263 Advances in diagnosis and management of equine polysaccharide storage myopathy (PSSM). M. E. McCue*, S. J. Valberg, and J. R. Mickelson, *University of Minnesota*, *St. Paul*.

PSSM is a debilitating muscle disease in diverse breeds of horses. Clinical signs range from exertional rhabdomyolysis in Quarter Horses, muscle atrophy and progressive weakness in Draft breeds to muscle soreness and gait abnormalities in Warmbloods. PSSM affects 10% of Quarter Horses and 36% of Belgian Draft horses and an unknown number of Warmbloods in both Europe and North America. The gold standard for diagnosis of PSSM is the presence of periodic acid Schiffã™ (PAS) positive inclusions in type 2A and type 2B muscle fibers which are resistant to amylase digestion. In addition, PSSM is characterized by 1.5-4 X normal glycogen concentrations in skeletal muscle. No defect in glycogenolysis or glycolysis have been identified in PSSM horses. Rather glycogen accumulation appears to be related to enhanced glycogen synthesis. In Quarter Horses enhanced insulin sensitivity is also reported. Through a limited breeding trial and a genetic association analysis of an extensive number of clinical cases, we recently identified an autosomal dominant genetic mutation that is highly associated with PSSM in both Quarter Horses and Belgian Draft horses. This mutation accounts for 80 and 89% of PSSM cases in each breed respectively. We anticipate a genetic test will be available for PSSM within the next year.

Dietary management of PSSM involves decreasing dietary starch and provision of a fat supplement as an alternative energy substrate. This stabilizes blood glucose, increases serum free fatty acids and lowers insulin concentrations. Fat supplementation should be used judiciously in overweight horses. Muscle stiffness and exertional rhabdomyolysis can be eliminated in most horses if this diet is combined with daily exercise. Quarter Horses have a low skeletal muscle oxidative capacity and low intramuscular lipid stores. Gradual training is essential to improve muscle function likely through increased glycogen metabolism, increased oxidative capacity to utilize fat and improved substrate flux.

Key Words: Genetic, Glycogen, Muscle

264 Management of obesity and insulin resistance in horses. R. J. Geor*, R. A. Carter, and K. H. Treiber, *Virginia Polytechnic Institute and State University*, *Middleburg, VA*.

Although epidemiological data are scant, it has been suggested that the prevalence of obesity in horse (and pony) populations is on the rise. There is no universal definition of obesity in equids but according to the body condition scoring system (BCS) developed by Henneke, horses or ponies with a BCS of 8 (fat) or 9 (extremely fat) can be defined as obese, while animals with a BCS of 7 might be considered overweight. Insulin resistance (IR) is associated with obesity in horses and this disturbance to metabolic regulation may underlie susceptibility to laminitis, particularly the pasture-associated form of this disease. In support of this hypothesis, Treiber et al. (2006) recently described a ″pre-laminitic metabolic syndrome″ (PLMS) in otherwise healthy ponies with high (>70%) sensitivity and specificity for identification of animals at increased risk for pasture-associated laminitis. The central features of the PLMS were hyperinsulinemia, IR and generalized and/or regional (e.g. a cresty neck) adiposity. A similar clustering of clinical conditions, referred to as the equine metabolic syndrome (EMS), likely occurs in mature horses. In susceptible horses and ponies, consumption of forage or feed rich in nonstructural carbohydrates (NSC; sugars, fructans, and/or starch) may exacerbate IR and risk of laminitis. The mechanisms linking IR and laminitis are unknown, but might involve impaired glucose delivery to hoof keratinocytes or vascular endothelial dysfunction associated with oxidative stress and/or inflammation. Specific quantitative characterization of IR can be used to identify horses and ponies in need of special measures to avoid laminitis, particularly interventions that target decreased body fat mass and improved insulin sensitivity, including a reduction in dietary energy (calories) and NSC, restricted access to pasture during high-risk periods, and increased physical activity. The administration of levothyroxine sodium may be justified for animals that do not respond to diet and exercise programs alone.

Treiber KH, Kronfeld DS, Hess TM et al. 2006. J Am Vet Med Assoc 228:1538-1545.

Key Words: Horse, Obesity, Insulin resistance

Lactation Biology: Metabolism and Gene Expression in Support of Lactation

265 Characterization of the utilization of trans octadecenoic acids in lactating dairy cows. C. Tyburczy*[1], A. L. Lock[1], D. A. Dwyer[1], F. Destaillants[2], Z. Mouloungui[3], L. Candy[3], and D. E. Bauman[1], [1]*Cornell University*, *Ithaca, NY*, [2]*Nestle Research Center*, *Lausanne, Switzerland*, [3]*Laboratoire de Chimie Agro-Industrielle*, *Toulouse, France*.

The biological activity of individual octadecenoic acids may be dependent on the location and orientation of the double bond. Therefore, our objective was to examine the affect of elaidic acid (trans-9 18:1; EA) and vaccenic acid (trans-11 18:1; VA) in relation to oleic acid (cis-9 18:1; OA) during lactation. Three mid-lactation Holstein cows were used in a 3x3 Latin square design, and treatments (>82% purity) involved abomasal infusion of 1) EA (41.7 g/d), 2) VA (41.4 g/d) and 3) OA (45.5 g/d). Treatment periods were 4 d, separated by a 7 d wash-out interval. Milk yield (24.2 ± 2.2 kg/d; mean ± SD) and yield of milk components were not affected by treatment. Incorporation of infused isomers into milk fat triglycerides (TG) plateaued by d 3 and transfer efficiency averaged 59.1 ± 0.1%, 54.2 ± 0.1% and 54.6 ± 0.3% for EA, VA and OA, respectively. For the VA treatment, milk fat content of cis-9, trans-11 conjugated linoleic acid (CLA) more than doubled and the ratio of VA to CLA did not change, consistent with mammary conversion of VA to CLA by delta-9 desaturase. Total lipid concentration of plasma lipid classes averaged 209.9 ± 10.5 mg/dl, 161.4 ± 15.4 mg/dl, 14.5 ± 2.0 mg/dl and 2.4 ± 0.5 mg/dl for phospholipids (PL), cholesterol esters (CE), TG and free fatty acids (FFA), respectively. Similar values for the proportion of fatty acids provided by each plasma lipid class were 60.3 ± 2.2%, 32.1 ± 1.8%, 6.4 ± 0.8% and 1.2 ± 0.3%. Infusion of EA, VA and OA increased their specific content in plasma PL, TG and FFA, but for VA the relative increase was much greater for plasma TG and FFA. Overall, data demonstrate that biological differences exist among individual octadecenoic acids in lactating dairy cows.

Key Words: Milk Fat, Trans Fatty Acids, Lactation

266 Expression of lipogenic genes in adipose tissue increases during milk fat depression induced by treatment with trans-10, cis-12 conjugated linoleic acid (CLA). K. J. Harvatine*, D. A. Dwyer, and D. E. Bauman, *Cornell University*, *Ithaca, NY*.

Trans-10, cis-12 CLA decreases milk fat synthesis through transcriptional down-regulation of genes involved in mammary fatty acid synthesis, transport and esterification. Intake is not decreased during CLA-induced milk fat depression, resulting in a calculated increase in energy balance. To investigate energy partitioning during milk fat depression, adipose tissue biopsies were taken from four cows arranged in a switchback design. Treatments were control and 4 day abomasal infusion of trans-10, cis-12 CLA (7.5 g/d). CLA decreased milk fat yield by 38% and milk fat content by 34%, but yields of milk and other milk components were unchanged. Adipose tissue was biopsied from adjacent to the tail head, and expression of lipogenic enzymes and transcription factors regulating lipogenesis was determined by Real-Time PCR. Expression of lipoprotein lipase, fatty acid synthase and stearoyl-CoA desaturase was increased more than one fold over control ($P < 0.002$). The lipogenic regulatory proteins sterol-response element binding protein 1 (SREBP1) and throid hormone responsive spot 14 were increased, and leptin and PPARgamma tended to increase. Thus, a CLA dose resulting in near maximal inhibition of mammary lipogenesis resulted in increased expression of lipogenic-related genes in adipose tissue. Overall, results are consistent with energy spared from the reduction in milk fat synthesis being partitioned towards adipose tissue fat stores during short-term milk fat depression.

Key Words: Milk Fat Depression, Fat Synthesis, Adipose Tissue

267 The relationship between trans-10 18:1 and milk fat yield in cows fed high oleic acid or high linoleic acid plant oil supplements. T. Hinrichsen[1], A. L. Lock*[2], and D. E. Bauman[2], [1]*Royal Veterinary & Agricultural University*, *Denmark*, [2]*Cornell University*, *Ithaca, NY*.

Trans-10 18:1 (t10) has been proposed to affect milk fat synthesis because its milk fat content is associated with diet-induced milk fat depression (MFD). We summarized data from 35 publications (109 treatments) and found an inverse curvilinear relationship between milk fat content of t10 and milk fat percent ($R2 = 0.54$). However, t10 may be a marker for the altered rumen biohydrogenation (BH) that occurs with MFD rather than having a direct inhibitory effect per se. In vitro studies have shown that the BH of oleic acid results in formation of a range of trans-18:1 fatty acids (TFA), whereas BH of linoleic acid produces both conjugated 18:2 and TFA. Therefore, we used plant oils enriched in either oleic or linoleic acid to examine potential effects of TFA on MFD. Cows ($n = 30$) were fed a basal TMR diet for 3 wk (Period 1). In Periods 2 and 3 (14 and 11 d, respectively) cows were divided into 3 groups: control group (C) that continued on basal diet, high-oleic (82%) sunflower oil supplemented group (O) and high-linoleic (75%) safflower oil supplemented group (L). Oils were added at 2.5 and 3.5 % of DM in Periods 2 and 3, respectively. There were no treatment differences for yield of milk, milk protein or milk lactose ($P > 0.05$). Milk fat yield was reduced by 14% ($P < 0.05$) and 34% ($P < 0.001$) in Periods 2 and 3, respectively, for treatment L compared to C; treatment O did not differ from C ($P > 0.05$). Milk fat t10 (g/100 g FA) increased 4-fold ($P < 0.01$) and 2-fold ($P = 0.17$) for L and O, respectively, in Period 2. Similar increases for Period 3 were 11-fold ($P < 0.001$) and 4-fold ($P < 0.01$) for L and O. A 4-fold increase in t10 correlated with MFD when cows received the linoleic acid supplement, but no MFD occurred with a similar increase and milk concentration of t10 induced by oleic acid supplement. Thus, the present study offers no support for t10 as a cause of MFD and highlights the limitation in concluding cause-effect relationships based on correlations between specific milk fatty acids and MFD.

Key Words: Milk Fat, Trans Fatty Acids, Lactation

268 In vivo treatment with xanthosine expands the mammary stem cell population. A. V. Capuco*[1], C. M. Evock-Clover[1], D. L. Wood[1], and A. Minuti[2], [1]*Bovine Functional Genomics Laboratory, USDA-ARS*, *Beltsville, MD*, [2]*Institute of Zootechnics, Catholic University*, *Piacenza, Italy*.

Mammary stem cells provide for growth and maintenance of the mammary gland and are therefore likely targets for means to improve the productivity and efficiency of dairy animals. Xanthosine treatment has been shown to promote expansion of hepatic stem cells in vitro. The objective of this study was to determine if in vivo treatment with xanthosine can increase the mammary stem cell population. Xanthosine was infused into the right mammary glands of four Holstein calves (3 mo old) for 5 consecutive days. The right rear quarter received a supplemental injection of xanthosine directly into the mammary parenchyma. Immediately after each xanthosine treatment, calves were injected intravenously with 5-bromo-2-deoxyuridine (BrdU). Forty days after the final treatment, mammary tissue was obtained at slaughter. BrdU-label retaining epithelial cells (LREC) were detected immunohistochemically and quantified. We and others have employed the retention of BrdU as a method for labeling putative bovine mammary stem cells. Infusion of xanthosine into the bovine mammary gland significantly increased the number of LREC in treated quarters compared to contralateral control quarters ($P = 0.06$). LREC averaged 0.4% of epithelial cells in control and 0.84% in xanthosine-treated quarters. Data indicate that in vivo treatment with xanthosine can be used to increase the number of mammary stem cells. This is the first demonstration of an in vivo treatment to increase the endogenous population of adult mammary stem cells in any species. Utility of this treatment for biomedical research and for dairy management is of considerable interest.

Key Words: Progenitor Cells, Lactation, Proliferation

269 Prepubertal nutrition effects on bovine mammary parenchyma and fat pad gene expression profiles. P. Piantoni*[1], D. Graugnard[1], K. M. Daniels[2], R. E. Everts[1], S. L. Rodriguez-Zas[1], H. A. Lewin[1], R. M. Akers[2], and J. J. Loor[1], [1]*University of Illinois*, *Urbana*, [2]*Virginia Polytechnic Institute and State University*, *Blacksburg*.

Nutrition prior to puberty appears to differentially affect bovine mammary parenchyma and fat pad development. Objectives were to evaluate gene expression profiles in parenchyma and fat pad due to enhanced nutrient intake to achieve widely-different rates of gain during the isometric growth phase in the first 63 d of life in Holstein heifers. Tissues from calves fed ($n = 6$/milk replacer diet) a control (20:20, protein:fat, fed at 450 g/d), high protein low fat (28:20, HPLF, fed at 970 g/d), HP high fat (28:28, HPHF, fed at 970 g/d), or 1.5X HPHF (HPHF+, fed at 1460 g/d) diet were used for RNA extraction. Calf starter (20% CP) was available ad libitum. A 13,257 bovine

oligonucleotide (70-mers) array and qPCR were used for gene expression profiling. Annotation was based on similarity searches using BLASTN against human, mouse and bovine RefSeq, human, mouse, and bovine UniGene, and bovine TIGR. Cy3- and Cy5-labelled cDNA from mammary parenchyma or fat pad and a reference standard were used for hybridizations (80 arrays). ANOVA (FDR-adjusted $P \leq 0.10$) identified 5,585, 203, and 20 differentially expressed genes due to tissue type, diet, and diet x tissue interaction, respectively. Among upregulated genes in HFHP+ vs. control or HFHP, regardless of tissue, Ingenuity Pathway Analysis identified cell assembly/organization, cell growth/proliferation, and cell death as modified families of related genes. However, analysis of downregulated genes between HFHP+ and HFHP showed major impacts in gene expression regulation, small molecule biochemistry, and immune response. Further, histidine metabolism, fatty acid metabolism, Val/Leu/Ile degradation, Arg/Pro metabolism, and IL2 signaling were the most significant canonical pathways among downregulated genes. We conclude that the mammary parenchyma and fat pad transcriptomes are impacted by nutrition during the first 2 mo of life. Genomic adaptations could at least in part explain tissue growth responses to enhanced nutrient intake.

Key Words: Calf, Genomics, Mammary Gland

270 Mammary gland expression of cell cyle, apoptosis, and immune response genes accompany progression through a prolonged lactation cycle. D. L. Hadsell*, D. Torres, and M. S. Bray, *Baylor College of Medicine*, *Houston TX*.

In the mouse mammary gland, the prolonged lactation cycle is a biphasic developmental process that is characterized by a wave of proliferation during the early postpartum period followed by decreased proliferation in mid-lactation and elevated apoptosis during prolonged lactation. The goal of this study was to identify the genes regulating secretory cell function and turnover during this cycle. Mammary samples (N=5 mice/time) were collected from mice on days 2, 8, 14, 21, 28, and 35 post-partum. Total RNA from these samples was analyzed using the Sentrix Mouse Ref 6 BeadChip (Ilumina, Inc.). Of the 46,119 genes and ESTs on the array, expression was detected for 17,028. One-way ANOVA identified 1,645 genes that changed ($P<0.05$) with time, and 1,056 genes that changed by at least 2-fold. Expressed genes were clustered into 10 distinct temporal patterns using k-means clustering. The 10 patterns were labeled based on the direction (Down, Flat, or Up) of each sequential change in expression for each of the pairwise comparisons between the 6 adjacent time points. Patterns 1 (DUUFF), 5 (UUFFU), 7 (UUUDU) and 9 (FUUFF) were enriched ($P<0.05$) in genes integral to immune response, defense response, cell motility, and cell death. These genes were low during early lactation and maximally expressed during prolonged lactation. Patterns 2 (DDUFU), 6 (DFUUU), 8 (DFUFU) and 10 (DDUUU) were at their highest expression on day 2 and decreased with time postpartum. These genes regulated primary metabolism, DNA metabolism, cellular protein metabolism, cell cycle, and mitosis. Patterns 3 (FDDFU) and 4 (UFDFU) were associated with metabolism and transport. These genes increased between days 2 and 8, and then decreased through the remainder of the study. These results demonstrate that previously observed changes in mammary cell turnover during the prolonged lactation cycle are supported by concomitant changes in the expression of cell cycle and cell death genes. The results also support the conclusion that the immune system is important to regulating the decline in milk synthesis during prolonged lactation.

Key Words: Mammary, Microarray, Lactation

271 SOCS3 and STAT3 are up-regulated and STAT5 down-regulated during induced involution of the bovine mammary gland. K Singh*, M Prewitz, J Dobson, and K Stelwagen, *AgResearch Ltd, Ruakura Research Centre*, *Hamilton, New Zealand*.

In dairy animals, gradual involution associated with a decline in milk yield occurs following peak lactation. In cows, abrupt termination of milking induces involution of the mammary gland which is characterized by alveolar engorgement, followed by decreased communication between mammary epithelial cells (MEC) and extracellular matrix, as well as cell-cell communication and subsequently increased apoptosis of the secretory MEC. The aim of this study was to investigate the role of STAT5, STAT3 and SOCS3 in the bovine mammary gland during this process, ultimately to understand mechanisms to improve milk production during late lactation. Alveolar tissue was obtained from non-pregnant cows in mid-lactation slaughtered at 0, 6, 12, 18, 24, 36, 72 and 192h (n=6/group) after the last milking. Western blot analysis showed STAT5a and phosphorylated STAT5 levels were decreased 2-fold by 24h post milking ($P<0.01$) and remained down-regulated to 192h by 4.4-fold and 7.7-fold ($P<0.01$), respectively, relative to 6h post milking. STAT3 expression was also down-regulated (2.4-fold, $P<0.05$), but only at 192h relative to 6h after the last milking. However, relative to 12h post milking, the level of STAT3 decreased from 36h onwards ($P<0.05$). In contrast, phosphorylated STAT3 was barely detectable at the early time points and was dramatically up-regulated by 36 and 72h post milking by 39- and 44-fold ($P<0.001$), respectively, and at 192h post milking by 22-fold ($P<0.05$), all relative to 6h. Real-time RT-qPCR analysis showed that SOCS3 mRNA levels were up-regulated by 72h post milking (2.3-fold, $P<0.05$). These results suggest that the up-regulation of SOCS3 and phosphorylated STAT3 and down-regulation of STAT5 play a key role during bovine mammary gland involution.

Key Words: SOCS3, STAT3 and 5, Bovine Mammary Involution

272 MammOmics™: transcript profiling of the mammary gland during the lactation cycle in Holstein cows. M. Bionaz*, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, and J. J. Loor, *University of Illinois*, *Urbana*.

Achieving greater understanding of the genomic adaptations in the mammary gland of high-producing dairy cows during lactation represents a formidable challenge. Our objective was to explore the mammary transcriptome using biopsies from 8 Holstein cows harvested at -30, -15, 1, 15, 30, 60, 120, 240, and 300 d relative to parturition. Milk composition and milk fatty acid profiles also were determined throughout lactation. A 13,257 unique oligonucleotide (70-mers) array was used for transcript profiling. Annotation was based on similarity searches using BLASTN against human, mouse and bovine RefSeq, human, mouse, and bovine UniGene, and bovine TIGR. Cy3- and Cy5-labelled cDNA from mammary tissue and a reference standard were used for hybridizations. ANOVA (false discovery rate-adjusted $P \leq 0.05$) identified 7,055 differentially expressed genes due to physiological state. A total of 701 of these genes had a ≥2-fold change in expression in at least one other time point examined relative to day -30. We verified key microarray results for 38 genes by qPCR. Expression patterns of the 701 genes relative to d -30 were grouped into 2 clusters of upregulated (283) and 4 clusters of downregulated genes (418). Ingenuity Pathway Analysis mapped 3,355 of 7,055 differentially expressed genes. Relative to d -30, network analysis of genes with ≥2-fold expression indicated that some of the most predominant

molecular functions were on d -15 immune response (6 genes), on d 1 (25) through d 60 (48) lipid metabolism and molecular transport, on d 120 (53) cell-to-cell signaling and tissue development, and on d 240 (10) and 300 (7) connective tissue development and function. Twenty-nine of 52 downregulated genes by ≥2-fold on d 60 were associated with cell-to-cell signaling. Similarly, 30 of 49 downregulated genes on d 240 and 300 were associated primarily with molecular transport. Transcriptome analysis highlighted the importance of genes associated with immune function, lipid metabolism, transport, and tissue remodeling during the lactation cycle in the bovine mammary gland.

Key Words: Gene Networks, Microarray, Genomics

273 Photoperiod alters metabolic gene expression in bovine liver potentially through suppressors of cytokine signaling. E. E. Connor*[1], E. D. Thomas[2], and G. E. Dahl[3], [1]*Bovine Functional Genomics Laboratory, USDA-ARS*, *Beltsville, MD*, [2]*Department of Animal and Avian Sciences, University of Maryland*, *College Park*, [3]*Department of Animal Sciences, University of Florida*, *Gainesville*.

Previous research has demonstrated effects of day length (photoperiod) on multiple physiological processes in cattle including reproduction, lactation, immune function, growth and carcass composition. Many of these effects are mediated by changes in prolactin (PRL) and PRL signaling. Recent research has shown a role of PRL-responsive suppressors of cytokine signaling (SOCS) in fatty liver and metabolic syndrome in rodents. Thus, to determine whether photoperiod manipulation could influence hepatic lipid metabolism in ruminants, we investigated the effects of short-day (8 h light:16 h dark; SD) and long-day (16 h light:8 h dark; LD) photoperiod exposure on hepatic *SOCS* and metabolic gene expression in Holstein steer calves (98 ± 4 d old). Liver biopsies were collected after 3 and 6 wks of exposure to SD (n = 6) or LD (n = 6) and evaluated for mRNA expression of *SOCS-1*, *SOCS-3*, enzymes of glucose and fatty acid metabolism (*phosphoenolpyruvate carboxykinase 1* [*PCK1*] and *2* [*PCK2*], *acetyl-coA carboxylase* α [*ACACA*], *fatty acid synthase* [*FASN*] and *very long chain acetyl-coA dehydrogenase* [*ACADVL*]), and a key transcription factor in lipid biosynthesis (*SREBP1-c*) by absolute quantitative real-time RT-PCR. Relative to LD, expression of *ACACA*, *ACADVL*, *SREBP-1c* and *PCK1* was decreased (P < 0.05) in steers exposed to SD for 6 wks. In addition, *SOCS-1* tended to be lower (P = 0.11) in SD steers after 6 wks. There was a tendency for an increase in *FASN* expression in SD steers at 3 wks (P = 0.06), but a suggested decline by 6 wks (P = 0.23). Expression of *PCK2* and *SOCS-3* was unaffected by photoperiod treatment. Based on our findings and those in rodents, we propose a mechanism whereby SD photoperiod lowers circulating PRL and *SOCS-1* expression, suppressing *SREBP-1c* and hepatic lipogenesis via reductions in *ACACA* and *FASN*. Suppressed hepatic lipogenesis may reduce the incidence or severity of fatty liver during metabolic imbalance. In conclusion, SD photoperiod treatment prior to calving may aid in the prevention of fatty liver and metabolic syndrome in dairy cows during the periparturient period.

Key Words: Photoperiod, Gene Expression, Fatty Liver

274 Effects of intramammary infusions of serotonin (5-HT) and methysergide (METH), a 5-HT antagonist, on milk production and composition in lactating dairy cows. L. L. Hernandez*[1], J. B. Wheelock[1], G. Shwartz[1], L. H. Baumgard[1], A. M. Parkhurst[2], and R. J. Collier[1], [1]*University of Arizona*, *Tucson*, [2]*University of Nebraska*, *Lincoln*.

The neurotransmitter 5-HT, synthesized from tryptophan, is a proposed feedback inhibitor of milk synthesis. We evaluated effects of intramammary infusions of 5-HT or METH on milk yield (MY) and composition in 6 multiparous lactating dairy cows. Cows were assigned to a repeated measures design of contralateral intramammary infusions with METH (20 mg/quarter/d) or 5-HT (50 mg/quarter/d). Udder halves were first treated with METH or saline (SAL) for 3d followed by a 7d washout period before administrating 5-HT or SAL. MY was recorded twice daily for each udder half and milk composition of each half was determined once daily. Daily blood samples were harvested for plasma to determine glucose and NEFA concentrations. Sweating rate (SR), respiration rate (RR), and left and right udder temperatures were obtained twice daily after milking. Infusions of METH and SAL increased MY 10.9% from beginning of infusion to end of infusion period (P<0.002). Infusions of 5-HT and SAL decreased MY by 11.1% compared to pre-5-HT infusion period and MY decreased further by 8.9% post-5-HT infusion (P<0.05). Infusions of SAL, METH, and 5-HT increased SCC (P<0.05). Infusing 5-HT tended to reduce mean lactose concentration (4.3%/vol) relative to SAL infusion (4.6%/vol; P=0.06). Milk protein was decreased by METH and SAL 2.0% compared to the post-infusion period (P=0.0001) and was increased 5.8% by5-HT and SAL compared to the pre-infusion period (P=0.02). SR increased 17% during intramammary infusion of 5-HT and decreased 33% post-infusion (P<0.0001). SR increased 11% by METH infusion and decreased 11% post-infusion (P<0.0001). No effect of 5-HT or METH infusions was detected on plasma NEFA or glucose concentrations, RR, or milk fat content. We conclude this data supports the concept of 5-HT as a feedback inhibitor of lactation.

Key Words: 5-HT, Milk Production, Feedback Inhibition of Lactation

275 Chitotriosidase activity in blood and colostrum at peripartum period in goats. N. Castro[1], J. Capote[2], A. Morales[1], C. Rodriguez[1], and A. Arguello*[1], [1]*Las Palmas de Gran Canaria University, Animal Science Unit*, *Arucas, Las Palmas, Spain*, [2]*Canary Agronomic Science Institute*, *La Laguna, Tenerife, Spain*.

Chitotriosidase (ChT) is a functional chitinase, with high homology to chitinases belonging to family 18 of glycosylhydrolases and present in different species. Predominantly it is a secretory protein but it is in part processed and stored in lysosomes. ChT mRNA is expressed only at a late stage of differentiation of monocytes to activated macrophages in culture indicating that the enzyme has a strongly regulated expression. Since ChT is able to cleave chitin present in the cell wall of fungi and nematodes, it is possible that this enzyme continues to play a role in defense mechanisms against parasites and fungi. There have been many studies of human ChT, but few of other mammalian endocrine chitinases. The aim of this study was to measure ChT activity in goat serum and colostrum around partum period. Blood from 30 Majorera breed goats was taken at -4, -3, -2, -1, 1, 2, 3, and 4 postpartum days, and colostrum was sampled at 1, 2, 3, 4, and 5 postpartum days. ChT activity was assayed in serum and colostrum using a fluorescence method. Blood serum ChT activity was 3887, 4023, 3682, 3333, 2658, 2955, 2575 and 3520 nMol/ml/h at -4, -3, -2, -1, 1, 2, 3, and 4 postpartum days respectively. No statistical effects of time were shown, but the lowest ChT activity level was measured around partum day.

Colostrum ChT activity was 3912, 2124, 737, 403 and 465 nMol/ml/h at 1, 2, 3, 4, and 5 postpartum days, respectively. Statistical differences ($P<0.05$) were shown between postpartum days.

Key Words: Chitotriosidase, Goat, Colostrum

276 Pre-pubertal nutrition affects mammary development and first lactation performance depending on growth potential in dairy sheep. A. Zidi[1], G. Caja*[1], M. Ayadi[2], V. Castillo[1], C. Flores[1], and X. Such[1], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Spain*, [2]*Institut Superieur de Biologie Appliquée de Medenine*, *Tunisia*.

A total of 57 ewe lambs of Manchega (MN, n = 35) and Lacaune (LC, n = 22) dairy sheep, born during winter and weaned at wk 5 of age, were used to evaluate the effects of pre-pubertal level of nutrition on long-term lactational performance. Nutritional treatments consisted of ad libitum (concentrate and alfalfa hay) or restricted (concentrate and straw) feeding to achieve the maximum ADG (MN, 254 g/d, n = 18; LC, 293 g/d, n = 12) or 65% ADG (MN, 164 g/d, n = 17; LC, 189 g/d, n = 10), respectively, from wk 5 to 22. After wk 22, ad libitum ewe-lambs joined the adult ewe flock for grazing (MN, 183 g/d; LC, 201 g/d; $P < 0.05$). Compensatory growth was applied to restricted ewe-lambs from wk 22 to 27 (MN, 223 g/d; LC, 279 g/d; $P < 0.05$) to reach puberty and pregnancy during first fall. All ewe-lambs were exposed to rams and mated under control conditions after the second estrus cycle. Computerized axial tomography (CAT) was done at wk 16 and 36. Puberty was reached earlier in ad libitum than in restricted fed ewe lambs (MN, -35 d; LC, -21 d; $P < 0.05$). CAT images at wk 16 showed greater fat pad ($P < 0.05$) due to ad libitum feeding in both breeds (MN, +54%; LC, +32%). Parenchyma percentage was lower in the ad libitum fed MN ($P < 0.05$), but no differences were detected between the other groups. Conception rate (50.9%), prolificacy (1.24 lambs/ewe) and lamb body weight at birth were not affected by the dietary treatments. Milk yield varied according to treatment and breed, the breed × treatment interaction being highly significant ($P < 0.001$). Restricted ewe lambs yielded more milk than ad libitum at first lactation (114 DIM) in MN (61.2 vs. 40.0 L; $P < 0.05$), whereas it was the opposite in LC (122.9 vs 143.5 L; $P < 0.05$). No significant differences in milk components were detected between feeding treatments, but milk of restricted MN had greater fat and protein contents.

Key Words: Dairy Sheep, Mammary Development, Lactation

Graduate Student Paper Competition: National ADSA Production Division

277 The relationship between negative energy balance and mastitis in dairy cattle during early lactation. K. M. Moyes*[1], T. Larsen[2], N. C. Friggens[2], J. K. Drackley[1], and K. L. Ingvartsen[2], [1]*University of Illinois*, *Urbana*, [2]*University of Aarhus*, *Tjele, Denmark*.

Our objective was to determine whether dairy cows experiencing more severe postpartal negative energy balance (NEB) are at a greater risk for developing mastitis during early lactation. Data from a total of 138 lactations from 117 cows were used in a case-control epidemiologic study. Cows were of 3 breeds (Danish Red, Danish Holstein and Jersey) ranging from parity 1 to 4. Blood samples were collected weekly from 56 d before expected calving date through 90 DIM. Blood was analyzed for insulin, aspartate aminotransferase (ASAT), NEFA, glucose and BHBA. Daily milk yield was measured and composite SCC were analyzed. Cows were classified as 1) healthy (H) if SCC < 100,000 cells/mL and they were not treated for mastitis; 2) sub-clinical mastitis (SM) if SCC > 800,000 cells/mL but were not treated for mastitis; or 3) clinical mastitis (CM) if SCC > 800,000 cells/mL and were treated for clinical mastitis. Cows that developed mastitis during the first 7 DIM were excluded from the dataset. The time of mastitis (TOM) was recorded as the DIM in which the first rise in SCC was observed and was recorded as TOM = 0. The time prior to and after TOM was distinguished as ± n wks relative to TOM = 0. Healthy cows were paired with either a SM or CM cow and the TOM for each H cow was equal to the TOM for their paired mastitic cow. Data from wk -2 relative to TOM were analyzed using the MIXED procedure of SAS. Cows that developed SM did not differ statistically from H cows. The CM cows had higher NEFA ($P<0.05$) and ASAT ($P<0.05$) than H cows. All other variables were similar among treatment groups. Cows in more severe NEB tended to have higher NEFA than cows experiencing 'normal' postpartal NEB. In addition, higher ASAT indicates that the CM cows may have experienced more liver tissue damage prior to the development of mastitis when compared with H cows. Our results indicate that cows experiencing more severe postpartal NEB may be at a greater risk for developing mastitis.

Key Words: Negative Energy Balance, Mastitis, Dairy Cattle

278 The use of the Rumensin Premix in dairy cows: factors influencing its effects on milk production and milk composition. J. Dubuc*[1], D. DuTremblay[1], M. Brodeur[1], R. Bagg[2], P. Dick[2], J. Baril[2], and L. DesCoteaux[1], [1]*Universite de Montreal*, *Saint-Hyacinthe, Quebec, Canada*, [2]*Elanco Animal Health*, *Guelph, Ontario, Canada*.

The goal of this field trial was to evaluate the effects of 16 ppm of monensin sodium (Rumensin Premix, Elanco Animal Health, Canada) on production (PROD) and milk fat percentage (MFP) of commercial dairy herds. Another goal of this study was to identify possible interactions between monensin and nutritional factors on PROD and MFP. A randomized clinical trial was conducted on 49 Holstein herds in Quebec (Canada) between Nov. 2005 and May 2006. The herd was considered as the unit of interest. Herds were balanced in two groups for milk production, housing system, feeding system and size of farm. Monensin treatment was allocated in a crossover designed trial for each group. Monensin premix was added to the lactating dairy cow rations for a consecutive 3-month period for every herd. PROD and MFP were from weekly averages of daily bulk tank data. PROD and MFP were considered as outcome variables in linear mixed models. PROD and MFP were treated as repeated measures in herds. All models included treatment, group, season, parity and days in milk as fixed effects. Majority of herds were fed total mixed rations (TMR; n=30; 61%) and were housed in tie-stalls (n=42; 86%). Overall monensin effect on PROD was not significant (P=0.54). However, herds having high non-fiber carbohydrate level (NFC; >41.0%) in their diet had a higher milk production (+0.84kg/d; P=0.03). Monensin had a decreasing effect (-0.12%) on MFP (P<0.01). Statistical interactions