energy generation, derived from glucose was not affected by glucose level. This study is the first to show that, within the physiological range of plasma glucose (3.33-5.55 mM), a significant portion (~55%) of galactose for lactose synthesis derives from non-glucose sources. Further, that essential AA are the major source for *de novo* AA synthesis, the supply of essential AA as precursors for mammary synthesis of non-essential AA, in addition to casein, may need to be considered as a potential limitation to milk protein yield by dairy cows.

**Key Words:** Mammary Gland, Lactose Synthesis, Glucose

### W127 The effect of using a teat sealant to decrease intramammary infections at calving and to compare microbiological results from quarter and composite milk sampling.

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A study was conducted at the University of Georgia Dairy in Athens to evaluate the effect of an internal teat sealant at dry-off on new intramammary infections (IMI) at calving and to compare microbiological results of composite and quarter milk sampling to determine IMI status. Quarter and composite milk samples were taken at dry-off, calving and 10 d post calving. At dry-off, 20 cows were infused with a standard dry cow antibiotic (Tomorrow, Fort Dodge, Inc.) and vaccinated with *Escherichia coli* J-5 vaccine (Novartis, Inc., Larchwood, IA). Twenty animals were divided into 2 equal groups based on parity (primiparous and multiparous). Animals with each group were then randomly assigned to either treatment (infused with Orbeseal, Pfizer, Inc., Exton, PA) or control groups. Quarter and composite samples were taken at dry-off from 10 teat sealed cows and 10 controls, and frozen until cultured. Animals in the study were dried off from 9/18/2004 until 12/15/2004. A total of 63 of 80 quarters sampled was bacteriologically negative, 2 samples had *Staph. aureus*, 9 samples had coagulase negative staph (CNS), and 6 samples had environmental streps. For the 40 quarters treated with a teat sealant, 35 samples were negative, 1 had *Staph. aureus*, 3 had CNS, and 1 had an environmental strep at dry off. For the 40 quarters that were not treated with a teat sealant, 28 samples were negative, 1 had *Staph. aureus*, 6 had CNS, and 5 had environment streps at dry-off. At dry-off, 14 of 20 composites were negative, 2 had environmental streps, and 4 had CNS. Preliminary results of sampling at calving and 10 d are 4 of the 4 fresh treated cows were bacteriologically negative with 0 new IMI. 5 of the 8 fresh control cows were negative and 3 had a new IMI. At 10 d post calving, 5 of 7 control cows were negative and 2 had a new IMI. 79% of the composite samples correctly categorized the infection status of the cow. Two composite samples were contaminated during the collection process.

**Key Words:** Teat Sealant, Milk Sampling, Mastitis

### W128 Composition and size of mammary glands of pregnant gilts according to gland anatomical location.

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This study was to characterize the growth of mammary glands individually or as grouped by anatomical location during gestation in gilts. Thirty-five pregnant gilts (158.2±3.8 kg, Camborough-22, PIC) were allotted randomly to seven slaughter groups: d 0, 45, 60, 75, 90, 102, and 112 of gestation. Gilts were fed 2 kg/d gestation diet (3.1 Mcal ME/kg, 12.2% CP, as fed basis) and slaughtered according to their assignments to obtain mammary glands. Skin and extraneous fat pad were removed from mammary glands to obtain parenchymal mammary tissues. Obtained mammary tissues were further separated into individual glands. Individual mammary glands were weighed and bisected in an approximate midsaggital section to measure the cross-sectional area (CSA). Half of the each mammary gland was sampled, ground, and pooled according to anatomical location. The first two pairs of glands were pooled as ′anterior′. The 3rd, 4th, and 5th pairs of glands were pooled as ′middle′. The 6th, 7th, and 8th pairs of glands were pooled as ′posterior′. Weight of individual glands, and CSA increased ($P < 0.01$) cubically from d 45 to 112 of gestation. Individual dry matter (DM) and crude protein (CP) contents in anterior, middle, and posterior increased ($P < 0.05$) cubically from d 45 to 112 of gestation. Weight of individual glands in middle (345.9 g) was higher ($P < 0.05$) than that in posterior (241.3 g) at d 112 of gestation. Content of CP in middle glands (138.8 g) was higher ($P < 0.05$) than those in anterior (101.5 g) and posterior (97.2 g) at d 112 of gestation. Weight gains of individual glands, CP accretions in individual glands, and CSA of individual glands accelerated ($P < 0.01$) after d 70.5, 81.6, and 67.0 of gestation, respectively based on non-linear regressions from NLREG program. This study indicates that the growth of individual mammary glands and CP accretion in individual mammary glands mainly occurred during late gestation (after d 70), and individual mammary glands located in the middle (3rd, 4th, and 5th pairs) gained more weight and proteins during gestation than those located in the anterior or posterior.

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**Key Words:** Mammary Glands, Gestation, Sows

### W129 Mineral and trace element content of porcine milk throughout lactation and comparison to human and bovine milks.

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The concentrations of minerals and trace elements in milk are tightly regulated through mammary transporters as well as their binding to milk proteins. The pig is an important production species and biomedical model, however the mineral or trace element content of pig milk and mammary transport systems have not been well characterized. We analyzed the mineral and trace element content of porcine milk throughout lactation and compared it to bovine and human milk. Milk was obtained from three sows at farrowing (0 h), 12 h and d 1-4, 7, 14, 18, 21 and 24 postpartum. Human milk (n=8) was obtained between 1 and 3 months postpartum and bovine milk (n=3) from cows in midlactation. Milk samples were analyzed by atomic absorption (Ca, Mg, Na and K), colorimetric assay (P) and trace elements by Inductively Coupled Plasma Emission Spectroscopy (Cu, Fe and Zn). Longitudinal changes in porcine milk were analyzed by repeated measures ANOVA using the MIXED model within SAS and data are expressed at means ± SEM. All minerals and trace elements were affected ($p<0.001$) by stage of lactation, with the exception of Fe. Ca increased ($P<0.001$) 3-fold from porcine colostrum (563 ± 87 ug/L) to mature milk (1664 ± 96 ug/L ). Mg (91 ± 4 vs. 121 ± 4 ug/L ) and P (1252 ± 40 vs. 1562 ± 31 ug/L ) also increased ($p<0.001$) from colostrum to mature milk. Milk K initially increased between 0 and 24 h, then declined from 1314 ± 46 ug/L in colostrum to 1035 ± 44 ug/L in mature milk ($p<0.001$). Na also decreased ($P<0.001$) from colostrum (651 ± 45 ug/L ) to mature milk (329 ± 17 ug/L ). Zn decreased from colostrum (10.2 ± 1.0 ug/L ) to mature milk (5.3 ± 0.2 ug/L ), as did Cu (2.6 ± 0.3 vs 1.1 ± 0.1; $P<0.001$). Compared to human milk, porcine milk contained 2- to 5-fold higher ($p<0.001$) concentrations of all minerals. Porcine milk was also higher in Ca, P, Cu, Fe and Zn than bovine. Mg was similar and Na and K were lower ($P<0.001$) between porcine and bovine. The high content of minerals and trace elements in porcine milk suggest high capacity transport systems in pig mammary gland that merit further investigation.

**Key Words:** Milk, Minerals, Pig

**W130 Effect of vaccenic acid/conjugated linoleic acid-enriched butter on plasma lipoproteins in the cholesterol-fed hamster.** A. L. Lock[1], C. A. M. Horne[2], D. E. Bauman*[1], and A. M. Salter[2], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Nottingham*, *Sutton Bonington, LEICS, UK.*

Butter naturally enriched in *cis*-9, *trans*-11 CLA (rumenic acid; RA) and vaccenic acid (VA) has been shown to be an effective anticarcinogen; however, there has been no examination of the effects of a naturally-derived source of VA and RA on atherosclerosis-related biomarkers. The current study was designed to determine the effect of VA/RA-enriched butter (VA/RA-BT) on plasma lipoproteins and tissue fatty acid profiles in the cholesterol-fed hamster as the biomedical model. Male Golden Syrian hamsters were fed diets containing 0.2% cholesterol and 20% added fat as, treatment (TRT) 1: control (20% standard butter; STD-BT), TRT 2: 5% STD-BT + 15% VA/RA-BT or TRT 3: 15% STD-BT + 5% partially hydrogenated vegetable oil (PHVO). The content of RA and VA was 3.61 and 15.36 g/100 g fatty acid, respectively, in the VA/RA-BT and 0.44 and 1.39 g/100 g in the STD-BT. Diets were fed for 4 wk after which plasma lipoproteins were isolated, cholesterol quantified, and tissue fatty acid profiles determined. The concentration of RA in the liver and epididimal and perirenal fat depots was 0.33, 0.52, and 0.58 for TRT 1; 2.07, 3.35, and 2.98 for TRT 2; and 0.67, 0.85, and 0.80 g/100 g for TRT 3, respectively ($P < 0.001$). The concentration of VA was 0.32, 0.74, and 0.64 for TRT 1; 2.41, 5.11, and 4.53 for TRT 2; and 0.78, 1.66, and 1.51 g/100 g for TRT 3 for liver and epididimal and perirenal fat depots, respectively ($P < 0.001$). Total ($P < 0.001$) and LDL ($P < 0.01$) cholesterol concentrations were significantly reduced in TRT 2 and 3 compared to TRT 1. However, VLDL concentrations were significantly reduced in TRT 2 animals compared to those in both TRT 1 and 3 ($P < 0.01$). HDL was not different among TRT. The ratio of potentially atherogenic lipoproteins (VLDL+IDL+LDL) to anti-atherogenic HDL was lower in animals fed VA/RA-BT (0.60, TRT 2) than those fed either control diet (1.70, TRT 1) or the diet containing PHVO (1.04; TRT 3; $P < 0.001$). Thus, increasing the VA/RA content of butter results in a beneficial plasma lipoprotein profile that is associated with a reduced risk of atherosclerosis.

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**Key Words:** CLA, Vaccenic Acid, Atherosclerosis

## Nonruminant Nutrition: Enzyme Supplementation and Methodology

**W131 Nutrient digestibility in microbial phytase supplemented corn-soybean based diets in two phases of growing pigs.** H. Krebs*[1], C. T. Kadzere[1], Z. Liu[1], and E. van Heugten[2], [1]*North Carolina A&T State University*, *Greensboro*, [2]*North Carolina State University*, *Raleigh.*

Phytate phosphorus (P) makes up 40 to 90% of P in cereal grains and in oilseeds and is unavailable to swine except when supplementary phytase is in the diet. In a 4 x 4 CRD study, 16 male castrated pigs were assigned to four homogenous groups of four animals each to evaluate the effects of microbial phytase on nutrient digestibility in pigs in Phase I (PI) and in Phase II (PII). Each group was fed one of four diets (DI to DIV) differing only in P, calcium (Ca), and phytase content. The average weights of pigs were 19 kg and 39 kg at the start of PI and PII collection periods, respectively. In PI, DI (negative control) contained 0.1% less P and Ca than DII and no phytase; DII (positive control) which had 0.6% P and 0.7% Ca as recommended for growing pigs (10-20 kg) by NRC and 0.0% phytase; DIII and DIV had both 0.1% less P and Ca than DII and had 0.0125% and 0.025% supplemental phytase, respectively. The amount of phytase in PII was similar to that in PI diets. PII diets had 0.1% less P and Ca in DI, DIII, and DIV than the NRC recommendation of 0.5% P and 0.6% Ca for growing pigs (20-50 kg) as in DII. A pig on DII in PI was removed from the study. Fecal samples were collected on d 25 to d 31 in PI and on d 60 to d 66 in PII and analyzed. There were no differences in nutrient digestibility in PI. There were differences ($P < 0.05$) in ash, protein, and fiber digestibility in PII. In PII, pigs on DIII had the highest (75.9%) and those on DI the lowest (65.8%) ash digestibility. Protein digestibility was highest (90.3%) in DIII pigs and lowest (83.0%) in DII. Fiber digestion was highest (68.6%) in DIII and lowest (57.8%) in DII. Nutrient digestibility was higher ($P < 0.05$) in PII than in PI. Microbial phytase in corn-soybean based diets did not influence nutrient digestibility in PI but did in PII. Data presented shows that phytase at the lower level improved digestibility of protein and fiber. It is hard to understand why this was not the case with the higher level.

**Key Words:** Phytase, Swine, Nutrition

**W132 Effect of microbial phytase in corn-soybean based diets on total and soluble fecal phosphorus excretion in two phases of growing pigs.** Z Liu[1], C. T. Kadzere*[1], H. Krebs[1], and E. van Heugten[2], [1]*North Carolina A&T State University*, *Greensboro*, [2]*North Carolina State University*, *Raleigh.*

The effect of microbial phytase in corn-soybean based diets on total phosphorus (TP) and soluble phosphorous (SP) excretion were evaluated in growing male castrate pigs in Phase I (PI) and Phase II (PII) in a 66-d 4 × 4 CRD study. Pigs (n = 16) were assigned to four equal groups of four pigs each and groups were fed one of four diets (DI to DIV) differing only in phosphorus (P), calcium (Ca), and phytase. The average pig weights were 19 kg and 39 kg at the start of PI and PII collections, respectively. In PI, DI (negative control) contained 0.1% less P and Ca and no phytase; DII (positive control) had 0.6% P and 0.7% Ca as recommended for growing pigs (10-20 kg) by the NRC and no phytase; DIII and DIV both had 0.1% less P and Ca than DII, and had 0.0125% and 0.025% supplementary phytase, respectively. Phytase levels in PII diets were the same for corresponding PI diets. PII diets had 0.1% less P and Ca in DI, DIII, and DIV than in DII with the NRC recommended level of 0.5% P and 0.6% Ca for grow-