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ABSTRACTS

American Dairy Science Association
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Sunday, July 12, 2009

SYMPOSIA AND ORAL SESSIONS

Triennial Reproduction Symposium: Challenges and Opportunities Facing Livestock Reproduction in the 21st Century:
Session 1: Global perspectives on animal health and livestock reproduction

1 A global perspective on the evolution of animal agriculture. R. D. Green*, *Pfizer Animal Genetics, Sutton, NE.*

As the end of the first decade of the new millennium approaches, the landscape of global animal agriculture appears to be changing more rapidly than ever. With the prediction that world demand for meat and dairy products is expected to increase by 40 to 50% by 2025, the challenges of the so-called *Livestock Revolution* to animal and dairy science cannot be understated. In previous generations, tremendous gains in the efficiency of production and product quality have been achieved through the advancement of the animal and dairy sciences across all disciplines. Most of these improvements came in the form of technologies that were developed based upon an improved understanding of farm animal biology and husbandry. However, the global animal agriculture of the future will require rapid science-based solutions to: 1) decrease the environmental footprint of livestock production including soil, range, water, and air quality; 2) reduce all aspects of energy utilization for production of animal products while increasing the efficiency of nutrient utilization; 3) capture energy from non-traditional sources for use in animal production systems; 4) enhance the well-being (as defined by a non-agrarian society) and adaptability of animals to efficient production environments; 5) improve the recycling of animal inputs and products; 6) enhance animal health and food safety in the face of a *smaller* planet; and 7) preserve and appropriately utilize plant and animal genetic resources. Additionally, while the trend of further consolidation, integration, and industrialization of animal agriculture is expected to continue in to the foreseeable future, there is also a growing differentiation toward small farms and production for local markets. Application of the new sciences of genomics and systems biology to address these challenges is a key strategy to meet the global needs for production of animal protein and by-products. Increasing reproductive efficiency and longevity, coupled with enhancing animal and human health in the face of greater disease challenge, are desired outcomes to meet the challenges which lie ahead.

Key Words: animal agriculture, global, technology

2 Impact of animal health on endocrinology and reproduction in dairy cows. D. Wolfenson*[1], Y. Lavon[1], R. Meidan[1], Z. Roth[1], and G. Leitner[2], [1]*The Hebrew University, Rehovot, Israel*, [2]*The Veterinary Institute, Bet-Dagan, Israel*.

Mastitis is an important health issue in dairy production. Both short-term clinical mastitis and chronic subclinical mastitis caused by Gram (+) or Gram (-) bacteria depress fertility. Yet, the detailed mechanisms underlying reproductive failure are not clear. In a series of studies, we examined the effects of subclinical, long-term mastitis, or short-term clinical mastitic events that ended weeks earlier, on ovarian follicle function. About 30% of mastitic (mainly subclinical) cows exhibited an extended (twice longer) estrus to ovulation interval than that of uninfected, or the remaining 70% of mastitic cows that exhibited a normal interval. This syndrome may lower fertilization rate. Delayed ovulation was associated with low follicular androgen and low follicular and circulating estradiol concentrations, resulting in low or delayed or no preovulatory LH surge. The one third of mastitic cows with low estradiol also exhibited low expression of steroidogenic genes in both theca and granulosa cell layers. The above syndrome is probably not related to attenuated pulsatile LH secretion, but rather to the direct disruptive effect of mastitis on follicle function. Delayed ovulation resulted, as expected, in a delayed rise of circulating progesterone. The factors affecting the variability in response among individual mastitic cows are unclear. In another study we found that the Gram-positive toxin (but not Gram-negative LPS), which is usually associated with subclinical mastitis, manifested a significant carryover disruptive effect on preovulatory steroid concentrations and steroidogenic gene expression. The disruptive effect of mastitis on oocyte competence was demonstrated in vitro. Blastocyst formation rate but not cleavage rate was significantly lower in oocytes obtained from mastitic cows. These studies indicate that mastitis has a profound disruptive effect on timing of ovulation, follicular steroidogenesis and oocyte competence, which may partially explain the low fertility of mastitic cows.

Key Words: mastitis, reproduction, cow

3 Challenges in matching the physiology and productivity of the modern commercial sow. G. R. Foxcroft*, *University of Alberta, Edmonton, Alberta, Canada*.

Current management practices are failing to capture the extraordinary reproductive potential of the modern commercial sow. This is partly due to a failure to meet the nutritional demands of the gilt and sow throughout her productive lifetime. Inappropriate management of gilt development results in unacceptable variation in the weight of the gilt at breeding. Over-weight, rather than under-weight sows at the time of farrowing their first litter is an increasing risk factor for lack of retention in the breeding herd due to locomotor problems. Selection pressures placed on dam-line females has resulted in gradual improvements in overall productivity (pigs born or weaned/sow/year) and less variability in post-weaning fertility. However, although a very high percentage of weaned sows in well managed herds are expected to show post-weaning estrus and be bred immediately after weaning, the short weaning-to-ovulation intervals appear to place a limitation on subsequent litter size, linked to inadequate pre-ovulatory follicle development at the time of ovulation. Delaying breeding of the weaned sow for 14 to 21 days after first estrus, using either pharmacological suppression of estrus or skip-a-heat protocols, results in up to a two-pig increase in subsequent litter size, and a greater retention of sows in the breeding herd. Finally, biology of more prolific sow dam-lines appears to be associated with increasing variation in average litter birth weight as sows mature. In this sub-population of low litter weight-bearing sows, we hypothesize that high ovulation rates, associated with moderate to high embryonic survival to d 30 of gestation, results in extreme intra-uterine crowding, inadequate placental development and hence intra-uterine growth restriction due to an inability to compensate for inadequate placental growth in the peri-implantation period. Therefore, although some sows can show excellent lifetime performance in well managed breeding herds, genetic selection programs and management practices must address the increasing variability in the quality of the litters born.

Key Words: sow, fertility, management

4 The impact of amino acid nutrition on pregnancy outcome in pigs: mechanisms and implications for swine production. G. Wu*[1], F. W. Bazer[1], G. A. Johnson[1], S. W. Kim[2], and T. E. Spencer[1], [1]*Texas A&M University, College Station*, [2]*North Carolina State University, Raleigh*.

Pigs suffer up to 50% embryonic/fetal loss during gestation and exhibit the most severe naturally occurring intrauterine growth retardation among livestock species. Placental insufficiency is a major factor contributing to suboptimal reproductive performance and low birth weights of piglets. We recently reported the unusual abundance of members of the arginine family of amino acids (e.g., arginine, ornithine, and glutamine) in porcine allantoic fluid during early gestation when placental growth is most rapid. Arginine is synthesized from glutamine and proline in swine and serves as the nitrogenous precursor for the synthesis of nitric oxide (a major vasodilator and angiogenic factor). Proline is the major substrate for placental synthesis of ornithine and polyamines (key regulators of protein synthesis and angiogenesis) in pigs, whereas branched-chain amino acids (BCAA) donate an amino group for glutamine production in placentae. Additionally, arginine, leucine and glutamine activate the mammalian target of rapamycin cell signaling pathway to enhance protein synthesis and cell proliferation in placentae. In support of a functional role for amino acids in improving pregnancy outcome, dietary supplementation with arginine to gilts fed a conventional diet beginning on d 30 of gestation to term increased the number and total litter weight of live-born piglets by 22% and 24%, respectively. In addition, formulating the diet for gestating gilts on the basis of optimal requirements of arginine and BCAA (relative to lysine) for fetal protein accretion decreased the oxidation of dietary amino acids, enhanced maternal tissue nitrogen balance, and reduced variation in piglet birth weight. We propose that amino acids, through the synthesis of nitric oxide and polyamines, stimulate placental angiogenesis and growth (including vascular growth), placental and uterine blood flow, and the transfer of nutrients from mother to fetus to promote fetal survival, growth and development. (Supported by USDA/NRI grants #2006-35203-17199 and 2008-35203-19120)

Key Words: amino acids, pigs, reproduction

Triennial Reproduction Symposium: Challenges and Opportunities Facing Livestock Reproduction in the 21st Century: Session 2: Genetic influences on animal reproduction

5 Application of genome based technologies for identifying genes and their expression that are important for livestock reproduction. J. F. Taylor*, S. D. McKay, J. E. Decker, D. Vasco, M. C. McClure, J. W. Kim, M. A. Rolf, T. Taxis, and R. D. Schnabel, *University of Missouri, Columbia*.

High-density single nucleotide polymorphism (SNP) genotyping platforms are beginning to revolutionize genetic improvement within the livestock industries. Because the effective population sizes of most breeds is small there are strong correlations between the alleles present at loci separated by hundreds of thousands of nucleotides. Consequently, even when unrelated animals are genotyped at high resolution, the presence of genes responsible for variation in a trait can be detected by associating individual SNPs with phenotypes. Genome-wide association (GWA) analyses using thousands of Holstein and Angus bulls have now been performed and have revealed that there are hundreds or thousands of loci contributing to phenotypic variation. However, the limiting factor in these studies is the availability of populations with a large number of high-quality phenotypes. We performed a GWA for Heifer Pregnancy Rate (HPR) in 1721 registered Angus bulls, of which only 855 had EPDs for HPR. At genome-wide $P<0.01$ we found only 13 regions on 9 chromosomes associated with HPR and none harbored the 'usual hormone suspects.' Variation within the gamma-aminobutyric acid A receptor cluster which is integral to gonadotropin production and release and therefore controls oocyte recruitment and ovulation was associated with variation in HPR. Unfortunately, variation within any of the four genes within this cluster may be causal for the detected HPR effect and technology does not yet exist to rapidly identify the causal mutations in genes/regulatory elements. This has led away from the concept of marker-assisted selection on casual mutations and towards a novel approach called genome-wide selection in which animals' breeding values are estimated from their high-density SNP genotype profiles. Genomic estimates of breeding value were officially incorporated into the USDA's genetic evaluation system in Spring 2009 and are currently under development for beef cattle.

Key Words: single nucleotide polymorphism, genome-wide association, genomic selection

6 Application of molecular and genetic tools for identification of reproductive traits to create and establish commercial lines of swine. T. Rathje*, *Danbred North America*, *Columbus, NE*.

Modern swine breeding programs seek to produce lines that optimize the efficiency of pork production systems. Pork production systems have increasingly utilized economic metrics that identify the key drivers of profitability for their operations. Providers of genetic material utilize these metrics to identify the phenotypes in pigs that contribute positively to the economic performance of customer businesses. Reproduction, and its numerous component traits, continues to be one of the main causes of success or failure in production systems. Improving these traits has been quite successful using quantitative genetic approaches (e.g., litter size, structure score) despite relatively low heritabilities. Application of molecular genetics holds the promise of increasing the rate of genetic improvement and permitting the inclusion of traits difficult to measure quantitatively on a routine basis. Two example traits, live pigs at five days of age and sow longevity, will be used to illustrate the research and development involved in generating new traits currently being used in a modern selection program. An example of pig survival will be used to demonstrate the combined impact of molecular and quantitative approaches to new trait development. The economic considerations of molecular and quantitative approaches will be discussed.

Key Words: trait development, pigs, marker-assisted selection

7 Epigenetics: A mechanism of adaptation to perinatal events. R. Lane*, R. McKnight, L. Joss-Moore, Q. Fu, and X. Ke, *Division of Neonatology, University of Utah Department of Pediatrics*, *Salt Lake City*.

Mammalian pregnancies have experienced threats throughout time from external environmental conditions and maternal pathophysiologies. These conditions and pathophysiologies threaten the life of the fetus. To survive, adaptations have arisen that increase the odds of survival in the fetus. Recent human epidemiological evidence and animal model studies suggest the price for these adaptations are postnatal morbidities such as diabetes. A molecular mechanism that links fetal adaptation to postnatal morbidities is epigenetics. Epigenetics are heritable changes in gene expression that occur in the absence of altered DNA sequence. Epigenetic determinants of gene expression are defined through modifications of chromatin structure, such as DNA methylation, covalent modifications of histones, and nucleosome repositioning. We have used multiple models of perinatal disease, ranging from intrauterine growth retardation (IUGR) to mechanical ventilation, to test the hypothesis that significant changes in the perinatal environment 1) modify chromatin structure of target relevant genes; 2) affect perinatal and postnatal gene expression of the same target genes; and 3) increase the risk of associated adult morbidities, such as diabetes. Relevant genes whose chromatin structure is known to be vulnerable to perinatal disease include insulin growth factor 1 and peroxisomal proliferator activated receptor gamma. Our studies of these genes and others have led us to the following conclusions. First, epigenetics as a mechanism of perinatal adaptation is different from the traditional dogma of embryonic imprinting epigenetics, in which genes are turned either off or on. Within the context of a perinatal adaptation, epigenetics acts as a rheostat and/or alters mRNA variant expression. Second, epigenetic perinatal adaptations modify chromatin structure along the whole gene and do not necessarily concentrate at the 5 prime end of a gene. Third, epigenetic perinatal adaptations are tissue and gender specific events. A goal in the field will be to understand how to moderate the consequences of the epigenetic perinatal adaptations to minimize the predisposition towards postnatal morbidities.

Key Words: epigenetics, histone, chromatin

8 Impact of dam nutrition on subsequent growth and reproduction in beef heifers. R. N. Funston*, *University of Nebraska, West Central Research and Extension Center*, *North Platte*.

Maternal stimuli or an insult during a critical period of fetal development having long term implications for the offspring is the concept of fetal programming. Much of the evidence regarding how maternal nutrient restriction impacts prenatal physiological parameters was generated in laboratory animals. Few studies have evaluated effects of maternal nutrient restriction on post-natal growth and development in livestock species. Very few experiments have restricted specific diet components during pregnancy, such as protein, and evaluated offspring growth and performance. In recent studies at the University of Nebraska, calf birth weights were unaffected while calf weaning weights were greater from cows gestated on dormant winter range receiving protein supplementation during late gestation compared to unsupplemented cows. These studies demonstrated gestational treatments may augment physiologic parameters in production scenarios in contrast to data generated from laboratory-based studies. It is valuable to note protein supplementation enhanced growth after birth. Protein supplementation of the dam increased weaning weight of heifer calves, without a change in birth weight, and the change persisted through pregnancy diagnosis and subsequent calving. More interestingly, age at puberty was not greatly affected, yet protein supplementation of the dam increased heifer calf pregnancy rates. In a subsequent study, more heifers from protein-supplemented dams were pubertal before breeding, possibly affecting pregnancy rate. Heifers from protein-supplemented dams appear less feed efficient compared to heifers from unsupplemented dams. These data provide evidence that heifer fetuses exposed to nutritionally restricted environments (non-supplemented dams) during gestation become more efficient in later life. This body of research provides compelling evidence of a fetal programming response in female progeny to maternal nutrition in beef cattle.

Key Words: fetal programming, heifer progeny, supplementation

Monday, July 13, 2009

POSTER PRESENTATIONS

Animal Behavior and Well-Being

M1 Validation of footprint analysis to describe sow gait. J. Grégoire*[1,2], R. Bergeron[3], S. D'Allaire[4], M.-C. Meunier–Salaün[5], and N. Devillers[1], [1]*AAFC, Dairy and Swine R&D Centre, Sherbrooke, QC, Canada*, [2]*University Laval, Ste Foy, QC, Canada*, [3]*University of Guelph, Alfred, ON, Canada*, [4]*University of Montreal, Faculty of Veterinary Medecine, St Hyacinthe, QC, Canada*, [5]*INRA–SENAH, St-Gilles, France*.

Locomotion disorders represent the second cause for culling breeding sows and affect up to 25% of sows and gilts. In order to study lameness, methods must be developed to objectively describe and assess sow gait and locomotion disorders. Five second-parity gestating sows were used in 3 trials per day over 2 days to validate the use of footprints to assess sow gait related to lameness. The method consisted of measuring footprints remaining after a sow was moved along a 4.9 m clay corridor. A digital panoramic photo of the footprint sequence was taken and analyzed with specialized software. Individual footprints were identified using a system which assigned a separate color to each leg. Footprints were accepted if the sow walked without stopping and had taken at least 3 strides. Footprints variables measured or calculated for assessment are shown in Table 1. Measurement variability was assessed for each sow. Spearman correlations were also calculated between each measure and the walking speed of sows. Speed was correlated with stride length ($r=0.50$, $P<0.01$) but not with other variables. Measurements from footprints are a promising tool to describe sow gait and quantify lameness. However, more data are needed to describe variations between sound and lame sows and to characterize locomotion disorders.

Table 1. Means and variability of measures on sow footprints

Distances	Mean (cm) [Range]	Intra–day CV% (Range)	Inter–day CV% (Range)
Contralateral	46 [36-55]	4–11	2–7
Ipsilateral front	58 [45-73]	4–11	3–10
Ipsilateral rear	31 [24-40]	7–16	1–2
Diagonal front	20 [11-27]	8–25	2–10
Diagonal rear	75 [68-85]	2–6	0.5–5
Stride length	88 [72-99]	2–7	2–7
Distance between fronts	15 [9-21]	2–31	3–19
Distance between rears	10 [5-14]	2–27	2–14
Surface area	327 cm^2 [171-500]	2–47	0.5–21

Key Words: behavior, lameness, clay

M2 Changes of serum HSP70 during weaning and effects of NCG and arginine on serum HSP70 in early-weaned piglets. X. Wu, X. Zhou, Y. Gao, Y. Yin*, and R. Huang, *Laboratory of Animal Nutritional Physiology and Metabolic Process, Institute of Subtropical Agriculture, the Chinese Academy of Sciences, Changsha, China*.

Stress-induced heat shock protein 70 (HSP70) functions to promote refolding and prevent aggregation of partially-denatured proteins, as well as tag irreversibly-damaged proteins for proteolysis to protect the cells in stress. L-Arginine is a nutritionally essential amino acid that is particularly important for piglets under stress conditions. N-Carbamylglutamate (NCG) is a metabolically stable analogue of N-acetylglutamate which activates a key enzyme in arginine synthesis in enterocytes. This study determined changes in serum HSP70 during weaning and the effects of N-Carbamylglutamate (NCG) and Arginine on serum HSP70 and TNF-α. On d 1, 2, 3, 5 and 7 after weaning, six piglets were selected after 12 hrs fasting on each day for blood sampling to evaluate serum HSP70 by ELISA. In another experiment, eighty-nine Landrace×Yordshire piglets from 12 pens (average pen weight 5.56±0.51 kg; weaned at 21 d) were grouped into 3 treatments, and fed one of the following diets for 7 days: a standard diet (SD), SD+NCG (0.08%), or SD+Arg (0.6%). On 8 d after weaning, six piglets were randomly selected from each treatment for serum samples. Results were statistically analyzed using one-way ANOVA. Serum HSP70 increased after weaning, reaching its highest concentration of 2.17 μg/mL on d 3 after weaning, and then decreased to 0.5 μg/mL ($P<0.05$). Serum HSP70 was higher in the NCG and Arg groups than the control group ($P<0.05$). NCG increased serum TNF-α ($P=0.046$). These findings indicated that weaning induced HSP70 production in piglets. Arginine and NCG maintained serum HSP70 concentrations in terms of supporting HSP70 synthesis. In conclusion, Arginine and NCG alleviated weaning stress, stimulated changes in HSP70 and may be useful in diets.

Key Words: N-carbamylglutamate, L-arginine, HSP70

M3 Effects of feed-borne *Fusarium* mycotoxins on histological changes in lymphoid organs of turkeys. C. K. Girish*, T. K. Smith, P. Anil Kumar, and G. N. Girgis, *University of Guelph, Guelph, Ontario, Canada*.

An experiment was conducted to investigate the effects of feeding grains naturally contaminated with *Fusarium* mycotoxins on histology of lymphoid organs including bursa of Fabricius, thymus and spleen of turkeys. The efficacy of a polymeric glucomannan mycotoxin adsorbent (GMA) was also determined. Seventy-two 1-d-old male turkey poults were fed corn, wheat, and soybean meal-based diets for 21 days. Diets included (1) control grains, (2) contaminated grains and (3) contaminated grains + 0.2% GMA. The major contaminant was deoxynivalenol (2.7-3.6 μg/g) with lesser amounts of zearalenone (0.67-0.75 μg/g) and 15-acetyldeoxynivalenol (0.26-0.31 μg/g). Histological changes were recorded at the end of 14 and 21 days of feeding. Data were subjected to arcsine transformation and analyzed by analysis of variance using a PROC GLM procedure of SAS. Histological examination of bursa and thymus revealed that the proportion of birds showing lymphocytolysis was numerically higher in the birds fed naturally contaminated diets compared to controls on both day 14 (0.46 vs 0, bursa; 0.78 vs 0.15, thymus) and 21 (0.39 vs 0, bursa; 0.23 vs 0, thymus). The feeding of contaminated diets significantly ($P = 0.003$) increased secondary follicles in spleen at the end of day 21 compared to controls. Lymphocytolysis as observed in bursa of Fabricius and thymus after feeding contaminated diets could result in immunosuppression. The formation of secondary follicles in the spleen could be attributable to an acute immune response to the feeding of naturally contaminated grains. It can be concluded

that the feeding of contaminated grains resulted in altered cellularity of lymphoid organs. The feeding of naturally contaminated grains to turkeys should be minimized.

Key Words: *Fusarium* mycotoxin, histology, lymphoid organs

M4 Seasonal cow behavior in a large dairy herd in central Iran. R. Kowsar[1], A. Nikkhah*[2,1], M. Khorvash[1], M. Alikhani[1], and G. R. Ghorbani[1], [1]*Isfahan University of Technology*, *Isfahan, Iran*, [2]*Zanjan University*, *Zanjan, Iran*.

Monitoring behavior helps to optimize nutritional, health, and social states of high-producing cows in mechanized and competitive environments. A study was conducted between December 2006 and February 2008 to determine seasonal eating, ruminating, and lying behaviors of dairy cows of different age and productivity. The herd had about 3000 dairy cattle housed in yards. A total of 415 multiparous, high-producing cows (MH), 166 multiparous, medium-producing cows (MM), 166 multiparous, low-producing cows (ML), 165 primiparous, high-producing cows (PH), 83 fresh cows (FC), 82 fresh heifers (FH), and 82 high milk somatic cell counts (HSCC) cows were monitored. The average daily air temperature and relative humidity were 2.53°C and 55.8% in Winter, 20.9°C and 36% in Spring, 26.8°C and 17.3% in Summer and 10.0°C and 43.9% in Fall. During each season, eating, ruminating, standing and lying behaviors were recorded weekly and on multiple days within weeks at 1000 h by 4 individuals. Each activity was expressed as the percentage of cows exhibiting the activity relative to the existing number of cows at each recording day. Across groups, a greater percentage of cows ($P<0.01$) were eating during Winter (25.7%) than during Spring (17.1%), Summer (15.4%), and Fall (14.5%). The percentage of cows neither eating nor ruminating was less ($P<0.05$) in Winter (48.1%) than in Summer (58.9%) and Fall (58.6%) but not in Spring (53.7%). More cows in PH (24.6%) and ML (21.3%) groups were observed eating than in MM (15.2%), MH (16.6%), and FC (12.3%) groups. Lying was observed more often ($P<0.01$) in FC (71%), MM (69.6%) and MH (64%) cows than in FH (54%), ML (55.7%) and PH (55.7%) groups. More cows were seen ruminating ($P<0.01$) in MM (31.7%), FC (31.3%), HSCC (28.7%), PH (27.2%) and MH (26.7%) groups compared to FH (20.5%) and ML (22.9%) groups. The HSCC cows did not behave in ways that would distinguish them from cows with normal milk SCC. In the light of the large sample size and prolonged experimental period, findings demonstrate significant effects of season, age, lactation stage, and production level on eating, ruminating, and lying behaviors of dairy cows.

Key Words: eating, behavior, season

M5 Automated recording of sow posture and locomotion using accelerometers. N. Devillers*[1], J. Déom[1,2], C. Corriveau[1], J. Grégoire[1,3], and R. Bergeron[4], [1]*AAFC, Dairy and Swine R&D Centre*, *Sherbrooke, QC, Canada*, [2]*University of Sherbrooke*, *Sherbrooke, QC, Canada*, [3]*University Laval*, *Ste Foy, QC, Canada*, [4]*University of Guelph*, *Alfred, ON, Canada*.

The aim of this study was to assess the efficacy of an alternative, automated technique to measure posture and locomotion. Accelerometers (HOBO® G Logger UA-004-64, Onset©, Pocasset, MA) were installed on the rear leg and back (between shoulder blades) of 11 sows, housed either in gestating stalls (n=3), individual gestating pens (n=4) or farrowing crates (n=4). The accelerometer measured its relative position in a 3D-space every 5 sec and provided angle data for the 3 axes. Optimal angle range was determined as the one giving the best percentage of agreement between video observations of postures and calculation from accelerometer data for a 6-hour period. However, optimal angle ranges for each posture varied between sows, and when adapted to fit each sow, the percentage of agreement between accelerometers and video observations averaged 98.0 ± 0.6%. An overall percentage of agreement of 91.0 ± 3.4% was obtained when an optimal angle range that could fit all sows was used. The percentages of agreement for each posture and for all sows were 79.1 ± 6.3%, 89.0 ± 4.4%, 82.5 ± 4.2% and 99.1 ± 0.3% for lying laterally, lying ventrally, sitting and standing, respectively. Rear leg accelerometers were also used to record accelerations on the vertical axis 5 times per sec on 2 sows during 10 and 20 min eating periods. Numbers of steps/10 sec were calculated from variations in accelerations. Steps for each leg of the sow were also counted by video observation. Total number of steps for all legs was correlated to the number of steps for the measured leg ($r=0.78$, $P<0.01$). Number of steps measured from acceleration and from video observation were highly correlated ($r=0.98$, $P<0.01$). Finally, precision of step counting was 0.03 steps/10 sec. In conclusion, accelerometers are efficient and precise devices to automate posture and locomotion recording in sows, but calibration is necessary for posture measurement.

Key Words: behavior, technique, posture

M6 The effects of farm-to-slaughter plant pig management on pork quality. L. N. Edwards*[1], T. Grandin[1], T. E. Engle[1], M. J. Ritter[2], A. Sosnicki[3], and D. B. Anderson[1], [1]*Colorado State University*, *Fort Collins*, [2]*Elanco Animal Health*, *Greenfield, IN*, [3]*PIC*, *Hendersonville, TN*.

Two studies differing in facility design and season (Exp. 1 & 2) were conducted to determine effects of pre-slaughter management on pork quality by monitoring blood lactate concentration ([LAC]) and rectal temperature TEMP throughout the marketing process, from loading at the farm to exsanguination. (Exp.1, n = 80; Exp. 2, n = 144). Blood lactate concentration and TEMP were sampled from each animal at seven points during the marketing process: (1) baseline at the farm, (2) post-loading on the truck, (3) pre-unloading after transport, (4) post-unloading at the plant, (5) post-lairage at the plant, (6) post-movement to the stunning area and (7) at exsanguination. Pearson correlations were used to determine relationships between [LAC] and TEMP at the seven sampling points and meat quality. Correlations were also used to relate the changes in [LAC] and TEMP between sampling points to meat quality. Increased [LAC] during loading at the farm resulted in improved meat quality, i.e. increased 24 hr pH ($P < 0.002$), decreased L* ($P < 0.03$) and decreased drip loss ($P < 0.02$) (Exp. 1 & 2). Exsanguination [LAC] was not related to ultimate meat quality (Exp. 1 & 2) even though previous work has demonstrated that higher exsanguination [LAC] is related to lower 45 min pH and increased drip loss. It is hypothesized that these results are due to calm handling in the stunning chute preventing excessive [LAC] production by the skeletal muscles at exsanguination. Also there was a correlation between [LAC] at loading and [LAC] at exsanguination ($P<0.002$, Exp. 2) suggesting that animals with high [LAC] at loading tended to maintain a high [LAC] at exsanguination. The data suggest that high [LAC] during loading is associated with higher ultimate pH, darker color, and lower drip loss. Therefore, improving pre-slaughter handling at the farm during loading will not necessarily translate to direct improvements in fresh pork quality traits.

Key Words: drip loss, handling, pre-slaughter

M7 Comparison of slaughter methods with or without previous stunning on animal welfare and bleeding efficiency in bulls. J. E. Gomes Neves[1], M. J. R. Paranhos da Costa[1], R. Roça[2], N. G. Gregory[3], and L. Faucitano*[4], [1]*Faculdade de Ciencias Agrárias e Veterinárias, Universidade Estadual Paulista Julio de Mesquita Filho*, *Jaboticabal, Sao Paulo, Brazil*, [2]*Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista Julio de Mesquita Filho*, *Botucatu, Sao Paulo, Brazil*, [3]*Royal Veterinary College*, *London, UK*, [4]*Agriculture and Agri-Food Canada*, *Sherbrooke, Canada*.

In Brazil, steers are mainly slaughtered by captive bolt stunning (with or without bolt penetration) and bleeding. However, in some plants religious slaughter consisting of bleeding without previous stunning is also used. Religious slaughter without stunning is criticized from an animal welfare standpoint. The objective of this study was to assess the effects of two slaughter methods (with vs without previous stunning) on brainstem function of steers during bleeding and bleeding efficiency. A total of 171 Nelore (pure and crossbred) bulls weighing 287 kg on average were either stunned using a penetrating captive bolt (A1; 84 bulls) or were not stunned (A2; 87 bulls) prior to slaughter. Brainstem function was evaluated at 20 and 60 sec after bleeding using parameters such as palpebral and corneal reflex, rhythmic breathing and response to potentially painful stimuli (nose and tongue pricking/pinching). Bleeding efficiency was assessed through the analysis of residual haemoglobin content in the Longus colli muscle. Signs of consciousness data were analysed by Fisher test, while bleeding efficiency data were analysed by Wilcoxon test. No A1 bulls showed signs of brainstem function or pain responsiveness during bleeding, while 98 and 54% of A2 bulls were showing one or more of these signs at 20 and 60 sec after bleeding, respectively (P<0.001). No difference in bleeding efficiency was observed between slaughter treatments. In conclusion, religious slaughter as it was implemented in this study was less appropriate from an animal welfare point of view and captive bolt stunning appears to be better practice if one wants to make sure animals are unconscious while bleeding.

Key Words: beef, slaughter, animal welfare

M8 Water access and the physiological well-being of Holstein slaughter cows. K. D. Vogel*[1], J. R. Claus[2], T. Grandin[1], G. R. Oetzel[3], and D. M. Schaefer[2], [1]*Colorado State University*, *Fort Collins*, [2]*University of Wisconsin*, *Madison*, [3]*University of Wisconsin*, *Madison*.

The objective of this study was to investigate the impact of water access on the physiological well-being of Holstein slaughter cows during marketing through analysis of serum components and body weight. Multiparous Holstein cows (n = 57, 613 ± 88 kg mean body weight, 2.9 ± 0.5 mean BCS, varying stage of lactation) were purchased from a Wisconsin terminal market and assigned to two water withdrawal treatments (Control, free access to water at all times; 36 h, 36 hours of continuous water withdrawal) following a completely randomized block design. Blood samples were collected by tail vein puncture at 0, 9, 18, 27, and 36 h of each treatment. Mean ambient temperatures were 1.9 ± 6.2°C during the trial period, which occurred in March and April. Mean serum glucose was greater (P< 0.05) with the 36 h treatment (79.09 ± 1.13 mg/dl) than the control (75.37 ± 1.13 mg/dl). Mean serum creatinine was greater (P< 0.05) with the 36 h treatment (0.61 ± 0.03 mg/dl) than the control (0.69 ± 0.03 mg/dl). Lack of water access for 36 h also increased (P<0.05) mean serum albumin, anion gap, calcium, chloride, sodium, and urea N. Mean body weight loss increased between 0 and 36 h, regardless of water access treatment. Greater (P<0.05) mean total body weight loss was observed in the 36 h treatment (5.16 ± 0.40%) when compared with the control treatment (3.27 ± 0.40%). As sampling time increased from 0 to 36 h, regardless of water access treatment, mean serum total bilirubin, anion gap, and phosphorus increased. Mean serum bicarbonate decreased (P<0.05) between the 18 h (27.74 ± 0.47 mmol/l) and 36 h (25.59 ± 0.47 mmol/l) sampling times. In conclusion, it was determined that water withdrawal in lairage should not exceed 18 h to prevent unnecessary weight loss during the marketing of Holstein slaughter cows under climatic conditions similar to those in this study.

Key Words: dairy cow, Holstein, welfare

M9 Changes in temperament score as a result of handling do not affect voluntary feed intake. T. D. Maddock*[1], J. L. Foster[1], M. A. Elzo[2], and G. C. Lamb[1], [1]*North Florida Research and Education Center*, *Marianna*, [2]*University of Florida*, *Gainesville*.

Beef cattle (bulls = 240, steers = 432, heifers = 641) were evaluated post-weaning for temperament and individual daily feed intake using a GrowSafe feed intake facility. Data were collected over a 4-yr period from 2005-2008. Cattle were weaned, inoculated for respiratory disease, and introduced to feed prior to entering the feeding facility. Cattle were assigned to pen (10 to 20 hd/pen) and acclimated to the feeding facility and diets for 14 d prior to initiation of a 70 d data collection period. Temperament scores were collected both objectively (exit velocity; m/s) and subjectively (chute score; 1 = very docile; 5 = very aggressive). During data collection cattle were handled either weekly (11x; n = 307) or every 2 wk (6x; n = 1006) and temperament scores were collected every two weeks (d 0, 14, 28, 42, 56, and 70) regardless of number of times handled. Independent variables were calf sex and working frequency; whereas, dependent variables measured were changes in exit velocity and chute scores. Temperament improved from d 0 to 70 with reductions in both chute scores (2.81 to 2.58; $P < 0.001$) and exit velocities (2.71 to 2.11 m/s; $P < 0.001$). Handling frequency did not affect differences in chute scores ($P = 0.11$), but cattle that were handled 6x (-0.68 m/s) had a greater reduction ($P < 0.001$) in exit velocity than cattle handled 11x (-0.08 m/s). Steers had a greater ($P < 0.01$) reduction in chute score (-0.35 m/s) than heifers (-0.17 m/s) and bulls (-0.05 m/s); however steers and heifers had similar ($P = 0.90$) reductions in exit velocity (-0.63 and -0.60 m/s, respectively) which were greater ($P < 0.01$) than bulls (-0.39 m/s). Feed intake (% of BW) was not correlated to improvements in chute score ($P = 0.12$) or exit velocity ($P = 0.94$). As cattle were handled, temperament improvement was partially dependent upon sex and handling frequency, however the improvements in temperament failed to enhance feed intake.

Key Words: beef cattle, feed intake, temperament

M10 Effect of group change on lying time and milk yield of dairy cattle. I. Guasch*[1] and A. Bach[1,2], [1]*IRTA-Ruminant Production*, *Caldes de Montbui, Spain*, [2]*ICREA*, *Barcelona, Spain*.

It is commonly believed that changing dairy cattle from groups results in social stress which may alter behavior and production performance. Forty-six (19 primiparous (PM) and 27 multiparous (MP)) lactating cows (milk yield = 38±8 kg/d) were monitored over a 48-d period to assess the effects of introducing a group change in lying behavior and milk production. After calving all animals were moved to a pen holding approximately 50 cows. When cows reached about 60 DIM were moved (in sets of 3-9 animals) to a different pen holding about 120 cows. During the study 26 cows changed groups. Individual daily milk production

was recorded electronically. Total daily lying time and number of lying bouts were also automatically recorded using a pedometer (Afikim, Israel). The accuracy of the automatically-collected lying behavior data was validated comparing the results from the pedometers with those acquired through video recordings of 3 animals for two 3-d periods. Comparisons between PM an MP cows and the effect of group change were analyzed using a mixed-effects model including animal as a random effect. Overall, PM cows spent less ($P < 0.05$) time lying (624±4.9 min/d) than MP cows (651±3.8 min/d), but they showed a greater ($P < 0.05$) daily number of lying bouts (14±0.2 bouts/d) than MP cows (11±0.1 bouts/d). Average daily lying time the first 3 d after a group change was reduced ($P < 0.05$) to 562±25.9 min/d from 651±25.9 min/d prior the change. This change in lying time tended ($P = 0.08$) to be more marked in PM (-116 min/d) than in MP cows (-31 min/d). However, average daily lying time between 4 and 6 d after the group change increased to 594±28.8 min/d and to 600±28.1 min/d between 7 and 10 d thereafter. The average number of lying bouts was unaffected by group change. Daily average milk production tended ($P = 0.06$) to be reduced by 0.8 kg/d during the 3 d following the group change, with this reduction being more marked ($P < 0.05$) in PM than in MP cows. It is concluded that when animals change pens in groups of 3 or more, the consequences on lying time and milk production are transient and relatively short, but tend to be more pronounced in PM than in MP cows.

Key Words: social, monitor, management

M11 Effect of rubber flooring in a freestall dairy barn on cow behavior and milk production. J. Pempek* and N. Botheras, *The Ohio State University*, *Columbus*.

Most dairy cows in the United States are housed on concrete floors, which has likely contributed to an increased incidence of hoof problems and lameness. The use of alternative flooring surfaces that should provide a soft and slip-resistant surface for cattle has recently been debated in the dairy industry. This study investigated the effects of rubber versus concrete flooring on dairy cow behavior and milk production. Six pens were included in this study. Three experimental pens were covered with interlocking rubber mats and the other pens remained solid concrete. Primiparous cows were randomly allocated into two groups and placed on concrete or rubber flooring. Older cows were blocked based on their level of milk production (high versus low producing) and cows within each block were randomly allocated to pens with different flooring surfaces. Thirty-six cows were observed (six focal cows from each pen) for a continuous period of 24 h every 4 wk for 7 mo. Every 15 min, the location, posture and behavior of each focal cow were observed and recorded. Cows were milked twice daily and milk yields of focal cows at each milking were obtained. Over a 24 h period, there was no significant difference in the percentage of time spent feeding between the cows housed on a concrete surface and those on a rubber surface (LSM ± SE: Concrete = 17.6 ± 0.01%; Rubber = 17.1 ± 0.01%; P = 0.57). Cows spent similar time lying in the freestalls (Concrete = 44.8 ± 0.03%; Rubber = 42.9 ± 0.02%; P = 0.21). Also, cows spent a comparable amount of time standing in the freestalls (Concrete = 17.8 ± 0.03%; Rubber = 18.1 ± 0.03%; P = 0.20) and standing anywhere in the pen while they were not feeding (Concrete = 19.0 ± 0.02%; Rubber = 22.2 ± 0.02%; P = 0.71). There was no significant difference in the milk yield of cows housed on concrete surfaces compared to cows housed on rubber surfaces (Concrete = 32.7 ± 1.54 kg/d; Rubber = 33.4 ± 1.38 kg/d; P = 0.25). In conclusion, a softer rubber flooring surface did not affect the behavior and milk yield of dairy cows.

Key Words: dairy cows, flooring, behavior

M13 Assessing within- and between-herd variation in lying behavior of dairy cows. K. Ito*, D. M. Weary, and M. A. G. von Keyserlingk, *Animal Welfare Program, University of British Columbia*, *Vancouver, BC, Canada*.

One of the most important design criteria for dairy cow housing is access to a comfortable lying area. Behaviors such as the time cows spend lying down and how often they lie down can be used to evaluate the quality of stalls; however, assessing lying behavior on farms can be challenging. Indices such as the Cow Comfort Index (CCI) and Stall Use Index (SUI) have been widely used in on-farm assessments. Our objectives were to establish reliable sampling and recording methods for measuring lying behavior, evaluate the adequacy of CCI and SUI as estimates for lying behavior, and to describe variation in the lying behaviors of freestall-housed dairy cows. Electronic data loggers recorded daily lying time and number of bouts at 1-min intervals for 5d for 2033 cows on 43 farms. CCI and SUI were calculated based on a single scan at 2h before pm milking on each farm. Subsets of data were created including 4, 3, 2 or 1d/cow and 40, 30, 20, 10, 5, or 1 cow(s)/farm. The estimate derived from each sample size was compared with the grand mean (5d and 44 cows/farm) for lying time and bouts, and CCI and SUI were compared to the farm mean lying time, bouts, and bout duration, using regression. Recording 30 cows for 3d represented the grand means with high accuracy (R^2=0.9), but using fewer cows or fewer d/cow resulted in poorer estimates of the farm average. CCI and SUI showed no association with the daily lying time (R^2<0.01, P>0.5), and CCI was only weakly associated with the number of bouts (R^2=0.16, P=0.01) and bout duration (R^2=0.09, P=0.05), suggesting that these indices should not be used as indicators of lying behavior. Cows lay down on average (±SD) 11.0±2.1 h/d in 9±3 bouts, with the average bout duration of 87.7±29.7 min. These values ranged from 9.5 to 12.9 h/d, 7 to 10 bouts/d, and 65.3 to 112.3 min/bout across farm means, and 4.2 to 19.5 h/d, 1 to 28 bouts/d, and 21.6 to 342.4 min/bout across individuals, showing that variation in lying behavior among individual cows within farm was far greater than differences across farms.

Key Words: dairy cow, lying behavior, cow comfort index

M14 Effects of pair versus single housing on behavior and performance of dairy calves before and after weaning from milk. A. De Paula Vieira*[1,2], M. A. G. von Keyserlingk[1], and D. M. Weary[1], [1]*University of British Columbia*, *Vancouver, BC, Canada*, [2]*Capes Foundation*, *Brasilia, DF, Brazil*.

This experiment tested the effects of pair versus single housing on the behavior and performance of dairy calves before and after weaning. Calves were assigned to either continued individual housing (n=9 calves) or pair housing (n=9 pairs). Before weaning calves had ad libitum access to grain, hay and water via buckets. Pasteurized whole milk was fed via a teat twice daily for 2 h until d 37. During this period pair-housed calves ate more grain than the individually housed calves (averaging 93 vs. 59 ± 11 g/d; P<0.04). Calves were weaned from milk starting on d 37 until d 42 by progressive dilution with water. From d 42 until d 49 only water was available from the teat and grain intake increased over this period (from 537 to 1.216 ± 91 g/d; P<0.0001). From d 49 onward the teat was no longer available. Paired calves increased their intake of water from the bucket more rapidly than did the individual calves (P<0.02). Intake averaged 1.73 vs. 1.53 ± 0.53 kg/d on d 49 and 6.08 vs. 3.74 ± 0.53 kg/d on d 50. Calves in both treatments vocalized in response to the teat removal on d 49, but this response was less in the paired than the individually housed calves (85 vs. 194 ± 9 calls/4 h period on d 49; P<0.0001); call rate declined in both treatments to 3

vs. 13 ± 9 calls/4 h period on d 55 (P<0.0001). There was no effect of treatment on calf BW from d 1 to d 55. On d 56, calves were moved to group pens, mixed with other calves and observed for 15 d; grain, water and hay were available ad libitum via automatic feeders. After mixing, paired calves spent more time at the feeder than did the individual calves (88 vs. 66 ± 3 min/d; P<0.004). Similarly, paired calves consumed more grain (3.46 vs. 2.29 ± 0.17 kg/d; P<0.006). Both differences were greatest on the d of mixing. Weight gains after mixing were higher for paired than individual calves (e.g. 0.02 vs. -2.40 ± 0.57 kg/d on the d after mixing; P<0.0002); after 5 d, gain in the 2 groups were similar, averaging 0.45 kg/d. The results indicate that pairing calves minimizes behavioural responses and improves performance of dairy calves before and after weaning.

Key Words: social behavior, group housing, calf management

M15 Flavors affect the feeding behaviour of ewes fed two unpalatable feeds. A. Mereu[1], V. Giovanetti[2], G. Molle[2], I. Ipharraguerre[3], and A. Cannas*[1], [1]*Dipartimento di Scienze Zootecniche, University of Sassari, Sassari, Sardinia, Italy*, [2]*Agris Sardegna, DiRPA, Olmedo, Sardinia, Italy*, [3]*LUCTA SA, Barcelona, Spain*.

In a previous experiment canola meal and oat grains resulted very unpalatable to ewes. The objective of this study was to enhance the acceptability by ewes of these two feeds through the addition of flavors. In a first experiment (Exp 1), the palatability of canola meal fed alone (control) or combined with 13 different flavors, formulated to elicit sweet (1 to 8), umami (9 to 12) or bitter (13) taste, was tested. A second experiment (Exp 2) resembled the first one except that oat meal instead of canola meal was used. In each experiment, one hour after being fed a basal diet (grass hay, barley meal and urea) each ewe entered alone a pen in which 200 g of a feed + flavor combination were supplied for 6 min. Then, the ewe was taken out and a new one tested another combination. The same 14 multiparous dry ewes were used for the two experiments, carried out in sequence with a 2-w resting period, following 14 (days/animals) x 14 (feed combination) Latin square designs. The statistical model included 3 fixed factors (feed combination, day, ewe). In Exp 1, the DMI of canola meal flavored with products 12 and 2 was higher (P<0.05) than that of canola meal flavored with products 6 and 9. However, none of the treatments was significantly different from the control (only canola meal). There was a significant (P<0.05) and positive relationship between DMI and experimental days for all treatments, except for treatment 12. For several treatments (5, 7, 8, 4 and 9 in decreasing order), mostly sweet-based additives, this association was very high, ranging from R^2=0.85 (P< 0.001) found for flavor 5 to R^2=0.69 (P< 0.01) for flavor 9. In Exp 2 (oat meal based), no differences in DMI among treatments were observed. The day effect was significant for fewer treatments (in decreasing order of association: 6, 3, 1, 2, 5, 4, 12, control, and 8). The R^2 ranged from 0.50 (P< 0.05) to 0.26 (P< 0.09) for treatments 6 and 8, respectively. The experiments showed that some flavors (mostly sweet-based flavors) favored the adaptation of the animals to initially unpalatable feeds, reducing the variability of DMI among ewes.

Key Words: canola meal palatability, oat meal palatability, flavors

M16 When and where do cows defecate? M. Villettaz Robichaud*[1], A. M. de Passillé[2], and J. Rushen[2], [1]*Université Laval, Québec, Québec, Canada*, [2]*Agriculture and Agri-Food Canada, Agassiz, British Columbia, Canada*.

Many environmental and animal health problems of dairy production are due to accumulation of feces but little research has been done on cow defecation and urination in the past fifty years. In exp. 1, we observed each occurrence of defecation and urination of 48 lactating Holstein cows (DIM = 144.7 ± 38.0 d., BW = 667.1 ± 72.0 kg, parity = 2.8 ± 2.3) in free-stalls over a period of 48h. There were large differences between cows in frequency of defecation (mean ± SD, range; 10.0 ± 4.17/d, 3–20/d) and urination (7.58 ± 3.21/d, 2–18/d) and these were positively correlated (r=0.39 P=0.01). The frequency of urination and defecation were not strongly correlated with parity (r=-0.13 P=0.37;r=-0.27 P=0.06), milk production (r=-0.03 P=0.83;r=-0.16 P=0.29), body weight (r=0.14 P=0.33;r=-0.01 P=0.97) and DIM (r=-0.05 P=0.76;r=0.34 P=0.02). We observed 27.8% of defecation and 19.1% of urination in the area behind the stalls, occurred, 33.4% and 28.3% respectively in the feeding area and 20.7% and 38.4% when cows were standing with two feet in the stall and two feet in the alley. In exp. 2, we tested ways of stimulating defecation and urination. Twelve lactating Holstein cows were walked through a) an empty footbath or b) a footbath filled with water once a day for 6d. Cows were more likely to defecate in the water filled footbath (mean ± SE 0.67 ± 0.08 vs 0.42 ± 0.08). However when repeated 23d later, there was no difference between the treatments. In further tests, the cows stood for 2 min. in a) a dry footbath, b) a footbath filled with still water, c) a footbath filled with running water, or had d) air or e) water sprayed over their legs . There were no significant effects of treatments. Defecation frequency during tests decreased from d1 to d29 (mean ± SD d1 0.50 ± 0.52, d29 0.08 ± 0.29). Large differences between cows in the frequency of defecation and urination suggest that some are disproportionately responsible for spreading manure throughout the barn. The frequency of defecation and urination are not strongly related to production traits. A better understanding of factors controlling defecation and urination may help in developing more effective cleaning routines.

Key Words: elimination, defecation, urination

Animal Health: Stress, Respiratory Disease, Small Ruminants

M17 Effects of dehydration and rehydration on the thermoregulation of heat stressed Angus steers. B. Scharf*, L. E. Wax, T. J. Evans, and D. E. Spiers, *University of Missouri, Columbia*.

Evaporative cooling via panting or sweating is the most effective means of maintaining core temperature of cattle exposed to heat for an extended period. Water restriction during heat stress alters this ability. Therefore, a study was conducted to determine if dehydration under a controlled heat challenge would compromise thermoregulation. Eight Angus steers were maintained for 5 days at thermoneutrality (TN; 19-21°°C) in the Brody Environmental Center (University of Missouri). This was followed by 14 days of cyclic heat stress (HS; 26-36°C). Water was removed starting on Day 5 of heat stress. After 3 days, water was returned starting the rehydration phase. Measurements included rectal temperature (Tre) and respiration rate (RR) measured six times daily. Body weight, feed and water intakes, and sweat rate at rump and shoulder were recorded daily during acclimation, dehydration and rehydration. During dehydration,

steers lost ~10% of their body weight, which they regained within 36 h of rehydration. As expected, feed intake decreased (~75%) within 24 h of dehydration, but quickly recovered during rehydration. Transition from TN to HS caused RR to double (40-80bpm; P<0.05). Dehydration reduced RR (~15bpm), which remained low throughout rehydration (P<0.05). Similar to RR, Tre increased during HS (0.6°C; P<0.05). However, no increase in Tre occurred during dehydration (P=0.41), while rehydration caused a 0.8°C drop before recovery. Shoulder and rump sweat rates sharply increased with HS, but dropped to TN levels during dehydration (P<0.05), before recovering when water was returned. Haematocrit did not provide a reliable indication of dehydration as it only slightly increased during dehydration, and was not different from TN level (P=0.08). Steers in the present study showed no lasting effects of dehydration, with the thermal status of the animal returning to normal after 48 hours of rehydration. Unexpectedly, core body temperature remained relatively unchanged despite dehydration, demonstrating their ability to adapt to changing conditions.

Key Words: dehydration, heat stress, cattle

M18 Heat stress augments plasma tyrosine-nitrated proteins and lactate-to-pyruvate ratio after repeated endotoxin (LPS) challenge in steers. T. Elsasser*[1], R. Rhoads[2], S. Kahl[1], R. Collier[2], L. Baumgard[2], C. Li[1], and T. Caperna[1], [1]*USDA-ARS, Beltsville, MD*, [2]*University of Arizona*, *Tucson*.

Nitrated proteins are usually function-impaired. Nitrotyrosine (NT) is the standard marker for nitrated proteins and proinflammatory nitrooxidative stress (PNoS) signifying the aberrant interactions between nitric oxide and superoxide anion that often result from tumor necrosis factor-(TNF) α-mediated mitochondrial dysfunction. We investigated whether heat stress altered the PNoS responses in Holstein steers after two LPS challenges. Ten steers (318 ± 49 kg BW) housed in climate chambers were subjected to either a thermoneutral (TN: constant 19°C) environment or heat stress (HS) conditions (cyclical daily temperatures; 32.2 to 40.0°C) for 9d. In order to minimize confounding effects of altered plane of nutrition, TN were pair-fed to HS. On d 4 and 7, steers received an LPS challenge (*E. coli* 055:B5, 0.2 µg/kg BW, i.v.) with blood samples collected at marker-appropriate times between 0 and 24 hours relative to the start of each challenge. Plasma concentrations of TNF-α, xanthine oxidase (XO), serum amyloid-A (SAA), lactate (L), pyruvate (P), nitrate + nitrite (NOx), NT, and IGF-1 were measured. Plasma TNF-α (P<0.002), XO (P<0.01), SAA (P<0.005), increased over time but were not different between TN and HS. The increases in NOx were higher in HS than TN (P<0.05); NT was increased transiently (P<0.05) over baseline in TN at 7 h after the first LPS challenge. Plasma NT remained elevated in HS through the entire first and second challenges. Plasma IGF-1 was lower (P<0.03) at time 0 in HS than TN and decreased more (P<0.05) following each LPS challenge. The plasma L:P (where higher values are indicative of impaired mitochondrial function) was higher in HS than TN at time 0 prior to either LPS (P<0.05) with a heat-stress-by-time interaction (P<0.01). The data are consistent with the concept that although heat stress leaves the primary PNoS response to low-level LPS administration intact (including the plasma markers of the tolerance response), energy functions of mitochondria may be challenged where heat stress exacerbates the interaction of PNoS mediators to form NT proteins.

Key Words: heat stress, oxidative stress, cattle

M19 Lack of adaptation to fescue toxicosis under thermoneutral and heat stress conditions. D. E. Spiers*, D. K. Kishore, P. A. Eichen, and E. Moran, *University of Missouri*, *Columbia*.

Intake of endophyte-infected tall fescue reduces feed intake, activity, and body weight gain. This study determined the potential for short-term adaptation to fescue toxicosis and heat stress. Male CD Outbred rats (n=24) were implanted with temperature transmitters (Respironics, Bend, OR) to measure core temperature (Tcore). Feed intake (FI) and body weight (BW) were measured daily. Experimental design included several shifts (7 days each) in treatment to detect adaptation. All rats were initially fed diets with ground, uninfected tall fescue seed (E-) and exposed to 21°C (thermoneutral; TN) to establish baseline values. In Period 1, all groups were maintained at TN for 7 days with one group fed a diet containing ground, infected tall fescue seed (E+; ~165µg ergovaline/kg BW/d) and two groups fed E- diet. This was followed by 7 days at 31°C (heat stress; HS; Period 2) on the same diets. All animals were fed E- diet during the second 7 days of HS (Period 3). In the final 7 days (Period 4), E+ diet was returned to the original group and fed to one E- group, with the third group remaining on E- diet. In Period 1, FI decreased by 40% with E+ treatment (α=0.05), with a comparable reduction in BW (α=0.05) after 4 days. Initial HS (Period 2) immediately reduced FI in all groups (α=0.05), and diminished differences between E+ and E- groups. Growth stopped in controls, and continued to decrease in E+ rats during HS. A shift from E+ to E- diets (Period 3) returned FI and growth to control levels. Treatment of the original E+ and one control group with E+ diet (Period 4) produced identical reductions in FI and BW (α=0.05). An expected reduction in Tcore with E+ treatment occurred at TN (α=0.05), followed by an increase during early HS (α=0.05). Removal of E+ in Period 3 produced a reduction in Tcore (α=0.05) that coincided with increase in FI. Both groups fed E+ in Period 4 exhibited similar Tcore responses with no increase from Period 3. Although feed intake and growth shows no sign of adaptation to fescue toxicosis, there is indication that adaptation to heat stress improves the thermal response.

Key Words: heat, fescue, toxicosis

M20 Cyclic heat stress alters the diurnal thermal status of sows during lactation. E. A. Coate*, M. C. Lucy, T. J. Safranski, P. A. Eichen, A. M. Williams, and D. E. Spiers, *University of Missouri*, *Columbia*.

We have shown in earlier studies that heat stress has different effects on the average daily thermal status of sows during gestation, lactation, and breeding, with the greatest impact during lactation. The present analysis focused on the lactation period, with emphasis on diurnal shifts in thermal status. Primiparous sows (n=58) were initially housed during the last 3 weeks of gestation in the Brody Environmental Center (University of Missouri) in either thermoneutral (17.5 – 19.3°C; TN) or heat stress (23.8 – 30.9°C; HS) environments. Several days before farrowing, sows were moved to farrowing crates in two different chambers. They either went to the same thermal environment (TN-TN or HS-HS) or were to the other environment (TN-HS; HS-TN) until weaning. Respiration rate (RR) and rectal temperature (Tre) were measured daily (0800, 1200, 1600, and 2000). Likewise, skin temperature (trunk, extremities) was measured at the same times using infrared thermometry. Daily Tre increased 0.4°C in all treatment groups (α=0.05) to plateau on Day 10. There was a treatment effect on Tre (α=0.05), with only the TN-HS displaying a significantly higher value (0.3°C; α=0.05) than TN groups. Previous HS exposure reduced heat impact during lactation. Although Tre for HS groups were higher than TN groups at 1200 to 2000, they did not differ at 0800 (α>0.05), when Ta difference was 6°C. In contrast,

RR was 40% greater (42 vs 29 bpm; α=0.05) in HS groups compared to TN groups at 0800, and increased to 100.4% during the day (71 vs 35 bpm; α=0.05). Average skin temperature was at least 3.3°C higher (α=0.05) in HS vs TN sows. This difference decreased during lactation, when the TN values approached HS level. Despite differences in ambient temperature, heat loss as indicated by skin temperature and respiration rate was sufficient to minimize differences in rectal temperature of sows in the two environments during morning hours. However, heat loss was ineffective in preventing a separation of rectal temperature during warmer times of day.

Key Words: sow, lactation, heat

M21 Effects of bluetongue virus infection on sperm quality in German test-bulls. K. Kemmerling[1], D. Straet[1], U. Mueller[1], U. Janowitz[2], and H. Sauerwein*[1], [1]*Institute of Animal Science, Physiology & Hygiene Group, University of Bonn, North-Rhine-Westphalia, Germany*, [2]*Rinder-Union-West, Borken, North-Rhine-Westphalia, Germany*.

Bluetongue virus (BTV) is an arthropod-borne pathogen that is transmitted by *Culicoides midges* between ruminant hosts. BTV-infected sheep are prone to develop severe clinical signs, whereas cattle show only mild or no clinically apparent symptoms. For sheep, the recent BTV outbreak of BTV serotype 8 in Germany and the Benelux was shown to transiently alter many semen characteristics (Kirschvink et al. 2008, Vet. J.oi10.1016/j.tvjl.2008.06.008). For cattle no such data were available and we therefore evaluated semen quality in bulls that were naturally infected with BTV-8 in fall of 2007. Ejaculate volume, sperm concentration and post-thawing motility were recorded from 6 infected test bulls (BT group). BT status was assessed by serology and PCR commencing in July 2007. At that time, the 6 BT bulls were still negative but turned BTV-PCR positive in September to November 2007 without showing clinical signs. Between April and May 2008, all 6 bulls were again PCR negative and remained seropositive. Semen data from 31 non-infected test bulls that were recorded between 06 and 08 were matched for season and age and used as controls.

Key Words: bluetongue virus, semen quality, bulls

M22 The use of infrared thermography in the non invasive, automated detection of calves displaying bovine respiratory disease. A. L. Schaefer*[1], C. Bench[2], J. Basarab[3], N. Cook[3], E. Okine[2], J. Colyn[1], B. Chabot[1], D. Froehlich[3], L. Holt-Klemic[1], T. Liu[1], and P. Lepage[1], [1]*Agriculture and Agri-Food Canada, Lacombe, Alberta, Canada*, [2]*University of Alberta, Edmonton, Alberta, Canada*, [3]*Alberta Agriculture, Lacombe, Alberta, Canada*.

Bovine respiratory disease (BRD) is one of the most common afflictions in receiver calves causing harm to production economics and animal welfare. The purpose of the present study was to evaluate a non-invasive, automated infrared (IRT) detection system in the identification of calves displaying BRD. A total of sixty one multiple sourced, commingled commercial receiver steer calves averaging 225 kg liveweight were used. The calves were weaned and transported to the Lacombe Research Centre where they were blood sampled and placed into a pen with wood shavings bedding and ad-libitum access to cereal silage and water. All calves were fitted with RFID ear tags. An infrared scanning system consisting of an RFID reader, FLIR S60 camera and a computer were housed near the water bowl and when triggered by the presence of an RFID tag collected orbital (eye) images of the animal. For the sixty one (61) calves in the study, twelve (12) animals were identified as true positive (TP) for BRD and forty nine (49) as true negative (TN) or healthy. TP animals displayed a score of 3 or 4 out of 4 for core temperature (CT, rectal) > 40 C, clinical scores (Cl Sc, digestive, respiratory, temperature, disposition) of > 3 out of 20, a white blood cell (WBC) count of > 10,000/ul or < 7,000/ul and a neutrophile/lymphocyte ratio (N/L) of < 0.1 (neutropenia) or > 0.8 (neutrophilia). By contrast, TN animals displayed a score of 0 or 1 out of 4 for the above aberrations in CT, ClSc, WBC and N/L ratio. The average values for CT and Cl Sc for TP calves were 40.0 (0.45 SD) and 8.8 (2.5) respectively and for the TN calves 38.8 (0.19) and 1.8 (0.8) (P<0.01) respectively. Corresponding orbital IRT data were 36.7 (0.9) for TP and 35.7(0.3) C for TN respectively (P<0.01). The data suggest that a non invasive, automatic infrared screening system can be effective for detecting BRD in calves.

Key Words: cattle, infrared, disease

M23 Orbital thermal topography in calves with bovine respiratory disease. A. L. Schaefer[1], C. Bench[2], N. Cook[3], J. Colyn*[1], T. Liu[1], E. Okine[2], M. Stewart[4], and J. Webster[4], [1]*Agriculture and Agri-Food Canada, Lacombe, AB, Canada*, [2]*University of Alberta, Edmonton, AB, Canada*, [3]*Alberta Agriculture, Lacombe, AB, Canada*, [4]*AgResearch, Hamilton, New Zealand*.

The fever response to viral infection in mammals is typically identified using core or rectal temperatures. However, this approach to diagnostics is usually invasive, inconvenient and often appears subsequent to fever presentation. The purpose of the present study was to examine the radiated thermal topography of the orbital or eye region in calves known to be true negative (TN) or true positive (TP) for bovine respiratory disease (BRD). Fourteen multiple sourced, commingled, transported and weaned steer receiver calves averaging 225 kg were used. The calves were maintained on conventional cereal silage diets. Calves were identified as TP if their core temperature was > 40 C, their white blood cell count was < 7,000 or > 10,000 /ul, the neutrophile/lymphocyte ratio was <0.1 (neutropenia) or > 0.8 (neutrophilia) and their clinical score for respiratory distress was > 3 out of 20. A TP animal had to display three out of the four aforementioned attributes and a TN could only display 0 or 1. Eight of the fourteen calves were verified as TP and six as TN. All calves were scanned daily with a broad band infrared camera (FLIR S60) from a distance of 1 m. An area of 2825 pixels basically covering the eye and approximately 1 cm of surrounding skin was analysed and divided into five thermal groups of 24-26.9, 27-29.9, 30-32.9, 33-35.9, and 36-38 C. In a healthy animal the proportion of pixel area was measured as; 24-26.9 C, 6.8%; 27-29.9 C, 15.1%; 30-32.9 C, 31%; 33-35.9 C, 40.1% and 36-38 C, 4.7%. On the day the TP calves were identified as clinically ill the thermal range of 36-38 C was significantly higher (10.5% of pixels, P<0.05) compared to TN calves. Of interest was the observation that the thermal profile for the 36-38 C was also significantly higher for the TP calves the day before apparent clinical illness (36.4% of pixels, P<0.05) and for two days before identified clinical illness for the 33-35.9 C profile (66.1% of pixels, P<0.05). The data suggest that a radiated thermal profile of the orbital area may assist in the diagnosis of BRD in calves.

Key Words: infrared, BRD, eye

M24 Relationship between ex vivo neutrophil function in response to an enteropathogenic *Escherichia coli* and measures of health and performance of dairy calves. L. G. D. Mendonça*[1], G. Lopes Jr.[1], M.

A. Ballou[2], and R. C. Chebel[1], [1]*Veterinary Medicine Cooperative Extension, University of California Davis*, *Tulare*, [2]*Department of Animal and Food Sciences, Texas Tech University*, *Lubbock*.

Calves are extremely susceptible to disease during the first few weeks of life, and neutrophils are an integral component of the innate immune system. The objective of this study was to evaluate the relationship between neutrophil function and measures of health and production. Calves (n=64) were fed colostrum after birth. At 36±6 h of life, body weight (BW) was recorded and blood sampled for total serum protein. From 2 to 25 d of age calves were fed hospital milk and from 26 to 60 d of age calves were fed hospital milk blended with milk replacer. Blood was sampled at 3, 24, 45, and 66 d of age to determine the percentage of neutrophils phagocytizing (PHAG) and producing an oxidative burst (OB) against an enteropathogenic *Escherichia coli*. Calves were weighted at 25 and 60 d of age. Starter intake, attitude and fecal scores, antibiotic (ATB), anti-inflammatory (AINF), and oral electrolyte treatments were recorded daily. Median percentage of PHAG and OB positive neutrophils were calculated for 3, 24, 45, and 66 d and calves were stratified as above or below the median. Proportions of neutrophils PHAG or producing an OB were affected by time ($P < 0.01$). Neither PHAG nor OB positive measurements at 3 d were correlated with health parameters. However, calves with above median PHAG over all sampling times were less likely to be treated with ATB (AOR=0.13, CI95%=0.03-0.53) and AINF (AOR=0.03, CI95%=0.01-0.34) drugs, and were less likely to experience fever (AOR=0.12, CI 95%=0.01-1.0). Calves with above median PHAG were treated with ATB (0.2±0.2 vs. 0.8±0.2d) and AINF (0.1±0.1 vs. 0.4±0.1d) drugs for fewer days. Similarly, calves with above median OB positive neutrophils received ATB (0.3±0.1 vs. 0.7±0.2d) and AINF (0.1±0.1 vs. 0.3±0.1d) drugs for fewer days. Neither neutrophil PHAG nor OB on d 3 of live were correlated with performance. These data indicate that the percentages of neutrophils PHAG or producing OB positive against an enteropathogenic *E. coli* are related to measures of health of neonatal dairy calves.

Key Words: dairy calves, immunity, health

M25 Replacing milk proteins with nucleotides in milk replacers for pre-weaned dairy calves. J. A. Elizondo-Salazar*[1,2], C. M. Jones[1], R. F. Leuer[1], and A. J. Heinrichs[1], [1]*The Pennsylvania State University*, *University Park*, [2]*Estación Experimental Alfredo Volio Mata*, *Facultad de Ciencias Agroalimentarias. Universidad de Costa Rica*.

Two experiments were carried out to evaluate the effect of substituting milk protein in milk replacer with nucleotides derived from cell contents of *Saccharomyces cerevisiae* (NuPro; Alltech, Inc.). The first trial utilized 16 Holstein bull calves (4/treatment), and nucleotide product replaced 0, 5, 10, or 20% of whey protein concentrate in milk replacer. The second trial utilized 20 Holstein bull calves (5/treatment), and 0, 25, 50 , 75, or 100% of whey protein concentrate was replaced by nucleotide product. For both trials, intake and health were monitored daily and growth measurements were taken weekly. At 6 wk of age, xylose absorption was determined, and, calves were slaughtered. Within 5 min of death, two 1-cm sections were taken from each of the duodenum, jejunum, and ileum for morphometric analysis. Calf health growth measurements, small intestinal villus height, and xylose absorption were not different ($P > 0.10$) between treatment groups in either trial. In Trial 1, small intestinal crypt depth was lowest ($P < 0.03$) for the 5% treatment, with no differences between 0, 10 and 20% nucleotide groups. Also the total intestinal weight was greater for calves in the 10 and 20% nucleotide groups than the other treatments. In these studies, substituting yeast cell contents for milk protein in milk replacer did not affect health or growth of neonatal dairy calves. Nucleotides in the yeast cell contents may have improved intestinal growth and increased small intestinal crypt depth; however, this effect was not consistent in both studies.

Key Words: nucleotide, small intestine, milk replacer

M26 Association of bovine Fc receptor alpha-chain promoter gene heliotypes with IgG transfer into milk of Chinese Holstein cows. S. S. Li, J. Q. Wang*, H. Y. Wei, D. P Bu, G. L. Liu, X. L. Dong, and K. L. Liu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

The Fc receptor α–chain gene (FCGRT, which encodes the α–chain of FcRn) transports immunoglobulin G (IgG) across the epithelial cell layers into the secretions of mammary gland. The purpose of this study was to detect the association of FcRn promoter gene heliotypes with milk IgG concentration and transfer. We collected 189 individual milk and blood samples randomly from more than 2,800 Chinese Holstein cows across six dairy farms in the greater Beijing area. Determination of IgG concentration in milk and blood samples was performed by a commercial sandwich enzyme–linked immunosorbent assay (ELISA) using the Bovine IgG ELISA Quantitation Kit. The SNP stream system (Beckman Coulter, USA) was used for identifying single nucleotide polymorphisms (SNPs) in promoter of FcRn gene, and genotyping the 189 individuals. Haplotype block and main diplotypes were inferred by phase 2.1 software. The results indicated that four SNPs, assorted into six haplotypes, were identified in promoter of FcRn. Duncan′s multiple–range test showed the least square mean of blood IgG concentration, milk IgG concentration and mass of different diplotypes were not significantly different ($P>0.05$). Therefore, the haplotypes of FcRn promoter were not correlative with milk IgG concentration and transfer.

Key Words: FcRn, SNP, immunoglobulin

M27 Predictive measures of fetal distress in calves during delivery. K. E. Hard* and H. D. Tyler, *Iowa State University*, *Ames*.

The objective of this experiment was to evaluate accuracy of changes in tongue parameters for determining the extent of fetal stress during parturition. Fifty eight calves (Holstein, Jersey, and Jersey × Holstein) were monitored during calving. From the time the tongue was first visible, measurements of tongue color, length, and reflex were taken approximately every two minutes until umbilical cord rupture. Tongue color was determined using a color chart with 17 discrete colors. Tongue length was measured from the middle point of the nose to the tip of the tongue. Tongue reflex was assessed with a sharp pinch on the tongue on a scale from 0 to 3. Arterial blood samples were drawn within 20 minutes after birth. Fetal oxygenation parameters were analyzed using a blood gas analyzer (ABL77; Radiometer, Copenhagen). Three color categories were determined from the original 17 colors. Both initial and final tongue colors were significantly different ($P<.0001$). However, parameters reflecting oxygen delivery were not correlated to color categories (P_{O2} P=.0843, P_{CO2} P=.2944, and pH P=.9461), suggesting that dark tongue color is a poor predictor of stress. Mean tongue length tended to be positively correlated with P_{CO2} (P=.0534) and tended to be negatively correlated with pH (P=.1369), indicating that calves with longer tongues tended to have lower pH and higher P_{CO2}. However, tongue length was not significantly correlated with oxygen delivery parameters (P_{O2} P=.6583). This suggests that tongue length is

a good predictor of acidosis but not hypoxia. However, tongue reflex was not correlated to parameters of acidosis or hypoxia suggesting that reflex alone is a poor predictor of stress. If a calf presents with a long tongue, reduced reflex, and dark color stress is more likely than if there is only a single indicator present. Six calves in the study that had long tongues (greater than 55 mm), dark color (color 3 or lower), and poor responsiveness (reflex equal to 1). Five out of the six calves were stressed (pH $\leq$ 7.25, P_{O2}< 50, and P_{CO2} > 60), however, there were an additional six stressed calves in which changes in tongue parameters were not predictive of fetal stress.

Key Words: birth stress, calves, tongue color

M28 Automated measurement of feeding behavior to detect illness in milk-fed calves. F. T. Borderas[1,3], J. Rushen[2], M. A. G. von Keyserlingk[1], and A. M. de Passillé*[2], [1]*University of British Columbia, Vancouver, BC, Canada*, [2]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada*, [3]*Universidad Autónoma Metropolitana-Xochimilco, Coyoacán, Mexico*.

There is a need for improved methods of detecting illness among group-housed milk-fed calves. Automated monitoring of feeding behavior may be one possibility. We examined whether illness in group-housed dairy calves fed with an automated milk feeder changed their feeding behavior, and whether these changes were affected by milk rations. Unweaned Holstein calves were housed in groups of 3 to 16 animals and fed either high (12L/d or ad libitum) or low (4-6L/d) amount of milk or milk replacer. From birth, calves were subjected to regular health checks that included general condition, rectal temperature, lung auscultation and faecal scoring. Forty-eight calves became ill from gastro-intestinal or respiratory problems or both before 21d of age, with no differences between feed level (P>0.10). We paired 22 calves that succumbed to only one bout of illness with healthy calves on the same feeding level and of the same age. During the 2d prior to the day of illness detection, there were no differences between the sick and healthy calves in any measure of feeding behavior (P>0.10). In the days following clinically identified illness, sick calves fed high levels of milk or milk replacer showed a decrease in milk or replacer intake (-2.59 ± 0.7 L/d), a reduced frequency of visits to the milk feeder (-2.43 ± 0.3 visits/d), and an increase in the duration of each visit to the milk feeder (1.66 ± 0.5 min/visit), as compared to the matched healthy calves (PROC MIXED; P<0.05). This was apparent up to 3d after illness detection. However, sick calves fed low levels of milk or milk replacer only showed a decrease in the duration of each visit to the milk feeder (-1.35 ± 0.2 min/visit; P<0.05) compared to healthy calves, with no differences in intake of milk or replacer or frequency of visits to the milk feeder (P>0.10). Illness results in changes in feeding behavior of calves which can be monitored with automated milk feeding equipment but feeding level affects the types of changes in feeding that occur.

Key Words: calf, Illness detection, welfare

M29 Age-dependent health status in the goat. M. Worku*, R. C. Noble, and H. Mukhtar, *North Carolina A&T State University, Greensboro*.

Animal health status and acquired resistance to infection can differ with age. The objectives of this study were to compare health and infection indicators in yearling and adult goats. Twenty eight (14 yearling and 14 adults) Boer × Spanish cross goats housed at the North Carolina Agricultural and Technical State University farm were used. Animals were maintained under the same management conditions. The body weight, packed cell volume, fecal egg counts, FAMACHA, and body condition scores of yearling and adult goats were evaluated. After sample collection and readings, the tabulated data of the above parameters for each age group was compared to that of the other using a t-test. Correlation analysis was also used to assess the correlation amongst the different parameters. The study showed that adult goats had better body condition (p<0.0006), heavier body weight (p<0.0001), and more resistance against internal parasites (FAMACHA p<0.047), than yearling goats. The correlation analysis results showed there was a weak negative correlation between the body condition and FAMACHA (r=-0.4023). Age specific management practices may be needed to ensure improvements in the health status of yearling goats.

Key Words: goat, health, age

M30 Effect of vitamin E supplementation on naturally acquired parasite infection in lambs. C. E. MacGlaflin[1], A. M. Zajac[2], K. A. Rego[1], C. S. Petersson-Wolfe[2], and K. H. Petersson*[1], [1]*University of Rhode Island, Kingston*, [2]*Virginia Tech, Blacksburg*.

The emergence of anthelmintic resistant nematodes is a significant problem for the sheep industry. The naïve immune system of lambs makes them particularly susceptible to gastrointestinal nematode infections. Host nutritional status has been identified as a key component of immune function. Vitamin E (VE) is known to have broad effects on immune function and a VE deficient diet has been shown to reduce resistance to helminth infections in mice. The objective of this study was to determine the effect of vitamin E supplementation on naturally acquired parasite infection in lambs. Dorset lambs were assigned to one of two treatment groups at birth, 30 IU d-α-tocopherol / kg body weight (VE, n=9) or placebo (P, n=9). VE or P injections were administered every two weeks from birth through 7 months of age. All animals were weaned at 3 months of age. At 3-4 months of age all animals were de-wormed with albendazole (10 mg/kg) and levamisole (8.8 mg/kg). Lambs were housed together and allowed to graze on a field that was known to be contaminated with free-living nematodes. Fecal egg counts (FEC) were estimated using the Modified McMaster′s method. Weekly jugular blood samples were used to determine PCV. Serum vitamin E concentration was determined every two weeks. Composite fecal cultures were taken at the beginning and end of the study for parasite identification. Lambs were weighed every other week throughout the study. At seven months, lambs were slaughtered and abomasal and intestinal contents were collected at necropsy for quantification and identification of nematodes. Preliminary results: *Haemonchus contortus* and *Trichostrongylus columbriformis* larvae were recovered from the pooled fecal culture prior to deworming. FEC increased over time (P < 0.05) and PCV decreased over time (P < 0.05). There was no effect of vitamin E supplementation on FEC, PCV or average daily gain. Ewe lambs had higher PCV than ram lambs (P < 0.05) and younger animals had greater FEC than older animals (P < 0.05). Larval identification from the final composite fecal cultures and quantification and identification of nematodes recovered at necropsy are pending.

Key Words: sheep, parasite, vitamin E

M31 Analysis of the lipopolysaccharide profiles of *Escherichia coli* O118 and O151 O antigen gene clusters. J. W. Allen*[1], C. DebRoy[2], L. P. Fratamico[3], and A. R. Byers[1], [1]*North Carolina A & T State Uni-*

versity, Greensboro, [2]*The Pennsylvania State University, University Park,* [3]*U.S. Department of Agriculture, Agricultural Research Service, Eastern Regional Research Center, Wyndmoor, PA.*

In an earlier study by the authors, the DNA sequence of the O antigen gene cluster of an *Escherichia coli* serogroup O118 strain was determined, and 13 ORFs were identified, encoding genes required for O antigen sugar biosynthesis, transfer, and processing. The wzx (O antigen flippase) and wzy (O antigen polymerase) genes in the O antigen gene cluster of *E. coli* O118 shared little homology with similar genes in other *E. coli*; therefore, PCR assays targeting these genes were designed for identification of these serogroups. Specificity testing using strains belonging to *E. coli* O118 isolated from various sources, representative strains of 167 other *E. coli* O serogroups, and 20 non-*E. coli* bacteria revealed that the PCR assays were specific for *E. coli* O118. The focus of this study was to further characterize the lipopolysaccharide (LPS) profiles of these *E. coli* O118 and O151 strains. Although the lipopolysaccharide (LPS) profiles of O118 and O151 showed differences, multilocus sequence typing (MLST) of *E. coli* O118 and O151 strains only revealed minor variation at the nucleotide level; over a total of 3753 bp, only 61 sites (1.6%) differed among the isolates examined. Since *E. coli* O118 strains are more frequently isolated from humans, animals, and the environment than *E. coli* O151, serogroup O151 may likely be a minor variant of *E. coli* O118.

Key Words: food safety, microbiology, swine

M32 Association of tumor necrosis factor-α *(TNF-α)* gene promoter polymorphisms with hyper-responsiveness to endotoxin (LPS) in calves. S. Kahl*, T. H. Elsasser, M. Proszkowiec-Weglarz, and E. E. Connor, *USDA, Agricultural Research Service, Beltsville, MD.*

Previously, we identified a subpopulation of beef calves that failed to develop normal immune tolerance as defined by the patterns and magnitude of changes in plasma *TNF-α* concentration after 2 repeated LPS challenges. In these hyper responding calves (HRC), impaired LPS tolerance was related to exacerbated metabolic and clinical signs and prolonged recovery time. Recently, we identified 2 linked SNP located in the promoter region of the *TNF-α* gene in Angus × Hereford calves and showed that G to A (-526) and C to T (-701) transitions were associated with increased *TNF-α* mRNA expression in white blood cells, increased plasma TNF-α concentration, and decreased tolerance to repeated LPS challenges. In the present investigation, we applied a logistic regression analysis (LRA) to retrospectively determine whether the G to A (-526) polymorphism may aid in identifying at-risk HRC. Altogether, across 5 separate trials over 8 yr, 96 Angus × Hereford calves were genotyped and challenged with 2 consecutive LPS injections 4 d apart (0.2 μg *E. coli* 055:B5/kg BW, i.v.). Blood samples were obtained at 0, 1, 2, 3, and 4 h relative to each LPS injection. Plasma TNF-α was measured by RIA with TNF-α response calculated as area under the time × concentration curve (AUC). Within each experiment, HRC were identified using an algorithm to normalize AUC after each LPS challenge. In total, 18.7% of calves were recognized as HRC; genotype frequencies were 21.9%, 45.8%, and 32.3% for AA, AG, and GG, respectively. The LRA indicated an AA genotype was associated with a 10-fold higher risk for HRC vs. a GG genotype (odds ratio [OR], 10.3; 95% confidence interval [CI], 2.4 - 44.5; $P < 0.001$) and an 11-fold higher risk for HRC vs. AG (OR, 11.0; CI, 2.9 - 41.9; $P < 0.001$). No differences in OR for HRC were found between AG and GG genotypes. The results suggest that this *TNF-α* gene promoter polymorphism may be useful in identifying calves with a propensity to exhibit excessive or prolonged pathological responses to LPS-related infections.

Key Words: cattle, SNP, tumor necrosis factor-α

M33 Effect of calf-specific *Bacillus* on health and growth of young calves. D. Wood*, J. Sowinski, and R. Blome, *Animix, Juneau, WI.*

There is considerable published data on probiotic use in calves; however, few studies investigate *Bacillus*. The objective of this study was to evaluate health benefits of supplementing calf-specific *Bacillus* to newly arrived Holstein bull calves. Three trials were conducted. Previously, *Bacillus* were screened to inhibit growth of *Salmonella, E. coli* and *Clostridia* found in feces of over 1000 scouring calves in CA, WI, OH, IN and PA. In the three trials all calves were auction sourced, app. 1 wk of age and were randomly placed and randomly assigned to one of two diets (Bac and Ctrl). Trial design and results are shown in table 1. In Exp. 1, calves (initial BW=44.5kg) were placed into individual raised, slatted stalls. Calf diets were 1) 1 billion cfu *Bacillus* fed twice daily in CMR until weaning d 55 (Bac), 2) no added supplement, only basal formula (Ctrl). In Exp. 2, calves (initial BW=45.2 kg) were placed into individual veal stalls. Calf diets were: 1) 1 billion cfu *Bacillus* fed twice daily in CMR until d 29 (Bac), 2) no added supplement (Ctrl). In Exp. 3, calves were placed into individual raised, slatted stalls. Calf diets were: 1) 3 billion cfu *Bacillus* fed twice daily in CMR for initial 4 d, and again at peak scours, d 11, for 2 d (Bac), 2) no added supplement (Ctrl). Calf specific *Bacillus* reduced incidence and severity of enteric disease when 20-33% of calves required treatments. The 6 day treatment regiment performed as well as 29 or 55 d. Under duress of severe enteric disease with treatment rates of 70%, there was no effect. There was no effect on ADG or mortality in any study.

Table 1.

Trial	n	Strategy	Calves Treated†	Treats/ calf†	Mort/ cull	ADG	Days	Type
Exp 1, Bac	60	2 B cfu, 52 d	14	1.78[a]	7	1.29	0-52	Grain Fed
Exp 1, Ctrl	60	0	20	2.85[b]	5	1.26	0-52	Grain Fed
Exp 2, Bac	100	2 B cfu, 21 d	68	3.6	6	1.66	0-49	Veal
Exp 2, Ctrl	100	0	71	3.55	7	1.66	0-49	Veal
Exp 3, Bac	75	6 B cfu, 6 d	8[a]	2.375[a]	1	N/A	-	Grain Fed
Exp 3, Ctrl	75	0	17[b]	3[b]	2	N/A	-	Grain Fed

†During the week of peak scours. Values within rows with different superscripts differ *(P=0.05)*

Key Words: calf, probiotic, *Bacillus*

M34 Feeding colostrum with an esophageal feeder does not reduce IgG absorption in neonatal dairy heifer calves. J. A. Elizondo-Salazar*[1,2] and A. J. Heinrichs[1], [1]*The Pennsylvania State University, University Park,* [2]*Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias. Universidad de Costa Rica.*

Esophageal feeders are used to administer colostrum to calves that are weak or reluctant to nurse or to ensure rapid delivery of a consistent quantity of colostrum. However, feeding colostrum with an esophageal feeder has been associated in some studies with lower apparent efficiency of IgG absorption and slightly lower serum IgG concentration compared to feeding colostrum by nipple bottle. For this reason 40

newborn Holstein heifer calves were studied to compare absorption of immunoglobulins, total serum protein concentration, and apparent efficiency of absorption. Calves were separated from their dams before suckling occurred and a single feeding of 3.8 L of pooled colostrum was fed by 1.5 to 2 h of age using a nipple bottle, an esophageal feeder, or a combination of both. A jugular blood sample was collected from each calf at 0, 24, and 48 h of age. There were no differences between treatments when examining total IgG concentration (P=0.84), total serum protein concentration (P=0.85) or apparent efficiency of absorption (P=0.89). In this study, feeding colostrum with an esophageal feeder did not reduce IgG absorption, total serum protein concentration or apparent efficiency of absorption in neonatal dairy heifer calves.

Table 1. Description of treatments and blood parameters at 24 h of age in calves fed colostrum by nipple bottle, esophageal feeder, or a combination of both.

	Treatment					
Item	1	2	3	4	5	SEM
Number of calves	13	6	7	7	7	-
Amount fed, L						
Nipple bottle	3.80	2.84	1.89	0.95	0.00	----
Esophageal feeder	0.00	0.95	1.89	2.84	3.80	----
IgG_1, g/L	22.3	23.4	24.2	22.8	24.6	1.64
IgG_2, g/L	1.1	1.2	1.4	1.2	1.2	0.08
Total IgG, g/L	23.4	24.5	25.6	24.0	25.8	1.69
TSP, g/L	63.0	66.0	65.0	66.0	63.0	1.50
AEA, %	35.4	34.6	35.5	31.8	35.2	2.73

Key Words: immunoglobulin, serum protein, esophageal feeder

M35 High bacterial concentration in colostrum does not interfere with IgG absorption in neonatal dairy bull calves. J. A. Elizondo-Salazar*[1,2] and A. J. Heinrichs[1], [1]*The Pennsylvania State University, University Park*, [2]*Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias. Universidad de Costa Rica*.

The objective of this study was to determine the effects of feeding heat-treated colostrum and unheated colostrum with differing bacterial counts on passive transfer of immunity in neonatal calves. First milking colostrum with > 50 g IgG/L was collected from Holstein cows. After pooling colostrum, one third was transferred to 1.89-L plastic containers and frozen at -20°C, (unheated-low bacteria); one third was heat-treated at 60°C for 30 min, transferred to 1.89-L plastic containers, then frozen at -20°C, (heat-treated). The final third was transferred to 1.89-L plastic containers and stored at room temperature (20°C) for bacteria to grow during 24 h (unheated-high bacteria). Colostrum was then placed into a freezer at -20°C until needed for feeding. Samples of all colostrum were examined for standard plate count, coagulase-negative staphylococci count, environmental streptococci count, coliform count, gram-negative noncoliform count, Streptococcus agalactiae count, and Staphylococcus aureus count. Thirty Holstein bull calves weighing ≥ 30 kg at birth were randomly enrolled into 1 of the 3 treatment groups (in blocks of 3). Calves were separated from their dams at birth before suckling occurred. For the first feeding, 3.8 L of colostrum were fed via esophageal feeder between 1.5 to 2 h of age. Blood samples were collected at birth, 24 and 48 h of age to determine serum IgG and total protein (STP) concentrations. Batch heat treatment of colostrum resulted in lower bacteria concentration while maintaining colostral IgG concentration. Calves fed heat-treated colostrum had greater (P<0.01) total protein, serum IgG, and apparent efficiency of absorption (AEA) at 24 h (STP = 62.5 g/L; IgG = 26.7 g/L; AEA = 43.9%) compared with calves fed unheated-low bacteria colostrum (STP = 57.0 g/L; IgG = 20.2 g/L; AEA = 35.4%) or unheated-high bacteria colostrum (STP = 56.2 g/L; IgG = 20.1 g/L; AEA = 32.4%). In this study, a high load of naturally occurring bacteria in colostrum did not interfere with IgG absorption, and heat treating colostrum significantly improved IgG absorption.

Key Words: immunoglobulin, passive transfer of immunity, apparent efficiency of absorption

M36 Abrupt weaning alters leukocyte subsets and functional activity of granulocytes in beef calves. E. M. Lynch*[1,2], B. Earley[1], M. McGee[3], and S. Doyle[2], [1]*Teagasc, Animal Bioscience Centre, Dunsany, Co. Meath, Ireland*, [2]*Department of Biology, National University of Ireland, Maynooth, Co Kildare*, [3]*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*.

The objective was to determine the effect of abrupt weaning on leukocyte subsets and functional activity of granulocytes using 16 beef calves (mean age and weight (s.d.): 227 (18.2) days (d) and 310 (31.1) kg, respectively) that previously grazed with their dams. At the end of the grazing season, calves were either abruptly weaned (AW, n=8) on d 0, housed in a slatted floor shed and offered grass silage *ad libitium* or not weaned (control) (NW, n=8), housed with their dam and offered the same diet. Blood samples were collected by jugular venipuncture at d -7, 0, 2, 7 and 14. Neutrophil, lymphocyte and monocyte number were determined. Lymphocyte subsets ($CD4^+$, $CD8^+$, $WC1^+$), MHC Class II^+ cells, $G1^+$ neutrophils, neutrophil CD62L (L-selectin) surface expression and the phagocytic and oxidative burst activity of granulocytes (neutrophils and monocytes) were characterised by flow cytometry. On d 2, neutrophil number increased (P<0.001) and lymphocyte number decreased (P<0.01) in AW compared with d 0, but did not differ (P>0.05) in NW during the study. Neutrophil CD62L surface expression, neutrophil phagocytic activity and % $WC1^+$ lymphocytes decreased (P<0.05) on d 2 compared with d 0 in AW and NW but the decrease was greater (P<0.001) in AW. Monocyte phagocytic activity decreased (P<0.05) on d 2 to 14 in AW but did not differ (P>0.05) in NW compared with d 0. Monocyte number, neutrophil and monocyte oxidative burst activity did not differ (P>0.05) in AW and NW during the study. On d 2, the % $CD4^+$ and $CD8^+$ lymphocytes decreased (P<0.001) in AW but remained unchanged (P>0.05) in NW compared with d 0. The % MHC Class II^+ cells and $G1^+$ neutrophils increased (P<0.01) on d 2 in AW and NW compared to d 0 but the increase was greater (P<0.001) in AW. In conclusion, abrupt weaning resulted in neutrophilia however the potential of neutrophils to traffic effectively and the ability of granulocytes to phagocytose efficiently were impaired. Together with the decreased lymphocyte number and larger changes in lymphocyte subsets and MHC Class II^+ cells, this suggests a greater transitory reduction in immunity in AW than NW beef calves.

Key Words: weaning, leukocytes, phagocytosis

Bioethics

M37 Measuring and managing for sustainability in dairy production: A stewardship scorecard. G. W. C. Clark*, A. A. Whitman, and J. M. Hagan, *Manomet Center for Conservation Science*, *Brunswick, ME*.

The dairy industry faces huge challenges as consumer values change, investors concerns extend beyond the financial bottom line, and society's expectations of agriculture are being transformed. We are developing a stewardship scorecard that will provide an objective, numerical, science-based assessment of the condition of social, economic and environmental services on farms. Our goal is to develop a tool that allows producers, processors and consumers to assess farm stewardship of dairy products. The key scorecard components and their science-based indicators are being selected in consultation with dairy farmers and stakeholders (including consumers). Indicator will be screened and selected to meet five criteria: practicality, utility, scientific merit, efficiency, and social relevance. The scorecard will be tested by applying it to 25 dairy farms in the U.S. After the testing phase, the scorecard will refined based on (1) the field test results, (2) farmer surveys, (3) stakeholder meeting s, and (4) scientific peer review. The final version will be distributed with a user's handbook that describes how to apply the scorecard and ways that farmers can change their scores and communicate their performance to stakeholders and processors. The scorecard will be another tool for fostering an awareness of farm stewardship issues.

Key Words: sustainability, scorecard, stewardship

Breeding and Genetics: Beef Breeding, Poultry Breeding, and Genetics of Disease

M38 Milk production and composition during the first 4 months of lactation of Hereford (HH), Angus (AA) and F1 crosses grazing on native pastures Uruguay. A. Espasandin*[1], A. Casal[2], A. Graña[2], V. Gutiérrez[2], and M. Carriquiry[1], [1]*School of Agronomy, UDELAR*, *Montevideo , Uruguay*, [2]*School of Veterinary, UDELAR*, *Montevideo, Uruguay*.

The objective of this study was measure milk yield and composition in 24 cows (8 HH, 8 AA, and 8 F1) once a month from 30 to 120 days post-partum (DPP), blocked by calving date and body condition at calving. Cows grazed together on native pasture paddock with an average forage mass available of 2400 kg DM/ha. In the morning, cows were drained and separated from their calves and after 6 hours were milked with a portable machine with previous injection of oxytocin (10 IU/cow). Milk was weighted and sampled for chemical composition analysis (protein, fat and lactose. A mixed model was applied to analyze milk yield and composition including cow and calf breed and calf sex as fixed effects, DPP as a covariate and cow within breed as random effect. Means were considered to differ when $P \leq 0.05$. Milk yield (3.8±0.6, 5.4±0.8, 4.4±1.1 kg/d for HH, AA, and F1, respectively), and fat (4.2±0.5, 2.5±0.6, and 5.0±0.9% for HH, AA, and F1, respectively) and lactose (4.9±0.1, 5.2±0.1, 4.9±0.1% for HH, AA, and F1, respectively) contents did not differ among cow breeds but protein percentage was greater from HH and F1 than for AA cows (3.2±0.1, 2.6±0.2, and 5±0.2% for F1, HH, and AA respectively). Milk yield was greater during the first 60 DPP and decreased thereafter (5.4, 5.2, 3.9, and 3.5 kg/d ±0.4 for 30, 60, 90, 120 DPP, respectively). Protein and lactose contents were affected by month of lactation, as protein was less and lactose content was greater during the first 60 DPP (3.0, 3.0, 3.3, 3.2% ±0.07 and 5.2, 5.0, 4.9, 4.9% ±0.05 for 30, 60, 90, 120 DPP, for protein and lactose contents, respectively). Fat percentage was not affected by DPP and averaged 3.8±0.04% during the first 4 months of lactation. Tendencies observed for milk production and composition along lactation were similar to the reported in literature for beef and dairy cattle. Cow breed did not affect milk production and composition except for protein in which F1 and HH showed superiority.

Key Words: milk yield, beef cattle, lactation

M39 Genetic relationships of monounsaturated fatty acid with image analysis traits in Japanese Black cattle. Y. Nakahashi*[1], T. Kato[2], M. Nakamachi[1], N. Murasawa[1], Y. Hamasaki[1], S. Hidaka[1], and K. Kuchida[1], [1]*Obihiro University of A & VM*, *Obihiro, Hokkaido, Japan*, [2]*Tokachi Federation of Agricultural Cooparatives*, *Obihiro, Hokkaido, Japan*.

Monounsaturated fatty acids (MUFA) in beef cattle were investigated in large numbers due to the positive correlation with the flavor of marbling. We have studied MUFA and image analysis traits in order to clarify relations between MUFA and marbling shape in the rib eye. However, there are few studies concerning the genetic parameter of MUFA and no investigations on the correlations of MUFA with image analysis traits. The objective in this study was to analyze the relationships of MUFA with image analysis traits genetically. Carcass data were collected from Japanese Black cattle (n=1,447) that shipped to a meat processing plant in Hokkaido, Japan. Fat tissues were sampled from the rib eye of every carcass and the fatty acid compositions were analyzed using gas chromatography. Image analysis was performed to calculate the marbling percent (MP), fineness index of marbling (FIM) in rib eye and so on. Using single/multiple trait animal models, genetic analysis was conducted to estimate the heritabilities of all traits and the genetic correlations of MUFA with the image analysis. The heritability of MUFA was estimated as 0.83, indicating the possibility of improvement of the MUFA of Japanese Black. Genetic correlation of MUFA with MP was 0.20, showing a preferable relationship in which increasing MP causes improvement of MUFA. On the other hand, an undesirable correlation between MUFA and FIM was recognized (-0.09), suggesting that the improvement of MUFA is stifled by the number of small marbling flecks preferred in Japanese Black cattle. Therefore, in order to improve MUFA while keeping the fineness of the marbling in rib eye, planned breeding programs considering sire attributes could be effective by using image analysis.

Key Words: genetic parameter, image analysis, MUFA

M40 Genetic analysis of growth traits considering the average numerator relationship matrix and a hierarchical Bayes model for Nellore cattle. L. Shiotsuki*[1], F. F. Cardoso[2], J. A. II V. Silva[3], and L. G. Albuquerque[1], [1]*Universidade Estadual Paulista*, *Jaboticabal, Sao Paulo, Brazil*, [2]*Embrapa Pecuaria Sul*, *Bage, Rio Grande do Sul, Brazil*, [3]*Alta Genetics*, *Uberaba, Minas Gerais, Brazil*.

The aim of the present work was to evaluate two statistical models to predict the genetic merit of animals with uncertain paternity, a linear mixed model based on average numerator relationship matrix (ANRM)

and a hierarchical animal model (HIER), that considers the uncertainty in paternity attributions of offspring of multiple-sires. Genetic parameter estimates for post-weaning gain (PWG) and yearling weight (YW) obtained with these two models were compared, based on 62,212 records of Nellore animals, offspring of 581 bulls and 27,743 cows. The pedigree data set included information from 75,088 animals. Both models included fixed effects of animal age and age of dam at calving (2-16 years) as linear and quadratic covariables and, as random the animal direct genetic and contemporary groups effects. For YW, maternal genetic and permanent environmental random effects were also included in the models. Deviance information criterion (DIC) and a deviance based on conditional predictive ordinates (DCPO) were used to assess model fit. For PWG, DIC values were 531,166 (ANRM) and 531,033 (HIER) and DCPO values were 522,262 (ANRM) and 522,022 (HIER). For YW, these values were 548,931 and 547,831 (DIC) and 532,536 and 530,366 (DCPO) for ANRM and HIER, respectively. Therefore, for both traits, the HIER was the best fitting model. Postweaning direct heritability estimates obtained with both models were virtually the same (0,20±0,01). For YW, direct heritability estimates were 0.38±0.02 (ANRM) and 0,44±0.02 (HIER) and maternal heritability estimates were 0.12±0.02 (ANRM) and 0.03±0.01 (HIER), showing a different partition of genetic effects in its direct and maternal components between these models. Moreover, the total heritability for YW was 0.37±0.02 (HIER) and 0.31±0.02 (ANRM). These results indicate that selection for growth in this population will achieve faster genetic progress when based on YW and on HIER.

Key Words: growth traits, uncertain paternity, Zebu

M41 Estimates of genetic parameters using random regression on B-spline functions for weights from birth to mature in Nellore cattle. A. A. Boligon*[1], L. G. Albuquerque[1], M. E. Z. Mercadante[2], and R. B. Lobo[3], [1]*Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal, São Paulo, Brazil*, [2]*Instituto de Zootecnia, Estação Experimental de Zootecnia de Sertãozinho, Sertãozinho, São Paulo, Brazil*, [3]*Faculdade de Medicina de Ribeirão Preto, USP, Ribeirão Preto, São Paulo, Brazil*.

The aim of this study was to estimate (co)variance functions using random regression on B-splines for birth to mature weight. A total of 82,064 records from 8,145 females beloning to Nellore Cattle Breeding Program were analyzed. Models included additive direct and maternal effects, and animal and maternal permanent environmental effects as random. Contemporary group was defined including animals born on the same farm, year and season of birth, and belonging to the same group of age at recording (birth and every 45 days of age). Fixed effects were contemporary group and the covariables age of dam at calving (linear and quadratic effect) and orthogonal Legendre polynomials of animal age (cubic regression). Random effects were modeled using B-spline functions, considering different combinations of linear, quadratic and cubic polynomials for each individual segment. Residual effects were modeled using five age classes (0; 1-216; 217-660; 661-960 and 961-2920 days of age). Up to seven knots (six segments) were used for modeling animal additive direct and permanent environmental effects. For maternal genetic and environmental effects only one segment, with two knows in the extremity of the curve, was considered. Fifteen models, with 17 to 81 parameters, were used. A model including quadratic B-spline function with three segments for direct and permanent environmental effects, and one segment for maternal genetic and permanent environmental effects fitted best (47 parameters). Estimates of (co)variances obtained with the B-spline function were similar to that obtained using a multitrait (9 traits) and a random regression on Legendre polynomials for all random effects. Direct heritability estimates ranged from 0.27 to 0.43. The largest estimates of maternal heritability were for weights close to 240 days of age. The genetic correlation estimates between weights from birth to 8 years of age were moderate to high (0.32 to 0.95). Selection for weight at any age will promote changes in female mature weight. Random regression on B-splines of age can be used for genetic evaluation of growth in beef cattle.

Key Words: beef cattle, growth traits, random regression

M42 Estimation of genetic parameters for weights, scrotal circumference and testicular volume in Nellore cattle. A. A. Boligon*[1], L. G. Albuquerque[1], J. A. V. Silva[2], R. C. Sesana[1], and J. B. Junqueira[1], [1]*Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal, São Paulo, Brazil*, [2]*Alta Genetics Brasil LTDA, Uberaba, Minas Gerais, Brazil*.

Data from 129,575 Nellore cattle born between 1993 and 2006, belonging to the Jacarezinho cattle raising farm, were used to estimate genetic parameters for scrotal circumference measured at 9 (SC9), 12 (SC12) and 18 (SC18) months of age and testicular volume measured at the same ages (TV9, TV12 and TV18) and to determine their correlation with weaning weight (WW) and yearling weight (YW), in order to provide information for the definition of selection criteria in beef cattle. Estimates of (co)variance components were calculated by restricted maximum likelihood method applying an animal model in multiple-trait analysis. The following heritability estimates and their respective standard errors were obtained for WW, YW, SC9, SC12, SC18, TV9, TV12 and TV18: 0.33±0.02, 0.37±0.03, 0.29±0.03, 0.39±0.04, 0.42±0.03, 0.19±0.04, 0.26±0.05 and 0.39±0.04, respectively. Genetic correlations between the growth traits and scrotal circumference measures were positive and of low to moderate magnitude, ranging from 0.23±0.04 to 0.38±0.04. On the other hand, high genetic associations were estimated between scrotal circumference and testicular volume at different ages (0.61±0.04 to 0.86±0.04). Correlation estimates between SC and TV measured at the same ages were 0.71±0.03, 0.75±0.04, 0.86±0.04, for 9, 12 and 18 month of age, respectively. Selection to increase scrotal circumference should result in higher WW, YW and testicular volume. In conclusion, in view of the difficulty in measuring testicular volume there is no need to change the selection criterion from scrotal circumference to testicular volume in Zebu breeds′ breeding programs.

Key Words: beef cattle, genetic correlation, heritability

M43 Heritabilities, genetic correlations, and genetic trends for age at first calving and calving intervals in a Colombian Blanco Orejinegro-Angus-Zebu cattle population. O. D. Vergara[1,3], M. A. Elzo*[2], and M. F. Ceron-Muñoz[1], [1]*University of Antioquia, Medellín, Colombia*, [2]*University of Florida, Gainesville,*, [3]*University of Córdoba, Monteña, Colombia*.

Age at first calving and calving interval are traits that have substantial impact on production costs of beef cattle operations in Colombia. However, assessment of genetic variation and evaluation of animals in multibreed populations for these traits is scant. Thus, the objectives of this research were to estimate genetic parameters and trends for age at first calving (AFC), interval between first and second calving (CI1), and interval between second and third calving (CI2) in a Colombian beef cattle population composed of Blanco Orejinegro, Angus, and Zebu

straightbred and crossbred animals. Data were analyzed using multiple trait mixed model procedures. Variance components and genetic parameters were estimated by Restricted Maximum Likelihood. The 3-trait model included the fixed effects of contemporary group (year-season of calving-sex of calf; sex of calf for CI1 and CI2 only), age of cow at calving (CI1 and CI2 only), breed direct genetic effects, and individual heterosis. Random effects were cow direct genetic and residual. Relationships among cows were accounted for. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.15 ± 0.13 for AFC, 0.11 ± 0.06 for CI1, and 0.18 ± 0.11 for CI2. Low heritabilities for AFC, CI1, and CI2 suggest that nutrition and reproductive management should be improved to allow fuller expressions of these traits. Correlations between additive direct genetic effects for AFC and CI1 (0.33 ± 0.41) and for AFC and CI2 (0.40 ± 0.36) were medium and favorable, suggesting that selection of heifers for AFC would improve calving interval. Cow direct genetic AFC, CI1, and CI2 yearly means from 1989 to 2004 showed negative trends, suggesting that some selection for these traits existed in this population during these years.

Key Words: cattle, reproduction, trends

M44 Genetic parameters and genetic trends for pre and postweaning growth in a Colombian Blanco Orejinegro-Romosinuano-Angus-Zebu cattle population. O. D. Vergara[1,3], M. A. Elzo*[2], and M. F. Ceron-Muñoz[3], [1]*University of Cordoba, Monteria, Colombia*, [2]*University of Florida, Gainesville*, [3]*University of Antioquia, Medellin, Colombia*.

Genetic parameters and trends for weaning weight adjusted to 240 d of age (WW240), and weight gain from weaning to 24 mo of age (GW730) were estimated in a Colombian beef cattle population composed of Blanco Orejinegro, Romosinuano, Angus, and Zebu straightbred and crossbred animals. Data were analyzed using multiple trait mixed model procedures. Variance components and genetic parameters were estimated by Restricted Maximum Likelihood. The 2-trait model included the fixed effects of contemporary group (herd-year-season-sex), age of dam (WW240 only), breed direct genetic effects, breed maternal genetic effects (WW240 only), individual heterosis, and maternal heterosis (WW240 only). Random effects for WW240 were calf direct genetic, dam maternal genetic, permanent environmental maternal, and residual. Random effects for GW730 were calf direct genetic and residual. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.20 ± 0.003 for WW240 and 0.32 ± 0.004 for GW730. Maternal heritability was 0.14 ± 0.002 for WW240. Low direct and maternal preweaning heritabilities suggest that nutrition should be improved to allow fuller expressions of calf direct growth and cow maternal ability. The genetic correlation between direct and maternal additive effects for WW240 was negative (-0.42 ± 0.009). The near zero (-0.04 ± 0.009) correlation between additive direct genetic effects for WW240 and GW730 suggested that genes affecting preweaning and postweaning growth may differ in this population. Calf, sire, and dam weighted yearly means showed negative trends for direct WW240 and GW730. Maternal WW240 showed near zero trends during these years. Trends for calf direct WW240 and GW730 followed sire trends closely, suggesting that more emphasis was placed on choosing sires than on dam replacements.

Key Words: beef cattle, genetic parameters, genetic trends

M45 Genotype by environment interaction in Nellore cattle for 450 day weight. M. G. Dib*[1], I. D. P. S. Diaz[2], F. R. de Araujo Neto[2], H. N. de Oliveira[1,2], R. B. Lobo[3], and L. A. F. Bezerra[3], [1]*FMVZ-UNESP, Botucatu, SP, Brazil*, [2]*FCAV-UNESP, Jaboticabal, SP, Brazil*, [3]*FMRP-USP, Ribeirao Preto, SP, Brazil*.

The object of the current study was to determine if there was a genetic by environmental interaction between the Brazilian states of Sao Paulo and Mato Grosso do Sul for the trait of 450 day weight. The data included weights from 42,160 progeny of 24,476 cows and 1,244 sires recorded from 1991 through 2006. Variance components were estimated using a multiple trait animal model in a Bayesian framework considering weights in the different locations as different traits. The model included fixed effects of contemporary group and effects of animal and residual as random. The genotype by environment interaction was verified through the genetic correlations. Results indicate that the genetic and residual components of variance differ between the two states. Estimates of heritability (SD) for Sao Paulo and Mato Grosso do Sul were 0.4367 (0.025) and 0.3634 (0.019), respectively. The genetic correlation (SD) was 0.9294 (0.031), which does not suggest an important genotype by environment interaction for 450 day weight.

Key Words: 450 day weight, genotype by environment interaction, Nellore cattle

M46 Random regression analyses using B-spline functions to model growth from birth to adult age in Canchim cattle. F. Baldi*[1], L. G. Albuquerque[1], and M. M. Alencar[2], [1]*Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal (SP), Brazil*, [2]*Embrapa Pecuária Sudeste, São Carlos (SP), Brazil*.

The objective of this work was to use random regression models on B-splines functions, to estimate covariance functions for weights from birth to adult age in Canchim cattle. Data comprised 49,011 weight records on 2,435 females belonging to Southeast - Embrapa Cattle. Fixed effects of contemporary groups (year and month at birth and at weighing), age of dam at calving (quadratic) and a cubic regression on Legendre polynomials of animal age covariable were included in the model. A random regression on b-splines functions of age at recording was applied to model animal and maternal genetic and permanent environmental effects. Residual variances were considered heterogeneous with 4 classes. The same data set was analyzed with a multi-trait model for weights at standard ages (birth, weaning, 12 , 18 , 24 and 30 months of age, and at 6 years of age). Genetic direct and maternal and maternal permanent environmental effects were considered as random for weights from birth to 24 months of age. For weights after this age only genetic direct effect was considered. A total of twenty analyses, considering linear, quadratic and cubic b-spline functions and up to nine knots, were carried out. Spline functions of the same order were considered for all random effects. A model fitting quadratic b-spline functions, with four knots or three segments for direct genetic and animal permanent environmental effects and two knots for maternal genetic and permanent environmental effects, was the most adequate to describe the covariance structure of the data. Direct and maternal heritability estimates obtained with random regression models were similar to those obtained by multi-trait models, ranging from 0.19 to 0.43 and from to 0.01 to 0.05, respectively. Similar direct and maternal genetic correlation estimates between weights from birth to adult age were obtained by random regression and multi-trait models, ranging from 0.42 to 0.97 and from to 0.14 to 0.96. Random regression models

using b-spline functions as base functions were adequate to describe the covariance structure of the data.

Key Words: covariance function, genetic parameters, piece-wise polynomials

M47 Genetic parameter estimates for growth traits in Canchim cattle using random regression models. F. Baldi*[1], M. M Alencar[2], and L. G. Albuquerque[1], [1]*Faculdade de Ciências Agrárias e Veterinárias, UNESP*, *Jaboticabal, São Paulo, Brazil*, [2]*Embrapa Pecuária Sudeste*, *São Carlos, São Paulo, Brazil*.

The objective of this work was to estimate covariance functions, using random regression models on Legendre polynomials of age, for weights from birth to adult age in Canchim cattle. Data comprised 49,011 weight records on 2,435 females belonging to Southeast - Embrapa Cattle. The model of analysis included fixed effects of contemporary groups (year and month at birth and at weighing) and age of dam as quadratic covariable. Mean trends were taken into account by a cubic regression on orthogonal polynomials of animal age. Animal and maternal genetic effects and animal and maternal permanent environmental effects were modeled by random regression on Legendre polynomials of age at recording. Residual variances were modeled by a step function with 4 classes. The same data set was analyzed with a multi-trait model for weights at standard ages (birth, weaning, 12, 18, 24 and 30 months of age, and at 6 years of age). Genetic direct and maternal and maternal permanent environmental effects were considered as random for weights from birth to 24 months of age. For weights after this age only genetic direct effect was considered. A total of 12 random regression models with order from two to seven, were used to model the random effects. The model with quadric, cubic, quintic and linear polynomial degrees for direct and maternal genetic and animal and maternal permanent environmental effects fitted the data best. Estimates of direct and maternal heritabilities obtained with random regression models agreed with those obtained by multi-trait model, ranging from 0.19 to 0.38 and from 0.02 to 0.05, respectively. Direct and maternal genetic correlation estimates between weights from birth to adult age obtained by random regression, ranging from 0.39 to 0.92 and from 0.10 to 0.97, respectively, and were similar to those from multi-trait model. Random regression models on Legendre polynomials are well capable to describe the covariance structure of the data.

Key Words: covariance functions, growth curve, orthogonal polynomials

M48 Performance group in G×E study for genetic evaluation of growth in Brazilian Nellore. L. O. C. Silva[1,2], S. Tsuruta*[1], J. K. Bertrand[1], A. Gondo[2], L. A. Josahkian[4], P. R. C. Nobre[4], and A. N. Rosa[2], [1]*University of Georgia*, *Athens*, [2]*EMBRAPA*, *Campo Grande, MS, Brazil*, [3]*CNPq*, *Brasilia, DF, Brazil*, [4]*ABCZ*, *Uberaba, MG, Brazil*.

The objective of this study was to analyze the importance of G×E interaction when evaluating Nellore in Brazil. Data included 588,461 weaning weights (WW) and yearling weights (YW) from 1,335,354 animals. Data were collected from 1979 to 2007 by Zebu Cattle Brazilian Association (ABCZ). Records from grazing were 97% of the total. A six-trait model was used that considered WW and YW within three performance groups (PG, 1-low; 2-medium; 3-high performance), including 1/3 of the contemporary group (CG) each. PG was created based on the averages of adjusted WW and YW for CG. CG was defined by sex, farm, year, season, and feeding management. Fixed effects besides CG included age of the animals at weighing within CG (linear covariable) and age of dams at calving (linear and quadratic). Random effects in the model were direct and maternal. Variance components of WW and YW were estimated with Gibbs sampling using five exclusive random samples with 60,000 animals each. The first 50,000 Gibbs samples were discarded as burn-in and the following 250,000 were used to calculate posterior means and SD of (co)variances. Prediction of breeding values and accuracy were also obtained. The ratios PG3/PG2 and PG2/PG1 were 1.15 for WW and 1.2 for YW. Direct and maternal heritabilities for WW (0.18±.01; 0.24±.01) and YW (0.29±.01; 0.14±.01) within each PG were similar with results from other Zebu breeds. Direct genetic correlations between different PGs for WW and YW were around 0.86±.03. Maternal correlations were close to the direct ones. These results showed that even in different PGs, similar sets of genes are responsible for expression of WW and YW. Rank correlations between PG1 and PG3 for direct and maternal effect for sires with accuracy ≥ 0.40 were 0.97 and 0.94 for WW and 0.96 and 0.85 for YW. Results indicate no substantial re-ranking of sires in environments with different level of production.

Key Words: Zebu beef cattle, growth weight, G×E interaction

M49 Residual feed intake and reproductive performance of heifers sired by high or low RFI EBV bulls. J. M. Bormann*[1], D. W. Moser[1], T. T. Marston[2], and K. C. Olson[1], [1]*Kansas State University*, *Manhattan*, [2]*University of Nebraska*, *Lincoln*.

Residual feed intake (RFI) is the difference between an animal's actual feed intake and its predicted intake based on its body weight and growth rate. The objective of this study was to determine differences in performance and fertility between heifers sired by high or low RFI EBV bulls. Bulls with low or high genetic merit for RFI were selected from the Australian Angus Association sire summary and mated to Angus cross commercial cows at the Kansas State University Cow-Calf Unit in 2006. The average RFI EBV for the low RFI (efficient) and high RFI (inefficient) bulls were -0.55 kg (n = 4) and 0.27 kg (n = 5). Heifers (n = 49) were sent to a commercial bull test station for a feed intake and gain test of 57 days. Heifers were allowed *ad libitum* intake of a high roughage, complete diet (approximately 1.05 Mcal/kg ME). Biweekly body weights were collected and used to calculate mid-test body weight and average daily gain. Actual feed intake was regressed on mid-test metabolic body weight and average daily gain to calculate an expected feed intake for each heifer. RFI was calculated by subtracting the expected intake from the actual intake. Heifers were synchronized and bred by AI one time followed by natural service. LSMeans for heifers sired by low and high RFI bulls were 0.11 kg and -0.09 kg (P = 0.62) for RFI, 11.65 kg and 11.46 kg (P = 0.65) for dry matter intake, 18.43 kg/kg and 14.86 kg/kg (P = 0.47) for feed conversion ratio, and 0.72 kg/day and 0.67 kg/day (P = 0.49) for average daily gain. Weaning weight, on-test weight, and off-test weight were also similar between groups (P > 0.05). There was no difference between groups in first service or overall pregnancy rate (P > 0.05). Heifers in this study were being developed at a relatively low rate of gain. Genetic differences in RFI calculated in growing bulls may not have been expressed on the lower plane of nutrition of these developing heifers. There appeared to be no detrimental effect of selection for RFI on reproductive performance of heifers.

Key Words: beef, residual feed intake, breeding value

M50 Association between carcass and meat quality traits, and phenotypic residual feed intake, breed composition, and temperament in Angus-Brahman multibreed cattle. M. A. Elzo*[1], D. D. Johnson[1], D. G. Riley[2], G. R. Hansen[3], G. C. Lamb[4], R. O. Myer[4], J. G. Wasdin[1], and J. D. Driver[1], [1]*University of Florida*, *Gainesville*, [2]*USDA-ARS STARS*, *Brooksville, FL*, [3]*North Carolina State University*, *Plymouth*, [4]*North Florida Research and Education Center*, *Marianna, FL*.

Increasing production costs emphasize the need to identify and multiply cattle that are efficient at converting feed into beef of desirable quality. The objective was to study the association between 6 carcass and 6 meat quality traits and breed group (Angus (A), Brahman (B), Brangus, ¾ A 1/4 B, 1/2 A 1/2 B, and 1/4 A 3/4 B), residual feed intake (RFI) group (high: RFI > 0.85 kg; medium: -0.85 kg ≤ RFI ≤ 0.85 kg; low: RFI < -0.85 kg; SD = 1.7 kg), and exit velocity (EV) in 170 steers born in 2006 and 2007. Carcass traits were hot carcass weight (HCW), dressing percent (DP), longissimus muscle area (LMA), fat thickness (FT), kidney, pelvic, and heart fat (KPH), and marbling score (MS). Meat quality traits were Warner-Bratzler shear force (SF), tenderness score (TS), juiciness (JU), flavor (FL), thaw loss (TL), and cooking loss (CL). Data for EV and RFI were from 70-d postweaning feeding trials at a GrowSafe automated feeding facility. Calves were finished at a feedlot in Texas and commercially slaughtered at roughly 14 mm of FT. Carcass data were taken at the slaughter facility, and meat quality data measured at the Florida Meat Processing Lab. Traits were analyzed using single-trait mixed models. Fixed effects were contemporary group (year-pen), RFI group, age of calf, B fraction of calf, calf heterozygosity, and mean EV. Random effects were sire and residual. High RFI steers had smaller LMA ($P < 0.005$) than low RFI steers. High and medium RFI steers had higher ($P < 0.0002$) MS than low RFI steers. Brahman had lighter HCW ($P < 0.0006$), smaller LMA ($P < 0.0001$), thinner FT ($P < 0.02$), lower MS ($P < 0.0001$), higher SF ($P < 0.0003$), and lower TS ($P < 0.0001$) than Angus. Exit velocity was non-significant for either carcass or meat quality traits.

Key Words: carcass, meat quality, feed intake

M51 Temperature and humidity as criteria of between states differences in beef cattle growth rate. M. Lukaszewicz[1,2], J. L. Williams*[1], J. K. Bertrand[1], and I. Misztal[1], [1]*University of Georgia*, *Athens*, [2]*Polish Academy of Sciences*, *Jastrzebiec, Poland*.

The division of the US into regions distinguishes between northern ("cold") and southern ("hot") regions, while from East to West three zones are defined (east, mid-west and west). The latter corresponds with humidity distribution across the US. Neither classification perfectly matches the accepted region division leaving, within regions, states that differ climatically from the others. On the other hand GxE studies in cattle address the problem only from the temperature (heat) point of view. The aim of this analysis was to find out whether GxE interaction can only be attributed to temperature differences or if humidity affects beef cattle growth as well. Data were provided by the American Angus Association. Only states which could have been attributed a class of temperature (lower or higher than 55o F annual average) and a class of humidity (lower or higher than 65%) were considered. That excluded states like Kansas, Kentucky, Oregon, Washington, and both Dakotas as either they were spread over two temperature or over two humidity zones. Post weaning gain was highest (169kg, n=680741) in states described as cold/humid, and lowest (146kg, n=420570) in hot/humid ones. Intermediate gains (ca 158kg, n=1077665) were found in hot/dry and cold/dry states. Thus, the difference in gain associated with temperature is only due to high humidity. Records in the 3 groups of states were treated as different traits. Three-trait model included the effects of contemporary group (sex, age, dam's age) as yearlings and genetic additive effect. Estimates were obtained with Gibbs sampling on 1,477,563 records after removing records with missing information. Heritabilities were 0.20, 0.18, 0.21 (se 0.01 to 0.02) in cold/humid (NE), hot/humid (SE), and "dry" (W) states, respectively. Genetic correlations were all around 0.75 (se=0.02); there may be moderate re-ranking among the regions. Three breeding value estimates could be needed if sires are to be used nationwide.

Key Words: post weaning gain, Angus, climate G×E

M52 Multiple-trait genetic analysis of weight at week 8, age at sexual maturity and initial egg weight in Iranian indigenous chickens. H. Farhangfar*, S. M. Hosseini, and M. E. Navidizadeh, *Birjand University*, *Birjand, Iran*.

A multivariate animal model was used to estimate variance and covariance components as well as genetic parameters of weight at week 8, age at sexual maturity and initial egg weight for Iranian indigenous chickens. Data set consisted of 3822 records collected from an indigenous chicken flock. The total of progeny was 3822 representative of 179 sires and 1106 dams respectively. In the model, fixed environmental factors of generation (at two levels) and hatch number (at eight levels) along with random direct additive genetic effect were included. The average weight at week 8 (W8), age at sexual maturity (ASM) and initial egg weight (at first week of laying, EW1) were 495 g, 160 d and 39.3 g respectively. The animal model was fit using DMU package for obtaining restricted maximum likelihood estimates of variance and covariance components. For all traits, design matrices were the same. Additive genetic variance components for W8, ASM and EW1 were 1774, 34.46 and 4.71 respectively while environmental variance components were 2234, 81.91 and 18.69 respectively. Heritability estimates of W8, ASM and EW1 were found to be 0.44, 0.3 and 0.2 respectively. Additive genetic correlation between W8 and ASM was -0.03 while it was positively correlated with EW1 (0.23). A positive genetic correlation was found between ASM and EW1 (0.42). At environmental level, W8 were negatively correlated with ASM (-0.14) and EW1 (-0.0008). ASM had a positive environmental correlation with EW1 (0.4). Positive phenotypic correlations were found between W8 and EW1 (0.07) and between ASM and EW1 (0.4) while W8 was negatively correlated with ASM (-0.1).

Key Words: Iranian indigenous chickens, genetic parameters, animal model

M53 Comparative analyses of some growth traits of straight-runs and separate sex reared broilers. O. T. F. Abanikannda[1], A. O. Leigh[1], M. O. Akinsola[1], M. Orunmuyi[2], O. N. Coker[3], and K. A. Binuyo*[1], [1]*Lagos State University*, *Ojo - Lagos, Nigeria*, [2]*Ahmadu Bello University*, *Zaria, Kaduna State, Nigeria*, [3]*S & D Farms Nigeria Limited*, *Odeda, Ogun State, Nigeria*.

Feeds and feeding are the largest sources of expenditure in commercial broiler production. The need to cut down on the cost of feed / feeding, by reducing wastages and improving feed conversion efficiency of the birds impels an investigation into some genetic and non-genetic factors affecting some growth traits of the birds. This study aims at evaluating growth traits of broiler birds reared as straight-runs (mixed) or reared separately in sex demarcated lots. A total of sixty broiler birds derived from three commercial strains (Anak, Marshall and Ross) were stud-

ied, with each strain contributing twenty birds comprising ten each for male and female. However, two of the Anak male birds died two weeks into the experiment. Measurements were taken over a period of eight weeks up to the point when the birds were slaughtered. Three traits of economic importance studied were initial weight, slaughter weight and average daily gain (ADG).

Key Words: mixed sex, separate sex, growth traits

M54 Analysis of androgen receptor gene in dairy bulls. C. Foresta[2], A. Garolla[2], D. Zuccarello[2], and M. Cassandro*[1], [1]*University of Padova*, *Agripolis, Legnaro (PD), Italy*, [2]*University of Padova*, *Padova, Italy*.

Aim of this study was to identify the complete sequence of the transcript of the androgen receptor (AR) gene in cattle. At present, no information on the whole sequence of the AR gene is available, both in the NCBI (www.ncbi.nlm.nih.gov) and in the scientific literature: in particular, only some fragments for the exons 1-4-8 are described. Reconstruction of the coding sequence (cDNA) of AR was performed by extraction of RNA from skin biopsy of 6 Holstein Friesian bulls, which was then converted in cDNA by random examers and amplified using primers designed on human AR sequence or partial sequence of bovine AR already existing in literature. All amplified fragments were then sequenced (both forward and reverse) and the chromatograms aligned with the sequence of 8 already known structures of the AR gene (both from human and other species). Through the prediction of the protein sequence and the protein alignment (Clustal W), it was possible to compare the sequences to highlight the differences between the different species under consideration. The results obtained showed that, except for exon 1 (coding for the transactivation domain - NTD) known to be hypervariable, the sequence is highly conserved compared to other animal species. In particular, the serine residues at position 16, 83, 96, 261, 313, 429 and 654, representing the sites of phosphorylation known to activate the receptor, are completely preserved, as well as the region FxxLF, essential for the correct folding of the quaternary structure of the protein. Finally, the analysis of repeated sequences showed that the bull has a shorter poly-GLN primary site (aa 58-91) and a longest poly-GLN secondary site (aa 195-200) compared to man, with a peculiar insertion of 4 additional amino acids in the poly-GLY site (aa 451-476). Moreover, the extension of the sample analyzed and the evaluation of bulls of other breeds will allow us to understand the impact of the sequence variations found in this study, in terms of change in the androgen receptor function of the bull.

Key Words: androgen receptor gene, fertility, Holstein cattle

M55 Evidence for a genetic contribution to bovine viral diarrhea vaccine response in beef calves. X. Fang*[1], T. A. Henrickson[1], C. Maltecca[2], and M. G. Gonda[1], [1]*South Dakota State University*, *Brookings*, [2]*North Carolina State University*, *Raleigh*.

In this study we hypothesized that Bovine Viral Diarrhea Virus (BVDV) vaccine response varies among calves and that genetics may contribute to this variation. To test this hypothesis, BVDV humoral vaccine response, as measured by antibody ELISA, was collected from Angus and Angus-Simmental calves (N=85) that were sired by a total of 8 bulls. Calves born between February and April 2008 at the SDSU cow-calf unit entered the study. All individuals were vaccinated with Bovi-Shield GOLD-5, which includes modified-live virus strains type 1 and 2 (Pfizer, Inc., Exton, PA). Two blood samples were collected at time of vaccination (d=0) and post-vaccination (d=41). Day 0 samples were used to measure maternal BVDV antibody and test for persistently infected (PI) BVDV calves, while d 41 samples were used to measure humoral BVDV response to the vaccine. PI calves were detected by real-time RT-PCR for BVDV on RNA isolated from plasma samples (Qiagen, Valencia, CA). Positive controls were included for real-time RT-PCR and viral RNA isolation methods. BVDV antibody ELISA (Idexx, Inc., Westbrook, ME) was used to measure total amount of antibody present at days 0 and 41. Day 0 and 41 antibody concentrations were converted to sample-to-positive (S/P) ratios, and maternal antibody S/P ratios (d=0) were subtracted from S/P ratios at d 41. To investigate a possible effect of genetics on BVDV vaccine response, an ANOVA model including effects of sire, month of birth, sex, and breed composition was fitted. None of the calves tested positive for BVDV by real-time RT-PCR. The mean d 0 and d 41 S/P ratios were 0.744 (σ = 0.400) and 0.509 (σ = 0.242), respectively. Sire, month of birth, and gender were significantly associated with BVDV vaccine response ($P < 0.05$). This study is the first to show that sire affects BVDV vaccine response in calves, suggesting that genetics contributes to BVDV vaccine response variation. If genetics contributes to variation of BVDV vaccine response, then selecting high responders to BVDV vaccines may be one strategy for improving calf health.

Key Words: bovine viral diarrhea virus, vaccine, ELISA

M56 Estimation of genetic parameters and transmitting ability for Minnesota Johne's milk ELISA test. S. A. Attalla*[1,3], A. J. Seykora[1], J. B. Cole[2], and B. J. Heins[1], [1]*University of Minnesota, Saint Paul*, [2]*Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*, [3]*Cairo University*, *Giza, Egypt*.

A total number of 45,907 results for Johne's Milk Enzyme-Linked Immuno Sorbent Assay (ELISA) test were received from Minnesota DHIA, of which 40,177 records were from herds with at least one positive Johne′s cow. Pedigree information was available for 19,304 Holstein cows from AIPL USDA representing 22,694 total records. Milk ELISA optical density was transformed using a natural logarithm (lnOD). Heritability, repeatability, and breeding values for lnOD were estimated fitting a linear animal model. Variables for statistical analysis were the fixed effects of test date, and age at test day and lab control OD were covariables. Herd, animal, and permanent environmental effects were random effects in the model. All fixed effects were highly significant ($P < 0.001$). Heritability of linOD was 0.06 ± 0.01, while repeatability was 0.34 ± 0.02. The correlations between the breeding values of linOD for 108 Holstein AI sires that had at least 30 daughters in this study and their corresponding USDA PTAs for milk, fat, protein, productive life (PL), daughter pregnancy rate (DPR) and Net Merit (NM) were calculated. The correlations between lnOD breeding values and corresponding PTAs were: milk (0.01); fat (-0.05); protein (0.0); PL (-0.26); DPR (-0.21); SCS (0.19); and NM (-0.26). These correlations suggest that selection for PL, DPR, SCS and NM could improve the resistance of Holstein cattle against Johne's disease.

Key Words: Johne's disease, genetic parameters, predicted transmitting ability

M57 Relationship between base and process cheese characteristics. A. Hassan* and N. Nigam, *South Dakota State University, Brookings*.

The objective of this research was to study the relationship between properties of base and process cheese food. Full fat Cheddar cheese was made with exopolysaccharides (EPS)-producing or nonproducing cultures. Process cheese food was made from 2 day or 1 month old EPS-positive and negative base Cheddar cheese. The EPS-positive base Cheddar cheese contained 2% higher moisture and 1.5% lower fat than the EPS-negative one. Process cheese food contained about 44% moisture, 23% fat, 2% salt, and 21% protein. There were no differences (P >0.05) in composition of process cheese made from EPS-positive and negative base Cheddar cheese. Texture profile analysis, meltability, and viscoelastic properties were evaluated in both base and process cheeses. The 2 day and 1 month old EPS-positive base Cheddar cheeses were softer, and less gummy and chewy (P <0.05) than the corresponding EPS-negative cheeses. No differences (P >0.05) were observed in the texture profile analysis of process cheese food made from 2 day old EPS-negative and positive Cheddar cheeses. However, process cheese food made from 1 month old EPS-negative Cheddar was harder, and more gummy and chewy (P <0.05) than that made from the 1 month old EPS-positive base Cheddar cheese. This is due to less extensive proteolysis in the former base cheese. Although lower viscoelastic moduli were seen in the 2 day old EPS-positive than in the EPS-negative base Cheddar cheese, no differences (P >0.05) were found in process cheese food made from these base cheeses. Interestingly, whereas the viscoelastic moduli in the base cheese were not affected by age (2 day or 1 month), they were higher (P <0.05) in process cheese food made from base cheese aged for 1 month. Also, aging of base cheese for 1 month improved softening and melting properties. However, such improvements were not seen in the corresponding process cheese food. Modifications in the base cheese texture do not necessarily reflect on process cheese characteristics. Proteolysis of base cheese is a major factor affecting process cheese physical properties.

Key Words: process cheese food, base cheese, texture

M58 Fate of aflatoxin M_1 during manufacture and brining of feta cheese. M. M. Motawee*[1] and D. J. McMahon[2], [1]*National Organization for Drug Control and Research, Cairo, Egypt*, [2]*Utah State University, Logan*.

Aflatoxins are toxic carcinogenic compounds that can be present in milk if there is growth of Aspergillus on feedstuffs consumed by livestock. Because of health risks from consuming large amounts of aflatoxins, maximum amounts allowable in milk are 0.50 μg/L in the United States and 0.05 μg/L in the European Union. Our objective was to determine the fate of aflatoxin M_1 (AFM_1) in milk after pasteurization followed by manufacture of feta cheese and its storage in brine, and whether this would reduce the level of dietary exposure of consumers to AFM_1. Feta cheese was made from 4 kg of milk spiked with 1 and 2 μg AFM_1 per kg and AFM_1 contents were studied using an enzyme immunoassay technique. Milk pasteurization at 63°C for 30 min caused minimal (<10%) destruction of AFM_1. The remaining AFM_1 in the pasteurized milk was partitioned between curd and whey during cheesemaking. The yield of curd was 0.22 kg per kg of milk, and AFM_1 levels in the curd were 2.95 and 6.00 μg /kg for cheese made from the 1- and 2-μg/kg AFM_1milks, respectively. The AFM_1 levels in the corresponding wheys were 0.37 and 0.69 μg/kg. Thus, the curd contained only 64% of the original AFM_1 added to the raw milk. Cheeses containing 2.95 μg/kg AFM_1 were placed in 8, 10 and 12% brine solutions for 60 d and stored at 6 and 18°C. There was a 22 to 27% reduction of AFM_1 during the first 10 d of storage, with slightly more loss as salt concentration increased and when the cheese was stored at 18°C. Further storage caused only slight decrease in AFM_1 and after 60 d of brining the cheeses contained 2.2 and 2.1 μg/kg AFM_1 for cheese brined at 6 and 18°C, respectively, for a loss of 25 and 29% of AFM_1 from the curd into the brine. Through the conversion of milk into feta cheese (brined for at least 50 d) there was a loss of about 50% of the AFM_1 originally present in the raw milk. Thus, for consumers in regions with high aflatoxin levels in milk, health risk could be reduced by converting the milk into a brined cheese. A 30-g serving of such cheese would contain only 0.07 μg aflatoxin compared to the 0.25 μg aflatoxin from a 250-g serving of such milk.

Key Words: aflatoxin, milk, cheese

M59 The ELISA test to determinate the κ-casein B contents in bulk milk samples: Practical use. A. Rossoni*[1], M. Malacarne[2], C. Nicoletti[1], and A. Summer[2], [1]*ANARB - Italian Brown Cattle Breeders' Association, Bussolengo, Verona, Italy*, [2]*Dip. Produzioni Animali B.V.Q.S.A Università degli Studi di Parma, Parma , Italy*.

κ-Casein is one of the most important part of milk casein involved in the cheese making. The κ-casein family consists of one major carbohydrate-free component and several "minor" glycosylated ones, with the same amino acid sequence but with different nature and number of the carbohydrate groups. The most frequent variants in dairy milk are A and B, which differ for two amino acids, one in position 136 and one in 148. Substantial differences in cheese making properties were found due to better coagulation properties; more cheese was obtained from milk samples with B variant compared with the same quantity of milk with A variant. The "test kappa" is a commercial ELISA test useful to quantify κ-casein B content in bulk milk samples. Using this test is possible to follow the yearly farm's variation of milk κ-casein B content. Four different ratio of milk dilution were tested: 1:1000, 1:1500, 1:2000 and 1:3000. The best results were obtained with the lowest dilution, due to the better matching of samples intensity color with the calibration curve.

Key Words: κ-casein, milk quality, cheese

M60 Aroma profile characterization of traditional Algerian Bouhezza cheese. S. Carpino*[1], T. Rapisarda[1], G. Belvedere[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*D.A.C.P.A. University of Catania, Italy*.

Bouhezza cheese is an Algerian traditional cheese from goat, sheep or cow milk. It can be also produced from mixed milks in different proportions. The manufacturing of Bouhezza cheese requires the preparation of a natural container "*chekoua*" and a spontaneous fermented milk, rather skimmed and little acid "*lben*". The chekoua is a bag prepared from goat or sheep skin, treated with salt and juniper berry. It has also an important role as separator of serum and solid phase (ultrafilter). The manufacturing process is curried out by addition of "*lben*" and raw milk, to correct the acidity and salty. The cheese making is completed after 70 days, on the average, when pepper spice is added. The aim of this preliminary study was to characterize the volatile organic compounds (VOCs) of

Bouhezza cheese produced in different farms. Five Bouhezza samples (F1-F5) were analyzed by SMart Nose (SN) system which allowed the direct analysis by MS of VOCs. The ion fragments obtained by SN were then processed by a multivariate statistical PCA). Dynamic headspace purge and trap apparatus (Tekmar 8900) in combination with a gas chromatograph olfactometry/mass selective detector to analyze the odour active compounds. PCA applied to SN results showed a good separation (PC1 77,93%; PC2 13,05%) among the Bouhezza cheeses indicating the uniqueness of the homemade products. Olfactometry results confirmed high variability for the aroma profile. Cheese F1 had the richest profile (23 VOCs), followed by F4 (19 VOCs), F2 (18 VOCs), F3 (15 VOCs) and F5 (13 VOCs). All cheese samples were mainly characterized by aldehyde and ester compounds. Among aldehydes there were octanal, nonanal, (E,E)-2,4-decadienal, (E)-2-nonenal that gave, respectively, orange, apple, hay, and green notes. Free fatty esters detected were: ethyl octanoate, ethyl hexanoate, ethyl butanoate and propyl-1-methyl-acetate that gave, respectively, wine, floral, and fruity notes. The high variability of Bouhezza cheese was clearly detected by SN and GCO analyses confirming that the farm traditional cheese-making process, the milk and the different spices used during manufacturing contribute to the uniqueness of this product.

Key Words: Bouhezza cheese, SMart Nose, GCO

M61 Molecular characterization of Algerian cheese Bouhezza by PCR-TTGE. C. Pediliggieri[1], S. Carpino*[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*D.A.C.P.A. University of Catania, Italy*.

Bouhezza cheese is an Algerian traditional cheese from goat, sheep or cow milk. It can be also produced from mixed milks in different proportions. The manufacturing of Bouhezza cheese requires at first the preparation of a natural container "*chekoua*" and a spontaneous fermented milk rather skimmed and little acid "*lben*". The chekoua is a kind of bag prepared from goat or sheep skin, treated mainly with salt and juniper berry. It has also an important role as separator of serum and solid phase (ultrafilter). The end of the manufacturing is characterized by the addition of whole raw milk, what allows to correct the acidity and salty of the cheese. The manufacturing process is carried out by addition of "*lben*" and raw milk and it is completed after 70 days, on the average, when pepper spice is added. The bacterial ecosystem of Bouhezza cheese was explored by PCR-temporal temperature gel electrophoresis (PCR-TTGE). PCR-TTGE is a rapid molecular method based on direct analysis of DNA in the environment and on the separation of DNA molecules that differ by singles based allowing to analyse diversity within bacterial communities. Molecular fingerprinting was carried out on cheese samples collectd at different time during two experimental cheese-making: cheese at 7 days, at 15d, 21d, 41d, 56d, and at 70 d with and without pepper. By the use of universal primers, PCR-TTGE revealed the predominance in all samples of *L. lactis*, which presence was confirmed by specific PCR tests. Furthermore the presence of *Lb. plantarum*, *Lb. haelveticus* and *Lb. delbruekii* was detected. More bands (correspondent *to S. equorum, Lb. delbruekii* , and a band maybe identifiable with *S. termophilus*), were detected in PCR-TTGE profiles of cheeses after 41 days probably due to addition of whole raw milk. The presence of a few high-GC-content species, like *coryneform bacteria*, were observed too.

Key Words: Bouhezza cheese, PCR-TTGE, lactic bacteria

M62 Characterization of bacterial ecosystem in Pecorino Siciliano cheese produced in different areas of Sicily. C. Pediliggieri[1], S. Carpino*[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*D.A.C.P.A. University of Catania, Italy*.

Pecorino Siciliano is a PDO ewe's milk cheese produced in Sicily. The aim of this study was to evaluate the influence of different production areas on the dynamics of the microbial communities of artisanal cheeses by Temporal Temperature Gel Electrophoresis (TTGE). PCR-TTGE is a rapid molecular method, allowing to analyse diversity within bacterial communities, based on direct analysis of DNA molecules that differ by singles based. Among 21 farms allocated in seven different areas of Sicily classed as: Iblean (I), Etnea (E), South Center (SC), North Center (NC), Western (W), Western Center (WC), and Peloritana (P) seven experimental cheeses were selected on microbiological composition of cheese samples. Cheese ripened at two, four and eight months were sampled from each farm. Comparison of TTGE profiles showed differences among the different areas, allowing a further classification amenable to three main areas of Sicily (East, Center and West) as confirmed by cluster analysis of milk samples. The TTGE profiles of cheese samples obtained from East area farms resulted richer of microorganisms than the others areas, specially for the high GC bacteria (Propionibacteria, Artrobateria and Corinebacteria). This result was further confirmed comparing the TTGE profiles of the rind of cheese samples. The main species detected in cheese samples from all areas were: *S. equorum*, *S. termophilus*, *S. gallolyticus* subsp. *macedonicus*, and *Lc. lactis*, subsp. *cremoris*, however these microorganisms were more consistent in East area. Furthermore, an high relationship between microorganisms detected in milk samples and those ones detected in cheese samples, was observed. These results indicated that the quality of starter milk, probably affected by geographic area, might be also directly related to variability development in bacterial ecosystem of cheese.

Key Words: Pecorino Siciliano cheese, PCR-TTGE, bacterial ecosystem

M63 Persistency of conjugated linoleic acid and vaccenic acid on Tybo cow cheese. G. A. Gagliostro*[1], M. Martínez[2], V. I. Cejas[3], M. A. Rodríguez[3], and M. Balán[4], [1]*Instituto Nacional de Tecnología Agropecuaria, Balcarce, Buenos Aires, Argentina*, [2]*Instituto Nacional de Tecnología Agropecuaria, Salta, Argentina*, [3]*Instituto Nacional de Tecnología Industrial, PTM MIguelete, Buenos Aires, Argentina*, [4]*PRODEO S.R.L., Chivilcoy, Buenos Aires, Argentina*.

The study was designed to test concentration of 9-cis 11-trans C18:2 (CLA) and trans-11 C18:1 (VA) on Tybo cheese elaborated from milk with high CLA and VA contents. Eight Holstein cows (570 kg liveweight, 109 days in milk) producing 23.4 kg milk consumed (DM) 7.3 kg /cow of concentrate, 1.9 kg of a TMR composed by corn silage (70%), soybean oil (22%), fish oil (5.4%) and urea (2.6%) and 8 kg of pasture. After 34 days of adaptation milk was collected and transformed into Tybo cheese reproducing industrial conditions. Fatty acid (FA) composition of milk and cheese was analyzed by GLC and differences in FA content between milk and cheese were stated using the T-test for paired observations. Milk fat, protein and lactose contents were 24.2, 34.5 and 46.6 g/kg. Intake of 418 g of soybean oil and 103 g of fish oil contained in the TMR reduced the atherogenicity index (AI = [(C12 + 4C14 + C16)/Total unsaturated FA)] of milk from a pre-supplementation basal value of 2.06 to 1.16 Basal concentration (g/100g) of the atherogenic FA C12:0 (4.04) C14:0 (12.52) and C16:0 (29,16) were decreased by feeding oils (C12:0 = -1,84, 45%, C14:0 = -3,64, 29% and C16:0 = -3,29, 11%). CLA increased in milk from a basal value of 1.42 to 2.86

g/100g and VA from 2.56 to 3.55 g/100g FA after oil supplementation. Elaborated cheese contained 21.6% fat and 26.8% protein (w/w) with an atherogenicity index of 1.29. Differences between milk and cheese FA content were detected only for C4:0, C14:0 and VA. Concentrations of C4:0 (+0,42 g/100g, 36%), C14:0 (+0.85 g/100g, 10%) and VA (+0.93 g/100 g, 26%) increased in cheese. Transfer of 9-cis 11-trans CLA to Tybo cheese was 95%. Assuming that the cheese fat contain 95% FA, intake of 143 g/d of Tybo cheese rich in CLA may allow to obtain the suggested anticancer dose (800 mg) of CLA achieving also the proposed dose (250 mg CLA) that confers protection against cardiovascular disease for the consumer.

Key Words: cheese, conjugated linoleic acid, vaccenic acid

M64 Influence of microfiltration and adjunct culture on quality of Egyptian soft white cheese. S. Awad*, N. Ahmed, and M. El Soda, *Alexandria University*, *Alexandria, Egypt*.

Classical techniques used to improve milk shelf life and safety are based on heat treatments, like pasteurization and sterilization. Those techniques modify some physic-chemical properties of milk, for example its coagulation by rennet. Microfiltration constitutes an alternative to heat treatment to reduce the presence of bacteria and improve the microbiological safety of dairy products without modifying the physic-chemical properties of milk. Pasteurization and/or microfiltration of milk are recommended before cheese making to improve the hygienic quality of cheese. These will have a negative impact on the natural flora present in raw milk. Eight adjunct cultures of lactic acid bacteria, isolated from Egyptian dairy products, were evaluated in experimental Egyptian soft white cheese for flavour development. The effect of microfiltration (MF) and pasteurization on proteolysis, lipolysis and flavor development in Egyptian soft white cheese during 4 months of ripening were also studied. The chemical composition of cheeses seems to be affected by microfiltration rather than the culture types. The moisture content was higher and the pH was lower in pasteurized milk cheeses compared to microfiltrated milk cheeses at day one of manufacture. Chemical composition of experimental cheeses was within the legal limit for Egyptian soft white cheese in Egypt. All adjunct cultures used in this study had no effect on chemical composition of Egyptian soft white cheese. Proteolysis and lipolysis during cheese ripening were lower in microfiltrated milk cheeses comparing to pasteurized milk cheeses. Very significant variations in free amino acids, free fatty acids and sensory evaluation have been found among the adjunct cultures used in Egyptian soft white cheese. Cheese made using adjunct culture of *Lactobacillus delbrueckii* subsp. *Lactis, Lactobacillus paracasei* subsp. *paracasei*, and *Lactobacillus plantarum* received the highest scores of flavor and texture.

Key Words: Egyptian soft white cheese, microfiltration, proteolysis

M65 Development of a flavor lexicon for processed and imitation cheeses. S. L. Drake*, M. D. Yates, and M. A. Drake, *North Carolina State University*, *Raleigh*.

Processed cheeses and cheese foods are made using natural cheese, but imitation products made with caseinate and nondairy proteins are also available. Functionality and meltability are primary characteristics of these products, but flavor is also important and can be a defining characteristic. Studies have not focused on flavor of these products. This study was conducted to identify and define the sensory properties of processed and imitation cheeses. An experienced sensory panel (n=9) evaluated an array of processed and imitation cheeses (n=48 products). Following language development and refinement, selected processed and imitation products (n=20) were evaluated in duplicate by each panelist. Data was evaluated by univariate and multivariate analyses. Twenty aromatics and five basic tastes were documented in the products. However, a language of fourteen attributes could be used to differentiate most products. Processed cheeses were characterized by sweet aromatic, cooked/milky, diacetyl, whey, and milkfat flavors. Processed cheeses labeled as sharp were characterized by the previous terms plus sulfur, fruity, free fatty acid, and brothy flavors. Processed cheese foods were characterized by similar flavors but lower or absent in cooked/milky flavor. Imitation cheeses with casein/caseinates were characterized by sweet aromatic, minty and hay flavors while imitation cheeses with other protein sources had cardboard, fatty, oxidized, and fishy flavors. This study demonstrated an array of flavor profiles among processed cheese and between processed and imitation cheeses. This flavor lexicon can help the industry to better define and differentiate processed and imitation cheeses and to understand consumer flavor preferences for these products.

Key Words: processed cheese, flavor, cheese food

M66 Effect of cream cheese made from freeze-dried milk powder on physicochemical properties. S. H. Kim[1], S. Y. Lee[1], J. Ahn[2], and H. S. Kwak*[1], [1]*Sejong University*, *Seoul, Korea*, [2]*Jungwon University*, *Chungbuk, Korea*.

The cream cheese was manufactured from freeze-dried milk powder (FDMP) that was made by newly developed continuous multi-stage process. Physicochemical properties examined were composition, specific gravity, color, short-chain fatty acides and texture during 4 week storage at 4°. The compositions of the FDMP cream cheese were 32.7% fat, 8.3% protein and 57.1% water which were comparable to that of the cheese from control and spray-dried powder milk, respectively. Specific gravity of the FDMP cream cheese was 1.072 and it was not significantly different ($P<0.05$) from others. In color observation, L-, a-, and b-value were slightly different in each samples, however, they were not significant. Total short-chain fatty acid of all samples increased significantly during storage up to 4 weeks, but the FDMP cream cheese showed the lowest concentration among samples. This result indicated that the FDMP cream cheese could be extended storage time longer than others. In texture study, hardness scores decreased significantly in all samples during storage. The FDMP cream cheese showed that the scores were lower than control but higher than the cheese from spray-dried milk powder. Cohesiveness scores of the FDMP cream cheese were significantly increased during storage period and were higher than that of control and similar to the cheese from spray-dried milk powder. In conclusion, the quality of the FDMP cream cheese is similar to that of control and better than that of the cheese from spray-dried milk powder.

Key Words: cream cheese, freeze-dried milk powder, spray-dried milk powder

M67 Optimization of recovery of key Cheddar cheese flavor compounds from full fat and reduced fat Cheddar cheeses. D. M. Watson*, R. E. Miracle, and M. A. Drake, *North Carolina State University*, *Raleigh*.

Fat reduction in the American diet concerns both consumers and food manufacturers. Studies indicate that cheese consumers are interested in low fat cheese if a similar flavor profile to full fat cheese is assured. Recent flavor chemistry studies have identified twenty key flavor compounds in full and low fat Cheddar cheeses. Precise and high throughput extraction and quantitation of these compounds are crucial to identify methods to improve flavor of low fat Cheddar cheese. The objective of this study was to optimize a headspace solid phase microextraction (SPME) method for the recovery and quantitation of these key aroma compounds from full and reduced fat Cheddar cheese. Commercial full fat and 75% reduced fat Cheddar cheeses were purchased and used for the study. Sample size, salt content, extraction time, and extraction temperature were evaluated for their effect on recovery of the twenty previously identified compounds in a response surface model – central composite design (RSM-CCD) design matrix. The entire design was repeated using three SPME fiber types (Polydimethylsiloxane, PDMS; Carboxen-PDMS, CAR/PDMS; and Divinylbenzene-CAR/PDMS, DVB/CAR/PDMS) to determine which fiber was most efficient for key volatile compound recovery. Compounds were identified by gas chromatography mass spectrometry. The 3-phase DVB/CAR/PDMS fiber provided the most complete recovery of volatile compounds from the full and reduced-fat Cheddar cheeses. Sample conditions of 51 C for 40 min resulted in optimal recovery of low molecular weight compounds, especially acetic and butyric acids and 3-methylbutanal. Increasing sample weight under the same conditions resulted in the highest recovery of higher molecular weight compounds such as hexanoic acid, two lactones and phenylethanal. In contrast, a lower temperature time profile (44C for 20 min) allowed the highest recovery of both low molecular weight and low boiling point compounds. These results indicate that different sample extraction conditions can be used to achieve rapid and precise quantitation of key cheese flavor volatiles.

Key Words: cheese flavor, volatile compounds, volatile recovery

M68 The influence of sodium chloride on flavor of natural Cheddar cheese. M. A. Drake*[1], R. E. Miracle[1], and D. J. McMahon[2], [1]*North Carolina State University*, *Raleigh*, [2]*Utah State University*, *Logan*.

Sodium reduction concurrent with fat reduction in the American diet are currently key issues for food processors. Dietary guidelines currently suggest a maximum intake of 2300 mg of sodium per day, while the average consumer intake is 9 g per day. Natural Cheddar cheese is not a low sodium food (~175 mg per serving) and salt plays a crucial role in Cheddar cheese ripening and flavor. The objective of this study was to evaluate the impact of sodium chloride on sensory properties of low fat Cheddar cheese. Duplicate batches of low fat Cheddar cheese (6.0% fat, 51% moisture) were manufactured with 1% sodium chloride and aged at 3C for 4 months. Following aging, cheeses were comminuted to particles of size 1 to 4 mm, divided into five 2.7-kg portions, and sufficient salt added to produce cheese containing 1.0, 1.4, 1.8, 2.2, and 2.6% salt. Cheeses were then re-formed, vacuum-sealed and stored at 3C for 1 mo prior to sensory testing. This procedure allowed the impact of sodium chloride on sensory properties to be evaluated without altering cheese biochemistry. A trained panel documented the sensory properties of cheeses. Consumer acceptance testing (n=75 consumers) was subsequently conducted to document consumer perception of cheeses with different salt contents. Salty taste, and to a lesser extent umami taste, increased with increasing sodium chloride concentration by descriptive sensory analysis ($p<0.05$). Sodium chloride addition and salty taste did not cross-modulate other trained panel sensory attributes. Consumers documented differences in salty taste intensity between all salt concentrations except 2.2 and 2.6% ($p<0.05$). Salty taste liking scores suggested that salt concentrations of > 1.8% resulted in cheeses with acceptable salty taste intensity. A salt reduction of as little as 25% from typical salt content (1.8 decreased to 1.4%) in low fat Cheddar cheese was noticed by consumers and negatively impacted acceptance ($p<0.05$). Salty taste intensity is a consumer expectation in Cheddar cheeses, and exploration of sodium chloride alternatives is warranted if sodium reduction in this product is desired.

Key Words: salt reduction, cheese flavor, low sodium

M69 Automatic detection of microstructural features using a statistical image processing method. G. Impoco[1], L. Tuminello[1], N. Fucà[1], M. Caccamo*[1], and G. Licitra[1,2], [1]*CoRFiLaC*, *Ragusa, Italy*, [2]*D.A.C.P.A., University of Catania*, *Catania, Italy*.

Detecting features in digital micrographs of cheese samples is an important pre-processing step for automated quantitative analysis. A statistical Image Processing algorithm has been developed for automated detection, requiring no user intervention. Scanning Electron Microscope (SEM) and Confocal Laser Scanning Microscope (CLSM) were used to acquire images of Ragusano pasta-filata cheese. SEM images were taken at 15kV, working distance 18mm, 1000×. Confocal images were taken at 10×, numerical aperture 0.30. The main microstructural features of the images were gathered into specific classes: fat globules, generic pores, protein matrix, and pore clusters, for SEM images; fat, protein, empty areas, and gas holes, for CLSM images. Images were manually labelled using an ad-hoc tool. The labelled pictures and the original micrographs were used to train a statistical algorithm, on the basis of pixel intensity and gradient neighborhoods, computed as multi-scale N,S,W,E circular sections around each pixel. The result of this learning stage was 51 probability density functions (PDFs), describing the probability of pixels to take certain numerical values for each feature class. Different PDFs were generated for SEM and CLSM images, and collected into two different libraries. After training, new images can be classified using the learned statistics. The algorithm associates to each pixel its probability to belong to a certain feature class. Notice that, although an intensive manual effort is necessary for training, this work is carried out only at the very beginning on a new type of cheese. Once the method has been trained, the operative stage requires no user intervention at all. Satisfactory classification results have been obtained for SEM images. Results for CLSM images were not accurate and can be probably improved using geometric features. Nevertheless, this statistical analysis suggested that in the observed images gas holes lie close to fat with high probability.

Key Words: cheese microstructure, image processing, feature detection

M70 Lactic acid bacteria enhance levels of conjugated linoleic acid in Cheddar cheese. A. J. Pandit, S. K. Anand*, A. N. Hassan, and K. F. Kalscheur, *South Dakota State University*, *Brookings*.

The present study was undertaken to produce Cheddar cheese with enhanced levels of conjugated linoleic acid (CLA) using two strains of lactic acid bacteria previously identified as high CLA producers (*Lactococcus lactis* 4b isolated from Cheddar cheese and produced 1.12 g CLA/100g fatty acids in milk, and *Lactobacillus helveticus* ATCC 15807, which produced 0.54 g CLA/100g fatty acid in milk). These cultures were evaluated for their suitability for cheese making by the

cheese slurry method. The four treatments employed were: 1) cheese made with a CLA negative culture (DVS), 2) cheese made with *Lc. lactis* 4b, 3) cheese made with a combination of DVS and *Lb. helveticus* ATCC 15807, and 4) cheese made with a combination of *Lc. lactis* 4b and *Lb. helveticus* ATCC15807. The control cheeses made with DVS had a CLA level of 0.62g/100g FA (day 1). The CLA levels in cheese manufactured using *Lc. lactis* 4b increased from 0.86g/100g FA on day 1 to 0.97g/100g FA after 6 months of ripening. The addition of *Lb. helveticus* (treatments 3 and 4) although showed an initial increase in CLA levels to 0.84 and 0.83 g/100g FA on day 1, did not show any significant enhancement throughout the ripening period. There was no difference (P>0.05) in the chemical composition of cheeses among treatments. Due to higher acid production, the pH values of cheeses made with *Lc. lactis* 4b were lower than those made with DVS. Proteolysis (water soluble nitrogen and trichloroacetic acid soluble nitrogen) was higher in the CLA-positive cheeses than in the control cheese. The CLA-positive cheeses had lower (P>0.05) levels of free oil and less meltability than control cheeses. Textural properties of CLA-positive cheeses differed from those in the control cheese during the first 3 months but not after 6 months of ripening. Bacterial counts on M17 and MRS agar were higher (P>0.05) in CLA-positive cheeses than in the control cheese throughout the ripening period. The CLA-positive cheeses had high sensory scores. Our study demonstrates the possibility of increasing levels of CLA in Cheddar cheese using lactic cultures without the need of substrate addition to milk.

Key Words: lactic acid bacteria, CLA, cheese

M71 Effect of aging on the rheology of full fat and low fat Cheddar-like caprine cheese. D. L. Van Hekken*[1], Y. W. Park[2], and M. H. Tunick[1], [1]*Dairy Processing & Products Research Unit, Agricultural Research Service, Wyndmoor, PA*, [2]*Agricultural Research Station, Fort Valley University, Fort Valley, GA*.

The rheological properties of aging full fat (FF) and low fat (LF) caprine milk cheeses were characterized to determine the changes in the cheese matrix during storage. Three batches each of high moisture, Cheddar-like caprine FF and LF cheeses were manufactured from whole or skim milk from the University's goat herd and were aged at 4°C for up to 6 months. Rheological properties (texture profile, torsion, and small amplitude oscillatory shear analyses) and protein distribution (SDS-PAGE) were measured after 1, 3, and 6 months of storage. The LF cheeses contained 55.1% moisture, 35.7% protein, and 1.3% fat while the FF cheeses contained 47.7% moisture, 22.5% protein, and 25.6% fat. Structurally, the LF cheeses were significantly harder, chewier, and more cohesive than the FF cheeses throughout storage; overall averages for LF versus FF cheeses were 160 N versus 17.4 N for hardness, 326 mJ versus 27.2 mJ for chewiness, and 0.24 versus 0.18 for cohesiveness, respectively. Higher values for the point of fracture and viscoelastic properties were noted as well for the LF cheeses when compared to LL cheeses; overall means were 92.8 kPa versus 17.8 kPa for shear stress, 108 kPa versus 23.6 kPa for shear rigidity, 96.6 kPa versus 34.7 kPa for elastic modulus, and 34.4 kPa versus 12.8 kPa for viscous modulus, respectively. Although overall changes between months 1 and 6 were not always significant, the LF cheeses showed more variation in their rheological properties than the FF cheeses. The LF cheeses demonstrated that fat is critical in creating a soft flexible cheese matrix and the results can be used to identify fat levels that will meet consumer demands for lower fat cheeses with acceptable texture.

Key Words: caprine milk, cheese, rheology

M72 Effect of renneting pH on calcium balance in cheese making process. N. Remillard* and M. Britten, *Food Research and Development Centre, Agriculture and Agri-food Canada*, *St-Hyacinthe, QC, Canada*.

Texture and melting properties of Italian cheese (Mozzarella) are influenced by calcium content. Decreasing whey drainage pH or curd washing are common practices to control calcium concentration in cheeses. In the present work, renneting pH was studied as a potential factor controlling calcium level in cheese. The effect of renneting pH (between 6.65 and 6.2) on: 1) the calcium transfer to the soluble phase during milk acidification, 2) the characteristics of rennet gels and 3) the cheese mass balance were determined. Cheese milk was standardized to a protein to fat ratio of 1.28 and a casein concentration of 2.65%. Decreasing the pH of milk was carried out by inoculation with thermophilic starter at 33.7°C. During the acidification and coagulation process soluble calcium concentration was monitored and calcium distribution between colloidal and soluble phases was established. The kinetics of gel formation as well as rennet gels permeability were determined as a function of renneting pH. Model cheeses were produced at a laboratory scale. Moisture, protein, fat and calcium distribution were determined from mass balance and composition of milk, cheese and whey. During acidification, the increase of soluble calcium concentration (d[Ca]/dpH) was 2-fold higher before renneting (liquid state) than after (gel state). As a consequence, decreasing renneting pH by 0.1 units reduced micellar calcium content by about 0.5mg per g casein in cheese curd at drainage. Lower renneting pH was associated with rapid gel formation and rennet concentrations had to be reduced to maintain constant gel formation kinetics. The permeability coefficient of rennet gels increased with decreasing renneting pH, suggesting faster dehydration of the gel matrix. Micellar calcium concentration in model cheese was significantly reduced by lowering renneting pH. Furthermore, cheese moisture and fat retention coefficients were both increased when the renneting pH was reduced.

Key Words: renneting pH, calcium, cheese

M73 Denaturation of proteins measured in liquid whey. M. Allen* and P. Tong, *California Polytechnic State University*, *San Luis Obispo*.

Protein structure affects the functionality of whey protein ingredients in food systems. The degree of denaturation of whey proteins has become important for characterizing how whey protein ingredients will perform in a food system. Several methods have been developed to quantify protein denaturation of purified whey proteins, whey protein concentrates and isolates, milk powders, fluid milk, liquid whey and other more complex dairy systems. The purpose of this experiment was to compare three different methods to measure denaturation of whey proteins in liquid whey obtained by various methods of separation and with varying degrees of heat treatment. A split-split plot experimental design was used. Raw bovine milk was skimmed and liquid whey was separated from the skim milk. Three separation methods: centrifugation, membrane filtration and enzyme coagulation, made up the first split plot. Each sub-plot of liquid whey was then divided into three split-split plots to receive heat treatment. Heat treatments were no heat, 76°C for fifteen seconds and 85°C for three minutes. Each of the resulting nine sub-sub plots was analyzed by polyacrylamide gel electrophoresis, bicinchoninic acid-soluble Protein assay and fluorescence spectroscopy to determine the amount of denatured protein in the liquid whey. The total protein in the liquid whey samples varied based on the separation method and ranged from 0.6%-1.0% protein by weight. To account for the differ-

ences in protein content, the amount of protein denatured was expressed as a percentage of the original total protein in each sample. Of the total protein, the amount of denatured protein ranged from 10%-40%. Differences in denaturation due to separation method and heat treatment were detected by all three methods of quantification. However, data indicates that each of the three methods of quantification yield different amounts of denaturation, which indicates there are also differences are due to the method of quantification. Subsequent work will attempt to gain a more complete understanding of how different methods of measuring whey protein denaturation can be used to characterize whey protein ingredients functionality.

Key Words: liquid whey, denatured, protein

M74 Use of fluorescence spectroscopy for monitoring changes and predicting browning reactions during whole milk powder storage. P. Salunke*, J. Amamcharla, and L. E. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Maillard reaction products and browning intermediates are products of a series of chemical reactions between lactose and proteins and have an impact on the quality of dairy based ingredients including whole milk powder (WMP). Maillard browning in dairy products can be determined by reacting furfural compounds with 2-thiobarbituric acid (TBA) to yield a yellow color which can be quantitatively measured by UV-VIS spectrometry. Using this approach the level of free hydroxymethylfurfural (FH), browning intermediates (BI) and total hydroxymethylfurfural (TH) can be determined. However, measurement of FH, BI and TH in WMP using this approach is tedious and time consuming. The objective of this study was to determine if front face fluorescence spectroscopy (FFFS) could be used to characterize the Maillard reaction products of WMP caused by manufacture and storage. Two WMP samples were collected from 4 different manufactures (total of eight samples) and stored for 12 months. At 0, 2, 10 and 12 months of storage the FH, BI and TH content were determined on each sample using the standard TBA based protocols. FFFS was also performed on each sample (emission scan at 400-600nm with excitation wavelength of 360nm) at each time point. For FFFS analysis three scans were performed on three sub-samples of each WMP sample (9 scans total). The nine scans were then averaged to obtain a single spectrum. The spectra were then normalized and used as input for the prediction of the FH, BI and TH. Root mean square error of cross validation (RMSECV) and relative standard error of prediction (RSEP) were used to evaluate the performance of the model. RMSECV of the samples were 1.53, 1.28 and 1.58 HMF μmoles/L, whereas RSEP was 10.48, 3.44 and 3.10% for FH, BI and TH, respectively. There was a good agreement between measured and predicted values of BI (R^2=0.92) and TH (R^2=0.87). However, the partial least squares (PLS) prediction model for FH had a high RMSECV and RSEP. The results indicate that FFFS has potential to characterize WMP and predict HMF values.

Key Words: whole milk powder, front face fluorescence spectroscopy, browning reaction prediction

M75 Profiling changes in amino acids and organic acids in Cheddar cheese during ripening using infrared spectroscopy. A. Subramanian*, J. Harper, and L. Rodriguez-Saona, *The Ohio State University*, *Columbus*.

Composition and flavor quality of Cheddar cheese, which influence the consumer acceptance, price and food processing application, develop during the ripening process. Organic acids and amino acids play important roles in flavor development. Therefore determination of their levels and the changes during ripening is important to understanding their influence on cheese quality. Fourier-transform infrared (FTIR) spectroscopy is an attractive technique for rapid and sensitive analysis of food composition. The goal of this research was to combine FTIR spectroscopy with a simple extraction technique to rapidly profile changes in organic acids and amino acids during cheese ripening. Twelve different cheese samples were ripened for a period of 73 days. Samples were collected on days 7, 15, 30, 45 and 73 during ripening, powdered and extracted with water, chloroform and ethanol. The extracts were analyzed by gas chromatography for amino acids, liquid chromatography for organic acids and FTIR for infrared spectra (4000-700cm^{-1}). The collected spectra were correlated with the amino acid and organic acid concentrations and analyzed by partial least squares regression (PLSR) analysis. Analysis of variance (ANOVA) of the chromatographic data was used to identify the compounds that exhibited significant changes during ripening. The FTIR spectra correlated well with amino acid and organic acid concentrations. The PLSR models showed excellent fit with coefficient of correlation >0.95. Amino acids and organic acids could be simultaneously determined in less than 20 min. The estimated standard errors for predicting unknown samples were <4%. Some of the prominent infrared marker bands that were responsible for the correlation were 1411 (amino acids), 1710-1450 (fatty acids), and 1200-1050 cm^{-1} (organic acids). Lactic acid, glutamic acid, leucine, asparagine, phenylalanine and valine are some of the compounds that exhibited significant changes during ripening. This method could potentially speed up amino acid and organic acid determination due to the possibility of simultaneous analysis and thereby save time and money.

Key Words: Cheddar cheese, rapid analysis, infrared spectroscopy

M76 Production of nisin-containing whey protein concentrate. H. Abd El-aal[1], R. Dave[1], A. Khattab[2], and A. Hassan*[1], [1]*South Dakota State University*, *Brookings*, [2]*Alexandria University*, *Alexandria, Egypt*.

The objective of this study was to optimize conditions for the production of nisin by two strains of *Lactococcus lactis* subsp. *lactis* in ultrafiltered (UF) whey, and study its stability in freeze dried whey protein concentrate. Pasteurized reconstituted (6% w/v) dried sweet whey concentrated 5 times by UF was fermented at 30°C for 24 hours by each of two strains of *Lactococcus lactis* subsp. *lactis* (ATCC 7962 and B10). The pH of the media was maintained at 6.5 using 5 M solution of ammonium hydroxide during the first 8 hours of fermentation followed by a free drop to a value of 4.7 to 4.9. Fermented media were freeze dried, packaged in polyethylene bags, and stored at 4 or 30°C for 3 months. Freeze drying was used as initial trials showed that the single stage drying decreased nisin activity by almost 50%. Freeze drying did not affect nisin activity. Nisin was determined by the agar well diffusion method in the fermented media before and after drying. No differences (P >0.05) in nisin production were seen between the two strains or in regular and UF whey. Boiling of cells prior to nisin assay increased (P <0.05) nisin activity. Whereas nisin activity in UF whey fermented with BS10 and ATCC 7962 was 183 and 167 UI/ml in the absence of yeast extract, it reached 1617 and 1667 UI/ml in the presence of 1% yeast extract, respectively. Nisin activity in the 1 month old whey protein concentrate powder stored at 4°C was about 40 to 45% of that before storage. This value further reduced to 30 to 35% during storage at 30°C. Boiling of reconstituted powder at pH 2 for 5 minutes released nisin from the producing cells and increased (P <0.05) activity. Boiled whey maintained 75% of the

original nisin activity after storage at 4°C for 1 month. By the end of the second month of storage, powder maintained only 15 to 20% of the initial activity. No differences (P >0.05) in nisin activity were observed between 2 and 3 months of storage. Whey protein concentrate powder containing nisin was successfully produced. Future research will study stability of nisin in whey protein concentrate produced using a multistage spray dryer and stored in modified atmosphere.

Key Words: nisin, whey protein concentrate, storage

M77 Bovine milk based infant formula promote the growth and acid production of bifidobacteria. K. Mohamedali* and S. A. Ibrahim, *North Carolina A & T State University*, *Greensboro*.

Several infant formulas are currently available in the market that are fortified with different nutrients to nourish infant development. Because recent research has demonstrated that bifidobacteria promote good health, it is important to determine the effects that infant formula may have on the growth of bifidobacteria. Therefore the objective of this research was to determine whether different commercial infant formulas are associated with differences in the growth and acid production of bifidobacteria in skim milk. Fifteen different strains of bifidobacteria were used in this study. Skim milk samples (100ml) were fortified with one of the 15 infant formulas and sterilized at 65 °C for 30 min. Samples were then cooled to 40°C and inoculated with individual overnight strains of bifidobacteria to achieve a final inoculum level of 3.0 log CFU/ml. Samples were then incubated at 37°C for 24 hrs. Bacterial growth was monitored at different time intervals by measuring pH values and total titratable acidity. At the end of the incubation period, samples were withdrawn and appropriate dilutions were surface plated on MRS agar. Results showed that the different rates growth of bifidobacteria were observed due to different formulas. Bovine milk protein hydrosylate based formulas enhanced the growth of bifidobacteria (as measured by the acid development and total bacterial population) significantly (P <0.05) compared with other formula base types. These results suggest that bovine milk protein hydrosylate based promote the growth of bifidobacteria and should be considered when selecting formula as an alternative for mother's milk.

Key Words: growth factor, bifidobacteria

M78 Induction of α and β galactosidases from *Lactobacillus reuteri* by different metal ions. A. Y. Alazzeh*[1], S. A. Ibrahim[1], D. Song[1], A. Shahbazi[1], and A. A. AbuGhazaleh[2], [1]*North Carolina A & T State University*, *Greensboro*, [2]*Southern Illinois University*, *Carbondale*.

Probiotics are food grade bacteria that could be used safely and directly as food supplements. Probiotics have many health benefits to the host such as better digestibility of sugars mainly lactose and raffinose, antimicrobial activity and decrease blood cholesterol of the host. Health benefits of probiotics are strain specific and *Lactobacillus reuteri* has been shown to have good potential for the production of digestive enzymes (α and β-galactosidases). Bacterial media could be an important factor in over producing these enzymes. The induction of α and β-galactosidases in probiotic bacteria is one of the interesting areas in food science. The objective of our study was test the induction of α and β-galactosidases by metal ions. 10 mM of Na^+, K^+, Fe^{2+}, Cu^{2+}, Mg^{2+} and 1 mM of Mn^{2+} were are added separately to the growth media to test the induction of α and β-galactosidases in six strains of *L. reuteri* (CF2-7F, DSM20016, MF14-C, MM2-3, MM7 and SD2112). Results showed that the activity of α and β galactosidases in *L. reuteri* in response to added metal ions is strain specific. The addition of Cu^{2+} lead to a complete inhibition of both enzymes, while the addition of Fe^{2+} lead to partial inhibition of both enzymes. *L. reuteri* (strain CF2-7F) showed the highest α and β-galactosidase activity when grown on a media with added Mn^{2+} ions (22.66 and 19.33 Gal U/ml, respectively). One mM Mn^{2+} ions could be added to the growth media of CF2-7F to induce the activity of both enzymes.

M79 Immobilization of *Lactobacillus acidophilus* in apple pieces (*Pyrus malus* L.) and mamey sapote (*Pouteria sapota*) for whey fermentation. M. E. Yañez-Villar[1], E. Paz-Gamoba*[1], A. Perez-Silva[1], H. S. García[2], and M. Montero-Lagunes[3], [1]*Instituto Tecnologico de Tuxtepec*, *Tuxtepec, Oax, Mexico*, [2]*Instituto Tecnologico de Veracruz*, *Veracruz, Ver, Mexico*, [3]*INIFAP Campo Experimental*, *Veracruz, Ver, Mexico*.

Lactobacillus acidophilus is a homofermentative probiotic bacterium which has been employed to treat digestive disorders. Immobilized cell preparations have been used to provide stability and better process conditions. In this work we evaluated cell viability of *L. acidophilus* immobilized on apple and mamey sapote chunks. Enriched whey was used as propagation medium with cell concentrations of 1, 5 and 10 gL^{-1}. *L. acidophilus* cells were immobilized at 37 °C for 12 h without stirring on fruit pulp cubes of 0.5 or 1 cm. The preparations fermented whey supplemented with 2% glucose and 1% yeast extract, and a control was included which contained free cells, under the same reaction conditions. Cell viability, pH values and acidity as % lactic acid were monitored in stored fermented whey samples that were kept at 4°C for 90 days. Fermented wheys developed acidity with decreased pH values and cell populations of 10^8 CFU/mL were reached with a 10 gL^{-1} inoculum in 8 h. Cells immobilized on mamey sapote cubes produced less acid but were more stable than free cell preparations and their populations reached >10^8UFC/mL with the same inoculum after 90 days of storage. Immobilized cell preparations showed good stability and re-usability, showed potential as carrier of probiotic bacteria as *L. acidophilus* and can be used to develop probiotic drinks containing fruit pulp and whey with a fermentation time of 6-8 h.

Key Words: probiotic, immobilization, *Lactobacillus acidophilus*

M80 A simple on-farm technique for early detection of foreign substances in milk. M. H. Hathurusinghe*[1], A. Alazzeh[1], A. Shahbazi[1], S. A. Ibrahim[1], and A. A. AbuGhazaleh[2], [1]*North Carolina A & T State University*, *Greensboro*, [2]*Southern Illinois University*, *Carbondale*.

High accessibility to dairy farms and poor level of biosecurity creates the possibility of intentional contamination of milk with biological or chemical agents. If such an event occurred contaminated milk from a single farm could affect large fraction of dairy output. Current available contamination detection methods require sophisticated techniques and cumbersome procedures. To improve detection capabilities, simple, robust, and rapid and effective techniques are needed. The main objective of this project was to investigate the use a simple and rapid test using Lactic Acid Bacteria (LAB) as indicator organisms to detect contaminants in milk. Preliminary studies have shown that LAB are sensitive to a number of toxins including arsenic, cadmium and cyanide. In this study, the ability of LAB to detect rat poison and its major component chemicals (Brodifacoum) was tested. Five strains of *Lactobacillus reuteri* were added to test tubes separately containing 10ml of MRS broth

and different concentrations of either a commercial brand of rat poison or a single chemical component. The test tubes were then incubated at 37 C. Growth of the bacteria was monitored by measuring the optical density. pH values of each sample was measured at the end of the incubation period. Four out of the five strains showed sensitivity for rat poison. Further studies will be carried out with the other LAB to select the strains that show fastest and greatest sensitivity and an organic dye will then be selected, which gives rapid color change for the pH change. This system will be improved to a highly sensitive, environmentally safe, quick and accurate test kit which could be used as a universal marker for early detection of terrorist attacks to the food supplies.

Key Words: biosecurity

M81 Fatty acid composition in ewe's milk fat produced in lowland, hill and highland areas of Sardinia. M. G. Manca, F. Puggioni, R. Boe, R. Rubattu, G. Battacone*, and A. Nudda, *Dipartimento di Scienze Zootecniche, University of Sassari, Italy*.

Aim of this work was to determine the fatty acid (FA) profile of sheep milk from farms located at different altitudes and characterized by different feeding practices. The FA profile, including the content of conjugated linoleic acid (CLA c9, t11), vaccenic acid (VA; C18:1 t11) and n3 FA, was determined by gas-cromatography. Milk bulk samples were collected every two weeks from April to July 2008 from 15 sheep farms of Sardinia: five farms in the lowland, five in the hill and five in the highland. Data were analyzed with a linear model using sampling period, altitude and sampling period × altitude as fixed factors. During the trial, sheep feeding was widely based on pasture, with some differences among the 3 areas. The FA composition was significantly affected by sampling period. The highest contents of CLA, VA and n3 FA (2.1, 4.6 and 2.0 g/100g of FAME, respectively) were observed in April when pasture availability was the highest, and the lowest ones were in July (1.1, 1.3 and 1.0 g/100g of FAME, respectively) when grass was more mature. Altitude influenced significantly all FA analyzed (Table 1). Interaction was significant for almost all FA, except for VA and CLA. The contents of VA, CLA, and C18:3 n3 were higher in lowland farms compared to hill and highland. A possible explanation for this pattern could be the differences in sheep farming system among the areas, especially the greater availability of fresh grass in the lowland, due to a larger presence of cultivated grass pasture.

Table 1. Fatty acid profile in milk produced in sheep farms localized at different altitude

	Altitude		
Fatty Acid (g/100g of FAME)	Lowland	Hill	Highland
C4-C16	52.1^{b}	51.6^{ab}	52.5^{a}
C18	10.9^{b}	12.53^{a}	12.21^{a}
C18:1 t11	2.7^{a}	2.5^{ab}	2.3^{b}
C18:1 c9	22.0^{b}	22.7^{ab}	23.1^{a}
C18:2 c9,c12	3.4^{a}	2.9^{b}	2.6^{c}
C18:3 n-3	1.5^{a}	1.2^{b}	0.8^{c}
CLAc9, t11	1.5^{a}	1.3^{b}	1.2^{b}
PUFA n-3	1.9^{a}	1.6^{b}	1.1^{c}
n6/n3	2.0^{b}	2.2^{b}	3.0^{a}

^{a,b,c}Means within a row with different superscripts differ.

Key Words: fatty acid, sheep milk, altitude

M82 Properties of nanopowdered chitosan-added and cholesterol-reduced yogurt during storage. M. H. Seo, Y. S. Lee, and H. S. Kwak*, *Sejong University, Seoul, Korea*.

The present study designed to develop the nanopowdered chitosan-added and cholesterol-reduced yogurt, and investigate the physico-chemical property and microbiological changes during storage. The percentages of powdered (PC, 150 μm) and nanopowdered chitosan (NPC, 500-600 nm) were 0.1, 0.3, 0.5 and 0.7%. The cholesterol removal was in the range of 92.7 to 93.5%. The pHs in PC and NPC-added yogurts were unchanged for 15 days, however, no chitosan added yogurt showed a pH decrease from 4.21 at 0 day to 4.05 at 10 days and was maintained thereafter. The counts of lactic acid bacteria decreased as percent of PC and NPC addition increased and storage time. At 15 day storage, the counts were 1.14 × 108 cfu/ml in no chitosan-added group, while in the range about 105 to 106 cfu/ml in both NPC and PC-added groups. In both PC and NPC-added yogurts, the viscosity decreased with storage period and it were significantly lower compared with that in no-chitosan-added group through the storage except 0.7% PC-added yogurt ($p < 0.05$). There was no trend found in color, however, a-value in the NPC-added yogurt was significantly different compared with other yogurts ($p < 0.05$). Especially, 0.7% PC or NPC-added yogurts showed a significant difference in most of sensory characteristics at all storage periods. The present study indicated that NPC or PC addition into yogurt resulted in pH maintenance during 15 day storage which was due to less counts of lactic acid, and less than 0.5% chitosan may be applicable to the nanopowdered chitosan-added and cholesterol-reduced yogurt development.

Key Words: functional yogurt, nanopowdered chitosan, storage

M83 Residual beta-cyclodextrin and entrapped nutrients in milk treated by crosslinked beta-cyclodextrin. H. J. Ha, J. E. Lee, and H. S. Kwak*, *Sejong University, Seoul, Korea*.

This study was carried out to investigate the residual beta-cyclodextrin(beta-CD) and entrapped nutrients, such as water-soluble vitamins(L-ascorbic acid, niacin, thiamine and riboflavin), free amino acids, short-chain free fatty acid and lactose when cholesterol was removed in milk (milk fat: 3.4%, cholesterol: 10.6mg/100ml) treated by various concentrations of crosslinked beta-CD (0.4, 0.6, 0.8, 1.0 and 1.2%). The beta-cyclodextrins provided average 92.7% removal of cholesterol when 1.0% of the beta-CD was added. The residual beta-CDs were 1.22 and 1.32 ppm when 0.4% of crosslinked and powdered beta-CD were added, respectively. And the residuals proportionally increased to 3.00 and 3.18 ppm in 1.0% both beta-CDs. In the loss of nutrients observation, the difference of loss was not found in any nutrients and the additions of crosslinked and powdered beta-CD in the milk. The content of lactose in control milk was 4.86% and the loss was ranged from 0.00 to 0.03%. The total concentration of free amino acid was 8.78 mol/ml and the loss was ranged from 0.26 to 0.71 mol/ml. The concentrations of L-ascorbic acid, niacin, thiamine and riboflavin were 3.24, 1.33, 0.51 and 1.31 ppm in the control milk and the losses of the vitamins were ranged 0.02~0.05, 0.01~0.06, 1.11~0.16 and 0.01~0.06 ppm, respectively. The concentrations of butyric, caproic, caprylic and capric acid in the control milk were 4.45, 2.26, 2.78 and 3.21 ppm and the losses ranged 0.00~0.03, 0.00~0.04, 0.00~0.05 and 0.00~0.04 ppm, respectively. In conclusion, this study indicated that the residual beta-CD was trace amounts and entrapped nutrients were negligible.

Key Words: residual beta-cyclodextrin, entrapped nutrients, cholesterol-removed milk

M84 Effect of reconstituted milk made from freeze-dried milk powder on physicochemical properties. S. H. Kim, S. I. Ahn, Y. H. Chang, and H. S. Kwak*, *Sejong University*, *Seoul, Korea*.

This study was carried out to investigate the reconstituted milk made from freeze-dried milk powder (FDMP) that was made by newly developed continuous multi-stage process. Physicochemical properties tested were composition, color, thiobarbituric acid value (TBA), short-chain free fatty acids, water-soluble vitamins and fat-soluble vitamins stored at 4C for 18 days. The compositions of FDMP reconstituted milk were 3.6% fat, 3.2% protein, 4.8% lactose and 87.2% water which were similar to that of the control and spray-dried milk powder (SDMP) origin. In color, L-, a- and b-value were slightly different among samples, however, they were not significant ($P<0.05$). TBA absorbance of FDMP reconstituted milk was not significantly different from that of SDMP milk, however, both products were higher than control milk. Total short-chain fatty acids of FDMP milk were similar to that of control during storage up to 18 days, however, SDMP milk showed significantly higher than FDMP milk in the fatty acids. The concentrations of water-soluble vitamins, such as L-ascorbic acid, niacin, thiamine and riboflavin showed decreasing trend during storage periods. The vitamins from FDMP were lower than that of control, but higher than that of SDMP milk. The fat-soluble vitamins, such as retinol and tocopherol showed similar decreasing trends to the water-soluble vitamins during storage. In conclusion, the results of this study indicated that the quality of reconstituted milk made from FDMP is much improved than that of SDMP milk.

Key Words: reconstituted milk, freeze-dried milk powder, vitamins

M85 Comparison of physico-chemical properties between freeze-dried and spray-dried milk powders during storage. S. H Kim, J. H. Park, and H. S. Kwak*, *Sejong University*, *Seoul, Korea*.

The present study was carried out to compare the physico-chemical properties between freeze-dried milk powder (FDMP) and spray-dried milk powder (SDMP) stored at different temperatures (4, 20 and 37°) during 80 days. There was no difference in moisture, protein, fat and ash between both milk powders ($p > 0.05$). Dispersibility and wetting time were higher in FDMP than in SDMP, which indicated the higher quality of FDMP in physical property. FDMP showed the slightly higher pH was found at 4 and 27° throughout the storage period compared with SDMP, however, a profound decrease was observed in both FDMP and SDMP at 37° after 50 day. Similarly, solubility was higher in FDMP than in SDMP at 4 and 27°, however, the solubility in FDMP decreased dramatically from 30 day storage when stored at 37°. As expected, FDMP showed the lower moisture content at 4 and 27°, and an increase after 40 day storage was found at both FDMP and SDMP. During 80 day storage, non-protein nitrogen (NPN) content was greater in SDMP at every temperature and increased continuously with the storage. In FDMP, after 60 day storage, NPN content was over 0.20, however, SDMP showed over 0.20 at the beginning of storage. Therefore, the present study indicated that the FDMP maintained the higher quality in physico-chemical properties including pH, spreadability, and solubility than SDMP, especially at 4 and 27° during 80 day storage.

Key Words: freeze-dried milk powder, spray-dried milk powder, physicochemical properties

M86 Phylogenetic analysis of dairy *Penicillium* rDNA. G. Petit* and S. Labrie, *Université Laval*, *Québec, Canada*.

Despite their industrial importance, little is known about the genetics of dairy *Penicillium* spp. At present, 13 *P. camemberti* (syn. *P. candidum* and *P. caseicolum*) genes and 13 *P. roqueforti* are available in public sequence databases. However, little information is available on the ribosomal DNA (rDNA) of either species since only the sequence of the ITS1-5,8S-ITS2 region has been deposited in databases. Based on this 600 bp sequence, it has been shown that *P. commune* and *P. camemberti*, which is considered a domesticated form of *P. commune*, are virtually identical at the phylogenetic level. The *P. commune* designation is still widely used in the scientific literature because of a number of differences at the phenotypic level, mainly growth rate and color variations. The objective of the present study was to determine the genetic variability over the entire rDNA operon sequence (4768 bp) of four terverticillate *Penicillium* spp. found in the dairy environment (*P. camemberti*, *P. commune*, *P. roqueforti*, and *P. chrysogenum*). Multiple sequence analyses revealed that there are clear phylogenetic similarities between the four species. In addition, the operons of *P. camemberti* and *P. commune* differed by a single nucleotide, confirming that there is no significant difference between these two species at the phylogenetic level. *P. chrysogenum* and *P. roqueforti* had the highest variability, with 26 polymorphisms. Overall, our results showed that rDNA is highly conserved among these four *Penicillium* species, with only 31 polymorphisms detected.

Key Words: dairy foods, phylogenetic analysis, *Penicillium* spp.

M87 Effects of culture conditions on the growth and autoaggregation ability of bifidobacteria and *Lactobacillus reuteri*. O. A. Hassan*[1], S. A. Ibrahim[1], A. A. AbuGhazaleh[2], A. Shahbazi[1], and Y. Murad[3], [1]*North Carolina A & T State University*, *Greensboro*, [2]*Southern Illinois University*, *Carbondale*, [3]*National Research Council-Canada*, *Ottawa, Canada*.

The use of bifidobacteria and lactobacillus as dietary adjuncts or as a source of probiotics is a subject of intense and growing interest. Several reports have indicated that probiotics have the ability to provide several health benefits. However, in order for these cultures to manifest beneficial effects, they need to achieve a viable mass through aggregation. A major factor affecting aggregation is the ability of these bacterial cells to adhere and grow within the host. This ability is a desirable property sought for use in commercial food preparations. The objective of this study was to evaluate the effects of different chemical factors on the growth and autoaggregating ability of bifidobacteria and *Lactobacillus reuteri*. Thirty-seven strains of bifidobacteria and eight strains of *L. reuteri* were cultivated in different culture media, (TPY, MRS) initial pH, and temperatures. Autoaggregation behavior was determined using the adhesion assay. Our results showed that the addition of calcium significantly induced autoaggregation for all of the strains in TPY media. We also observed that autoaggregation ability increased mainly at low initial pH levels (pH 5.5) and lower incubation temperatures (30-34 C). These findings indicate that autoaggregation ability can be significantly affected by several host environment factors including initial pH value and calcium. To achieve effective aggregations of probiotic bacteria, emphasis should be placed on optimizing growing conditions through introduction of calcium and pH lowering foods.

Key Words: autoaggregation, *Lactobacillus reuteri*

M88 80% whey (WPC) and serum protein (SPC) concentrate and 95% serum protein (SP) reduced micellar casein concentrate (MCC): Production and composition. J. Zulewska*[2], D. M. Barbano[1], M. Newbold[1], M. Drake[3], E. A. Foegeding[3], and C. Moraru[1], [1]*Cornell University, Ithaca, NY*, [2]*University of Warmia and Mazury, Olsztyn, Poland*, [3]*North Carolina State University, Raleigh*.

The research objective was to compare the production characteristics and composition of 80% WPC and 80% SPC. Raw whole milk (ca 1900 kg) was split into 2 portions: one was pasteurized (72C, 15s) and made into Cheddar cheese and whey and the other was cold separated into skim milk (SM) and cream. The SM was pasteurized (72C, 15 s), microfiltered (MF) to 3X (0.1 μm ceramic uniform transmembrane pressure) and diafiltered (DF) to 3X twice by adding reverse osmosis (RO) water back to the original SM weight to produce 95% SP reduced MCC. Separated whey (640 kg) and MF permeate (705 kg) from the first stage of MF of skim milk were ultrafiltered (UF) and DF using a spiral-wound 10 kDa polyethersulfone membrane to produce liquid 80% WPC and SPC. Whey and MF permeate were UF 5.2 and 5.5 X, respectively. Protein content [measured by infrared spectrophotometer (IR)] was 47 and 41% of protein plus lactose in the retentate for whey and MF permeate after UF, respectively. Next, UF retentates from whey and MF permeate were diluted to their original weight with RO water and DF until the retentate protein content measured by IR was close to 90% of protein plus lactose. The DF retentates (ca 55 kg) were kept frozen (-40C) prior to spray drying (200C and 95C at inlet and outlet, respectively). All processing was replicated 3 times. Mean UF and DF flux was higher for WPC than SPC, but flux decreased more per hour for WPC than SPC over a 135 min run. Over a longer run, the WPC flux may be lower. Liquid SPC was clear while WPC was opaque; L-value was 18.5 vs. 52.5 for liquid SPC and WPC, respectively. Liquid SPC pH was higher than WPC (6.9 vs. 6.5, respectively). Spray dried (SD) 80% WPC contained more fat on a dry basis (db) than SPC, 0.5 vs. 8% and this may cause sensory differences between products. WPC contained more glycomacropeptide than SPC (about 4.9 vs. 0% of protein) and this may cause differences in functionality. The SD 95% SP reduced MCC contained 2.7% fat and 84.6% protein on db.

Key Words: whey protein, serum protein, micellar casein

Forages and Pastures: Forage Compostition, Analysis and Utilization

M89 Utilizing near infrared (NIR) spectroscopy to predict carbohydrates (sugars) in forages. J. Horst*[1,2] and G. Ayangbile[1,2], [1]*Agri-King Inc., Fulton, IL*, [2]*Analab, Fulton, IL*.

The objective of this study was to determine if Near Infrared (NIR) can define the concentrations of carbohydrates in the cell contents of forages better than past methodologies. Total water soluble carbohydrates (WSC) and other acidic methods have been instituted in the past to quantify sugar contents. These methods are plagued with reproducibility problems, trying to determine a proper reference standard and numerous matrix interferences. NIR calibrations can be developed to assess carbohydrate concentration of mono and disaccharides in forages. The ability to rapidly predict Xylose, Fructose, Glucose and Sucrose in both fermented and non-fermented forages can provide useful nutritional information for optimizing animal performance. NIR also can provide accurate mannitol (sugar polyol) predictions on fermented silages, indicating undesirable heterofermentation. Calibrations were derived from reproducible wet chemistry techniques with extractions subjected to High Pressure Liquid Chromatography (HPLC) for analysis. The quantification of cell contents in feedstuffs including hay, haylage, corn silage, small grain silages and grain sources can potentially reduce incidents of laminitis in horses while improving feed efficiency in dairy, swine and poultry rations. NIR has achieved strong statistical correlations exceeding ≥.90 1-VR (validation R-squared) on most analytes and forage matrices.

Key Words: carbohydrates, sugars, NIR Calibrations

M90 Investigation into the use of NIR predicted 12 and 30 hr IVNDFD as a measure of corn silage quality. R. T. Ward[1] and R. A. Patton*[2], [1]*Cumberland Valley Analytical Service, Maugansville, MD*, [2]*Nittany Dairy Nutrition, Inc., Mifflinburg, PA*.

NDF digestibility in corn silage is important in determining the amount of nutrients provided in high producing dairy cattle with low rumen residence times. There is poor understanding of how to utilize available NIR predicted in vitro NDF digestibility (IVNDFD) evaluations to infer differences in digestibility rates at rumen appropriate time points. This study characterized relationships between common nutrients in corn silage and IVNDFD at 12 hrs and 30 hrs measured by NIR to determine if the use of an earlier IVNDFD time point (12 hrs) allows for better characterization of rates of NDF digestibility. This study involved 14,576 samples of corn silage, including both normal and BMR types, for which both 12 and 30 hr NIR measured IVNDFD were reported for 3 crop years. Samples were analyzed for DM%, and CP%, soluble protein%, lignin%, ADF% and NDF% of DM. All nutrients were measured with NIR. The equations for 12 hr and 30 hr INVDFD had R^2 of .883 and .853 for samples run by rumen incubation with digestibility of 36.7±1.57% and 60.9±2.41% respectively. Data were analyzed using proc mixed and proc reg of SAS. Fixed effects were crop year, geographic area (Northeast, Southeast, Midwest and Far West) and DM group. Dependent variables were IVNDFD at 12 and 30 hrs, the hourly rate of digestion for the first 12 hr and the last 18 hr. The Far West had lower 12 hr IVNDFD compared to other regions. Means for 12 hr and 30 hr IVNDFD were 38.7% and 58.3% respectively. Regression of 12 hr IVNDFD on 30 hr had R^2=.51. Regression of rate of 12 hr IVNDFD with the final 18 hr yielded an R^2 of .18; thus speed of 12 hr digestibility was unrelated to speed of the last 18 hrs. Using all items analyzed, the maximum R^2 was .55 for 12 hr IVNDFD and .60 for 30 hr. We conclude 12 hr NIR predicted IVNDFD has the potential to be more appropriate than 30 hr NIR IVNDFD for characterizing NDF digestibility differences in corn silage. There appears to be a consistent geographical and DM% effect on NIR predicted 12 hr IVNDFD.

Key Words: NIR, IVNDFD, geographic effects

M91 Ethanol or amylase pretreatments affect estimates of in vitro NDF digestibility. A. L. Miller, J. P. Goeser, and D. K. Combs*, *University of Wisconsin, Madison*.

Our objective was to determine if pre-treating feed samples with ethanol or amylase affects estimates of NDF or in vitro NDF digestibility (iv NDFD). We also tested whether pre-rinsing Ankom F-57 fiber bags with

acetone affects estimates of NDF and ivNDFD. An alfalfa and a mixture of 70% alfalfa and 30% corn grain were dried (60 C), ground (1mm), and weighed (0.5 g) into Ankom F57 fiber bags. Half the bags were pre-rinsed in acetone and dried at 100 C prior to adding sample. Both sets of bags were sealed and pretreated as follows: untreated (control), bags with feed sample were rinsed in 70% ethanol prior to NDF and iv NDFD analysis (ETOH), bags and feed were hot water-rinsed with amylase prior to NDF iv NDFD analysis (AMYLASE), or samples were sequentially rinsed with ethanol and amylase prior to NDF and iv NDFD analysis (ETOH-AMYLASE). In vitro NDF digestibility (24 h) was calculated as: ivNDFD (% of NDF) =100 X [(NDF0h –NDF residue 24 h)/(NDF0h)]. NDF concentration of alfalfa (43.1% of DM) or the alfalfa and corn mix (35.7% of DM) was not affected by acetone, or ETOH, AMYLASE, or ETOH-AMYLASE pretreatments. Estimates of in vitro NDF digestibility (% of NDF) were higher from samples that had been pretreated with acetone (alfalfa; 28.6 v 30.9, P<0.1, alfalfa-corn mix; 21.1 v 26.8, P<0.05)) than control. The 24 h ivNDFD for alfalfa (control: 29.7% of NDF) increased (P<.01) when feeds were pretreated with ETOH, AMYLASE, or ETOH-AMYLASE (36.8, 36.3, 38.9% of NDF, respectively). The iv NDFD values of bags containing the alfalfa-corn control (23.9% of NDF) were lower than from samples that had been pretreated with ETOH, AMYLASE or ETOH-AMYLASE (35.6, 38.5, 37.6% of NDF, respectively). Acetone pretreatment of Ankom F57 forage bags had little effect on estimates of NDF, but did influence the estimate of 24h iv NDFD. Pre-treatment of the alfalfa or the alfalfa-corn mix with ethanol, amylase or a sequential treatment of ethanol and amylase did not affect estimates of NDF. Estimates of iv NDFD were higher when samples were pretreated with amylase, ethanol or the sequential combination of ethanol and amylase.

Key Words: forage fiber, NDF digestibility, neutral detergent fiber

M92 Condensed tannins from purple prairie clover inhibit growth of *Escherichia coli* O157:H7. Y. Wang*[1], T. A. McAllister[1], S. N. Acharya[1], and A. D. Iwaasa[2], [1]*Agriculture & Agri-Food Canada Research Centre*, *Lethbridge, Alberta, Canada*, [2]*Agriculture & Agri-Food Canada, Semiarid Prairie Agricultural Research Centre*, *Swift Current, Saskatchewan, Canada*.

The capacity of purple prairie clover (*Petalostemon purpureum*) condensed tannins (PCT) to inhibit growth of *Escherichia coli* O157:H7 was assessed in vitro. PCT were obtained from whole plant, full bloom forage by methanol extraction followed by Sephadex LH20 purification. One strain (25922) of generic *E. coli* and eight strains of *E. coli* O157:H7 of different origins and possessing different antibiotic resistance traits (strains 3081, E318N, E319N, H4420, H4420nal, R508N, R508N2006 and EDL933) were cultured individually in M9 medium in 70-mL Kimax glass tubes, with PCT included at 0, 25, 50, 100 or 200 μg/mL (n = 4). Bacterial growth was assessed by measuring the optical density of the cultures at 600 nm (OD_{600}) after 4, 6, 8, 12 and 24 h of incubation. Including PCT in M9 medium at levels as low as 25 μg/mL reduced (P < 0.01) growth of all nine strains of bacteria examined, demonstrating a broad range of activity of the tannins. Inhibition of all bacterial strains increased linearly (P < 0.01) with PCT concentrations from 0 to 200 μg/mL. In all of the cultures, inhibition by PCT was greater during rapid growth (at 4 to 8 h; up to 97%) than during the stationary phase (at 24 h; up to 50%). Among the strains tested, EDL933, R508N2006 and H4420nal were most susceptible to PCT, and 3081 and E319N were least inhibited. By 24 h, optical densities of 0.6 were achieved in all PCT cultures (compared with OD_{600} of 0.85 to 1.15 in control cultures), indicating that the anti-*E. coli* O157:H7 activity of PCT at levels up to 200 μg/mL was bacteriostatic, rather than bactericidal. Dietary incorporation of condensed tannins from purple prairie clover could be a potential tool for mitigating *E. coli* O157:H7 in beef cattle.

Key Words: *E. coli* O157:H7, purple prairie clover, condensed tannins

M93 Evaluation of tannins from forages for their capacity to inhibit growth of *Escherichia coli* O157:H7. Y. Wang*[1], T. A. McAllister[1], K. H. Ominski[2], D. O. Krause[2], and K. M. Wittenberg[2], [1]*Agriculture & Agri-Food Canada Research Centre*, *Lethbridge, Alberta, Canada*, [2]*University of Manitoba*, *Winnipeg, Manitoba, Canada*.

Antimicrobial activity of plant tannins against rumen bacteria is well documented, but their potential for mitigating *E. coli* O157:H7 in beef cattle production is not known. Tannins from 10 forages growing on the western Canadian prairie, two commercially available products, and a brown seaweed (*Ascophyllum nodosum*; positive control) were extracted and purified, and their inhibitory effects on *E. coli* O157:H7 were determined. The bovine isolate, *E. coli* O157:H7 strain 3081 kan^R amp^R (resistant to kanamycin and ampicillin, each at 100 μg/mL), was cultured in 150-mL serum vials in M9 medium supplemented with each tannin type (n = 3). The tannins were added to medium individually at 400 μg/mL, except those from brown seaweed (50 μg/mL). Bacterial growth at 39°C was assessed throughout a 24-h incubation by measuring optical density at 600 nm (OD_{600}) after 0, 2, 4, 6, 8, 10, 12 and 24 h of incubation. Tannin from seaweed exhibited stronger anti-*E. coli* O157:H7 activity than did any of the other 12 tannins, inhibiting growth completely over the 24-h incubation. Among the terrestrial forages, purple prairie clover tannins showed the greatest activity against *E. coli* O157:H7 (i.e., lowest OD_{600}). Bacterial growth in cultures supplemented with tannins from three cultivars of sainfoin (Metrose, Erryr and Nova) and from Oxley cicer milkvetch was similar (P>0.05) to that observed in the control (no added tannins). In the presence of tannins from Aurora Alsike clover, white clover and birdsfoot trefoil, growth was reduced (P < 0.05) only at 10 and 12 h, compared with control, whereas tannins extracted from cicer milkvetch and trefoil languile inhibited (P < 0.05) growth at 8, 10, 12 and 24 h of incubation. Commercially available tannic acid and Quebracho tannins inhibited (P < 0.05) bacterial growth at 10, 12 and 24 h. Anti-*E. coli* O157:H7 activity of plant tannins varied greatly among the species examined, depending on their origin. Only tannins from purple prairie clover and brown seaweed possessed significant activity against *E. coli* O157:H7 and warrant further evaluation.

Key Words: tannins, *E. coli* O157:H7, forage

M94 Comparing mathematical models to estimate *in vitro* gas production parameters of hydroponic forage. E. Herrera-Torres, A. Cerrillo-Soto, M. Murillo-Ortiz, O. Reyes-Estrada, and A. S. Juarez-Reyes*, *Universidad Juarez del Estado de Durango*, *Durango, Dgo. Mexico*.

The goodness-of-fit test of four mathematical models: Gompertz, Richards, Logistic, and Ørskov and McDonald to describe the kinetic parameters of *in vitro* gas production from wheat hydroponic forage harvested at 12 days was evaluated. Samples were incubated in 100 ml glass syringes. Gas production was registered at 0, 3, 6, 12, 24, 48, 72, and 96h. The residual mean square (RMS) and the coefficient of determination (R^2) were used as selection criteria. Gas production data were obtained by the non lineal regression procedure using the NCSS 2000

program. Gas parameters from models were analyzed using ANOVA. Tukey´s test was used to compare means. The Gompertz model had the best goodness-of-fit according to values of 0.99 for R^2 and 4.28 for RMS. Highest gas production was obtained using Ørksov and McDonald model and was different among models (P<0.05). Similarly, the constant rate of gas production varied among models (P<0.05). Utilization of different models to evaluate *in vitro* gas production might avoid possible bias due to under or overestimation of *In vitro* gas production parameters.

Table 1. Statistical criteria for fitting of the models to evaluate *in vitro* gas production in hydroponic forage

Model	RMS	R^2
Logistic	14.56	0.98
Gompertz	4.28	0.99
Richards	11.78	0.99
Ørskov and McDonald	18.39	0.98

Key Words: mathematica models, *in vitro* gas production, hydroponic forage

M95 Effect of citrate synthase genes transformed into alfalfa on aluminum tolerance of its cells. F. F. Fan*, J. J. L. Li, Y. M. W. Wu, and J. X. L. Liu, *Zhejiang University*, *Hangzhou, China*.

This study was carried out to investigate the effect of bivalence citrate synthase genes transformed into alfalfa (*Medicago sativa* L.) on aluminum tolerance of its cells. Two different kinds of citrate synthase genes (CS) were cloned from *E.coli* (CSI, 1284bp) and *Oryza sativa* L (CSII, 1425bp), respectively, and then bivalence expression vector, containing CSI, CSII and the phosphomanose isomerase (PMI) gene isolated from Escherichia coli as the selectable marker gene, was constructed and transferred into *Agrobacterium tumefaciens* LBA4404 strain through electrotransformation method. The expression vector containing CSI alone was also constructed with the same method. Leaf disks of *Medicago sativa* L cultivar Youke were inoculated with *Agrobacterium tumefaciens* LBA4404 and selected on the mannose(30g/l). The callus were grown on the solid SH medium for 6 weeks in a chamber at 250C, 75% relative humidity, and exposed to 14 h of light and 10 h darkness. Integration of the transgene was detected by PCR with genomic DNA of the callus as template. Transcription of the transgene was determined by cDNA dot blotting analysis. The callus tissues of transgene were cultured in the liquid SH medium under the shake at 150 r.p.m and 250C for 2 days. The activity of the cells and their ATPase were detected when stressed under the different concentrations of Al3+. The specific PCR products of expected size (1284bp and 1425bp) were found in the genomic DNA from all transformed callus but not occurred in the non-transformed callus, indicating that two CS genes were integrated into the transformed callus. The cDNA dot blotting of the transformed callus revealed that the interested genes were transcripted. The activity of both the cells and their ATPase was significantly (P<0.05) higher in the transformed cells than that in the non-transformed cells, and with significantly (P<0.05) higher activity in the transformed cells of CSI and CSII as compared with those of CSI. It is suggested that the expression of the CS gene in the transformed cells could improve the aluminum tolerance of alfalfa (*Medicago sativa* L.) cells.

Key Words: citrate synthase gene, aluminum tolerance, alfalfa (*Medicago sativa* L.)

M96 Total digestible nutrient and energy values of new crossed and winter-hardy proanthocyanidin-containing alfalfa populations transformed with the maize bHLH (Lc) regulatory gene in ruminants: Comparison with non-transgenic alfalfa. A. Jonker*[1], P. Yu[1], Y. Wang[2], and M. Gruber[3], [1]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Lethbridge Research Centre, Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [3]*Saskatoon Research Centre, Agriculture and Agri-Food Canada*, *Saskatoon, SK, Canada*.

The objectives of this study were to determine digestible nutrients and energy values of three new crossed and winter-hardy proanthocyanidin-containing alfalfa populations transformed with the maize bHLH (Lc) regulatory gene in ruminants in a 3×2 factorial treatment design. Three new crossed Lc-transgenic alfalfa populations included 88-19×Rangelander, 88-09×Ramber, and 88-01×Beaver with two phenotypes of each (green, purple). The green phenotype contained no Lc-gene as non-transgenic control alfalfa (NT). The purple phenotype contained Lc-gene as Lc-transgenic alfalfa (LC). All samples were collected during two consecutive years (2007, 2008) in AAFC research field, Saskatoon, Canada. The items assessed include digestible nutrients (tdNFC, tdCP, tdFA, tdnNDF, TDN) and energy values (DE3X, ME3X, NEL3X for dairy; NEm and NEg beef). The results showed that there were no population effect (P>0.05) and no population × phenotype interaction effect (P>0.05). Averages of three population were 34.9, 23.4. 2.5. 7.2, and 64.2% of DM for tdNFC, tdCP, tdFA, tdnNDF and TDN respectively and 2.77, 2.35, 1.46, 1.58 and 0.98 for DE3X, ME3X, NEL3X, NEm and NEg, respectively. There were phenotype effects only on tdCP (NT vs. LC: 24.5 vs. 22.2% DM, P =0.014) and tdnNDF (NT vs. LC: 6.4 vs. 8.1% DM, P=0.056<0.10), but no phenotype effect on all energy values. In general, Lc-transformation did not affect on the energy values of the new crossed and winter-hardy proanthocyanidin-containing alfalfa.

Key Words: proanthocyanidin-containing alfalfa, TDN and energy values, beef and dairy

M97 Chemical profiles and protein and carbohydrate subfractions of new crossed and winter-hardy proanthocyanidin-containing alfalfa populations transformed with the maize bHLH (Lc) regulatory gene in ruminants: Comparison with non-transgenic alfalfa. A. Jonker*[1], P. Yu[1], Y. Wang[2], and M. Gruber[3], [1]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Lethbridge Research Centre, Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [3]*Saskatoon Research Centre, Agriculture and Agri-Food Canada*, *Saskatoon, SK, Canada*.

The objectives of this study were to determine chemical profiles and protein and carbohydrate (CHO) subfractions of three newly developed winter-hardy proanthocyanidin-containing alfalfa populations transformed with the maize bHLH (Lc) regulatory gene, in comparison with non-transgenic alfalfa in ruminants in a 3×2 factorial treatment design. Three new crossed Lc-transgenic alfalfa populations included 88-19×Rangelander, 88-09×Ramber, and 88-01×Beaver with two phenotypes of each (green, purple). The green phenotype contained no Lc-gene as non-transgenic control alfalfa (NT). The purple phenotype contained Lc-gene as Lc-transgenic alfalfa (LC). All samples were collected during two consecutive years (2007, 2008) in AAFC research field, Saskatoon, Canada. The CP and CHO fractions were partitioned according to the CNCPS system and included PA, PB1, PB2, PB3 and PC for protein fractions, and CA, CB1, CB2 and CC for carbohydrate fractions. Each fraction has different degradation behaviour (degradation rate) which is highly related to component nutrient availability. In chemical profile study, the results showed no population effect (P>0.05) and no population × phenotype interaction effect (P>0.05), but significant phenotype

effect (P<0.05) on chemical contents of anthocyanidin (0 µm/g DM in the Green vs. 197.4 µm/g DM in the purple), CP, CHO, ADICP and NDSF. Anthocyanidin had negative correlation (P<0.10) with CP, CHO, Hemicellulose, SCP, EIRCP and ratio of N to CHO. In CNCPS fraction study, there were no population effect (P>0.05) and no population × phenotype interaction effect (P>0.05), but phenotype effect (P<0.05) on carbohydrate CB2 and CB3 as well as ratio of PB to CB fraction. Anthocyanidin had negative correlation (P<0.10) with PB1, PB2, CB2 and ratio of PA to CA fraction. In conclusion, Lc-gene transformation partially affected chemical profile and carbohydrate subfractions of the newly developed proanthocyanidin-containing alfalfa.

Key Words: proanthocyanidin-containing alfalfa, protein and carbohydrate fractions, forage quality

M98 Sugarcane stalk proportion effects on dairy cow performance. S. Siécola Júnior[1], L. L. Bitencourt[1], V. A. Silveira[1], N. M. Lopes[1], G. S. Dias Júnior[1], J. R. M. Silva[2], R. A. N. Pereira[3], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, MG, Brazil*, [2]*Centro Federal de Educação Tecnológica*, *Januária, MG, Brazil*, [3]*Better Nature Research Center*, *Ijaci, MG, Brazil*.

Previous *in situ* digestibility data has shown that among sugarcane clones there is a positive correlation between the stalk to leaf ratio and whole plant digestibility. Stalk proportion is a high heritability trait; however it has not been used to select clones for alcohol and sugar production. This trial evaluated if there would be gain in dairy cow performance by acting upon this trait. Treatments were: Whole sugarcane plant or plant with complete leaf removal to simulate a clone with extremely high stalk to leaf ratio. Removing leaves decreased sugarcane NDF content from 52.7 to 42.3% of DM and forage particle size. The TMR ingredient composition was (% of DM): Sugarcane 18.3, corn silage 37.6, soybean meal 21.9, urea 0.2, citrus pulp 9.7, hydrated and ensiled mature ground corn 9.3, and a buffer-mineral premix 2.9. Diets nutrient composition was (No Leaves and Whole, respectively): CP 17.3 and 16.6, NDF 32.9 and 34.7, NFC 37.7 and 36.3. Fourteen Holsteins (256 DIM) were paired blocked and randomly assigned to a sequence of the two treatments in a crossover design with 21-periods and 14 days of adaptation. Daily milk yield was 18.4 kg for No Leaves and 18.2 for Whole (P=0.65) and DMI was 18.0 and 17.5, respectively (P=0.28). Differences in milk solids content and production, MUN, milk energy secretion, and chewing activity were not detectable (P>0.40). The removal of leaves tended do increased the intake of total tract digestible OM (P=0.10) and the ratio of milk energy secretion to digestible OM intake (P=0.08). The total tract DM digestibility was 75.1% for No Leaves and 71.4% of consumed for Whole (P=0.06). Although a positive response in dairy cow performance was not observed at this dietary sugarcane inclusion, digestibility variables suggest that sugarcane leaf removal may be advantageous. *Funded by Fapemig*.

Key Words: sugarcane, feed efficiency, digestibility

M99 Sugarcane stalk proportion effects on heifer growth. J. R. M. Silva[2], S. Siécola Júnior[1], L. L. Bitencourt[1], G. S. Dias Júnior[1], N. M. Lopes[1], V. A. Silveira[1], I. R. Rios[1], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, MG, Brazil*, [2]*Centro Federal de Educação Tecnológica*, *Januária, MG, Brazil*.

Previous *in situ* digestibility data has shown that among sugarcane clones there is a positive correlation between the stalk to leaf ratio and whole plant digestibility. Stalk proportion is a high heritability trait; however it has not been used to select clones for alcohol and sugar production. This trial evaluated if there would be gain in heifer growth by acting upon this trait. Thirty two Holstein-Zebu heifers were paired blocked and randomly assignment to a treatment for 42 days, following a 14-day standardization period used as covariate in the statistical model. Data obtained over time was analyzed using the repeated measures approach of the mixed procedure of SAS. Eight sugarcane clones were daily harvested in rotation from the same field. Treatments were: Whole plant or plant with complete leaf removal to simulate a clone with extremely high stalk to leaf ratio. Removing leaves decreased the NDF from 53.6 to 46.8% of DM, DM from 35.3 to 30.7% of fresh, and forage particle size. Diets composition was (No Leaves and Whole, respectively): Sugarcane 77.1 and 78.6, soybean meal 19.2 and 17.9, urea 1.0 and 0.9, CP 14.1 and 13.7, NDF 38.8 and 45.3, NFC 43.6 and 36.4 (% of DM). Body weight was 333 kg for No Leaves and 328 for Whole (P=0.14). There was an interaction between body weight and experimental week (P=0.07), the treatment effect got more pronounced with time. Daily body weight gain was 1.395 kg for No Leaves and 1.125 for Whole (P=0.05). Daily DMI was 8.4 kg for No Leaves and 8.7 for Whole (P=0.30), resulting in a ratio of daily gain to DMI of 0.158 and 0.122, respectively (P=0.05). Removing leaves reduced the daily ingestion time (P=0.04), had no effect on chewing time (P=0.96), and tended to decrease rumen pH (P=0.07). Intake of total tract digestible non-NDF OM was increased by leaf removal (P=0.03). Acting upon the sugarcane stalk to leaf ratio, genetically or mechanically, seems to be a promising avenue to accelerate heifer growth. *Funded by Fapemig.*

Key Words: sugarcane, heifer, digestibility

M100 Early-lactation cows fed concentrate do not respond to high-total nonstructural carbohydrates alfalfa. A. F. Brito*[1], G. Régimbald[2], G. F. Tremblay[3], A. Bertrand[3], Y. Castonguay[3], G. Bélanger[3], R. Michaud[3], and R. Berthiaume[1], [1]*Agriculture & Agri-Food Canada*, *Sherbrooke, QC, Canada*, [2]*Université Laval*, *Québec, QC, Canada*, [3]*Agriculture & Agri-Food Canada*, *Québec, QC, Canada*.

In late-lactation cows fed only forage, we reported that high-total nonstructural carbohydrate (TNC) alfalfa increased milk yield and N efficiency. The current study examines the effects of feeding high-TNC alfalfa on performance of early-lactation cows fed a high-concentrate diet. Alfalfa was cut at sundown or at sunup and conserved as baleage (46% DM). Ten multiparous (MC) and 8 primiparous cows (PC) were blocked by milk yield and parity and randomly assigned to treatments in a crossover design. Cows were fed high- or low-TNC alfalfa (59% of diet DM) plus a common concentrate (41% of diet DM). Alfalfas were fed once daily and concentrate (13.5% CP) 3 times a day. High- and low-TNC alfalfa baleage contained (% DM): 19 vs. 20 CP and 6.53 vs. 3.52 TNC. DMI and milk yield did not differ across treatments. However, 4% FCM was lower in the high- vs. low-TNC treatment due to reduced milk fat concentration with the former diet. The decrease in milk fat concentration with the high-TNC treatment was greater in MC than in PC (-0.26 vs. -0.10 unit of %) as evidenced by the significant TNC x parity interaction. MC fed low- vs. high-TNC diet possibly mobilized more body fat as shown by their lower BW gain, which might explain the increase in milk fat concentration. Reduced MUN with the high- vs. low-TNC treatment, particularly in PC, suggests better N utilization. Overall, high-TNC alfalfa had no effect on performance of early-lactation cows fed a high-concentrate diet.

Table 1.

	PC			MC				P	
Item	High-TNC	Low-TNC	SED	High-TNC	Low-TNC	SED	TNC	Parity	TNC× Parity
DMI, kg/d	18.9	20.1	0.70	23.6	23.9	0.59	0.13	<0.01	0.31
Milk yield, kg/d	25.0	26.1	0.81	34.4	33.9	0.68	0.58	<0.01	0.16
4% FCM, kg/d	22.9	24.3	0.85	31.2	32.1	0.71	0.05	<0.01	0.61
Fat, %	3.44	3.54	0.06	3.40	3.66	0.05	<0.01	0.76	0.05
Fat, kg/d	0.86	0.92	0.04	1.16	1.24	0.03	0.01	<0.01	0.91
Protein, %	2.74	2.83	0.05	2.71	2.74	0.04	0.07	0.42	0.37
Protein, kg/d	0.69	0.74	0.03	0.93	0.93	0.03	0.23	<0.01	0.23
MUN, mg/dL	11.6	13.5	0.40	9.92	10.0	0.33	<0.01	<0.01	<0.01
BW change, kg/d	0.21	0.82	0.30	0.34	0.05	0.29	0.46	0.25	0.05

Key Words: alfalfa, dairy cows, TNC

M101 Effects of variety and maturity at harvest time in the composition and *in vitro* kinetics of ruminal degradability of alfalfa hays. C. Arzola*[1], A. Muro[2], M. R. Murphy[4], O. Ruiz[1], J. Salinas[3], C. Rodriguez[1], Y. Castillo[1], and J.A. Payan[5], [1]*Universidad Autonoma de Chihuahua, Chihuahua, Chihuahua, Mexico*, [2]*Universidad Autonoma de Zacatecas, Zacatecas, Zacatecas, Mexico*, [3]*Universidad Autonoma de Tamaulipas, Cd. Victoria, Tamaulipas, Mexico*, [4]*University of Illinois, Urbana*, [5]*INIFAP, Delicias, Chihuahua, Mexico*.

To determine the effect of variety and stage of maturity upon the nutritional value of alfalfa hay, two varieties of alfalfa harvested at three different stages of maturity (SM) were utilized, with a completely randomized design; being the dependent variables neutral detergent fiber (NDF), acid detergent fiber (ADF) and crude protein (CP), and two varieties and three SM the independent variables. An ANOVA was carried to determine differences among varieties and/or SM. Two alfalfa varieties were used, CUF-101 and Excellent (multileaf), harvested in one of three phenotypic stages (PS): bud, early flowering or flowering stage. The effect of composition of the alfalfas in terms of concentration of NDF, ADF and CP upon the parameters of in vitro fermentation (A, B and C parameters of Groot's mono phase model) was evaluated, using a STEPWISE multiple regression analysis. NDF of the different PS showed differences (P≤0.05), with values of 33.97% for the CUF-101 variety in bud PS, 34.12% in the multileaf variety at bud PS, 29.66% in the CUF-101 variety at early flowering PS, 27.11% in the multileaf variety in early flowering PS, 42.88% in the CUF-101 variety at flowering PS, and 43.26% in the multileaf variety at flowering PS. The varieties registered a similar behavior in ADF, 22.23% for the CUF-101 variety in EF bud PS, 20.83% in the multileaf variety bud PS, 18.87% in the CUF-101 variety at early flowering PS, 18.74% in multileaf at early flowering PS, 26.13% in the CUF-101 variety at flowering PS, and 27.27% in the multileaf variety at flowering PS (P≤0.05). CP had values of 21.67% for the CUF-101 variety at bud PS, 20.44% in the multileaf variety at bud PS, 23.44% in the CUF-101 variety at early flowering PS, 22.02% in multileaf variety at early flowering PS, 20.10% in the CUF-101 variety at flowering PS, and 19.46% in the multileaf variety at flowering PS, corresponding the highest value to the CUF-101 variety at early flowering PS (P≤0.05). NDF and CP correlated positively with the parameters A and B of ruminal fermentation (P≤0.05), whereas ADF, NDF and CP were negatively associated with parameter C (P≤0.05).

Key Words: alfalfa hay, NDF, ADF

M102 Diurnal variation of non structural carbohydrate concentrations in alfalfa. C. Morin*[1,2], G. Bélanger[2], G. F. Tremblay[2], A. Bertrand[2], Y. Castonguay[2], R. Michaud[2], R. Berthiaume[3], and G. Allard[1], [1]*Université Laval, Québec, QC, Canada*, [2]*Agriculture and Agri-Food Canada, Québec, QC, Canada*, [3]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*.

Low concentrations of readily available energy combined with fast and intensive degradation of proteins in forages contribute to a low N use efficiency in dairy cows. Non structural carbohydrates (NSC) in forages are a major source of readily available energy for rumen bacteria. NSC are known to accumulate in forages during the day but few studies have established the time at which maximum NSC concentration is reached. Our objective was to study the diurnal variation of NSC in fresh alfalfa forage to determine the best harvest period to maximize NSC concentration. Field-grown alfalfa (cv. AC Caribou) in Lévis (QC, Canada, 46°48′N) was sampled every two hours between 6h00 and 20h00 on six different days around the recommended stage of development at harvest in each of the spring and summer growth cycles of 2007. A split-plot design with days as main plots and sampling times as sub-plots was used with three replications. All forage samples (n = 288) were scanned using near infrared reflectance spectroscopy and 75 samples were selected as calibration and validation sets and chemically analyzed for NSC [soluble carbohydrates (SC) + pinitol + starch]. Concentrations of NSC, SC, and starch in all samples were successfully predicted. Our results showed that they increased during the day in both growth cycles. In the spring growth period, NSC concentration averaged over the six days increased from 95 mg/g DM at 6h00 to a maximum value of 133 mg/g DM at 16h00 whereas, in the summer regrowth cycle, it increased from 74 at 6h00 to 129 mg/g DM at 18h00 (P = 0.01). This increase in NSC concentration was mainly due to an increase of 68% in starch concentration in spring and 156% in summer, and an increase of 24% in SC concentration in spring and 38% in summer. Our results confirm that NSC in alfalfa accumulate during the day under the Québec conditions and that the period when NSC concentration is maximum is between 16h00 and 18h00.

Key Words: sugars, *Medicago sativa*, legume forages

M103 Subjectivity of qualitative assessment of corn silage by dairy nutritionists. K. E. Griswold*[1], P. H. Craig[1], R. C. Goodling[1], and A. J. Heinrichs[2], [1]*Penn State Cooperative Extension, University Park*, [2]*Penn State University, University Park*.

To evaluate the accuracy and variability of sensory evaluation of forages, nutritionists attending the Penn State Dairy Nutrition Workshop were asked to qualitatively assess corn silage (CS) using their visual and tactual senses. In 2006, 34 nutritionists evaluated 12 samples, and in 2007, 21 nutritionists evaluated 8 samples. Nutritionists were allowed 2.5 min. to evaluate each sample for moisture content (MC) and particle size (PS). For MC, nutritionists could choose the descriptors, too wet, just right, or too dry. For PS, nutritionists were asked to evaluate PS for impact on fermentation and on rumen health with the descriptors, too fine, just right, or too coarse. Dry matter (DM) was determined by Koster Crop Tester, and PS distribution using a Penn State Particle Separator (PSPS). Data were analyzed using PROC MIXED and RSREG within SAS. The MC model included fixed effects of year and DM. The PS model included fixed effects of % of CS retained on each PSPS screen. Both models included the random effects of participant and sample. Assessment of MC was related (P < 0.01) to CS DM. Regression analysis showed an inverse linear relationship (P < 0.01, R^2 = 0.67) of the % of nutritionists labeling a sample as too wet compared to CS DM, and a

linear relationship (P = 0.03, R^2 = 0.44) of too dry classification to CS DM. The results showed nutritionists were better able to assess too wet CS compared to too dry CS. Evaluations of PS for both fermentation and rumen health were related (P < 0.01) only to the % of the CS retained on the PSPS top screen. For fermentation, the % CS retained was linearly (P = 0.02, R^2 = 0.29) related to the % of nutritionists ranking a sample as too coarse, but for rumen health, it was an inversely (P = 0.04, R^2 = 0.22) related to the % of nutritionists ranking a sample as too fine. These weak relationships indicate the reason for evaluating forage (e.g. effect on fermentation or on rumen health) will affect its assessment. The results indicate that nutritionists who routinely evaluate forage quality cannot adequately assess the value of CS without actual analysis.

Key Words: moisture, particle size, corn silage

M104 Use of *Pleurotus oestreatus* to change the nutritional quality of wheat straw. O. D. Montañez Valdez*[1], J. H. Avellaneda- Cevallos[2], J. M. Tapía-Gonzalez[2], G. Rocha-Chavez[2], E. Guerra-Medina[3], and E. O. Garcia-Flores[3], [1]*Centro Universitario del Sur de la Universidad de Guadalajara, Ciudad Guzmán, Jalisco*, [2]*Universidad Técnica Estatal de Quevedo, Santo Domingo. Quevedo, Los Ríos, Ecuador*, [3]*Centro Universitario de la Costa Sur de la Universidad de Guadalajara, Autlán, Jalisco*.

A study was conducted to evaluate the effect of *Pleurotus oestratus* on chemical composition of wheat straw. Wheat straw treated and untreated with *Pleurotus oestratus*, were obtained from a commercial facility. Ten samples plastic bags of wheat straw used previously as substrate to culture edible fungus were collected at random. The negative control group consisted of the pasteurized wheat straw untreated with *Pleurotus oestratus*. All samples were analyzed to dry matter (DM), organic matter (OM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), cellulose and hemicellulose of each wheat straw. Data were analyzed by mean comparison using a T Student test. No differences (P≥0.05) between treatments were found for DM, CP and hemicellulose; however, treated straw (P≤0.05) showed higher percentages of OM, NDF, and ADF. *Pleurotus oestratus* increased OM, NDF and ADF and increased soluble carbohydrates content of the wheat straw. The growth of *Pleurotus oestratus* on wheat straw changes its chemical composition by increasing organic matter content and modifying cell wall components, this may improve the nutritional quality of agricultural byproducts. This process may allow using *Pleurotus oestrarus*-treated straw for ruminant feeding.

Key Words: agricultural byproducts, *Pleurotus*, chemical composition

M105 Effects of wilting, molasses and inoculants on alfalfa silage nutritional properties. F. Hashemzadeh Sigari[1], M. Khorvash[1], G. R. Ghorbani[1], and A. Nikkhah*[2], [1]*Isfahan University of Technology, Isfahan, Iran*, [2]*Zanjan University, Zanjan, Iran*.

The objective was to determine the effects of wilting, molasses and inoculants on alfalfa silage nutritional characteristics. Fourth-cut, pre-bloom alfalfa crop with a DM of 20% was ensiled as either fresh or wilted to 37% DM. The fresh and wilted alfalfa were chopped into particles with a theoretical length of 2.5 cm and divided to three portions, added with 0, 5% and 10% molasses. Each portion was treated with either distilled water, or with Ecosyle containing *Lactobacillus plantarum* and *Propionibacterium*, or with Lalsil containing *Lactobacillus plantarum* MTD1. The experiment had a 2 × 3 × 3 factorial arrangement of wilting, molasses addition, and inoculants application. Each alfalfa treatment was ensiled in 3 replicates in 3-L PVC laboratory silos. After 90 days of preservation, silage was sampled for nutrient composition, in vitro digestion and gas production at 2, 4, 6, 8, 12, 16, 24, 36, and 48 h post-incubation as well as for 48-h in situ rumen degradation using fistulated sheep. Wilting alfalfa increased silage DM, tended to decrease CP and decreased silage NDF. Molasses increased silage DM linearly in fresh alfalfa and quadratically in wilted alfalfa. Silage NDF% increased with 5% but not 10% molasses. Molasses increased silage water soluble carbohydrates, and did not affect lactic acid content in wilted alfalfa while decreasing it in fresh alfalfa. Wilting reduced silage ammonia and acetate contents and increased silage pH. Adding 5% molasses to wilted but 10% to fresh alfalfa lowered silage pH. Lalsil in wilted alfalfa and both inoculants in fresh alfalfa reduced silage acetate. Inoculants did not affect silage ammonia in fresh alfalfa, but Lalsil decreased it in wilted alfalfa. Lalsil decreased silage pH in wilted alfalfa and increased it fresh alfalfa. Inoculants enhanced 48-h rumen degradation of silage OM. Adding 10% molasses to improved in vitro silage OM digestion at 6, 8, 36, and 48 h post-incubation. As incubation time progressed, gas production rose only in control and treated silos. Results suggest determining effects of wilting, molasses and inoculants on alfalfa silage nutritional properties.

Key Words: alfalfa, wilting, additive

M106 Effect of drying methods on chemical composition kinetics of ruminal fermentation and digestibility of *Leucaena leucocephala* in goats. R. Rojo-Rubio*[1], O. Vázquez-Mendoza[1], A. Z. M. Salem[1,2], D. López-Aguirre[1], D. Cardoso-Jiménez[1], B. Albarrán-Portillo[1], S. Rebollar-Rebollar[1], J. Hernández-Martínez[1], F. Vázquez-Armijo[1], and L. M. Camacho-Díaz[1], [1]*Universidad Autónoma del Estado de México, Temascaltpec, Estado de México, México*, [2]*Alexandria University, Alexandria, Egypt*.

The aim of the study was to determine the effect of drying methods: shadow at 25°C (SH), oven dry at 45°C (OD) and lyophilized at -27°C (LP) on chemical composition and nutritive value of *Leucaena leucocephala* leaves collected during dry season (April, 2007). Free condensed tannins (FCT), tannins binding-fiber (CT-fibre), tannins binding-protein (CT-protein)]; and chemical composition were determined. In vitro gas production of leaves was recorded after 1, 2, 4, 6, 8, 10, 12, 15, 19, 24, 30, 36, 48, 72 and 96 h of incubation. Two goats fitted with ruminal cannula were used in a randomized complete block design. Overall, drying method did not affect crude protein, acid detergent lignin and FCT content. Drying method affected NDF, ADF, CT, CT-fibre, CT-protein content and gas production (P>0.05). IVOMD and IVDMD were similar between drying methods (P>0.05). Metabolizable energy increased with LP method (P>0.05). Drying method affected chemical composition and nutritive value of *Leucaena leucocephala*.

Key Words: *Leucaena leucocephala*, drying method, tannins

M107 Timothy dietary cation-anion difference, grass tetany index, and mineral concentrations predicted by near infrared reflectance spectroscopy. G. F. Tremblay*[1], Z. Nie[2], G. Bélanger[1], S. Pelletier[1], and G. Allard[3], [1]*Agriculture and Agri-Food Canada, Québec, QC, Canada*, [2]*China Agricultural University, Beijing, China*, [3]*Université Laval, Québec, QC, Canada*.

The mineral concentration of forage grasses is involved in two metabolic disorders in dairy cattle production, namely clinical hypocalcaemia (milk fever) and hypomagnesaemia (grass tetany). Risks of occurrence of these two metabolic disorders can be evaluated by determining the dietary cation-anion difference (DCAD) and the grass tetany (GT) index of forages and specific rations. The objective of this study was to evaluate the feasibility of predicting timothy (*Phleum pratense* L.) mineral concentrations (Na, K, Ca, Mg, Cl, S, and P), DCAD, and GT index using near infrared reflectance spectroscopy (NIRS). Timothy samples (n = 1018), from an experiment with N and Cl fertilizers conducted at four sites in eastern Canada, were scanned using NIRS and analyzed for their mineral concentrations. Calculations of the DCAD were made using three formulas [DCAD1 = (Na + K) - (Cl + S); DCAD2 = (Na + K + 0.15 Ca + 0.15 Mg) - (Cl + 0.6 S + 0.5 P); DCAD3 = (Na + K) - (Cl + 0.6 S)]. The GT index [K/(Ca + Mg)] was also calculated. Samples were divided into calibration (n = 240) and validation (n = 868) sets. The calibration, cross validation, and prediction for mineral concentrations, DCAD, and GT index were performed using modified partial least squares regressions. Concentrations of K, Ca, Mg, Cl, and P were successfully predicted with coefficients of determination for prediction (R^2_P) of 0.69 to 0.92 and coefficients of variation for prediction (CV_P) ranging from 6.6 to 11.4%. The prediction of Na and S concentrations failed with respective R^2_P of 0.58 and 0.53, and CV_P of 82.2 and 12.9%. The three calculated DCAD and the GT index were successfully predicted with $R^2_P > 0.90$ and $CV_P < 20\%$. Our results confirm the feasibility of using NIRS to predict K, Ca, Mg, Cl, and P concentrations, as well as DCAD and GT index, in timothy.

Key Words: near infrared reflectance spectroscopy, dietary cation-anion difference, mineral concentration

M108 The effect of maturity stage on in vitro digestibility and energy utilization of mesquite (*Prosopis laevigata*) pods in goats. R. Rojo-Rubio*[1], A. Z. M. Salem[1,2], L. M. Camacho-Díaz[1], D. Cardoso-Jiménez[1], and S. Rebollar- Rebollar[1], [1]*Universidad Autónoma del Estado de México*, *Estado de México, México*, [2]*Alexandria University*, *Alexandria, Egypt*.

The aim of this study was to determine the in vitro digestibility, ruminal volatile fatty acids (VFA), in situ disappearance and energy utilization of Mesquite (*Prosopis laevigata*) pods at different stages of harvest using ruminal inoculums of two fistulated goats of Criollo × Nubia (40 ± 0.5 kg LW) fed on 40:60 ratio of forage (alfalfa) to concentrate (corn, soybean, mineral), respectively. Mesquite pods were harvested during the year 2008 at different maturity sages: young (YO, in May); and the semi-mature (SM- in August) and mature (MA- in October) pods, from the sub arid region in the Mezquital Valley, Hidalgo, México. DM and CP disappearance were determined after 24h of pods samples incubation, whereas the energy utilization of metabolizable and net energy (e.g. ME and NE) were estimated used a previous data recorded of ruminal gas production after 24h. VFA were increased (P = 0.001) in MA and SM than in YO pods, whereas IVDMD and ruminal disappearance of DM and CP, followed the opposite trend by increasing (P = 0.001) in YO than in MA or SM pods. Energy utilizations (ME or NE) were not affected by the maturity stage of pods, except the NE had tended (P = 0.089) to increase in MA and SM than in YO pods samples. On the basis of these results, it is assumed that, Mezquite pods of the semi-mature or mature stage have a higher nutritive value than young pods, which may be an important constraint for the use of these tree pods by ruminants browsing upland areas of Mexico where this tree species is predominant.

Key Words: mesquite, maturity stage, digestibility

M109 Nutritive value, in situ degradability and intake of forage soybean and Lablab by weanling goats. E. Valencia*, A. Rodríguez, and F. Rivera Melendez, *University of Puerto Rico*, *Mayaguez, Puerto Rico*.

Information is limited on nutritive value [crude protein (CP), neutral detergent fiber (NDF) and acid detergent fiber (ADF)] of forage soybean (FS; *Glycine max*) and lablab (LL; *Lablab purpureus*) when baled at approximately 20% DM. The objectives of this study were to determine their nutritive value, in situ DM and NDF degradability, and intake of FS and LL. Triplicate samples (500 g) from each forage were analyzed to determine CP and cell wall components (NDF, ADF, hemicellulose, and ADIN). Data were analyzed using the ANOVA procedure of SAS and mean separation was conducted with LSMEANS. The in situ degradability study was conducted in fistulae cows (2) maintained on grass diets utilizing the suspended nylon bags technique. Triplicate samples of each forage species were incubated after 0, 3, 6, 24 and 48 hrs and analyzed for rate of degradation and DM and NDF disappearance. Data were analyzed using the non-linear model; Degradation = a+b*(1– exp(c*t), where; a = soluble fraction, b = degradable fraction, c = rate of degradation, and t = time. Forage intake was determined using eight weanling Boer goats (average 17 kg BW). Goats were fed with FS and LL (at 3% of animal daily LW), 5-d adaptation and 5-d collection period in a crossover design with four goats per treatment. Crude protein concentration was similar (P>.05) for both FS and LL (averaging 17%). However, NDF and ADF were lower (P<.05) in FS than in LL (35.7 and 16.0 vs. 46.6 and 32.4%), and hemicelluloses and ADIN values were higher (P<.05), (19.7 and .62 vs. 14.16 and .41%). Ruminal DM degradation rate (kd) was faster in FS (.03) than in LL (.05), but NDF kd values were similar for both FS and LL (.09). After 48h of incubation, in situ DM disappearance was higher in FS (73.21%) than in LL (59.2%). Hay intake (FS = 439.9 and LL = 428.9 g/d) and intake as % of animal live weight (FS = 2.49, LL = 2.42%) were similar (P<.05). Both FS and LL differ in nutritive value and in situ DM degradability rate and disappearance, but forage intake was similar.

Key Words: legumes, in situ dry matter degradability, voluntary intake

M110 Inclusion of nopal (cactus) in diets for finishing lambs in Mexico. G. Aranda-Osorio*, M. Segundo-Espejel, C. A. Flores-Valdez, and F. M. Cruz-Miranda, *Universidad Autonoma Chapingo*, *Chapingo, Mexico, Mexico*.

The objective of this study was to evaluate the inclusion of nopal in diets of finishing lambs and its effect on animal performance and profitability. There were used 72 crossbred (Pelibuey × Damara × Rambouillet) lambs with inicial live weight of 22.10 ± 2.96 kg. Three diets were used in which nopal constituted: T1=0, T2=15, and T3=25% of the dry matter (DM), fulfilling the requirements for a daily gain of 250 g (NRC 1985), with similar nutritional composition. The nopal (cladodes of Atlixco variety, one years old) was chopped (2×3 cm) and offered in a separate feedbunk from concentrate. The total feed was offered (50–50%) twice a day (07:00 and 14:00 h). Feed rejected was collected and weighed every day before morning feeding. Four lambs were assigned per pen (3×3 m), which constituted the experimental unit, each treatment had 6 replicates. Lambs were weighed every 14 days. The experiment lasted 84 d. Data was analyzed under a mixed model of completely random design for repeated measures of SAS. The response variables were: total liveweight gain (TLG), daily liveweight gain (DLG), dry matter intake (DMI), feed conversion (FC), hot carcass yield (HCY) and profitability. The TLG was different (P≤0.05) between T1=0% (21.34 kg) vs. T2=15%

(18.62 kg) and T3=25% (17.19 kg), but similar (P≥0.05) among T2 and T3. Similar to ADG (T1=0.254 vs. T2=0.218 and T3=0.219 kg lamb^{-1} day^{-1}). The concentrate intake (DM) was different (P≤0.05) between treatment T1 (1.43 kg) vs. T2 (1.02) and T3 (0.90 kg) lamb^{-1} day^{-1}, as well as for the nopal (DM) (T1=0, T2=0.123 and T3=0.201 kg lamb^{-1} day^{-1}). The FC values were not different (P≥ 0.05) between T1 (5.74) and T2 (5.99), but different (P≤0.05) for T3 (5.29). There were no differences (P≥>0.05) on HCY (48.1, 47.4 and 47.8% for T1, T2 and T3, respectively). The profitability (USD) was similar among treatments (T1=$22.50, T2=$22.02 and T3=$20.38), as well as the cost: benefit ratio (T1=1.39, T2=1.43 and T3=1.40). Concluding that the inclusion of nopal in diets for finishing lambs in percentages between 15 to 25% (DM) could be an important alternative for producers in arid and semiarid lands.

Key Words: cactus pear, sheep, performance

M111 Nopal (cactus) fresh versus proteinically enriched in diets for finishing lambs in Mexico. G. Aranda-Osorio*, Y. Campos-Anzures, F. A. Salinas-Garcia, C. A. Flores-Valdez, L. A. Miranda-Flores, and F. M. Cruz-Miranda, *Universidad Autonoma Chapingo, Chapingo, Mexico, Mexico*.

The objective of this study was to evaluate the productive performance and profitability of finishing lambs fed with a diet containing fresh chopped or protein enriched nopal. Crossbred (Pelibuey × Damara × Rambouillet) male lambs (n=72) with an initial live weight of 23.22 ± 1.20 kg were used. Three diets were formulated (isoenergetic and isoproteinic) to fulfill the requirements of lambs growing at 250 g day^{-1} (NRC 1985), in which nopal was included (25% dry matter) in the following manner: T1=0, T2=fresh nopal and T3=enriched nopal. Cladodes of Atlixco variety one year old were used, chopped (2×3 cm) for the fresh manner or aerobically fermented for protein enrichment (addition of microorganisms such as fungus, yeast, and bacteria), which had a liquid consistency. Each treatment had 6 replicates and a pen (3×3 m) with 4 lambs constituted the experimental unit. The lambs were weighed every 14 days. The collected data was analyzed under a mixed model of completely random design of repeat measures by the statistical package of SAS. The analyzed variables were: total liveweight gain (TLG), average daily gain (ADG), dry matter intake (DMI), feed conversion (FC), and profitability. There were differences (P≤0.05) in TLG among treatments T1 (12.93 kg) and T3 (9.77 kg) but they were similar (P≥0.05) to T2 (10.33 kg). In ADG the T1 (238 g) was higher (P≤0.05) than T2 (174 g) and T3 (158 g), although T2 and T3 were similar (P≥0.05). The average DMI was higher (P≤0.05) for T3 (1,015 g) than for T1 (935 g), and they were similar (P≥0.05) to T2 (975 g). Treatments were different (P≤0.05) in FC (T1=4.08, T2=6.31 and T3=7.93). The profitability (USD) per lamb was higher for T1=$21.17 than for T2=$16.24 and T3=$14.90. It is concluded that the inclusion of nopal to finishing diets at levels of 25% (DM) could decreased performance and profitability and protein enrichment process needs to be reviewed before it could be recommended to producers.

Key Words: cactus pear, proteinic enrichment, sheep

M112 Chemical composition, in vitro gas production kinetics of mesquite (*Prosopis laevigata*) pods at different stages of maturity in goats. A. Z. M. Salem[1,2], R. Rojo-Rubio*[1], O. Vazquez-Mendoza[1], D. Cardoso-Jiménez[1], and B. Albarrán-Portillo[1], [1]*Universidad Autónoma del Estado de México, Estado de México, México*, [2]*Alexandria University, Alexandria, Egypt*.

The effect of the maturity stage on chemical composition and in vitro gas production as well as the energy utilization of Mezquite (*Prosopis laevigata*) pods were evaluated using ruminal inoculums of two fistulated goats of Criollo × Nubia (40 ± 0.5 kg LW) fed on 40:60 ratio of forage (alfalfa) to concentrate (corn, soybean, mineral), respectively. Mezquite pods were harvested during the year 2008 at different maturity stages: young (YO, in May) and the semi-mature (SM- in August); and mature (MA- in October) pods from the sub arid region in the Mezquital Valley, Hidalgo, México. Chemical composition and tannins levels [extractable condensed tannins (CT), free condensed tannins (FCT) and tannins binding fiber (CT-fibre) and protein (CT-protein)] in pods were determined. Gas production of pods samples was recorded at 1, 2, 3, 4, 6, 8, 12 and 24 h after incubation. Crude protein content was significantly increased (P = 0.001) in YO pods than in SM or MA, while the NDF, ADF, OM as well as the EE contents were increased (P < 0.05) in MA and SM than in YO samples. The SM samples were recorded a high concentration (P = 0.006) of fiber free carbohydrate (FFC) than the other groups of pods. Tannins contents (e.g. CT, FCT, CT-fiber, and CT-protein) in pods, at the different harvest stages, were ranked in the order MA = SM > YO. Seasonal differences in tannin contents may have been related to the phenology of plant species and to the temperatures prevailing during the different stages of growth. Gas production kinetics (G24, b and c) were increased (P < 0.05) in SM and MA than in YO samples, while the lag time as well as the partitioning factor were increased (P < 0.05) in YO pods than SM or MA. These results may be due to the type and structure of tannins at different stages of harvest. Based upon the results presented herein, it is concluded that the Mezquite (Prosopis laevigata) pods of the semi-mature or mature stage may represent a high quality feeding resource for grazing ruminants in the rangelands of Mexico, particularly during dry seasons.

Key Words: mesquite, maturity stage, chemical composition

M113 Using in vitro gas production technique to calculate total digestible nutrients value of native forage in southern Texas. A. D. Aguiar*[1], L. O. Tedeschi[1], F. M. Rouquette[2], A. Ortega[3], D. S. Delaney[3], and S. Moore[4], [1]*Texas A&M University, College Station*, [2]*Texas AgriLife Research, Overton, TX*, [3]*Texas A&M University, Kingsville*, [4]*King Ranch, Kingsville, TX*.

A major challenge in grazing beef production is to maintain nutritive value and production of forages in the pasture at an adequate level to meet animal requirements throughout the year. Therefore, proper and rapid forage analyses are needed to accurately determine the availability of energy and nutrients of the forage. The in vitro fermentation (ivF) of forages obtained from native forage pastures of the King Ranch, Kingsville, TX for two consecutive years (2006-2007) was evaluated. The objectives of this study were (1) to study the relationships between ivF parameters of isolated NDF, feed chemical composition, intestinal digestibility of NDF (idNDF), and passage rate (kp) to calculate total digestible nutrients (TDN), (2) to study the variation of TDN throughout the year, and (3) to correlate TDN with climatic variables. Twenty one samples were fermented using the gas production technique. The pressure of the cumulated gas production was collected every 5 min for 48 h. A theoretical equation using fractional rate of fermentation (kd) of NDF and kp were used to estimate digestible NDF. A combination of kp (4, 6, and 8% h-1) and idNDF (0, 10, and 20%) were used to compute TDN. This TDN was compared with a published empirical TDN equation, assuming 0.8 and 0.75 digestion coefficients for NDF (kdNDF).

The best combinations to calculate TDN were those assuming 0%, 6% h-1, and 0.75 (r2 = 0.48, mean square error or prediction (MSEP) = 3.83%) and 10%, 8%, 0.75 (r2 = 0.48, MSEP = 3.65) for IDNDF, kp, and kdNDF; respectively. Because a kp of 8% h-1 was assumed to be too fast to be effective for grazing cattle, the combination with kp of 6%/h was selected. A mixed model analysis indicated no differences among months (P = 0.08) and seasons (P = 0.39; year as random). Temperature, relative humidity, and rain had weak correlation with TDN. The TDN distribution was lognormal with a 90% confidence interval between 40.7 and 55.5%. The lack of correlations was likely due to large variation and small sample size.

Key Words: evaluation, forage, fermentation

Graduate Student Paper Competition-CSAS Poster Competition: CSAS Graduate Student Competition 1

M114 Variation in antibody and cell-mediated immune responses between Canadian Holsteins and Norwegian-Red crossbred first calf heifers. S. Cartwright*[1], E. B. Burnside[3], N. Karrow[2], L. Schaeffer[2], and B. A. Mallard[1], [1]*University of Guelph Department of Pathobiology, Guelph, Ontario, Canada*, [2]*Centre for Genetic Improvement of Livestock, Guelph, Ontario, Canada*, [3]*Gencor Inc., Guelph, Ontario, Canada*.

Inbreeding in the Holstein (HF) population has been steadily increasing and is thought to contribute to reduced fertility, decreased production and increased disease occurrence. The problems associated with inbreeding may be resolved by crossbreeding with more robust breeds. Previous research has shown superior udder health and reproductive efficiency of the Norwegian Red (NR) breed. The objective of this study was to evaluate antibody (AMIR) and cell-mediated immune response (CMIR) as well as production and differential cell count data on purebred and crossbred(HF, n=50; NRxHF, n=50) first calf heifers. Therefore heifers were immunized 6-9 days post-calving using type-1 and type-2 test antigens. Sera were obtained on days 0 and 7 for antibody detection using ELISA. On day 7, background skin-fold measurements were taken of the tail-fold and intradermal injections of PBS (control) and test antigen were administered. Forty-eight hours later any increase in skin-fold measurements were taken to assess delayed type hypersensitivity (DTH) as an indicator of CMIR. Whole blood samples were taken on day 7 for differential cell count analysis. Data on production was obtained from Dairy Comp 305. A SAS general linear model that includes the effects of breed, month and herd will be used to determine any statistical significance in AMIR, CMIR, and production or cell counts between breeds. Preliminary results show crossbreds (least squares mean = 78.24%) had a significantly greater DTH response compared to purebreds (least squares mean = 50.56%) (p = 0.0474). However there was no significant difference between crossbreds (least squares mean = 1.10 OD) and purebred (least squares mean = 1.16 OD) for antibody response (p = 0.7830). These results suggest crossbreds have a greater cell-mediated immune response compared to purebreds and therefore enhanced defence against intra-cellular pathogens.

Key Words: immune response, purebred, crossbred

M115 Translation efficiency mediated by untranslated region of bovine beta casein mRNA. J. Kim*, M. Bakovic, J. Li, J. Bag, and J. P. Cant, *University of Guelph, Guelph, Ontario, Canada*.

Regulation of protein translation in milk secretory cells of the mammary glands may influence milk protein production. It is generally accepted that untranslated regions (UTR) of mRNA play an active role in determining translational efficiency. Some of the characteristics of UTR involved in regulation of gene expression include secondary structure, length, and GC content. We hypothesized that the milk protein translation efficiency is influenced by characteristics of the 5′ and 3′ UTRs. The objectives were to test this hypothesis with *in vitro* translation assays, and to identify characteristics of 5′ and 3′ UTR of β-casein. Total RNA extracted from mammary gland of a Holstein dairy cow was first reverse transcribed to cDNA using oligo(dT), followed by 5′ and 3′ RACE-PCR to obtain the complete sequence of β-casein mRNA. Using different pairs of gene-specific primers, various recombinant transcripts spanning fragments of 5′ and/or 3′ UTR with the entire β-casein coding region were constructed. The amplified products were cloned into a pTZ19R vector to add a regulatory element sequence required for *in vitro* transcription and subsequent translation in rabbit reticulocyte lysate. Efficiency of translation was indexed as incorporation of biotinylated lysine residues into nascent β-casein which was detected by chemiluminescence. The quantity of extracted RNA from 100 mg of mammary gland was 884.7 ng/μl. The quality of RNA was illustrated by stained 28S and 18S ribosomal RNAs as well as the 260/280 and 260/230 ratios, both within the range of 2~2.05. The complete sequence of β-casein mRNA obtained by RACE-PCR was identified as 1095 bp in length where its 5′ and 3′ UTRs were 61 bp and 359 bp long respectively. Each of various recombinant transcripts incorporated in the pTZ19R vector were successfully transcribed and translated *in vitro* at optimal reaction times of 60 min and 40 min, respectively. The identification of sites on the UTR of mRNA of a milk protein that are responsible for translation efficiency improves our understanding of the mechanisms of translational control of milk protein.

Key Words: UTR, beta casein, translation efficiency

M116 Impact of an extended photoperiod in farrowing houses on sow and litter performances. M.-P. Lachance*[1], J.-P. Laforest[2], N Devillers[1], A. Laperrière[3], and C. Farmer[1], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R & D Centre, Sherbrooke, QC, Canada*, [2]*Animal Science Dept., Laval University, Québec, QC, Canada*, [3]*LTE, Hydro-Québec's Research Institute, Shawinigan, QC, Canada*.

The current project studied the effect of an extended photoperiod around parturition and throughout lactation on the performance of sows and piglets. Fifty-four sows were assigned to two light regimens: 1) standard (CTL, n = 28) consisting of 8 h of light daily from d 112 of gestation until d 23 of lactation; 2) extended (TRT, n = 26) consisting of 23 h of light from d 112 of gestation to d 4 of lactation and 16 h thereafter. On d 4 and 21 of lactation, (between 1000 and 1115), milk samples were obtained for compositional analyses and blood samples were collected to measure prolactin and melatonin. Feed intakes were noted during lactation for sows and during the 35 d following weaning for piglets. Colostrum intake was estimated based on a 24 h piglet weight gain starting at the end of farrowing. Litter size was standardized to 10 ± 1 pigs. Piglets were weighed at birth and on d 2, 4, 7, 14, 21 (weaning), 35 and 56. Behavior of sows was recorded using scan sampling every

5 min for 24 h on d 3 and 19 of lactation. Behavior data were analyzed with the Wilcoxon test and all other data with PROC MIXED of SAS, according to a one-way factorial design. TRT sows had lower concentrations of melatonin on d 4 of lactation (6.76 vs. 9.51, SEM = 0.88 pg/mL, $P < 0.05$) but prolactin concentrations, milk composition, piglet colostrum intake and sow feed intakes were not affected by treatment ($P > 0.1$). Litter growth during lactation was also unaffected ($P > 0.1$) but TRT piglets consumed less feed in the 2 weeks after weaning ($P < 0.05$) and weighed less on d 35 ($P < 0.05$) than CTL piglets. CTL sows tended to spend more time standing up than TRT sows on d 19 of lactation ($P < 0.1$). In conclusion, increasing the light period in farrowing houses did not lead to beneficial effects on sow and litter performances. *Thanks to Hydro-Québec and the Québec Federation of Swine Producers for financial support*.

Key Words: photoperiod, sows, lactation

M117 Effects of low-voltage electrical stimulation and aging on heavy lamb meat tenderness. E. Pouliot*[1], C. Gariépy[2], M. Thériault[1,3], C. Avezard[2], J. Fortin[2], N. J. Simmons[4], and F. W. Castonguay[1,3], [1]*Université Laval, Québec, QC, Canada*, [2]*Food Research and Development Centre, AAFC, St-Hyacinthe, QC, Canada*, [3]*Dairy and Swine Research and Development Centre, AAFC, Lennoxville, QC, Canada*, [4]*Carne Technologies Ltd, Cambridge, New Zealand*.

Chilling is a post-slaughter process that can affect meat quality. In some instances, chilling of lamb carcasses in Quebec might be too fast, potentially causing muscle shortening, hence toughening of the meat. The aim of this study was to evaluate the effect of electrical stimulation (ES) and aging time on meat tenderness of heavy lamb in Quebec. Seventy-six Suffolk-sired crossbred male lambs were slaughtered at a target weight of 48-52 kg. Half of them were electrically stimulated at 5 min *post-mortem* (21 V; 0.25 A; 60 sec; Jarvis, Model ES-4, Middletown, CT, USA). During the first 24 h of chilling, temperature and pH fall were monitored in the *longissimus dorsi* (*LD*) and samples were taken for enzymes analyses. After carcass cutting, *LD* sections were randomly assigned to aging periods of 1, 3 or 8 d. Ultimate pH (48 h), Warner Bratzler shear force (WBSF), sarcomere length, myofibrillar fragmentation index (MFI), calpains and calpastatin activities and sensory evaluation were also carried out on the samples. Data were analysed using the MIXED procedure of SAS (2001). Temperature fall was the same for both treatments, however ES carcasses always had a lower pre-rigor pH value than controls ($P < 0.001$) while the ultimate pH was equivalent. Tenderness was enhanced both by ES ($P < 0.001$) and aging ($P < 0.001$) according to WBSF and sensory evaluation. At each aging time, tenderness was greater for ES meat and only 3 d of aging was necessary to achieve the same tenderness level as the controls at 8 d. Sarcomeres were longer ($P < 0.001$) in ES samples than in controls. Neither MFI nor calpains and calpastatin activities were affected by ES treatment. These results provide the first evidence that ES could enhance the tenderness of heavy lambs in Quebec, mostly through cold shortening reduction.

Key Words: electrical stimulation, tenderness, lamb meat

M118 Lysine and energy maintenance requirements in modern, high productivity sows are greater than previous estimates. R. S. Samuel*[1], S. Moehn[1], P. B. Pencharz[2], and R. O. Ball[1,2], [1]*Swine Research and Technology Centre, University of Alberta, Edmonton, Alberta, Canada*, [2]*Research Institute, Hospital for Sick Children, Toronto, Ontario, Canada*.

Selective breeding of sows may have affected maintenance requirements due to increased lean tissue and decreased lipid content in the whole body. The objectives of exp. 1 and 2, respectively, were to determine the maintenance energy (ME_m) and lysine (LYS) requirements of modern sows. Exp. 1: non-pregnant sows (n=5, 174 kg±11 kg) were fed a barley-wheat-SBM diet of 12.5 MJ ME/kg, 0.65% total lysine, and 15% crude protein for one week at about 1.0 ME_m (473 kJ/$BW^{0.75}$) and 2.0 ME_m (925 kJ/$BW^{0.75}$). Heat production was measured by indirect calorimetry for 24 h. Sows fed 1.0 ME_m deposited protein but lost body lipid and body weight (BW). When fed at 2.0 ME_m, sows gained 1292 g/d. The calculated ME_m at 1.0 ME_m and 2.0 ME_m (515±8 vs. 495±9 kJ/$BW^{0.75}$) were similar (P=0.15), with a mean value of 506±7 kJ/$BW^{0.75}$. Exp 2: non-pregnant sows (n=4; 222.6±0.7 kg BW) were adapted to 2.2 kg of a semi-synthetic diet containing 14.0 MJ ME/kg and 1.09 g/kg LYS. Each sow received 6 test diets in random order, providing LYS intakes of 19.8, 25.2, 30.6, 41.4, 46.8 and 52.2 mg/$kg^{0.75}$. After adaptation to each diet, indicator amino acid oxidation using L-[1-^{13}C]-phenylalanine (PHE) was determined simultaneously with indirect calorimetry for 4 h. Plateaus in oxidation were achieved within 1.5 h. PHE oxidation decreased as LYS intake increased and was lowest ($P<0.05$) at 46.8 mg/$kg^{0.75}$ LYS. Maintenance LYS requirement, calculated by regression analysis, was 49 mg/$kg^{0.75}$. Heat production was linearly correlated ($r^2 = 0.54$) with PHE oxidation and was lowest ($P<0.05$) at LYS intake of 46.8 mg/$kg^{0.75}$. The mean respiratory quotient (1.029±0.028) showed that dietary energy was not limiting. Energy and LYS maintenance requirements of modern sows were 10% and 30% greater than previously reported. Sows were energetically most efficient when fed to meet the LYS requirement. Requirements for energy and protein in modern, high productivity sows require further characterization.

Key Words: maintenance, energy, lysine

M119 A modified Ovsynch protocol using pLH or hCG in lactating dairy cows. M. B. Gordon*[1], R. Rajamahendran[1], M. G. Colazo[2], and D. J. Ambrose[2,3], [1]*Department of Animal Science, Faculty of Land Food Systems, University of British Columbia, Vancouver, BC, Canada*, [2]*Dairy Research and Technology Centre, Alberta Agriculture and Rural Development, Edmonton, AB, Canada*, [3]*University of Alberta, Edmonton, AB, Canada*.

The Ovsynch program for timed insemination (TAI) is commonly used by dairy producers as a reproductive management tool because it allows for the control of ovarian follicular and corpus luteum development without the need for estrus detection However, some studies have reported that pregnancy losses occur at a higher rate after timed insemination using a GnRH-based Ovsynch protocol, than after insemination at detected estrus, in dairy cattle. Endogenous levels of progesterone and estrogen in plasma have been shown to have an inhibiting affect on LH release from the pituitary gland when treated with exogenous GnRH. This study compared the effects of 100 µg of Fertiline (GnRH) versus 25 mg of Lutropin-V (pLH), or 1,000 USP units of Chorulon (hCG) on ovarian response, conception rate and embryonic losses in lactating dairy cows subjected to a timed insemination protocol. Lactating Holstein cows were assigned to 3 treatment groups. Group 1 (n=57) received Ovsynch protocol with two treatments of GnRH 9 days apart with a treatment of PGF2α 48 hours before the second GnRH treatment and TAI 16-18 h later. Groups 2 (n=57) and 3 (n=53) received LH or hCG in place of the GnRH treatments, respectively. Pregnancy was diagnosed at 42 ± 3 d post-TAI. No differences in pregnancy rates were observed

between groups (28.1%, 22.6%, 22.8% for the GnRH, pLH, and hCG groups, respectively). Parity, DIM at TAI, and BCS had no effect on PR. Presumptive embryonic loss between days 28 and 42 was 16.7%, 9.3% and 8.3% for GnRH, pLH, and hCG groups, respectively (P=0.43). Animals were presumed pregnant on day 28 post-TAI if progesterone concentrations were > 1 ng/mL on days 14, 21, 25, and 28 post-TAI. Although this study did not find any advantages of replacing GnRH with pLH or hCG in a modified Ovsynch protocol, the number animals was small. As well, understanding the follicular and luteal patterns of animals treated with pLH or hCG during the modified Ovsynch protocol may also be important.

Key Words: Ovsynch, pLH, hCG

M120 Dairy farm sustainability in Quebec, Canada: The social aspect. V. Bélanger*, D. Parent, A. Vanasse, G. Allard, and D. Pellerin, *FSAA, Université Laval, Québec, Canada*.

Over the last two decades, the number of dairy farms has declined and the viability of the family farm and their rural communities has been questioned. To be sustainable, a farm should be viable, liveable, transmissible, and ecologically reproducible. Thus the assessment of farm sustainability should always be based on its economic, environmental and social aspects. As part of a comprehensive research project on the assessment of Quebec dairy farm sustainability, our objective was to develop indicators to evaluate the social aspect of farm sustainability; a concept rarely accounted for in the literature. To identify these indicators, experts (researchers, farmers, stakeholders) were consulted using a modified Delphi method. Our method uses a qualitative sequential approach: each expert submits his own indicators which are later debated in a focus group; the chosen indicators are then classified, ranked and, for each indicator, different threshold levels are established by the group to determine a score value for each. Indicators are selected based on their sensitivity to describe the social aspect of dairy farm sustainability considering the availability and easiness of on-farm acquisition. From the 166 statements initially submitted by the experts, 30 were selected and debated in the focus group. The relative weight of each indicator in a component and of each component remained to be determined by the focus group. To define the social aspect of dairy farm sustainability, indicators are grouped in four components for a total of 100 points: quality of life, social integration, farm succession and entrepreneurial skills. Results are presented as a radar diagram for each farm with axis representing indicators; for example, we have axis for farmer education level, leadership, innovativeness and risk-taking that describe the entrepreneurial skills component. This new assessment tool serves to evaluate the sustainability of a farm at a given point in time and could be used periodically to follow its evolution over the years.

Key Words: sustainability, social indicators, farms

M121 Characterization of rumen epithelial structure and function in lambs fed rapidly fermentable carbohydrates. M. A. Steele*, S. Greenwood, S. E. Hook, O. AlZahal, and B. W. McBride, *University of Guelph, Guelph, Ontario, Canada*.

The rumen epithelium performs vital roles in the absorption and metabolism of organic acids, yet very little is known about how it may adapt to compensate for shifts in rapidly fermentable dietary carbohydrates. Therefore, the objective of this study was to characterize the effect of increasing the proportion of rapidly fermentable dietary carbohydrates on rumen epithelial histology, ultrastructure and ketogenesis. Rideau-Arcott lambs (n=8) were randomly divided into a complete block design and assigned to a control (CON) diet consisting of 29% mixed grain and 71% alfalfa pellets (as-fed), or a high-grain (HG) diet comprised at a maximum carbohydrate challenge of 79% mixed grain and 21% alfalfa pellets (as-fed). The HG lambs were transitioned to their diet in a stepwise manner over 12 days and blood plasma was collected every third day, while rumen tissue was collected at slaughter on day 13. Plasma BHBA levels were significantly higher (P<0.01) in HG lambs compared to CON lambs once the dietary grain level reached 60% (as-fed). In spite of elevated levels of plasma ketones, the mRNA expression of two key enzymes involved in the metabolism of organic acids to BHBA (HMG-CoA Synthase and Acyl-CoA Synthase) were not differentially expressed between the CON and HG. Analysis of rumen tissue collected at slaughter by scanning electron and light microscopy revealed structural damage to the strata granulosum and corneum in the HG lambs but not the CON. To further investigate structural alterations, the mRNA expression of Desmoglein1, an important component of desmosomes, was quantified. Interestingly, the mRNA expression of Desmoglein1 was decreased 10-fold (P<0.05) in HG lambs which corresponds to the histological observation of demarcation in the exterior strata. The results from this study demonstrate that rumen epithelial ketone body production and structural integrity can be quickly altered by increasing the quantity of rapidly fermentable carbohydrates in the diet.

Key Words: rumen epithelium, ketogenesis, gene expression

M122 The influence of fish oil diets on insulin metabolism in adult male pig. C. A. Castellano*[1,2], I. Audet[1], J. -P. Laforest[2], P. Y. Chouinard[2], and J. J. Matte[1], [1]*Dairy & Swine R & D Centre, Agriculture and Agri-Food Canada, Sherbrooke, Qc, Canada*, [2]*Department of Animal Sciences, Québec city, Qc, Canada*.

The aim of this study was to evaluate the effects of long term dietary supplementation of n-3 polyunsaturated fatty acids (n-3 PUFAs) on plasma fatty acid profile, body weight (BW) and back fat thickness (P2) as well as on glucose, insulin and C-peptide responses to an oral glucose tolerance test in adult male pigs. Fifteen Duroc boars aged of 204.5 ± 1.8 days (145.8 ± 3.3 kg BW) received daily 2.5 kg of basal diet with a supplement of: 1) 62 g of hydrogenated animal fat (C, n=5); 2) 60 g of menhaden oil containing 17% of docosahexaenoic acid (DHA) and 15% of eicosapentanoic acid (EPA) (M, n=6) and 3) 60 g of tuna oil containing 30% of DHA and 7% of EPA (T, n=4). Rations were balanced to be isocalorics. After 7 months of experiment, a catheter was fit in the jugular vein and repeated blood samples were collected during 6 h following the oral glucose bolus (1 g/kg BW). Data were analysed using MIXED and CORR procedures of SAS. Data were considered significant at P<0.05. There were no difference among treatments for BW (275.4 ± 2.8 kg, P=0.07) and P2 (17.7 ± 1.1 mm, P=0.20). Dietary supplementation with n-3 PUFAs altered blood plasma profile: DHA and EPA increased whereas arachidonic acid decreased (P<0.01). Following the glucose tolerance test, plasma glucose, insulin and C-peptide were not affected by treatments (P>0.34). For all animals, correlations were found between P2 and C-peptide (an indicator of insulin secretion) (r=+0.50) and between P2 and glucose/insulin ratio (an indicator of insulin sensitivity)(r=-0.54). In conclusion, long term supplementation with dietary n-3 PUFAs did not affect insulin metabolism in healthy adult pig. The relationship between body fat and insulin sensitivity, well documented in human, suggests that adult male pig could be a promising animal model for studies on insulin metabolism.

Key Words: pig, fish oil, insulin

M123 Use of ash and nitrogen concentrations in manure to estimate loss of ammonia over time. H. A. Paz* and W. P. Weiss, *The Ohio State University*, *Wooster*.

The aim of this study was to validate a mass balance method based on N and ash in manure to estimate NH_3 losses from manure. Six multiparous Holstein were used in a replicated 3 x 3 Latin square with three 14 d periods. Two diets were balanced to contain 15.5% CP but in one the forage (58% of diet DM) was mainly corn silage (CS) and alfalfa silage in the other (AS). A third diet (CSU) was the same as the CS diet except that 0.5% of urea was added (17.3% CP). During total collection digestion trials (last 4 d of each period), urine and feces samples were used to prepare a slurry mixture (1200 g) in the same proportion as excreted by each cow. Slurries were sampled immediately after mixing, incubated at ambient temperature (12 °C) for 3 d and sampled again. Initial and final N concentrations and slurry masses were used to determine N losses. Nitrogen loss was estimated using the mass balance method as: (N Intake - N Milk) - N/Ash*(Ash Intake - Ash Milk), where N and Ash Intake and N and Ash Milk are g/d and N and Ash concentrations in slurry samples at 3 d constitute the N/Ash ratio. Average daily DM intake and milk yield were 22.4 and 32 kg/d, respectively, and were not affected by treatment. Average manure output was 65.4 kg/d with cows fed AS and CSU excreting an average of 18.6 kg/d of urine followed by CS at 14.5 kg/d (P= 0.02). Manure N excretion was highest for cows fed CSU followed by AS and CS (422, 392 and 343 g/d, P<0.01). Urinary N as percent of excreted N was 34, 41, 53% for AS, CS, CSU, respectively (P<0.01). Ash excretion in manure was highest for cows fed AS (1134 g/d); CS and CSU had similar ash excretion (936 g/d) (P<0.01). Urine contributed 46, 42, and 40% of excreted ash for AS, CSU and CS. Measured NH_3-N loss was 30, 41, and 70 g/3 d for AS, CS, and CSU diet and calculated losses were 17, 31, and 75 g/3 d, respectively (AS = CS < CSU for both measured and calculated losses, P<0.01). Average estimated NH_3-N losses did not differ from measured losses (P= 0.15), but calculated values averaged 6 g less. The method underestimated NH_3-N losses in cows with negative N balance and overestimated it for cows in positive N balance.

Key Words: nitrogen, ash, NH_3

M124 The effects of metaphylactic therapy on health and growth of neonatal Holstein bull calves. K. S. Holloway*, G. A. Holub, J. E. Sawyer, and M. A. Tomaszewski, *Texas A&M University, College Station*.

A study evaluating effects of metaphylaxis and milk replacer additives on health and growth was conducted with newborn Holstein bull calves (n = 52; mean BW = 42.28 ± 3 kg) < 7 d of age. Calves were randomly assigned to receive tilmicosin phosphate (TIL), ceftiofur crystalline free acid (CEF), or saline (CON). All calves received a commercial milk replacer program (25% CP, 20% fat), and within metaphylaxis treatment, were randomly assigned to receive milk replacer with: 1) 4 g/d for 7 d and then 2 g/d for the next 14 d of an egg-based additive (PR); 2) 2 g/d of 96% betaine (BE); 3) both PR and BE (BP); or 4) without additives (NA). Calves were housed in individual fiberglass hutches with ad libitum access to a commercial calf starter and water. Body weight was recorded twice weekly and fecal scores (1=firm, 4=watery) were recorded daily for 54 d. Number of treatments per calf for scours, incidence of respiratory symptoms, and febrile events were recorded on a daily basis, and the cumulative incidence of each response was used as an index of morbidity. All data were analyzed as a completely randomized design with a 3 X 4 factorial treatment arrangement. Neither metaphylaxis, additives, nor their interaction affected ADG (P>0.60); overall, calves gained .45 kg/d. Fecal scores were reduced by 39% for CEF compared to CON (P<0.01), but were not affected by additives. Metaphylaxis influenced neither incidence of fever (P>0.3) or respiratory symptoms (P>0.2) nor were they reduced by additives. Overall, calves were treated an average of only 0.39 times for respiratory symptoms and 0.66 times for fever. Scours were not influenced by metaphylaxis (P>0.6), additives (P>0.5), nor their interaction (P>0.8). Other than fecal score, metaphylaxis did not enhance productivity or reduce morbidity in this study, but disease challenge may have been mild. Feed additives influenced neither measures of health and performance nor did the metaphylaxis and feed additive interaction.

Key Words: calf, metaphylaxis

M125 Effects of single nucleotide polymorphisms in stearoyl CoA desaturase on milk fatty acid profile in lactating Holstein cows fed diets varying in fat content. L. Clark*, S. Moore, and M. Oba, *University of Alberta*, *Edmonton, Alberta, Canada*.

The objective of this study was to determine the effect of a single nucleotide polymorphism (SNP) in the stearoyl CoA desaturase (SCD) gene on the ability of dairy cows to produce 9*c*, 11*t*-18:2 (CLA), and to determine whether the CLA to 11*t*-18:1 (VCA) ratio can be used as a phenotypic indicator for CLA production capability. A SNP in SCD found on the fifth exon of chromosome 26, which encodes an amino acid change from alanine to valine, was evaluated in this study. Twelve lactating dairy cows in mid-lactation (180 ± 44 days in milk) were blocked by SCD genotype (AA, AV, and VV; n=4 for each genotype) and fed either a high or low fat diet in a cross-over design with 21-d periods. The high fat diet contained 5% sunflower seed oil on a dry matter basis, and dietary fat content was 3.2 and 8.3% for the low and high fat diet, respectively. Milk yield and milk fat concentration were not affected by dietary treatment or genotype, averaging 29.0 kg/d and 3.61%, respectively. The CLA concentration in milk fat was greater for cows fed the high fat diet compared with those fed the low fat diet (4.4 vs. 0.6%; $P < 0.0001$), but was not affected by genotype. The CLA-to-VCA ratio was 0.62 when AV and VV cows were fed the low fat diet, but decreased to 0.50 when they were fed the high fat diet. However, the CLA-to-VCA ratio was not affected by dietary fat content for AA cows, averaging 0.57 ($P < 0.06$ for diet × genotype interaction). These results indicate that AA animals maintained consistent activity of SCD when they were fed the high fat diet. Because the CLA-to-VCA ratio is affected by dietary fat content, it may not be used as a phenotypic indicator to identify animals with greater capability for CLA production in the field, in which animals are fed diets varying in dietary fat content.

Key Words: CLA, SNP, stearoyl CoA desaturase (SCD)

M126 Influence of subclinical hypocalcemia on plasma biochemical parameters in dairy cows. W. G. Chamberlin*, J. R. Middleton, and J. N. Spain, *University of Missouri*, *Columbia*.

The purpose of this study was to evaluate the effects of calcium status at calving on plasma biochemical parameters and fat mobilization in

Holstein cows. It was hypothesized that cows with subclinical hypocalcemia at calving would have greater elevations in liver associated biochemical parameters and non-esterified fatty acid (NEFA) concentrations compared with normocalcemic cattle. Forty-four multiparous Holstein cows were assigned to one of two groups 1) hypocalcemic (n=28; ionized calcium [iCa] < 1.0 mmol/L) or 2) normocalcemic (n=16; iCa > 1.0 mmol/L) based on whole blood iCa concentrations on the day of calving. Blood samples were collected from all cattle for measurement of iCa concentrations, NEFA concentrations, and serum chemistry profiles at -14 d, 0 (calving), 3, 7, 14, 21, 28, and 35 d. Data are reported as LSMeans ± SE. On d 0, [iCa] differed between groups with hypocalcemic cows having a lower [iCa] (0.87 ± 0.01 mmol/L) compared with normocalcemic cows (1.10 ± 0.01 mmol/L; P < 0.001). Hypocalcemic cows also had lower total plasma [Ca] on d 0 (7.17 ± 0.09 mg/dL vs. 8.26 ± 0.12 mg/dL). Hypocalcemic cows had greater blood pH on d 0 (7.37 ± 0.02 vs. 7.27 ± 0.03; P = 0.01). Total plasma bilirubin concentration tended to be greater in hypocalcemic cows on d 21 (0.24 ± 0.02 mg/dL vs. 0.17 ± 0.03 mg/dL, respectively; P = 0.08). Gamma-glutamyl transferase activity was greater in hypocalcemic cows on d 0, 3, and 7 (18.8 ± 0.8 vs. 16.0 ± 1.0 U/L; 18.4 ± 0.8 vs. 15.2 ± 1.1 U/L; and 20.8 ± 0.9 vs. 17.1 ± 1.0 U/L, respectively; P ± 0.03). These results indicate a relationship between hypocalcemia at calving, blood pH, and altered liver associated biochemical parameters.

Key Words: hypocalcemic, NEFA, transition cows

M127 Risk factors for multi-drug resistance of *Staphylococcus aureus* obtained from cases of mastitis. L. Oliveira*, H. Langoni, and P. Ruegg, *University of Wisconsin*, *Madison*.

The objective was to study risk factors for multi drug resistance (MDR) of *Staphylococcus aureus* isolated from milk samples obtained from cows with mastitis. Minimum inhibitory concentrations (MIC) of 12 antimicrobials were determined for S. aureus obtained from clinical (n = 58) and subclinical (n = 58) cases of mastitis that occurred on commercial dairy herds (n = 13). Of isolates, 76 (66%) did not exhibit resistance to any of the antimicrobials tested, 22 (19%) exhibited single drug resistance (SDR) and 18 (15%) exhibited multi drug resistance. Isolates with SDR were observed in 9 farms and MDR was exhibited in 18 isolates obtained from 4 farms. Farms could present isolates with SDR and MDR. Among resistant isolates, the distribution of MDR was 15 (66.7%) to two antimicrobials, and 3 (33.3%) to three antimicrobials. No isolate demonstrated resistance to more than three antimicrobials. MDR were observed in 7 (12%) and 11 (19%) of *S. aureus* obtained from subclinical and clinical cases, respectively. The combination of MDR to erythromycin and tetracycline (30.0%), and ceftiofur and enrofloxacin (27.8%) accounted for 57.8% of all MDR combinations. Enrofloxacin resistance was found in 7 isolates obtained from clinical cases that originated on one farm. Oxacillin resistance (indicating resistance to methicillin) was observed in a single isolate. Resistance type (SDR or MDR) was not associated with case type (P = 0.75), colony forming units (P = 0.12), somatic cell count (P = 0.98), days in milk (P = 0.30), or milk yield (P = 0.63). In this study, MDR was uncommon among the *S. aureus* isolated from bovine mastitis and there was no association between MDR and selected risk factors.

Key Words: *Staphylococcus aureus*, antibiotic resistance, multi-drug resistance

M128 Evaluating the impacts of a ruminally protected lysine product in dairy cows. N. Swanepoel*[1,2], P. H. Robinson[2], and L. J. Erasmus[1], [1]*University of Pretoria*, *Pretoria, South Africa*, [2]*University of California*, *Davis*.

The objective was to estimate the rumen escape potential of a prototype ruminally protected lysine (Lys) product (RPL; Ajinomoto Co., Tokyo, Japan) and to determine its effects on milk production and composition of high producing dairy cows. Rumen Lys escape of the RPL (42% L-Lys, 42% fatty acids) was estimated to be 18-23% using an in situ bag technique, increasing calculated intestinal absorption of Lys by 8-10 g/cow/d (the RPL was fed at 97 g/cow/d). The design was a double (early and mid lactation) 2x2 factorial with RPL crossover in two 28 day periods. Multiparity cows, grouped according to days in milk (DIM), allocated to one of two similar pens (~180 cows/pen), were fed the same total mixed ration (TMR), except for the RPL mixed into the treatment TMR. Both TMR were based on alfalfa hay, corn silage, steam flaked corn and dried corn distillers grains. Metabolic model evaluation suggested the TMR were limiting in Lys due to the high inclusion of corn products (47.6% of DM) causing a low model predicted Lys:Met ratio (i.e., ~3.1) in intestinally delivered protein of control cows. Dry matter intake was not impacted by RPL feeding in either early or mid DIM cows. Milk and true protein yields were reduced (41.8 vs. 40.9 kg/d and 1.27 vs. 1.25 kg/d; P = 0.05) by RPL in mid DIM cows but remained unchanged for early DIM cows. RPL decreased milk fat yield (1.86 vs. 1.77 kg/d and 1.56 vs. 1.43 kg/d; P<0.01), as well as fat concentration (3.50 vs. 3.29% and 3.74 vs. 3.54%; P<0.01) in early and mid DIM cows. Reduced concentrations of most essential amino acids (AA) in blood plasma with RPL feeding suggest that Lys was limiting. Since leucine (Leu) and isoleucine (Ile), as well as methionine (Met) and tryptophan (Trp) share intestinal transport systems, supplementary Lys from RPL may have reduced absorption of Ile and Trp through stimulation of Met and Leu absorption. Due to the involvement of these AA in metabolic processes (i.e., fatty acid synthesis, the citric acid cycle, muscle protein degradation), this could have changed energy metabolism in this study, reducing milk fat and/or protein synthesis when a small amount of Lys as RPL was supplemented.

Key Words: amino acids, milk protein, rumen bypass

M129 Effect of two CIDRs on progesterone concentrations and LH secretion in lactating dairy cows. C. Tritsch*, W. Silvia, S. Hayes, D. Ray, H. Hamilton, and A. Sanders, *University of Kentucky*, *Lexington*.

The concentrations of progesterone (P) maintained by 0, 1 or 2 EAZI-BREED CIDR® Cattle Inserts (Pfizer, New York, NY) were examined in lactating Holstein cows. Cows were presynchronized using prostaglandin (PG) F2a (Lutalyse® Sterile Solution, Pfizer, 25 mg each, i.m.) given at 50-120 days postpartum. Ten days later, ovaries were scanned ultrasonographically to confirm the presence of mature corpra lutea. CIDRs (0 CIDR controls n=5; 1 CIDR n=6; 2 CIDRs n=6) were inserted into each animal on the day of CL detection (experimental day 0). Animals received two injections of PGF2a as above, the first on the morning of day 1, the second 12 h later. Caudal blood samples were collected twice daily on days 0-2, then at 6 hr intervals beginning at 8 AM on day 3 for 24 h to quantify P. The concentration of P maintained by the CIDR (CIDR-P) was defined as the mean concentration in samples collected from 8 AM on day 3 through 8 AM on day 4. Jugular venous catheters were inserted on day 2. Blood samples were collected at 10 min intervals for 8 hours beginning at 8 AM on day 3, then an injection of GnRH (Cystorelin ®; Merial, Duluth, GA, USA; 100 ug, i.m.) was administered and blood sampling continued for 4 h at

30 min intervals. The effect of number of CIDRs (0, 1, 2) on CIDR-P, LH interpulse interval and the magnitude of the LH response to GnRH were determined by ANOVA. There was an effect of CIDR number on CIDR-P ($p < 0.0001$). There was no effect of CIDR number on the LH interpulse interval ($P = 0.4$). There was suppression in the amount of LH released in response to GnRH in the presence of 1 CIDR ($P < 0.01$). An additional CIDR had no further effect. These data suggest that 1) implanting 2 CIDRs leads to a significant increase in P compared to implanting a single CIDR, 2) increasing the concentration of P using two CIDRs failed to exert a negative feedback effect on pulsatile secretion of LH and 3) increasing the concentration of P with one CIDR exerted a significant suppression in the ability of GnRH to induce secretion of LH. *This research was supported by Kentucky Agricultural Experiment Station and KABA/Select Sires.*

Key Words: progesterone, dairy cow, LH

M130 Effects of increasing glycerin in the diet on ruminal fermentation during continuous culture. D. E. Rico*, Y. -H. Chung, C. M. Martinez, T. Cassidy, K. S. Heyler, and G. A. Varga, *The Pennsylvania State University*, *University Park*.

The objective of this experiment was to evaluate the impact of increasing levels of glycerin on ruminal fermentation during continuous culture. A 4 × 4 Latin square design was used to study four levels (0, 3, 5, and 8% of ration DM) of dry glycerin (min. 65% food grade glycerol) in the diet when replacing corn starch. The trial had 4 experimental periods of 9 d each, the first 6 d for adaptation and the last 3 d for sampling of effluent for DM content. Samples for VFA and ammonia were taken hourly for 5 h after feeding on day 9. Fermenters (1015 to 1040 ml in volume) were incubated with ruminal fluid (1 L) and ruminal digesta (25 g) from a cow receiving a diet with 16% CP, 32% NDF, and 25% starch. Fermenters were fed 25 g DM of the experimental diets three times per day and the solids retention time was set at 24 h. During the first 5 h after feeding, production of total VFA increased linearly ($P <0.05$) (76, 81, 86 and 87 mmol/L) while ratio of acetate to propionate decreased linearly ($P < 0.01$) (2.7, 2.3, 1.8 and 1.5) by increasing level of glycerin in the diet. Ammonia concentrations (11.7 15.1, 12.8, and 14.3 mg/dl) increased linearly ($P < 0.05$) with increasing glycerin level during the first 5 h after feeding. Dry matter digestibility increased linearly ($P < 0.01$) with glycerin level and was 37, 38, 41, and 40% for 0, 3, 5, 8% glycerin treatments, respectively. Higher ammonia concentration may indicate lower efficiency of nitrogen utilization by the ruminal microorganisms. Under the present experimental conditions, replacement of starch with glycerin seemed to have positive effects, as shown by increased total VFA production, decreased acetate to propionate ratio, and higher DM digestibility.

Key Words: dry glycerin, ruminal fermentation, continuous culture

M131 Evaluation of the economic impact of Optigen® use in commercial dairy herd diets with varying feed and milk prices. J. F. Inostroza*[1], V. E. Cabrera[1], R. D. Shaver[1], and J. M. Tricárico[2], [1]*University of Wisconsin*, *Madison*, [2]*Alltech Inc.*, *Brookings, SD*.

The objective of this study was to evaluate the impact of Optigen® (blended, controlled-release urea) use in commercial dairy herd diets on feed cost and milk income minus feed cost. Results from a field trial with 16 Wisconsin herds randomly assigned to treatment sequences of either Optigen® (OPT; 114 g/cow/d replacing an equivalent amount of supplemental CP to provide iso-nitrogenous TMR; TMR formulation space created by the use of OPT was filled with either corn grain or corn silage DM) to control (CON) or CON to OPT in a cross-over design with two 30-d feeding periods, showed that milk yield was 0.5 kg/d/cow greater ($P < 0.01$) for OPT than for CON; data were analyzed using the mixed model procedure of SAS with period, sequence and treatment as fixed effects and herd as a random effect. An economic simulation analysis was performed using the OPT feeding rate and milk yield response from the field trial and monthly soybean meal-48 ($0.373±0.054/kg), dry corn ($0.188±0.020/kg), corn silage ($0.059±0.005/kg), and high-moisture corn ($0.149±0.016/kg) prices (as-fed basis) and milk prices ($0.38±0.03/kg) for January through December, 2008. The cost of OPT was set at $1.63/kg. A total of 32 combinations of varying feed and milk prices were simulated. Results are provided in Table 1. Under the conditions of the simulations performed in this study, OPT reduced feed cost only when corn silage was used to fill formulation space while milk income minus feed cost was increased by OPT for all scenarios. A decision tool spreadsheet was developed to allow for further economic simulation analyses with the ability to vary the milk yield response to OPT, the cost of OPT, and the CP and energy supplements evaluated.

Table 1. Economic impact of Optigen® use in dairy herd diets.

CP Supplement Replaced by OPT	Ingredient Used to Fill Formulation Space	Feed Cost OPT - CON ($/cow/day)	Milk Income OPT - CON ($/cow/day)	Milk Income - Feed Cost ($/cow/day)
SBM-48	Dry Corn	0.047 (± 0.027)	0.192 (± 0.016)	0.145 (± 0.039)
SBM-48	Corn Silage	-0.020 (± 0.039)	0.192 (± 0.016)	0.212 (± 0.051)
SBM-48	HM Corn	0.042 (± 0.028)	0.192 (± 0.016)	0.150 (± 0.040)

Key Words: controlled-release urea, feed cost, dairy cows

M132 Dry matter intake measurements in commercial tie-stall dairy herds. M. W. Dekleva*[1], C. D. Dechow[1], J. M. Daubert[1], J. W. Blum[2], and G. A. Varga[1], [1]*The Pennsylvania State University*, *University Park*, [2]*University of Bern*, *Bern, Switzerland*.

The objective of this study was to determine the relationships among fat corrected milk (FCM), measured dry matter intake (DMI), and DMI predicted from National Research Council equations (NDMI) in order to determine if DMI could be measured with sufficient accuracy in commercial tie-stall dairy herds to facilitate genetic research. There were 1091 intake measurements made for 543 cows from 11 herds in Central Pennsylvania. All herds participated in monthly Dairy Herd Improvement Association testing, and intakes were measured once monthly over a 24-hour period within 7 days of a test date. Herd managers were instructed to follow their normal feeding routine and to distribute feed evenly to all cows. Intakes were then calculated by recording the total feed distributed to a group of cows, adjusting for observed variation, recording the amount of feed that was moved to or from individual cows, and subtracting weights of individual refusals the following morning. Feed samples were collected on each visit and analyzed for dry matter percentage. Body weights were estimated from hearth girth measurements at four points during lactation. Least-squares-means (LSM) for FCM, DMI and BW were estimated for week of lactation 1 to 40 using a four-trait model in ASREML. Fixed effects included herd-test day, herd-lactation and week of lactation. Random effects were cow and error. Least squares-means for BW and FCM were used to derive weekly

NDMI. The correlation between DMI and NDMI was 0.52 (P<0.001) and were most strongly associated during the first 10 weeks of lactation, after which point DMI was less than NDMI. The correlation between FCM and DMI across all herds was 0.23 (P<0.001). However, there was considerable variation among herds, with correlations between FCM and DMI within herd ranging from -0.14 (P=0.32) to 0.66 (P<0.001). Dry matter intake can be estimated in commercial tie-stalls with moderate accuracy, which could facilitate genetic research for feed intake in commercial herds.

Key Words: intake, commercial, dairy

Graduate Student Paper Competition-National ADSA Production PhD Poster: National ADSA Production Poster PhD Only (Graduate)

M133 Metabolism of ferulic acid in ram lambs. M. A. Soberón* and D. J. R. Cherney, *Cornell University*, *Ithaca, NY*.

Little is known about the metabolism of free ferulic acid (FA) in the ruminant once FA leaves the rumen. Due to its soluble nature, FA may be absorbed into the bloodstream and metabolized. This study was conducted to elucidate the metabolic pathway of free FA in sheep. Eight male lambs were randomly assigned to one of four treatment levels (0g, 3g, 6g or 9g of free FA) as part of a replicated 4x4 Latin square design. Lambs were housed individually and fed chopped alfalfa hay (22.8% CP, 39.3% NDF, 0.73 Mcal/kg NE_G) ad libitum and 0.35 kg corn grain (9.1% CP, 11.2% NDF, 1.52 Mcal/kg NE_G) once daily. Basal levels of FA in hay, grain, blood, feces and urine were established following a 14 d adjustment to diet and housing. Sampling was repeated at the conclusion of five continuous days where an oral dose of free FA was administered via bolus after each morning feeding. Feed, refusal and fecal samples were dried (60°C), ground to pass through a 2mm screen and analyzed for [FA] and NDF. Plasma and urine were frozen (-20°C) until analysis for [FA]. Body weights were taken weekly and DMI was measured daily. In addition to treatments, each lamb ingested FA in its bound form via the offered hay (2.67 mg/g FA) and corn (3.17 mg/g FA). Hay DMI was different among treatments (P=0.039) with DMI averages of 0.903 kg (0g), 1.06 kg (3g), 1.06 kg (6g), and 0.938 kg (9g). Refusals across treatments were not different in NDF level (P=0.347) or [FA] (P=0.848), indicating that sorting had no effect on free FA ingested. Free FA treatment level did not affect lamb body weight (P=0.281), fecal NDF levels (P=0.111), or fecal [FA] (P=0.294). No free FA was found in the plasma analyzed, indicating that during the five hours that passed between bolus dosage and blood collection, free FA in the blood was metabolized. Urine [FA] increased with increasing levels of free FA fed (P<0.001; averages were 1.66 μm/mL, 100 μm/mL, 240 μm/mL, and 592 μm/mL respectively for 0g, 3g, 6g, and 9g doses). These data indicate that free FA in lambs is fully metabolized from the blood by five hours post-dosage and primarily excreted in the urine.

Key Words: phenolic, ruminant

M134 Effects of acetate and essential amino acids on protein synthesis signaling in bovine mammary epithelial cells in-vitro. J. A. D. R. N. Appuhamy*, C. T. Bray, J. Escobar, and M. D. Hanigan, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Protein synthesis responds to various signals such as hormones, amino acids and energy supply. Acetate plays a major role as an energy source for milk synthesis in bovine mammary glands. The objective of this study was to investigate the effects of essential amino acids (EAA) and acetate on the phosphorylation status (PS) of mammalian target of rapamycine (mTOR), and ribosomal protein S6 (rpS6) which are involved in cellular signaling associated with protein synthesis and the cellular energy sensor AMP-activated protein kinase (AMPK). Bovine mammary epithelial (BME) cells from the MacT cell line were deprived of EAA and acetate overnight and then cultured in complete or EAA-deprived DMEM/F12 with and without acetate (5 mM sodium acetate) in a 2×2 factorial design repeated in 2 experiments. After 1 h of incubation, BME were lysed in the presences of protease and phosphatase inhibitors. Cell lysates were subjected to Western immunoblotting with antibodies against phosphorylated mTOR (Ser^{2448}), rpS6 ($Ser^{235/236}$), and AMPK (Thr^{172}). The PS of each signaling protein was determined as a ratio of the phosphorylated form and total forms. Acetate deprivation increased PS of AMPK (PS_{AMPK}) by 34% (P<0.05) and reduced PS of mTOR (PS_{mTOR}) by 42% (P<.05). There was a weak correlation between PS_{AMPK} and PS_{mTOR} (r=-0.32). Acetate had no effect(P>.10) on PS of rpS6 (PS_{rpS6}). In the absence of EAA, PS_{mTOR} and PS_{rpS6} were reduced (P<.01) by 55% and 75%, respectively. The correlation between PS_{mTOR} and PS_{rpS6} was 0.74 (P<.05). There was no interaction (P>.10) between EAA and acetate on PS_{mTOR} and PS_{rpS6} suggesting their regulatory effects on cell signaling were independent of each other. Extracellular EAA availability appeared to have a stronger effect on protein synthesis signaling in BME cells compared to the effect of extracellular acetate availability mediated by AMPK.

Key Words: cell signaling, acetate, amino acid

M135 Molecular cloning, distribution and ontogenetic expression of b0,+AT and the oligopeptide transporter PepT1 mRNA in Tibetan suckling piglets. W. Wang*[1], G. Wu[4], W. Gu[1], T. Li[1], M. Geng[1], W. Chu[2], R. Huang[1], M. Fan[3], D. Fu[1], Z. Feng[1], and Y. Yin[1], [1]*The Chinese Academy of Sciences*, *Changsha, Hunan, P. R. China*, [2]*Changsha University*, *Changsha, Hunan, P. R. China*, [3]*University of Guelph*, *Guelph, Ontario, Canada*, [4]*Texas A & M University*, *College Station*.

The AA transporter system b0,+ mediates apical uptake of basic amino acids, especially lysine and arginine. But some dietary protein digestion products are absorbed as oligopeptides rather than free AA. The aim of our study was to clone Tibetan porcine AA transporter b0,+AT and PepT1 for comparing the sequences of Tibetan pig with other species, and investigating tissue distribution and ontogenetic expression in the small intestine of Tibetan suckling piglets. Purebred Tibetan piglets (n=42) were obtained from multiparous sows and slaughtered randomly at 1, 4, 7, 14, 21, 28 and 35 d of age (6 piglets/age). The Tibetan porcine b0,+AT cDNA cloned from the small intestine was described first. The ORF of b0,+AT is 1464 bp and codified 487 AA residues, having a higher degree of sequence similarity with common pig (99.59%) and horse counterparts (91.2%) than with human (88.7%). The tibetan porcine PepT1 cDNA encodes 708 deduced AA residues that have high sequence similarity with its ovine and bovine counterparts. Both 2 putative proteins have 12 putative transmembrane domains. In this study, both b0,+AT and PepT1 mRNAs were detected in duodenum, jejunum, ileum, and liver by PCR. We investigated the expression of two genes in

duodenum, anterior jejunum, posterior jejunum and ileum from 1 to 35 d. The b0,+AT mRNA in duodenum and jejunum was greatest and least, respectively. It has a similar pattern in duodenum and anterior jejunum, which level decreased early in the suckling period and increased until d 35. Posterior jejunum expression uncreased steadily with age, except d 7. The ileum had the greatest expression at d 14 and became steady after d 28. The jejunum also had the greatest expression of PepT1 compared with the duodenum and ileum. PepT1 mRNA expression in the duodenum and proximal jejunum increased continuously from d 1 to 14; expression was greatest ($P<0.01$) at d 14 and then decreased from d 21 to 35. Our findings show that PepT1 expression in the distal jejunum increased gradually with age and the jejunum is the major absorption site for AA in Tibetan suckling piglets.

Table 1. b0,+ and PepT1 expression from d 1 to 35

tissue/ages	duo(b0,+/PepT1)	proximal jeju	distal jeju	ileum
1	$1.028^{a}/1.009^{bc}$	$1.025^{b}/1.244^{b}$	$1.019^{c}/0.785^{b}$	$1.061^{b}/0.573^{c}$
4	$0.346^{bc}/1.035^{c}$	$0.468^{b}/0.727^{b}$	$1.332^{c}/1.113^{b}$	$2.072^{b}/0.975^{ab}$
7	$0.113^{c}/1.294^{b}$	$0.437^{b}/0.730^{b}$	$3.127^{b}/1.729^{ab}$	$2.106^{b}/1.093^{ab}$
14	$0.459^{b}/3.575^{a}$	$0.809^{b}/2.257^{a}$	$1.178^{c}/2.588^{a}$	$6.483^{a}/0.177^{d}$
21	$0.475^{b}/1.709^{b}$	$0.759^{b}/1.090^{b}$	$2.367^{bc}/3.072^{a}$	$4.035^{ab}/0.819^{bc}$
28	$0.498^{b}/0.531^{c}$	$0.528^{b}/0.885^{b}$	$3.682^{ab}/2.784^{a}$	$2.969^{b}/0.527^{c}$
35	$0.857^{a}/0.424^{c}$	$4.511^{a}/1.023^{b}$	$5.212^{a}/2.850^{a}$	$3.704^{ab}/1.411^{a}$

Key Words: amino acid transporter, PepT1,b0,+, Tibetan pig

M136 Milk fatty acid composition of whole fluid milk in the United States. A. M. O'Donnell*, D. M. Barbano, and D. E. Bauman, *Cornell University*, *Ithaca, NY*.

Consumers are increasingly aware that food components have the potential to influence human health maintenance and disease prevention, and dietary fatty acids (FA) have been of special interest. It has been 25 years since the last survey of US milk fatty acid composition, and during this interval there have been substantial changes in dairy rations, including increased use of total mixed rations and by-product feeds as well as the routine use of lipid and FA supplements. Furthermore, analytical procedures have improved allowing greater detail in the routine analysis of FA, especially *trans* fatty acids. Our objective was to survey US milk fat and determine its fatty acid composition. We obtained samples of fluid milk from 56 milk processing plants across the US every 3 months for one year to capture seasonal and geographical variations. Processing plants were selected based on the criteria that they represented the major volume of milk produced in that area. An overall summary of the milk fat analysis indicated that saturated fatty acids (SFA) comprised 63.7% of total milk FA with palmitic and stearic acids representing the majority (44.1% and 18.3% of total SFA, respectively). Unsaturated fatty acids (UFA) were 33.2% of total milk FA with oleic acid predominating (71.0% total UFA). *Trans* FA (TFA) represented 3.2% of total FA, with vaccenic acid being the major *trans* isomer (46.6% total TFA). *Cis*-9, *trans*-11 18:2 conjugated linoleic acid represented 0.56% total milk FA, and the major omega-3 FA (linolenic acid, 18:3) composed 0.39%. Analyses for seasonal and regional effects indicated statistical differences for some FA, but these were minor from an overall human nutrition perspective as the FA profile for all samples were numerically similar. Overall, the present study provides a valuable database for current fatty acid composition of US fluid milk, and results demonstrate that the milk fatty acid profile is remarkably consistent across seasons and geographic regions from the perspective of human dietary intake of milk fat.

Key Words: fatty acids, milk fat composition, survey

M137 Polymorphisms in lipogenic genes and variations in milk fatty acid composition in Holstein dairy cows. R. A. Nafikov*[1], J. P. Schoonmaker[1], J. M. Reecy[1], D. Moody-Spurlock[1], J. Minick-Bormann[2], K. J. Koehler[1], and D. C. Beitz[1], [1]*Iowa State University*, *Ames*, [2]*Kansas State University*, *Manhattan*.

The objective of this study is to determine variations in single nucleotide polymorphisms (SNPs) in lipogenic genes that are associated with differences in milk fatty acid composition in Holstein dairy cows. Three genes, sterol regulatory element binding protein 1 (SREBP1), SREBP cleavage-activating protein (SCAP), and insulin induced protein 1 (Insig1) that are involved in the transcriptional regulation of stearoyl-CoA desaturase (SCD) and other lipogenic genes, were sequenced in exonic and intronic regions to detect SNPs. Five hundred cows were genotyped for discovered SNPs using Sequenom MassARRAY system. Phenotypic data were comprised of milk samples that were collected once per month throughout a ten month lactation period for all the cows and analyzed for fatty acid composition using gas chromatography. The PROC MIXED procedure of SAS with a month of lactation as a repeated statement was used to analyze the data. The mixed model included genotype as a fixed effect, sire line as a random effect, and milk production, percentage of milk fat, and lactation number as covariates. Multiple numbers of SNPs from SREBP1, SCAP, and Insig1 were significantly associated with differences in unsaturated fatty acid composition in milk. In particular, depending on the SNP, the percentages of monounsaturated fatty acids, polyunsaturated fatty acids, total unsaturated fatty acids, saturated fatty acids, and/or the ratio of unsaturated to saturated fatty acids were affected. The effects of SNPs from the earlier mentioned genes might be explained by differential regulation of the SCD transcription in cows with different genotypes for those genes. The results of this study indicate the potential of using associated SNPs as DNA markers to select breeding stocks that have a healthier milk fatty acid composition.

Key Words: SNP, fatty acids, candidate genes

M138 Regulation of bovine pyruvate carboxylase promoters by fatty acids. H. M. White*, S. L. Koser, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Pyruvate carboxylase (PC) is a critical enzyme in gluconeogenesis and TCA cycle carbon flux. Bovine PC (EC 6.4.1.1) gene contains three promoter sequences (P3, P2, and P1 from 5′ to 3′) which regulate its expression. Physiological stressors that evoke changes such as elevated NEFA or elevated glucocorticoid levels, including the onset of calving and feed restriction, also activate PC. The objective of this experiment was to determine the direct effects of stearic, oleic and linoleic acids (1 mM), dexamethasone (1 μM) and Wy14643 (10 μM; a PPAR aganonist) on promoter activity. Rat hepatoma (H4IIE) cells were transiently transfected with bovine PC promoter-luciferase constructs containing either P1, P2 or P3 and exposed to treatments for 23 h. Activity of P1 was suppressed ($P \leq 0.05$) with exposure to stearic acid (1.75 vs. 5.85 arbitrary units for stearic vs. control, respectively), and enhanced ($P \leq 0.05$) with exposure to Wy14643 (9.31 vs. 5.85 arbitrary units for Wy14643 vs. control, respectively). Conversely, stearic acid enhanced

($P \leq 0.1$) P3 activity (1.87 vs. 0.34 arbitrary units for stearic vs. control, respectively). Activity of P2 was not altered ($P \geq 0.05$) by any treatments and there was no response to glucocorticoids or unsaturated fatty acids for any of the promoters tested. Stearic acid suppresses the activity of bovine PC promoter 1 but enhances the activity of promoter 3 creating a net increase in promoter activity. These data demonstrate the role of fatty acids in regulating PC expression. The specificity of response for PC promoter function to stearic acid in the current data suggests a physiological role for elevated stearic acid concentrations previously observed in transition cows at calving.

Key Words: pyruvate carboxylase, promoter, fatty acids

Lactation Biology

M139 Effects of restricted feeding of prepubertal ewe lamb on growth performance, mammary gland development and first lactation. L. Villeneuve*[1], D. Cinq-Mars[2], and P. Lacasse[3], [1]*Centre d'expertise en production ovine du Québec*, *LaPocatière, QC, Canada*, [2]*Laval University*, *Québec, QC, Canada*, [3]*AAFC, Dairy and Swine Research and Development Center*, *Sherbrooke, QC, Canada*.

The aim of this study was to determine the effects of restricted feeding before puberty on growth performances, mammary gland development and milk production in replacement ewe lambs. At weaning, 72 Dorset ewe lambs were assigned to either an ad libitum diet (A), a restricted diet with good quality forage (14.8% CP, 2.15 Mcal ME/kg DM, 34.7% ADF) (F), or a restricted diet with medium quality forage (13.3% CP, 1.81 Mcal ME/kg DM, 42.8% ADF) (R). The quantity of feeds offered to ewe lambs of group R and F was adjusted in order to get an ADG representing 70% of that of ewe lambs of A group. These diets were offered during 75 d following weaning to cover the allometric phase of mammary gland development. During this period, ADG were respectively 223 and 229 g/d for R and F group compared to 305 g/d for A group ($P<0.0001$). At the end of this period, 28 ewe lambs were slaughtered and their mammary gland was collected. Parenchymal tissue weight tended to be higher for R and F groups with 27,86g and 24,37g respectively compared to 19,34 g for A ($P<0.10$). Stroma weight was greater ($P<0.05$) for A lambs (91.2, 61.9, and 64.4g for A, R and F, respectively). Total DNA and total protein in parenchymal tissue tend to be greater ($P=0.09$ and $P=0.07$ respectively) for R and F. Dry fat free tissue were greater for R and F averaging 1.81mg and 1.50mg respectively against 1.19mg for A ($P<0.05$). The remaining ewe lambs were fed a diet composed of silage and barley until their first lambing. During this period, compensatory growth occurred and ADG were greater ($P<0.01$) for R and F (179 and 175 g/d) than for A ewe lambs (147 g/d). Feed conversion was better ($P<0.01$) for R and F while the DMI was similar for all three groups. Milk fat and protein content were comparable for all animals but standardize milk yield tend to be better for R and F group ($P=0.07$). The results of this study suggest that restricted feeding before puberty improve mammary gland development and milk production without compromising growth performances in ewe lambs.

Key Words: ewe lamb, mammary development, restricted feeding

M140 Effects of intravenous infusion of *trans*-10, *cis*-12 18:2 on mammary lipid metabolism in lactating dairy cows. R. Gervais*[1], J. W. McFadden[2], A. J. Lengi[2], B. A. Corl[2], and P. Y. Chouinard[1], [1]*Université Laval*, *Québec, QC, Canada*, [2]*Virginia Tech*, *Blacksburg*.

It has been previously established that supplementation of *t*10*c*12 18:2 reduces milk fat content and fat deposition in a number of species. The objectives of the study were 1) to examine whether potential mechanisms by which *t*10*c*12 18:2 is reported to affect lipid metabolism in adipose tissue of different species could be partly responsible for the inhibition in milk fat synthesis observed in dairy cows; 2) to investigate the effects of *t*10*c*12 18:2 on the expression of a newly identified isoform of stearoyl-CoA desaturase in bovine mammary tissue. Four primiparous lactating Holstein cows fitted with a jugular catheter were used in a 2×2 crossover design. For the first 5 d of each period, cows were infused intravenously with a 15% lipid emulsion providing 10 g/d of either *c*9*c*12 18:2 (CTL) or *t*10*c*12 18:2 (CLA). On d 5 of infusion, mammary gland biopsies were performed and tissues were analyzed for mRNA expression of acetyl-CoA carboxylase (ACC), fatty acid synthetase (FAS), lipoprotein lipase (LPL), stearoyl CoA desaturase-1 (SCD1) and -5 (SCD5), sterol regulatory element-binding protein-1 (SREBP1), interleukin-6 (IL6) and -8 (IL8), and tumor necrosis factor-α (TNFα) by real-time RT-PCR. Compared to CTL, CLA reduced milk fat content and yield by 46 and 38%, respectively ($P<0.05$), and increased the *t*10*c*12 18:2 content in milk fat from 0.05 to 3.53 mg/g ($P<0.05$). Milk yield, milk protein, and DMI were unaffected by treatments ($P>0.15$). Infusion of the CLA treatment reduced the mRNA expression of ACC and FAS by 46 and 57%, respectively and tended to reduce the expression of SCD1 ($P=0.06$) and LPL ($P=0.14$). Abundance of SREBP1 mRNA was reduced by 59% in the CLA treatment ($P<0.05$). However, infusing *t*10*c*12 18:2 did not affect the expression of transcripts for SCD5, TNFα, IL6, and IL8 ($P>0.15$). Results from the current study corroborate the idea that effects of *t*10*c*12 18:2 observed on adipose tissue in animal models and humans are not part of the response in the inhibition of milk fat synthesis in dairy cows. They also support the hypothesis that SCD1 and SCD5 present important differences in their regulation and physiological roles.

Key Words: CLA, lipid metabolism, desaturase

M141 Selection of reference genes for quantitative real-time PCR in mouse mammary gland during different lactation days. X. L. Dong[1,2], J. Q. Wang*[1], D. P. Bu[1], K. L. Liu[1], H. Y. Wei[1], and L. Y. Zhou[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*Yangzhou University*, *Yangzhou, China*.

Real-time quantitative PCR (qPCR) is a method for rapid and reliable quantification of mRNA transcription. Selection of high quality reference genes is crucial to interpret the data generated by this method. The aim of this study was to investigate the expression stability of reference genes in the mammary gland of mouse during lactation circle. Six reference genes (*B2M*, *ACTB*, *GAPDH*, *SDHA*, *HPRT1* and *ARBP*) were chosen. The mammary gland samples were obtained from thirty lactating mice that were at 0, 1, 4, 8 and 12 days relative to parturition. Gene expression levels were measured by qPCR. During the different lactation days, the expression of the gene was analyzed by the ANOVA procedure of SAS (Version 6.12, SAS). The expression of *ACTB*,*GAPDH*, *SDHA*,

HPRT1 and *ARBP* was relatively stable (P>0.05), but the *B2M* shows a significant difference (P<0.05). The stability of the selected genes was investigated using geNorm Visual Basic application for Microsoft Excel. Based on geNorm algorithm, the range of expression stability in the genes analysed was (from the most stable to the least stable): *GAPDH/ HPRT1*, *ARBP*, *ACTB*, *SDHA* and *B2M*. We propose the use of two genes *GAPDH* and *HPRT1* as references for normalization of real-time qPCR in mice mammary gland for different lactation days.

Key Words: lactation, reference gene, qPCR

M142 Responses of milk protein and mammary amino acids metabolism to duodenal soybean small peptides and free amino acids infusion in lactating goat. H. Liu, Z.-J. Cao, L. Wang, S.-L. Li*, and L.-B. Wang, *College of Animal Science and Technology, China Agricultural University*, *Beijing, China*.

The effects of infusing soybean small peptides (SSP) or their free amino acids (FAA) into milk protein and the mammary amino acids (AA) metabolism of lactating goats were investigated using duodenal perfusion technique. Six Saanen goats with silicon catheters implanted into their carotid artery and mammary veins were used in crossover design. Blood samples were collected from carotid artery and mammary vein. The AA concentrations in the plasma, as well as in mammary uptakes of AA were monitored. The results showed that all AA concentrations in arterial plasma tended to be increased by SSP and FAA infusion. Differences in the concentrations of most essential amino acids (EAA) were significant between SSP and FAA infusion treatment, except for Val, Ile and Met ($p<0.05$). The concentration of all nonessential amino acids (NEAA), measured after FAA infusion treatment, was the higher ($p<0.05$), and the concentration of Asp, Glu, Ala and Tyr were significantly different ($p<0.05$). The concentration of most EAA in the mammary vein was the higher after FAA treatment, and the concentration of Val, Lys, Leu and Arg were significantly so ($p<0.05$). The mammary uptake of EAA was increased by SSP and FAA infusion. The mammary uptakes of other NEAA were increased by SSP and FAA infusion, except for Asp, Glu and Gly. Most EAA were taken up in excess in the SSP and FAA treatment. The rations of the EAA (except for Met) were low in the SSP treatment, compared to the FAA treatment. Ratios of all NEAA varied among treatments. Compared to the control treatment, significant increases in milk protein yield and milk protein content after the FAA infusion were observed ($p<0.05$); with the SSP infusion treatment, milk yield and milk protein were numerically increased, the difference was not significant. The results suggested FAA could improve milk protein synthesis.

Key Words: soybean small peptides, free amino acid, mammary metabolism

M143 Characterization of the bovine mammary FcRn receptor in mammary cells *in vitro*. C. R. Baumrucker*, Y. Wang, W. Liu, and C.D. Dechow, *The Pennsylvania State University*, *University Park*.

Bovine IgG1 is specifically transported by a process of transcytosis across the mammary epithelial cells during colostrogenesis and the neonate intestinal epithelia by the bovine FcRn receptor [bFcRn]. The FcRn receptor is composed of α heavy chain [FCGRT] and it is non-covalently associated with β2 microglobulin [β2M] in the plasma membrane. Mammary IgG1 appearance in cow colostrum is extremely variable in mass and concentration. We show concentration variance is inversly correlated to lactose mass while total mass of IgG1 remains variable suggesting differences in FcRn capacity. Data with bovine mammary cells in vitro (BME-UV1 & primary cells [MeBo]) shows strong expression of both bFCGRT and bβ2M mRNA when compared with bovine mammary and liver mRNA. In whole mammary tissue, but not the cells, we detected the expression of a bFCGRT variant. With the cellular expression, we set the objectives to characterize the 1) hormonal regulation of the bFCGRT mRNA and 2) to characterize IgG1 binding to the bFCGRT component *in vitro*. We show that the two messages (bFCGRT & bβ2M) were regulated (real time PCR) by hormone combinations that regulate mammary proliferation and differentiation *in vivo*. While insulin (I), cortisol (F), and prolactin (Prl) was not different from control (2% FBS), the absence of Prl showed significant reduction in bFCGRT expression. The application of 17β-estradiol accounted for >2 fold increase in both FcRn components in MeBo cells while the BME-UV1 cells did not respond. Biotinylated bIgG1 binding assays with the mammary cells in vitro indicated specific binding and receptor characteristics. Our findings suggest that bovine mammary cells may be utilized to understand the regulation of the FcRn to bind, internalize, and transcytoses IgG1 into colostrum. Furthermore, it is likely that the use of cell culture will provide a better understanding of the phenotype of FcRn variants and how they may contribute to the difference in IgG1 mass during colostrogenesis.

Key Words: mammary, FcRn, IgG1

M144 *In vitro* culture and characterization of a mammary epithelial cell line from Chinese Holstein dairy cows. H. Hu[1], D. P. Bu[1], J. Q. Wang*[1], Q. Chen[1], X. Y. Li[1], H. Y. Wei[1], L. Y. Zhou[1], and J. J. Loor[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*University of Illinois*, *Urbana*.

The objective of this study was to establish an in vitro bovine mammary epithelial cell line as a system that could be used to study mammary epithelial cell biology. Mammary tissue from a 3-y old lactating (ca. 100 DIM) Chinese Holstein dairy cow was used as a source of epithelial cells. Tissue was plated on collagen-coated (35 mm) plastic culture dishes and incubated in DMEM/F12 media containing 10% fetal bovine serum (FBS). Fibroblasts and epithelial cells successively grew and extended from mammary tissue during a 3-d culture period after which epithelial cells were obtained by continuous culture and digestion with 0.25% tripsin and 0.02% EDTA. Immunocytochemistry revealed a strong positive response of cytokeratin-18 suggesting that cells harvested exhibited the specific character of epithelial cells. Epithelial cells cultured in growth medium supplemented with supraphysiological concentrations of bovine insulin (5 μg/mL) and hydrocortisone (10^{-7} mol/L) maintained a normal diploid chromosome modal number ($2n = 60$) and were capable of synthesizing and secreting β-casein. Frozen preservation in 90% FBS and 10% DMSO did not influence the growth character, chromosome number, or protein secretion ability of the epithelial cell line. Results indicated that the obtained mammary epithelial cell line is normal in morphology, growth, and cytogenetic characteristics. Thus, this resource might aid in the controlled study of bovine mammary cell biology.

Key Words: mammary epithelial cells, Chinese Holstein dairy cow, tissue culture

M145 Transcriptomics comparison of MacT cells and mammary tissue during pregnancy and lactation. R. Sharma, M. Bionaz, A. K. G. Kadegowda, R. E. Everts, H. A. Lewin, and J. J. Loor*, *University of Illinois*, *Urbana*.

Use of immortalized bovine mammary epithelial cell lines (e.g., MacT) has enriched knowledge on the molecular aspects of bovine mammary physiology. The degree of similarity between these cell lines and mammary tissue at the mRNA level remains unknown. A 13K bovine oligonucleotide microarray was utilized to compare gene expression in bovine mammary tissue prepartum (-30 d) and postpartum (60 d) with MacT cells cultured in lactogenic medium. We identified transcripts which were similar as well as those highly-expressed in mammary tissue (MG) or MacT cells through direct hybridization. Overall, 30.4% (3,073) of transcripts had similar abundance between MG and MacT (FDR ≤ 0.2). Similarity was higher at 60 d (55%) compared with -30 d (43%). Results at 60 d were mainly related to insulin sensitivity, metabolism (e.g., hormones, anion), oligomerization of proteins, and arrest in proliferation. In contrast, at -30 d similarities were related to production of ATP and lipids (e.g., eicosanoids), activation of transcription (e.g. androgen and E2F). Overall, there were comparable numbers of highly-expressed genes (HEG; FDR ≤ 0.05) in MG (822) or MacT (852). The same trend was observed at 60 d (1,380 for MG; 1,350 for MacT). Interestingly, at -30 d the proportion of HEG in MG vs. MacT was nearly doubled (2,092) than that of MacT vs. MG (1,269). Overall HEG in MacT vs. MG were involved in cellular movement, apoptosis, cellular growth and proliferation, morphogenesis and development. In contrast, HEG in MG vs. MacT were related to increases in carbohydrate and lipid metabolism, transport of lipid and Ca2+, morphology of leukocytes, and decreased cell death. Most of HEG in MacT vs. MG at 60 d code for elements of the protein synthesis machinery even though milk protein transcripts were expressed at >12-fold in MG vs. MacT. Results suggest that MacT cells could be useful to study transcriptional regulation of nonlactating mammary tissue. Furthermore, they appear suitable for studies of proliferation, differentiation, and survival and death during lactation.

Key Words: microarray, genomics, epithelial cell

M146 Chinese women dietary behavior in different lactating stages and breast milk levels of fatty acids and iron. L. Xu*[1], Q.-H. Sheng[2], Z.-G. Zhang[3], Q. Gen[3], and L.-W. Zhang[1], [1]*School of Food and Science and Engineering , Harbin Industry University*, *Harbin city, China*, [2]*National Dairy Engineering & Technical Research Center, Northeast Agriculture*, *Harbin city, China*, [3]*Hebei Dairy Engineering & Technical Research Center*, *Shingjiazhuang city, China*.

Doing-the-month is a popular traditional behavior for Chinese mothers after delivery. During this period, lactating women prefer to meat and egg, and have a sedentary traditional habit. These unusual behaviors of mothers make a possible of change in fatty acids and iron compositions in human milk during the early stage of lactating, compared with follow-up months. Therefore, forty volunteers were recruited and assigned into two groups, the postpartum first month group (n=13) and postpartum 2-6 months group (n=27), respectively. The data were analyzed using SPSS version 10.0. This protocol and procedure were approved by Peking University Ethics Committee. The special changes in diet were assessed with indictors of protein, fat, and carbohydrate. Higher protein and lower carbohydrate intakes were indicated in the postpartum first month group, compared with that in postpartum 2-6months group. The fat intakes are similar between the two groups. Compared with "Chinese Dietary Reference Intakes", over 60% of women exceeded the standard in the intake of protein and fat in the postpartum first month group. However, there were over 20% women who had under standard intakes in energy, protein, and carbohydrate in the postpartum first month. For the postpartum 2-6months group, more than 50% of lactating women had lower intakes in protein and carbohydrate than the standard. Furthermore, the individual average content of 13 fatty acids and iron from human milk in different lactating stages were identified. There are no significant differences in the concentration of reported breast milk fatty acids in two groups, except for LA. There is significantly higher concentration of LA in the postpartum first month group than that in postpartum 2-4months group. The decrease in the content of iron was indicated in postpartum 2-6 months group, comparing with the postpartum first month group, from 126.82 μg/100ml to 80.85 μg/100ml. However, there is no statistical significant difference from two groups.

Key Words: lactating women, human milk, fatty acids

M147 Effect of staged ovariectomy on mammary histology and transcript abundance in prepubertal heifers. B. T. Velayudhan*[1], R. M. Akers[1], B. P. Huderson[1], A. Rowson-Baldwin[2], R. C. Hovey[2], and S. E. Ellis[3], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*University of California*, *Davis*, [3]*Clemson University*, *Clemson, SC*.

Previous studies suggest that the magnitude of reduction in mammary growth in response to ovariectomy depends on the age at which surgery was performed. We hypothesized that ovariectomy will reduce mammary epithelial cell proliferation and the magnitude of response will be greater in early ovariectomy. The objectives were to determine the effect of staged ovariectomy on epithelial cell proliferation as well as gene expression in bovine mammary gland. Prepubertal dairy heifers either at 2, 3 or 4 m of age were randomly assigned to one of two treatments, ovariectomized n = 8) or sham operated (n = 12), and mammary parenchyma were harvested 30 d after surgery. Epithelial area measurements and localization of progesterone receptors (PR) and Ki67 positive epithelial cells were determined by histological and immunohistochemical analyses. Gene expression of estrogen receptor-α (ERα), estrogen responsive genes such as stc1 and tfpi, PR and proliferating cell nuclear antigen (PCNA) were determined by quantitative real time PCR using comparative Ct method. Data were analyzed using Mixed model procedure of SAS. Expression of PR was reduced ($P < 0.05$) in ovariectomy at both protein and message level, but there was no difference in the proliferation of epithelial cells ($P = 0.652$) or the percent area of epithelium present ($P = 0.845$). Expressions of stc1, tfpi, and PCNA mRNA were down regulated by ovariectomy ($P < 0.05$) but ERα mRNA was not affected ($P = 0.196$). We did not find an interaction between ovariectomy and age at surgery for epithelial proliferation or transcript abundance. Our data suggest that a 30 d period after ovariectomy in prepubertal dairy heifers is insufficient to produce a marked reduction in proliferation rates in mammary epithelial cells despite the changes in estrogen related gene expression.

Key Words: epithelial proliferation, gene expression, ovariectomy

M148 Variation in expression of genes involved in glucose production and transport in mammary gland, liver and muscle of lactating cows. R. Weikard*, K. Krappmann, B. Brand, T. Goldammer, R. Brun-

ner, and Ch. Kühn, *Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*.

To identify regulatory mechanisms necessary to accommodate changes associated with lactation, analysis of mRNA expression levels of metabolic key enzymes of gluconeogenesis and glucose transport in mammary gland, liver and muscle of lactating cows was performed using quantitative RT-PCR. Three groups of animals (10 per group) differing in their metabolic status due to high differences in milk production (high, medium, low) were analyzed. In mammary gland of high-lactating (HL) dairy cows, the mRNA expression level of PCK2 known to catalyze the rate-controlling step of gluconeogenesis was significantly upregulated ($p<0.001$). Because in mammary gland mRNA expression levels of other genes included in gluconeogenesis did not vary significantly between groups, an additional metabolic function for PCK2 could be assumed in this tissue. Differences in glucose transport in mammary gland were reflected by divergent in transcript levels of glucose transporters. Whereas GLUT1 was higher expressed in mammary gland of HL cows ($p<0.05$), insulin-responsive GLUT4 and GLUT12 were downregulated in mammary tissue of this group ($p<0.005$ and $p<0.001$). In liver, significant differences of mRNA expression levels were detected for PCCA, which revealed a higher level in the HL group ($p<0.001$). This would indicate on an accelerated propionate metabolism. Furthermore, GLUT8 and GLUT4 showed a marked decrease in mRNA expression ($p<0.001$ and $p<0.001$) in the liver of HL cows. A considerably lower level of gene expression of PCK2 ($p<0.001$) and a substantial increase in the transcript level of FBP2 ($p<0.001$) were observed in muscle of HL cows pointing to affected gluconeogenesis or suggesting specific, yet unrecognized functions of these genes in muscle metabolism. The results presented could provide a basis for the elucidation of the physiological role of the enzymes of gluconeogenesis and glucose transport in different tissues in response to lactation-associated metabolic challenges in dairy cows.

Key Words: lactation, gene expression

M149 Effects of increased milking frequency on milk fatty acid composition in early lactation dairy cows. S. L. Shields*, D. Sevier, J. E. Williams, S. Zaman, P. Rezamand, and M. A. McGuire, *University of Idaho, Moscow*.

Milk production can be increased by more frequent milking; however, it may alter milk fatty acid (FA) composition. Our objective was to determine the effects of increased milking frequency on milk FA profile in early lactation cows, using a unilateral frequent milking (UFM) model. After parturition, sixteen Holstein cows were assigned to UFM in which the left udder half of each cow was milked four-times daily (4×; at 0500, 0900, 1600, and 2000 h) and the right udder half was milked twice daily (2×; at 0500 and 1600 h) with milk yields recorded from 1 through 21 days in milk (DIM) and samples were collected on d 3, 7, 10, 14, and 21. Milk FA composition was determined using gas chromatography (GC). Data were statistically analyzed by paired t-test using SAS (v. 9.2). Milk fat yield (milk yield × milk fat percent) was greater for the udder half milked 4× compared with the udder half milked 2X (0.60 vs 0.39 ± 0.01 kg/day; $P < 0.001$). Milk protein yield was also greater for the udder half milked 4× compared with the udder half milked 2× (0.42 vs 0.31 ± 0.006 kg/day; $P <0.001$). No significant difference was, however, detected in FA (wt% of total FA) synthesized via de novo synthesis for the udder milked 4× compared with the udder half milked 2× including 4:0 (3.91 vs 3.84 ± 0.1), 6:0 (1.75 vs 1.74 ± 0.06), 8:0 (0.91 vs 0.91 ± 0.04), 10:0 (1.86 vs 1.90 ± 0.12), 12:0 (2.10 vs 2.13 ± 0.14), and 14:0 (0.14 vs 0.13 ± 0.01; $P \geq 0.15$ for all). In addition, no significant difference was detected in 18:0 (11.83 vs 11.86 ± 0.28; $P = 0.76$) or two major products of desaturase enzyme, 18:1 c9 (27.0 vs 27.1 ± 0.68) and 18:2 c9 t11 (0.37 vs 0.37 ± 0.01; $P \geq 0.75$ for both), between the udder half milked 4X and the udder half milked 2×. We conclude that using a UFM model, increased milking frequency resulted in greater milk fat yield; however, increased milking frequency did not affect the FA synthesized via *de novo* synthesis, through the action of the desaturase enzyme or from preformed FA. Increased milk fat content, due to increased milking frequency, may have been related to increased FA uptake by the mammary gland.

Key Words: milking frequency, milk composition, milk fatty acid

M150 Energy deprivation inhibits protein synthesis in mammary epithelial cells through an AMPK- and mTOR-dependent pathway. S. A. Burgos* and J. P. Cant, *University of Guelph, Guelph, Ontario, Canada*.

Restriction of energy availability results in decreased milk yield and activity of enzymes involved in milk synthesis. To determine the involvement of the AMP depedent protein kinase (AMPK) and mammalian target of rapamycin (mTOR) signaling pathways in regulation of protein synthesis by energy deprivation, we examined the effects of 2-deoxy-D-glucose (2DG), a glucose analog that inhibits glycolysis, in the activation state of AMPK and mTOR signaling on effector mechanisms of mRNA translation in Mac-T cells. Subconfluent Mac-T cells were incubated in DMEM containing 2.5 mM D-glucose for 16 h and then treated with 10 mM 2DG for 15 min. Cell were harvested by scraping in lysis buffer. For immunoprecipitation, cell lysates were incubated with antibody for 2 h at 4°C with rotation and then protein A sepharose was added for 1 h. Beads were washed in lysis buffer and the precipitates were eluted in SDS sample buffer. For determination of protein phosphorylation state, cell lysates were boiled in SDS sample buffer for 5 min. Equal amounts of immunoprecipitated samples or cell lysate protein were separated by SDS-PAGE and transferred to PVDF membranes. Membranes were blocked, incubated with primary antibody overnight at 4°C, washed, and incubated with secondary antibody. Blots were visualized by enhanced chemiluminescence. We observed that energy depletion by 2DG stimulates AMPK activity, as measured by its phosphorylation at Thr172 and by the phosphorylation of the AMPK target acetyl-CoA carboxylase at Ser-79. The activation of AMPK was associated with downregulation of mTOR signaling, as determined by phosphorylation state of the mTOR translation effectors ribosomal protein S6 kinase and eukaryotic initiation factor (eIF) 4E-binding protein-1 (4E-BP1). In addition, 2DG treatment resulted in the enhanced association of eIF4E with the translational repressor 4E-BP1 and reduced formation of the active eIF4E-eIF4G complex. The results suggest that energy deprivation inhibits protein synthesis in mammary epithelial cells through an AMPK- and mTOR-dependent pathway.

Key Words: energy deprivation, mammalian target of rapamycin, protein synthesis

M151 Effect of milking frequency (1 vs. 4x) on milk yield, composition and numbers of gene transcripts for alpha-lactalbumin and beta casein in milk. A. P. Alex*[1], J. L. Collier[1], D. L. Hadsell[2], and R. J. Collier[1], [1]*University of Arizona, Tucson*, [2]*Baylor College of Medicine, Houston, TX*.

Recently published information indicates cytoplasm associated with milk fat globule membranes contains messenger RNA for the milk

proteins casein and alpha-lactalbumin. Furthermore, differences in the concentrations of these transcripts in mammary epithelial cells are reflected in differences in the concentration of these transcript in milk. Objective was to evaluate the effect of 1 vs 4x milking frequency on milk yield & composition as well concentration of messenger RNA transcripts for beta casein and alpha lactalbumin. Mean milk yield (kg/d) on d15, d60, d120 and d230 was 19.0, 18.2, 15.9 and 9.1 from the 4× half and 6.8, 7.2, 5 and 2.7 from the 1x half. Milk fat percent was on average slightly lower (3.34) in milk from 4× halves versus 1× halves (3.7) while protein per cent was slightly higher (2.83 vs. 2.68). Lactose and solids not fat (SNF) percentages were higher in milk from 4× halves than 1x halves. Beta-casein expression in 4× milk at d15, 60, 120 and 230 was 3.2, 2.2, 4.8 and 2.4 fold higher than 1× milk. Alpha-lactalbumin gene expression in milk from 4× halves was 2.9, 3.6, 8.8 and 2.1 fold higher than 1× at d15, 60,120 and 230. Thus transcript numbers were higher in milk from udder halves milked 4x despite slightly lower fat concentrations in milk from these halves versus milk from 1× milked halves. We conclude that transcript concentration for the milk proteins alpha-lactalbumin and beta-casein reflected differences in milk yield associated with differences in milking frequency. *This project was supported by National Research Initiative Competitive Grant no. 2007-35206-17831 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: beta casein, alpha lactalbumin, milking frequency

M152 Lactational effects of once- versus twice-daily milkings throughout lactation in two breeds of dairy ewes. A. Santibañez, X. Such*, G. Caja, V. Castillo, and E. Albanell, *G2R, Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

The effects of once- (1×) vs. twice-daily (2×) milkings throughout lactation on milk yield, milk composition, SCC, lactose, cisternal size and milk fractioning were studied in 2 breeds of dairy ewes differing in milk yield, udder compartments and milkability (Manchega, MN, n = 29; Lacaune LC, n = 37). After the weaning of the lambs (wk 5), ewes were machine milked at 2× and blocked into 2 groups to which milking treatments were applied: 1× (MN, n = 15; LC, n = 18) and 2× (MN, n = 14; LC, n = 19). Individual milk recording was conducted weekly (wk 5 to 25) for milk yield, biweekly for milk composition, monthly for SCC, and 2 times (wk 5 and 14) for lactose. Cisternal area and udder compartments were measured using an oxytocin receptors blocking agent (wk 5 and 14). Reducing milk frequency throughout lactation impaired milk yield differently in each breed (MN, -46%; LC, -25%; $P < 0.01$). A dramatic drop in milk yield was observed between wk 5 and 6 of lactation in the ewes passing from 2× to 1×. Milking frequency did not affect ($P > 0.05$) percentages of major milk components (fat, protein, total solids and casein), the milk of MN ewes being richer in components than LC. During lactation, lactose in blood was not affected by milking frequency, but LC ewes had greater levels of lactose than MN (33.9 vs. 19.5 µml/L, respectively; $P < 0.05$). The SCC was not affected ($P > 0.05$) by milking frequency, but LC ewes had greater values than MN ($P < 0.01$) and, for both breeds, a linear increase ($P < 0.01$) in SCC from 1st to 3rd parity was observed (5.01, 5.02, 5.62 log10 cells/mL). Cisternal and alveolar milk decreased ($P < 0.05$) throughout lactation (wk 4 to 14; 503 to 270 mL; 450 to 164 mL, respectively). Area of the cistern decreased (44.5 to 34.6 cm^2) as lactation progressed, affecting ($P < 0.01$) the fractioning of cisternal milk (S, 282 mL; L, 476 mL). Ewes LC showed greater cisternal area and cisternal milk ($P < 0.05$) than MN (483 vs 267 mL; 46.9 vs. 30.3 cm^2), respectively) which were related to the ability of each breed for adapting to 1× milking frequency.

Key Words: milking frequency, milk fractioning, dairy ewes

M153 Activation of mTOR signaling by insulin-like growth factor-I stimulates translation initiation in mammary epithelial cells. S. A. Burgos* and J. P. Cant, *University of Guelph*, *Guelph, Ontario, Canada*.

In several mammalian systems, the insulin-like growth factor I (IGF-I) mediates its effects through the phosphatidylinositol-3-kinase (PI3K) and mammalian target of rapamycin (mTOR) signaling pathways to regulate protein translation. The objective of this study was to determine the involvement of PI3K and mTOR signaling pathways in regulation of translation initiation by IGF in bovine mammary epithelial cells. Subconfluent Mac-T cells were serum starved for 16 h and then treated with 50 ng/ml IGF-I for 0, 5, 10 or 15 min. For inhibition of PI3K, cells were pretreated with 1 mM wortmaninn for 30 min. Cell were harvested by scraping in lysis buffer. For immunoprecipitation, cell lysates were incubated with antibody for 2 h at 4°C with rotation and then protein A sepharose was added for 1 h. Beads were washed in lysis buffer and the precipitates were eluted in SDS sample buffer. For determination of protein phosphorylation state, cell lysates were boiled in SDS sample buffer for 5 min. Equal amounts of immunoprecipitated samples or cell lysate protein were separated by SDS-PAGE and transferred to PVDF membranes. Membranes were blocked, incubated with primary antibody overnight at 4°C, washed, and incubated with secondary antibody. Blots were visualized by enhanced chemiluminescence. IGF treatment led to increased phosphorylation of protein kinase B at Ser 473was maximal within 5 min of IGF treatment. The effect of IGF on PKB phosphorylation was blocked by wortmannin. IGF treatment resulted in phosphorylation of the tuberous sclerosis complex 2 protein at Thr 1462 and the proline-rich Akt substrate of 40 kDa at Thr 246 by 5 min and was maximal by 10 min. Phosphorylation of ribosomal protein S6 kinase phosphorylation and eukaryotic initiation factor (eIF) 4E-binding protein-1 (4E-BP1) increased progressively up to 15 min. Hyperphosphorylation of 4E-BP1 led to the release of eIF4E and enhanced formation of the active eIF4E-eIF4G complex. IGF-I stimulates translation initiation through mTOR signaling in mammary epithelial cells.

Key Words: insulin-like growth factor, mammalian target of rapamycin, protein synthesis

M154 An intact SREBP pathway is essential for the *trans*-10, *cis*-12 CLA-induced inhibition of de novo fatty acid synthesis in the murine lactating mammary gland. M. R. Foote*[1], K. J. Harvatine[1], J. Monks[2], M. C. Neville[2], Y. R. Boisclair[1], and D. E. Bauman[1], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Colorado*, *Aurora*.

Trans-10, *cis*-12 conjugated linoleic acid (CLA) is a potent inhibitor of de novo fatty acid synthesis in the lactating mammary glands of many species. In dairy cows and mice, this inhibition of milk fat synthesis is accompanied by a coordinated decrease in the expression of key lipogenic genes within the mammary gland, including the sterol response element binding protein 1 (SREBP1), a transcription factor involved in the regulation of hepatic lipid synthesis in rodents. To evaluate the functional role of SREBP in the regulation of milk fat production, we examined CLA-induced inhibition of milk fat synthesis using mice expressing a floxed version of the escort protein SCAP (SREBP cleavage-activating protein), which is necessary to activate the SREBP pathway. Control mice and mice with disrupted SCAP expression were orally dosed with water (n = 8) or with 20 mg of *trans*-10, *cis*-12 CLA (n = 8) for four days during lactation. CLA decreased ($P<0.05$) growth of litters from control dams but had no effect on growth in dams with disrupted SCAP expression. CLA decreased ($P<0.01$) the proportion of de novo fatty acids (C<16:0) in milk of control mice but had no effect

on milk fatty acid composition of mice with disrupted SCAP expression. In addition, CLA decreased (P<0.05) the mammary expression of key lipogenic genes (e.g., SCD1, SREBP1c) in control dams but not in SCAP-disrupted dams. These results demonstrate a functional role for the SREBP signaling pathway in the regulation of mammary synthesis of fatty acids and indicate that an intact SREBP pathway is essential for the *trans*-10, *cis*-12 CLA-induced inhibition of de novo fatty acid synthesis in the mammary gland.

Key Words: CLA, mouse

M155 Low dosage oxytocin treatment induces milk ejection in dairy cows. C. J. Belo and R. M. Bruckmaier*, *University of Bern, Vetsuisse Faculty, Veterinary Physiology*, *Bern, Switzerland*.

Oxytocin (OT) treatment is frequently used in dairy practice to overcome disturbed milk ejection. However, the chronic use of high OT dosages can reduce the response to endogenous OT. We have investigated the use of OT in practical farms and we have tested the suitability of low dosage OT for milk removal. Based on the information from 82 dairy farms the used OT dosages were high, especially when injected i.m. (23 ± 2 IU and 7 ± 1 IU for i.m. and i.v. injections, respectively). We have studied low dosage OT treatment in cows with disturbed milk ejection, twenty six cows routinely treated with OT during milking (group T) and 17 cows without previous OT treatment (group C). After cessation of spontaneous milk flow, OT (0.2, 0.5 or 1 IU in group T; 0.2 or 0.5 IU in group C) was i.v. injected. The time from the injection until cessation of the OT induced milk flow was recorded (response phase). The response phase and the amounts of removed milk in response to the OT injection increased with increasing OT dosage and were 198 ± 27 s and 302 ± 18 s and 3.4 ± 0.7 kg and 6.5 ± 1.3 kg for 0.2 and 0.5 IU in group C, respectively, and 157 ± 15 s, 221 ± 16 s and 288 ± 22 s and 3.2 ± 0.5 kg, 5.5 ± 1.0 kg and 9.7 ± 1.3 kg for 0.2, 0.5 and 1 IU in group T, respectively. Within 20 min from injection OT, plasma concentrations returned to basal levels except for 1 IU where the OT plasma concentrations were still slightly elevated as compared to basal concentrations (P<0.05). The threshold OT concentration at cessation of milk flow after injection of 0.2, 0.5 or 1 IU of OT was calculated based on the OT plasma half-life. The threshold increased with increasing dosages of OT and was higher in group T (88 ± 11 pg/ml, 14 ± 1pg/ml, and 23 ± 2 pg/ml for 0.2, 0.5 and 1 IU, respectively) than in group C (7 ± 1 pg/ml and 11 ± 1 pg/ml for 0.2 and 0.5 IU, respectively). Obviously there is a desensitization of the udder towards OT when the udder is exposed to elevated OT plasma concentration, both short-term during the actual milking and long-term due to chronic high-dosage OT treatment. However, low dosage OT treatments to induce normal milk removal are possible.

Key Words: oxytocin, milk ejection, dairy cow

M156 Effect of exogenous growth hormone and ovariectomy on protein expression of aromatase in prepubertal bovine mammary gland. B. P. Huderson*[1], S. E. Ellis[2], and R. M. Akers[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Clemson University*, *Clemson, SC*.

Recent studies have shown an important role for locally produced estrogen in both humans and transgenic mice. Currently there is limited literature examining local estrogen production in the bovine mammary gland with most concentrating on periparturient animals. The purpose of these studies was to evaluate the effects of administering exogenous bovine somatotrophin (bST) and ovariectomy (OVX) on local aromatase production in mammary gland of prepubertal heifers. In the first experiment, 19 Holstein heifers (7 ± 4 d of age) were randomly assigned to one of two treatments bST (500 mg; n=10) or placebo (0.9% saline; n=9). Animals were administered subcutaneous treatments every three weeks beginning on day 23 of life. All animals were fed milk replacer and calf starter for 8 wk and starter and hay thereafter. Mammary parenchyma (PAR) and fat pad (MFP) were harvested for Western blot analysis. In both PAR and STR, local aromatase production was not affected by bST. In the second study, 22 Holstein heifers were randomly assigned to one of two treatments, ovariectomy (OVX; n=10) or sham (INT; n=12). Treatments were applied at 60, 90, or 120 d of age. Heifers were fed milk replacer and calf starter for the first 8 wk of life, and hay and calf starter thereafter. In PAR, animals operated on at 120 d had more aromatase detected compared to animals operated on at 60 and 90 d. Aromatase was detected in MFP but expression was not affected by treatment. In conclusion, local mammary production of aromatase was not effected by either bST or OVX and was predominantly expressed in MFP as opposed to PAR. Previously our lab reported no effect of OVX on the expression of genes involved in mammary gland proliferation and morphogenesis. Based on our current findings it is plausible that gene expression was not affected because there was no actual change in local aromatase production and therefore no change in local estrogen concentration.

Key Words: aromatase, bST, ovariectomy

M157 Removal of histidine from an intravenous amino acid infusion depresses milk protein and stimulates milk fat production by dairy cows. N. G. Purdie*, C. E. A. Borsy, C. Chui, J. Imada, P. Stahel, C. Longo, A. K. Shoveller, V. R. Osborne, and J. P. Cant, *University of Guelph*, *Guelph, Ontario, Canada*.

A selective decrease in histidine supply to the duodenum of dairy cows has been shown to stimulate milk fat production. To further characterize this response, four Holstein cows in their second lactation (122 ± 9 DIM) were fed a 50% forage TMR (12.1% CP, 1.53 Mcal/kg NELp). They were continuously infused i.v. with 0.9% saline as a negative control (NC), 300 g/d of a mix of essential amino acids in the profile found in milk protein as a positive control (PC), PC minus histidine (PC-His), and PC minus His plus 100 g/d Glu (PC-H+G). Treatments were given in a 4 x 4 Latin square, balanced for carryover effects, of 5-d infusion periods followed by 2 d of rest without infusion. Treatment differences were detected after analysis of variance with PROC MIXED of SAS. Pre-planned orthogonal contrasts were used to detect effects of PC vs. saline, imbalance (PC-His and PC-H+G vs. saline) and His deficiency (PC-His and PC-H+G vs. PC). There were no effects of treatment on feed intake or milk production of cows during the last 2 d of infusion ($P < 0.20$). Infusion of PC increased ($P < 0.05$) plasma concentrations of the essential amino acids Met, Phe, Thr, Ile, Leu, and Val and had no effect on non-essentials ($P > 0.17$) compared to saline. Infusion of the mixes without His caused a similar increase compared to saline in plasma concentrations of Met, Phe, Thr, Ile, Leu, and Val but also increased Arg, Tyr, Ser and Gln ($P < 0.05$). Compared to PC, the removal of His caused plasma His concentration to fall ($P = 0.033$) and branched-chain amino acids to increase ($P < 0.05$). Except for Arg, non-branched chain essential amino acids were not affected by His deficiency ($P = 0.318$). A milk fat stimulation of 95 g/d was observed with His deficiency ($P = 0.077$) but was not significant with imbalance ($P = 0.126$). Milk protein yield decreased 100 g/d with His deficiency ($P = 0.014$) and was not

affected by imbalance (P = 0.478). The protein:fat ratio of milk fell from 0.91 to 0.75 due to His deficiency (P = 0.012).

Key Words: milk composition, milk yield, histidine

M158 Effects of a shortened dry period on milk production and composition in early lactating Holstein cows. S. Safa[1], A. Heravi Moussavi*[1], M. Danesh Mesgaran[1], A. Golian[1], and A. Soleimani[1,2], [1]*Department of Animal Science, Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran*, [2]*Islamic Azad University-Kashmar Branch, Kashmar, Khorasan Razavi, Iran*.

The study was designed to test the effects of a shortened dry period on milk production and composition in early lactating Holstein cows. Cows were randomly assigned in 1 of 2 treatments: 1) traditional 60 d dry period (n=12) and 2) a shortened 20 d dry period (n= 12). Holstein cows were blocked in pairs based on their previous 305 d milk, parity and expected calving dates. All cows were fed by routine ration of farm (total mixed diet) twice a day and had at all time free access to water. Milk samples were collected from each milking on 1 d per week until 50 d after parturition and composited for analysis of milk composition. The data were analyzed using the MIXED procedure of SAS for a completely randomized design with repeated measures. The reduction in dry period reduced milk production dramatically ($p<0.01$; 38.11 and 28.57 ± 1.1kg/d, respectively). The effect of time was significant and the milk yields increased over the time ($p<0.01$). The cows in different dry periods behaved similarly over the time. Milk protein content tended to increased in the shortened dry period group ($p=0.066$; 3.07 and 3.17 ± 0.04%, respectively). The lactose content was numerically higher in the shortened dry period group ($p=0.07$; 4.59 and 4.73 ± 0.05%, respectively). Milk fat content was similar among the groups. The yields of milk fat ($p<0.01$; 1.45 and 1.09 ± 0.09 kg/d, respectively), protein ($p<0.01$; 1.17 and 0.92 ± 0.06 kg/d, respectively) and lactose ($p<0.01$; 1.76 and 1.36 ± 0.09 kg/d, respectively) were all decreased due to the reduction in dry period. The milk fat content was decreased and yields of protein and lactose increased over the time ($p<0.01$). The results of this study demonstrated that reduction of dry period to 21 d significantly reduced milk production and milk components yields compare with the convention 60 d dry period.

Key Words: dairy cows, dry period, milk production

M159 Udder morphology of the Holstein cows, primiparous and multiparous. M. Porcionato*, J. Negrão, F. Paiva, and T. Delgado, *University of São Paulo*, *Pirassununga, São Paulo, Brazil*.

This trial aimed to evaluate the morphological characteristics of udder and teats with ultrasound, estimate the cisternal areas of mammary gland and teats, as well as the relation between these images and the productive parameters. One hundred lactating primiparous and multiparous Holstein cows at the beginning and at the end of 1st, 2nd, and 3rd, lactations were milked twice a day with mechanical milker. Data were analyzed using SAS (version 8.2). Differences were considered significant at $P<0.05$. The ultrasonography showed higher ($P<0.05$) teat channel in 3rd (12.74 mm) than 1st (14.64 mm) lactation. The distance for the teat to floor was lower ($P<0.05$) in 3rd (48.82 cm) than 1st (57.07 cm) lactation. It was observed high and positive correlation ($r = 0.84$) between cisternal area and cisternal milk. The number of lactation had influence on the morphology of their mammary gland and teats, as well as in the milking duration and milk yield of the Holstein cows. The ultrasound technique used in this trial, carried before early milkings at minimum intervals of eight hours between milkings, presented satisfactory results of cisternal areas estimation of the mammary gland and teats in the primiparous and multiparous cows.

Key Words: adaptation, cisternal milk, morphology

M160 Effects of increased milking frequency on milk yield and selected measures of mammary gland health in lactating cows. S. L. Shields*, D. Sevier, J. Peak, K. S. Seo, P. Rezamand, and M. A. McGuire, *University of Idaho*, *Moscow*.

Increased milking frequency during early lactation increases milk yield; however, it may alter milk composition and measures of mammary gland health. The objective of this study was to determine the effects of increased milking frequency on milk yield and composition, and measures of mammary gland health in a unilateral frequent milking (UFM) model. Sixteen Holstein cows at parturition were assigned to UFM, in which, the left udder half of each cow was milked four-times daily (4×; at 0500, 0900, 1600, and 2000 h) and the right udder half was milked twice daily (2×; at 0500 and 1600 h). Milk yields were measured from 1 through 21 days in milk (DIM) and samples were collected on d 3, 7, 10, 14, and 21. Milk composition and somatic cell count (SCC) was determined. In addition, flow cytometric analysis with bovine monoclonal antibodies was used to identify the composition of leukocytes from the milk samples collected. Data were statistically analyzed in a paired t-test setting by SAS (v. 9.2). No clinical case of mastitis was observed. Milk yield was greater during the first 21 DIM for the udder halves milked 4× as compared with those milked 2× (13.3 vs 9.91 kg/d; $P < 0.001$). Milk fat percent was greater for the udder half milked 4× as compared with the udder half milked 2× (4.96 vs 4.57%; $P = 0.009$). No significant difference was observed in SCC ($P = 0.20$) or the SCC linear score (3.54 vs 2.77 for 4× vs 2×, respectively; $P > 0.9$) between milking frequencies. In addition, no significant difference was detected for cell population of total leukocytes (45.5 vs 40.5% for 4× vs 2×, respectively), granulocytes (12.7 vs 8.75% for 4× vs 2×), mononuclear cells (30 vs 29.2% for 4× vs 2×), or CD4 to CD8 ratio (2.90 vs 2.75 for 4× vs 2×) for the udder halves milked 4× as compared with the udder halves milked 2× ($P \geq 0.46$ for all). We conclude that using a UFM model, increased milking frequency resulted in greater milk yield and milk fat percent; however, milking frequency did not affect selected measures of mammary gland health.

Key Words: milking frequency, somatic cell count, milk leukocyte

M161 Regulation of CYP17A1 activity and its potential implications on the development of boar taint. M. J. Billen and E. J. Squires*, *University of Guelph, Guelph, Ontario, Canada*.

Male pigs are routinely castrated to prevent boar taint from the accumulation of 16-androstene steroids, in particular 5α-androstenone. Our objectives were to investigate how the two forms of porcine CYB5, CYB5A and CYB5B, and the phosphorylation status of porcine CYP17A1 modulate 17α-hydroxylase, C17,20 lyase and andien-β synthase activity of CYP17A1. We were especially interested in systems that would maintain the normal production of sex steroids (through the 17α-hydroxylase and C17,20 lyase reactions) while decreasing the production of the 16-androstene steroids (through the andien-β synthase reaction), since this might lead to methods for controlling boar taint. HEK-293 cells that were over expressing CYP17A1, cytochrome P450 reductase (POR), cytochrome b5 reductase (CYB5R3) and cytochrome b5A (CYB5A) or cytochrome b5B (CYB5B) were used. Increasing the ratio of CYB5A to CYP17A1 caused a decrease in 17α-hydroxylase, a transient increase in C17,20 lyase, and an increase in andien-β synthase activity ($p<0.0001$). Increasing the ratio of CYB5B to CYP17A1 also decreased 17α-hydroxylase ($P<.004$), but did not affect the andien-β synthase activity; however, the C17,20 lyase was significantly increased ($P<.004$). In cells over expressing CYB5A, treatment with the phosphatase inhibitor, okadiac acid (OA) increased C17,20 lyase activity ($P<.004$)and decreased 17α-hydroxylase and andien-β synthase activities ($P<.003$) , while co-transfection with an expression vector for protein phosphatase 2A (PP2A) increased 17α-hydroxylase and decreased C17,20 lyase and andien-β synthase activities ($P<.020$). Using site directed mutagenesis to change wild type CYP17A1-Ser106 to CYP17A1-Ala106 resulted in an increase in 17α-hydroxylase and decrease in C17,20 lyase activities ($P<.05$) in the presence of CYB5A. These results point to the different isoforms of CYB5 and phosphorylation status of CYP17A1 as selective targets for producing entire male pigs with a normal production of sex steroids and decreased production of the 16-androstene steroids that contribute to boar taint

Key Words: boar taint, cytochrome b5, phosphorylation

M162 Effects of dietary energy level and slaughter weight on carcass quality traits and grades in finishing pigs. M. J. Park[1], J. Y. Jeong[1], D. M. Ha[2], J. C. Han[2], B. C. Park[3], S. T. Joo[1], and C. Y. Lee*[2], [1]*Gyeongsang National University, Jinju, Korea*, [2]*Jinju National University, Jinju, Korea*, [3]*CJ Corps., Seoul, Korea*.

In Korea, pig carcass is valued according to its quality and yield grades mainly determined by the fat:muscle balance and backfat thickness, respectively. The present study was undertaken to investigate the effects of dietary energy level and slaughter weight (SW) on carcass grades, physicochemical characteristics and sensory quality traits of belly, ham and loin in lean-type, cross-bred finishing gilts and barrows beginning from 80-kg BW under a 2 (sex) × 2 [diet; 3.2 Mcal (medium energy; ME) vs 3.0 Mcal (low energy; LE) DE/kg] × 3 (SW; 110, 125 & 138 kg) factorial arrangement of treatments. Backfat thickness, which increased with increasing SW ($P<0.01$), was not affected by sex or diet. Carcass marbling score was greater ($P<0.01$) in gilts and LE than in barrows and ME, respectively. Carcass quality grade, which was greater in barrows and LE vs gilts and ME, respectively ($P<0.01$), had no relation to SW, whereas the yield grade decreased remarkably ($P<0.01$) between 125- and 138-kg SW primarily due to the upper limits of carcass wt imposed on the A & B grades. Physicochemical characteristics including pH, drip loss, and variables pertaining to color of belly, ham and loin were not affected significantly by the treatments, albeit statistically significant in some cases, in terms of quality criteria. In sensory evaluation for the primal cuts, the fat:muscle balance of fresh belly improved between 110- and 125-kg SW, but it did not change further between 125- and 138-kg SW. Marbling score of fresh ham was greater in LE vs ME ($P<0.01$) and tended to increase between 110- and 125-kg SW ($P=0.10$), whereas in loin, the increase of this variable between the two SW was significant ($P<0.01$). In the acceptability, LE was superior to ME in cooked belly and ham, but the effect of SW was insignificant in these and cooked loin. In conclusion, SW can be increased up to 138 kg without compromising carcass quality, whereas carcass yield grade decreases between 125- and 138-kg SW. Moreover, LE has some beneficial effects on quality of the whole carcass and the major primal cuts.

Key Words: finishing pig, slaughter weight, carcass

M163 Feedlot performance and carcass traits of Nellore, Simmental, Simbrasil and F_1 Simmental × Nellore bullocks. S. R. Baldin[1,2], C. L. Martins[1], R. D. L. Pacheco*[1], D. D. Millen[1], R. S. Barducci[1], L. M. N. Sarti[1], T. M. Mariani[1], J. P. S. T. Bastos[1], M. D. B. Arrigoni[1], and J. C. Hadlich[1], [1]*FMVZ/Unesp, Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP, São Paulo, Brazil*.

The objective of this study was to evaluate feedlot performance and carcass traits of *Bos indicus* and *Bos taurus* breeds: Nellore (NE), Simmental (SM) and its crosses. The experiment was conducted at São Paulo State University feedlot, Botucatu campus, Brazil. It was used 54 8-mo-old bullocks (250.4 ± 32.7 kg) randomly assigned to one of 27 pens (two animals per pen) according to genotype: 18 NE, 12 SM, 12 Simbrasil (SB; 5/8 SM, 3/8 NE) and 12 F_1 Simmental × Nellore (SN). Pens were considered the experimental unit. Bullocks were fed 80% concentrate after 21-d of adaptation, and were weighed every 28-d to calculate the ADG. After slaughter, rib eye area (REA) and back fat thickness (BFT) were measured to evaluate muscle growth and fat deposition. Meat samples were harvested between twelfth and thirteenth ribs to evaluate tenderness measured by Warner-Bratzler shear force (WBSF) of the steaks at 0, 7 and 14-d of ageing. SM had greater ($P < 0.05$) ADG when compared to the others genotypes (NE = 1.06, SM = 1.67, SB = 1.32, SN = 1.22 kg), while SN and SB had ($P < 0.05$) greater ADG than NE. No differences were observed ($P > 0.10$) for dressing percentage (NE = 54.5, SM = 53.6, SB = 54.4, SN = 53.9%). NE presented smaller ($P < 0.05$) REA, measured in square centimeters, than others genotypes (NE = 54.43, SM = 67.03, SN = 64.59, SB = 71.89). On the other hand, NE, SB and SN presented in millimeters ($P < 0.05$) greater BFT when compared to SM (NE = 3.46, SB = 3.42, SN = 3.25, SM = 2.55). At day 0, steaks from NE and SM presented ($P < 0.05$) higher shear than SB and SN (NE = 4.98, SM = 4.45, SB = 3.13, SN = 3.33 kg), however these differences were not detected ($P > 0.10$) when steaks were aged for 7 and 14-d. Means WBSF among genotypes were 3.97, 2.72 and 2.53 kg for steaks aged for 0, 7 and 14-d, respectively. Steaks aged for 7 and 14-d had lower shear ($P < 0.05$) than those steaks without ageing. The thinnest group evaluated was SM, which performed better than NE and its crosses (SB and SN). Seven days of ageing seem to be sufficient time to improve meat tenderness of beef cattle regardless of genotype.

Key Words: Nellore, Simmental, WBSF

M164 Effects of vitamin D supplementation on carcass traits of Nellore and Canchim bullocks fed high concentrate diets. F. S. Parra[1,2], S. R. Baldin[1], M. D. B. Arrigoni[1], C. L. Martins[1], J. R. Ronchesel[1], N. R. B. Consolo[3], A. L. Campanini[1], R. S. Barducci[1], L. M. N. Sarti[1], D. D. Millen[1], R. D. L. Pacheco*[1], D. Tomazella[1], H. D. Rosa[1], T. Leiva[1], E. N. Andrade[1], [1]*FMVZ/Unesp, Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP, São Paulo, Brazil*, [3]*UD/Unesp, Dracena, São Paulo, Brazil*.

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test the effects of vitamin D supplementation (VDS) on final BW, HCW, dressing percentage and carcass pH of Nellore (NE) and Canchim (CC; 5/8 Charolais, 3/8 NE) bullocks fed high concentrate diets. The experiment was designed as a 2 × 2 factorial arrangement, replicated 9 times, in which 18 8-mo-old bullocks (209.4 ± 23.3 kg) of each of two breeds evaluated were fed diets with or without vitamin D at 7.5×10^6 UI•animal^{-1}•d^{-1} for 10-d prior to slaughter. Animals were adapted for 21-d to the high concentrate diets fed. Diets contained 47.5% high moisture corn, 20% citrus pulp, 12.8% soybean meal, 13.7% sugarcane bagasse, 4.6% *Cynodon* hay and 1.5% supplement. Bullocks were withheld from feed for 16-h before every weight assessment. Carcass pH was measured on *Longissimus dorsi* muscle at 0 and 24-h after slaughter with a meat pH meter (Hanna Instruments model 99163). No significant (P > 0.10) breeds and VDS main effects or interactions between breeds and VDS were observed for any of the carcass traits parameters evaluated (Table 1). In conclusion, vitamin D supplementation did not affect the carcass traits of NE and CC bullocks in this study.

Table 1. Effects of vitamin D supplementation on carcass traits of NE and CC bullocks

Item	NE	CC	VIT D[3]	NONE[4]	P value Breeds	P value VIT[5]	SEM
Final BW, kg	365.3	384.1	375.6	373.1	0.20	0.90	44.6
HCW, kg	194.1	201.3	197.1	198.3	0.39	0.88	25.2
Dressing, %	53.1	52.4	52.4	53.0	0.15	0.21	1.4
pH0[1]	6.84	6.88	6.85	6.87	0.46	0.61	0.16
pH24[2]	5.57	5.59	5.58	5.58	0.73	0.95	0.17

[1] Carcass pH at time 0; [2] Carcass pH after 24-h of chilling; [3] VDS; [4] No VDS; [5] P value for VDS.

Key Words: bullocks, carcass, vitamin D

M165 Interaction of dietary vitamin D_3 and sunlight exposure on meat tenderness and color of *Bos indicus* cattle. A. R. Lobo Jr.[1], E. F. Delgado*[1], G. B. Mourão[1], A. Berndt[2], and J. J. A. A. Demarchi[2], [1]*Escola Superior de Agricultura, Piracicaba, SP, Brazil*, [2]*Agência Paulista de Tecnologia do Agronegócio, Andradina, SP, Brazil*.

Beef tenderness improvement through dietary vitamin D_3 supplementation has been challenged by null results and negative impacts on animal performance. The animal is able to synthesize vitamin D by action of ultraviolet (UV) radiation from the sunlight. Therefore, sunlight exposure may modulate the effectiveness of vitamin D_3 supplementation to increase active metabolites of that vitamin in the body fluids. Hence, this work aimed to verify whether dietary vitamin D_3 modifies meat tenderness and color in *Bos indicus* cattle under natural sunlight exposure or protected conditions. Forty-one castrated bulls (411±38 kg) were confined and fed high concentrate diet, after assignment to 6 treatments: 1) neither vitamin D_3 supplementation (NV) nor shade (NS); 2) NV with shade (WS – 50% UV filtration); 3) 2×10^6 IU of vitamin D_3 for 2 days pre-slaughter (WV2) + NS; 4) WV2 + WS; 5) 2×10^6 IU of vitamin D_3 for 8 days pre-slaughter (WV8) + NS; and 6) WV8 + WS. The myofibrillar fragmentation index and shear force were measured at 1, 7 and 21 days (d) *postmortem* (*pm*). The meat color was measured at 24 hours *pm* using the CIELab parameters *L**, *a** and *b**. Plasma and muscle calcium were also measured. The WV8 increased fragmentation index (P = 0.09) in NS (22.3±1.5) compared to WS (18.3±1.5), even though cattle under NS had lower (P < 0.05) muscle calcium concentration. There was no effect of either vitamin or sunlight exposure (P > 0.05) on shear force, which decreased (P < 0.01) during *pm* storage (1 d*pm*: 10.4±0.4 kg; 7 d*pm*: 8.8±0.5 kg; 21 d*pm*: 6.8±0.5 kg). The WV8 (32.3±0.5) increased (P = 0.065) *L** values compared to WV2 (30.5±0.5), while both were similar (P > 0.05) to NV (31.6±0.5). Higher *a** (P = 0.02) and *b** (P < 0.001) values were observed for WV8 (17.1±0.4 and 4.5±0.2, respectively) than for both WV2 and NV (15.8±0.4 and 3.6±0.2; and 15.5±0.4 and 3.4±0.2, respectively). NS (34.5±0.5) animals presented (P < 0.05) higher *L** values than WS (32.6±0.5) at 24 hours *pm*. Vitamin D_3 or sunlight exposure can alter beef color. Both factors interacted to change the myofibrillar fragmentation, but were not sufficient to impact shear force in *Bos indicus* cattle.

Key Words: aging, calcium, shade

M166 Expression of calpastatin isoforms and meat tenderness of pure-bred Large White and Duroc animals fed different doses of ractopamine. E. F. Leonardo, E. F. Delgado*, I. L. Stella, L. L. Coutinho, and G. B. Mourão, *Escola Superior de Agricultura, Piracicaba, SP, Brazil*.

Calpastatin is a specific endogenous inhibitor of calpains and it is coded by a single gene. Studies had demonstrated that exons 1xa, 1xb and 1u of the calpastatin XL domain are functional and generate three differentiated isoforms which might be related with muscular growth and meat tenderness. The objective was to verify the impact of calpastatin isoforms on pork tenderness and whether they are responsive to beta adrenergic agonist. Sixty animals (30 barrows and 30 gilts) being 30 Large White (LW) and 30 Duroc (DU) were randomly assigned to different doses of ractopamine (RAC): 0 (control), 10 ppm (RAC 10) and 20 ppm (RAC 20) in the diet. The RAC was given to the animals from 85 kg to 110 kg of live weight in a period of 4 weeks. Samples of muscle *L. dorsi* had been collected immediately after slaughter and frozen in liquid nitrogen for quantification of relative mRNA abundance of three calpastatin isoforms (CAST1: 1xa; CAST2: 1xb; CAST3: 1u). The myofibrillar fragmentation index (MFI) was measured at 1, 3 and 5 days *postmortem* (d*pm*), while shear force (SF) was measured at 1 and 5 d*pm*. Rib eye area (REA) was obtained in those animals. Only CAST1 had differential expression between breeds and RAC doses, with higher (P < 0.05) expression in the LW animals and RAC fed pigs. CAST2 presented low relative expression. CAST3 had similar expression with no effect (P > 0.05) of gender, breed or RAC. MFI was lower (P < 0.01) for LW on d 1 and 5 *pm* [(LW 1 d*pm*: 32±1.1; 5 d*pm*: 52±1.2) and (DU 1 d*pm*: 37±0.7; 5 d*pm* 58±0.9)] and for 20 ppm of RAC at all times *pm* [(Control/1 d*pm*: 40±1.1 ; 3 d*pm*: 49±1.4 ; 5 d*pm*: 60±0.4); (RAC 10 / 1 d*pm*: 36±1.3; 3 d*pm*: 48±1.2; 5 d*pm*: 57±0.7) and (RAC 20 / 1 d*pm*: 31±1.1; 3 d*pm*: 39±0.5; 5 d*pm*: 47±0.9)]. There was a positive correlation (r = 0.81; P < 0.01) between CAST1 mRNA abundance and shear force 1 d*pm*. There was also a positive correlation (r = 0.58; P < 0.01) between REA and CAST1 expression for the LW pigs. RAC or LW pigs produced muscled loin and tougher meat that could be related to higher CAST1 expression

Key Words: myofibrillar fragmentation, growth, shear force

M167 Heat shock protein β-6 emerges as a potential biomarker to predict meat tenderness. I. Zapata*, H. N. Zerby, and M. Wick, *The Ohio State University*, *Columbus*.

The mechanisms controlling meat tenderness involve a multitude of cellular functions, which have proven difficult to develop into a coherent model. A novel approach is the use of functional proteomics, a combination of electrophoretic, image, statistical and protein sequencing technologies that identifies the protein(s)/peptide(s) bands associated with tenderness measured by Warner Bratzler Shear (WBS). The aim of this study was to statistically associate the staining intensity of electrophoretically separated bands from a myofibrillar fraction with WBS and determine the sequence of the protein(s)/peptide(s) within those bands. Twenty two Angus crossbred steers were harvested. Muscle samples were taken from the *Longissimus dorsi*. Samples for functional proteomics and for WBS were taken at 36h and 72h postmortem, respectively. The myofibrillar fraction was resolved on a 10% to 20% acrylamide gradient gel. Gel images were analyzed by a stepwise multiple linear regression model fitted using the dependent variable of 72h WBS. Significant bands were analyzed by capillary liquid chromatography nanospray tandem mass spectrometry (nano-LC/MS/MS). The regression model significantly identified two bands (R^2 = 0.508). In the first band, myosin heavy chain along with myosin light chain 2 were identified. The second band contained multiple isoforms of myosin light chain 2 and the heat shock protein β-6 (hspb6). This heat shock protein has never been associated to tenderness variability. Hspb6 has been related, *in vivo*, to muscle relaxation during high calcium concentration events during situations of acute stress. Hspb6 is known to be intimately related to the stability of the actin thin filament. The band that contained this protein was found to be negatively associated with 72 h WBS which suggests that higher levels of hspb6 lead to tougher meat while lower levels lead to more tender meat. By identifying the mechanisms through which tenderness is mediated, it will be possible to implement breeding strategies to produce cattle with greater and more consistent tenderness.

Key Words: functional proteomics, heat shock protein, tenderness

M168 Evaluating the application of dual x-ray energy absorptiometry (DEXA) to assess dissectible fat and muscle from the 9–11th rib section of beef cattle. F. R. B. Ribeiro*[1], R. D. Rhoades[2], L. O. Tedeschi[3], S. E. Martin[3], and S. F. Crouse[3], [1]*Texas A&M University*, *Commerce*, [2]*The King Ranch Institute*, *Kingsville, TX*, [3]*Texas A&M University*, *College Station*.

The objective of this study was to evaluate the adequacy of measuring dissectible fat and muscle from the 9–11th rib section of beef cattle using a dual x–ray energy absorptiometry (DEXA) scanner (GE Lunar Prodigy Advance, General Electric, Madison, Wisconsin). Data were obtained from 52 animals (20 steers, 16 bulls and 16 heifers) from two trials. Trial 1 was composed of Angus steers (n = 24) and Trial 2 had Angus bulls (n = 16) and heifers (n = 16). The 9–11th rib section samples were removed from the carcasses and digital images were obtained using the DEXA scanner. The outputs of the DEXA scanner were total fat percentage and lean muscle amount. The lean muscle percentage was calculated in order to compare with the rib dissection composition. Then, the 9–11th rib samples were physically dissected and chemical analyses were performed following the Hankins and Howe procedure. Regression analysis was performed with PROC REG. The DEXA fat prediction explained 84 and 86% of the variation in the physical and chemical rib fats, respectively. For both predictions, the regression analysis indicated that the intercept and the slope were not different from zero and one ($P < 0.001$), respectively. However, the mean biases were significantly different from zero and underpredicted (3.4 and 2.3% for physical and chemical rib fats, respectively). The DEXA lean prediction explained 82% of the variation in the physically separable lean with a mean bias of -16% (overpredicted). These results indicated that DEXA scanners can precisely predict the 9–11th rib section fat and lean tissue of beef cattle, but accuracy is lacking. More calibration might be needed to improve accuracy of DEXA scanners.

Key Words: DEXA, carcass composition, cattle

M169 Age entering the feedlot and implant potency: I. Post-weaning-weaning and feedlot performance. P. Beck*[1], B. Barham[2], S. Gadberry[2], J. Apple[3], M. Miller[4], and L. Hughes[4], [1]*University of Arkansas*, *Hope*, [2]*University of Arkansas Coop. Ext. Ser.*, *Little Rock*, [3]*University of Arkansas*, *Fayetteville*, [4]*Texas Tech University*, *Lubbock*.

According to the National Beef Quality Audit, beef exporters and beef producers have cited carcass quality as a primary challenge facing the industry. This research focused on animal age and implant status and their effects on animal performance. Spring-born calves (n = 80, BW, = 220 ± 5.7 kg) were weaned at 7 months and backgrounded for 63-d. Backgrounding diets were fed at a rate to promote ADG of 1 kg/d. Fifty percent of the calves were then sent directly to the Texas Tech University research feedyard for finishing (CALF), the remainder were placed on small grain pasture for 133-d prior to finishing (YRLNG). One-half of each feeding group received an aggressive implant regimen (AGG), where cattle were implanted at the beginning of backgrounding (Synovex S or H), at the start of grazing (Synovex S or H), at the initiation of feeding (Synovex S or H), and 50-d prior to the end of the finishing (Synovex Plus). The remainder received a low potency implant regimen (LOW) where the initial implant was delayed until 50-d prior to the end of finishing (Synovex S or H). Feedyard cattle received steam-flaked corn based finishing diets until the average backfat thickness for each group reached 1.5 cm. Data were analyzed as a 2 × 2 factorial arrangement of treatments by the mixed procedure of SAS. During backgrounding, AGG calves gained 0.13 ± 0.06 kg/d more ($P = 0.03$) than LOW. Forage allowance restricted grazing performance and there was no effect ($P = 0.88$) of implant on ADG, but AGG YRLNG were still 17 ± 7.6 kg heavier ($P = 0.03$) than LOW YRLNG at the end of grazing. During finishing, ADG of LOW was 0.30 ± 0.04 less ($P \leq 0.01$) than AGG and CALF gained 0.26 ± 0.06 less ($P \leq 0.01$) daily than YRLNG (ADG 1.65, 1.92, 1.89, 2.21 ± 0.05 kg, for LOW CALF, AGG CALF, LOW YRLNG, and AGG YRLNG, respectively). Implanting in early stages of production do not reduce performance enhancement in subsequent stages. Implantation increases beef production when nutrient dense diets are fed to growing and finishing cattle, this increased productivity becomes essential when feed costs increase cost of production.

Key Words: beef cattle, finishing, implants

M170 Age entering the feedlot and implant potency: II. Carcass quality, shear force and sensory panel characteristics. B. Barham*[1], P. Beck[2], S. Gadberry[1], J. Apple[3], W. Whitworth[4], and M. Miller[5], [1]*University of Arkansas*, *Little Rock*, [2]*University of Arkansas*, *Hope*, [3]*University of Arkansas*, *Fayetteville*, [4]*University of Arkansas*, *Monticello*, [5]*Texas Tech University*, *Lubbock*.

The objective of the study was to evaluate the effects of age of calf entering the feedlot and implant treatment on carcass characteristics.

Spring-born calves (n = 80, BW, = 228 ± 5.7 kg) were weaned at 7 mo. of age and backgrounded for 63-d. Backgrounding diets were fed at a rate to promote ADG of 1 kg/d. Fifty percent of the calves were sent directly to the Texas Tech University research feedyard for finishing (CALF) and the remainder stayed at the SWREC for a 133-d small grain grazing program prior to finishing (YRLNG). One-half of each feeding group received an aggressive implant regimen (AGG), where cattle were implanted at the beginning of backgrounding (Synovex S/H), at the start of grazing (Synovex S/H), at the initiation of feeding (Synovex S/H), and 50-d prior to the end of the finishing (Synovex Plus). The remainder received a low potency implant regimen (LOW) where the initial implant was delayed until 50-d prior to the end of finishing (Synovex S/H). Cattle were fed corn based finishing diets until the average backfat thickness for each group reached 1.5 cm. Ribeye area was increased (P < 0.01) by AGG implant program of both CALF and YRLNG. Marbling scores were decreased in AGG compared to LOW (P = 0.03) and in YRLNG compared to CALF (P < 0.01). The percent choice was not different (P = 0.58) between LOW and AGG CALF (86 ± 8.8 and 78 ± 9.3%, respectively). The percentage choice was decreased (P < 0.01) from 94 ± 8.7% for LOW YRLNG to 46 ± 8.4% in AGG YRLNG. Sensory panel scores for initial and juiciness, flavor intensity, and beef flavor were lower for AGG when compared to LOW (P<0.01). Initial and sustained tenderness were lower in AGG YRLNG compared to LOW YRLNG (P<0.01), AGG CALF compared to LOW CALF (P<0.01), LOW CALF compared to AGG YRLNG (P<0.01) and AGG CALF compared to LOW YRLING (P<0.01). Shear force values were lower in AGG compared to LOW (P<0.01). This research indicates that implantation should be delayed if cattle are placed on a grazing program when a nutrient restriction may occur and cattle are to be marketed on a grid that places economic emphasis on carcass quality.

Key Words: beef cattle, implants, carcass characteristics

M171 Enhancing pork loin quality attributes through genotype, chilling method and ageing time. M. Juarez*, W. R. Caine, J. L. Aalhus, W. M. Robertson, and M. E. R. Dugan, *Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, Alberta, Canada*.

Opportunities to niche market pork with enhanced quality attributes are expanding. One method used in other species to enhance quality attributes, such as tenderness and flavour, is guaranteed ageing. Pork can suffer from excessive purge losses and oxidative rancidity during extended ageing, which might be controlled through management of genotype and chilling regimes. To examine the opportunity to enhance pork quality through ageing, alternate sides from carcasses from Large White (LW, n = 24) and Duroc × Large White (Duroc, n = 24) barrows were either conventionally or blast chilled. The longissimus thoracis et lumborum muscle was dissected from the carcass sides (24 h post-mortem) and trimmed of cover fat. Three sections (15 cm length) were vacuum packaged and assigned to 2, 7 or 14 days of ageing (2°C) controlling for muscle location. Blast chilled meat had lower purge (P<0.01) and drip (P<0.001) losses and higher hue (P<0.05) than conventionally chilled meat. However chilling by conventional or blast-chilling methods had no effect on sensory characteristics (P>0.2). When breeds were compared, meat from Duroc barrows had lower moisture (P<0.001) and higher intramuscular fat content (P<0.001), L* (P<0.001) and hue (P<0.01) values than LW. Overall tenderness (P<0.01) and palatability (P<0.001), as well as flavour intensity (P<0.001) and desirability (P<0.001) and juiciness (P<0.001) values were higher and undesirable flavours were lower (P<0.001) for meat from Duroc pigs, when compared with LW. Days of ageing dependent increases were observed for purge loss (P<0.001), L* (P<0.001), hue (P<0.001), chroma (P<0.001) and content of protein (P<0.01), with corresponding decreases (P<0.001) in drip loss and moisture content. Instrumental (P<0.001) and sensory (P<0.01) tenderness increased from day 2 to 14. Therefore independent of chilling method, ageing seemed to improve pork quality of loins. Moreover ageing had greater effect on tenderness, while breed, due to differences in intramuscular fat content, had greater effect on flavour.

Key Words: blast chilling, ageing, breed

M172 Effects of dry-ageing on pork quality of vitamin E enhanced loins. M. Juarez*[1], W. R. Caine[1], J. L. Aalhus[1], M. E. R. Dugan[1], N. Hidiroglou[2], and B. E. Uttaro[1], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada*, [2]*Health Products and Food Branch, Health Canada, Sir Frederick G. Banting Research Centre, Ottawa, ON, Canada*.

Presumably, dry-ageing enhances flavour attributes of meat by surface desiccation to increase fatty acid content and other organoleptic molecules. However information regarding dry-ageing of fresh pork is limited. Supplementation of vitamin E to pigs prior to slaughter has been shown to enhance DL-α-tocopherol level in muscle and reduce lipid oxidation. To examine the effects of vitamin E dietary supplementation and dry-ageing on pork quality, Large White (LW, n=24) and Large White x Duroc (Duroc, n=24) barrows were assigned to control or high vitamin E (addition of 600 mg vitamin E kg-1) dietary treatments, slaughtered and three longissimus thoracis et lumborum sections from each side of the carcass were wet or dry-aged for 2, 7 or 14 days. Dry-aged meat had lower (P<0.001) moisture and higher (P<0.001) protein content due to higher drip and purge losses when compared with wet aged meat. Dry-ageing also increased (P<0.001) TBARS content in pork, but no effect (P>0.05) was observed on sensory characteristics. Vitamin E dietary supplementation resulted in lower (P<0.05) purge loss and L* values and higher (P<0.05) tenderness and flavour desirability and intensity, however TBARS content was not affected (P>0.05). The increase in duration of ageing decreased moisture content and drip loss and increased (P<0.001) protein and TBARS content, purge loss and L*, chroma and hue values. These changes were more accentuated in dry-aged meat (P<0.01). Moreover days of ageing dependent increases (P<0.001) were observed for instrumental and sensory tenderness, juiciness and overall palatability. The increase (P<0.01) in flavour desirability and intensity and the decrease in off-flavour for meat from LW barrows were higher (P<0.05) in day 7 than in day 14. Meat from Duroc barrows had lower (P<0.001) moisture and protein content, and higher (P<0.01) fat and TBARS content and L* and hue values. Instrumental and sensory tenderness, juiciness, flavour and palatability were higher (P<0.01) in meat from Duroc than LW barrows. Therefore while duration of ageing affected most quality and sensory characteristics, there were only variable changes to quality attributes of dry versus wet-aged pork.

Key Words: tocopherol, blast-chilling

M173 Age at the beginning of the free-range fattening period affects meat quality of Iberian pigs. M. A. Latorre*, J. A. Rodríguez-Sánchez, and G. Ripoll, *Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain*.

The traditional productive cycle for Iberian pigs includes a final free-range fattening phase (from November to February) in which animal intake natural feed resources, mainly acorns and grass. This period has

important consequences on the meat quality, which is determinant for elaboration of dry-cured products. The high amount of intramuscular fat (IMF) is one of the most relevant quality aspects in meat from Iberian pigs. The reproductive planning of the traditional system is based on two births per year (spring and autumn), beginning the free-range period with different age (18 or 12 months) but similar weight (110 kg BW) and being slaughtered with 160 kg BW (21 or 15 months of age, respectively). In this context, a total of 40 Iberian pigs were used to study the effect of age at the beginning of the outdoor fattening period on loin characteristics; 18 months old (OP) and 12 months old (YP). The YP fed higher quantity of concentrates than P22 (4.5 vs. 2.5 kg/day) during the growing phase to achieve the finishing period at similar weight. Each treatment was replicated twenty times (barrows and gilts in the same proportion in each treatment). The carcass weight was not affected by age (130.4 vs. 130.7 kg for OP and YP, respectively; $P > 0.10$). However, carcasses from YP had thicker backfat between the last 3rd and 4th last ribs than carcasses from YP (64.8 vs. 60.6 mm; $P < 0.01$). Meat from OP had less protein content (2.12 vs. 2.18%; $P < 0.05$) but tended to show higher IMF content (5.9 vs. 5.1%; $P < 0.10$) than meat from YP. Loin from OP was more red (a*) (8.5 vs. 6.8; $P < 0.05$) but showed lower H° value (63.3 vs. 68.8; $P < 0.01$) than loin from YP. Meat from OP had higher water holding capacity than meat from YP because of lower thawing (1.34 vs. 2.17%; $P < 0.001$) and cooking losses (16.5 vs. 17.3%; $P < 0.10$). It is concluded that meat quality of pigs that began the outdoor fattening period with 12 months of age was better than that of pigs that did it with 18 months of age.

Key Words: age, meat quality, free-range Iberian pigs

M174 Effects of electrical stimulation and aging on beef tenderness of dairy cows. A. A. Souza*[1], T. I. Ferreira[2], and J. C. Hadlich[3], [1]*UNIDERP/ANHANGUERA, Campo Grande, Mato Grosso do Sul, Brazil*, [2]*IAGRO, Campo Grande, Mato Grosso do Sul, Brazil*, [3]*UNESP, Botucatu, Sao Paulo, Brazil.*

Tenderness is considered by consumers the most important characteristic related to meat quality. The use of electrical stimulation (ES) is thought to be useful in increasing meat tenderness. Besides ES effects, aging may also have the same effects on meat tenderness, and potentially additive effects when associated with ES. Therefore, the aim of this study was to evaluate ES and aging influence on meat tenderness. Slaughter and meat processing were performed at Sao Paulo State Institute of Food Technology (ITAL). A total of 400 samples were collected from 80 crossbred dairy cows, 12-15 years old and finished on intensive grazing. At slaughter, each carcass was subjected to electrical stimulation on the right side of the carcass. Left side was used as control. After chilling, samples were obtained between 12^a and 13^a ribs of *Longissimus dorsi* muscle. Reading of pH values were made on hours 1, 3, 5 and 24 during chilling time. Meat tenderness and pH decline were evaluated for different treatments: Control=no ES/no aging; ES = electrical stimulation; AG = Aging; ESAG = electrical stimulation + aging. Electrical stimulation consisted of 100 v and 60 Hz during 90 seconds, with pulses of 3 s followed by 3 s resting interval. The aging time used was 14 days at 0-2^0C. The ES increased meat tenderness whereas aging alone or combined with ES showed no beneficial effects on tenderness. Early decline in pH using ES or aging was not observed. High initial pH values at this trial suggests animals were well rested at time of slaughter. These results suggest ES must be used to improve carcass quality from old cows, and meat can be made available to consumers without further aging processing.

Table 1. Carcass tenderness and pH decline

	Control	Electrical stimulation	Aging	Electrical stimulation + aging
Shear Force (kgf/cm^2)	11.24±1.88^a	7.82±1.68^b	8.56±1,72^{ab}	8.66±1.03^{ab}
pH (24h)	5.56±0.72^a	5.68±0.084^a	5.58±0,11^a	5.75±0.14^a

*means with different superscripts are statistically different (P< 0,05)

Key Words: electrical stimulation, meat quality, aging

M175 Relationship between raw breast meat color lightness values and functionalities of broiler fillets deboned six to eight hours postmortem. H. Zhuang* and E. Savage, *ARS-USDA*, *Athens, GA*.

The relationships between International Commission on Illumination (CIE) color lightness (L*) measurements and pH, drip loss, cook yield and Warner-Bratzler (WB) shear force of broiler breast fillets deboned 6-8h postmortem were investigated. In each of three replicate trials, broiler fillets were collected from a commercial processing plant and separated based on CIE L* values (measured using a Minolta spectrophotometer on the medial side) into three color groups: light, $L^* > 60.5$; median, $56.0 < L^* < 58.8$; and dark, $L^* < 54.5$. For each fillet within each color group, pH and drip loss of the raw meat and cook yield and WB shear force of the cooked meat were determined. Our results showed that there were significant differences in pH, drip loss and shear values between the light, median and dark fillet groups. There were significant differences in cook yield between the light group and both the middle and the dark groups which were not different from each other. There were significant negative Pearson's correlations between L* and pH and cook yield, and positive correlations between L* and drip loss and WB shear force values. These results demonstrate that functionality parameters of fillets removed from broiler carcasses at 6-8h postmortem are related to their CIE L* values.

Key Words: broiler breast, fuctionality, color

M176 *In vitro* analysis of effect of time–temperature combinations on viability of *Taenia hydatigena* eggs. B. S. Buttar*, M. L. Nelson, J. R. Busboom, D. P. Jasmer, D. D. Hancock, and D. Walsh, *Washington State University*, *Pullman*.

In the Pacific Northwest USA, potato co-product has been incriminated as a source of infection of *Taenia saginata* for beef cattle. The parasite leads to serious carcass defects and condemnation. Potato co-product have been heat treated at processing plants and feedlots which resulted in gelatinization of the starch and an increased incidence of acidosis. *Taenia hydatigena*, a canine tapeworm, was used as a surrogate organism to study the minimum amount of heat required to inactivate *Taenia spp.* eggs. A supply of eggs was obtained by maintaining the sheep-dog life cycle of the tapeworm under laboratory conditions. The parasite eggs were heat treated in a Completely Randomized Design with a 4×4 factorial arrangement of time-temperature combinations (5, 10, 15, 20 min. at 40, 50, 60, 70°C) in a heating block and further processed for ex-shelling (with 1% NaClO) and activation (with 50% sheep bile) to release activated oncospheres. Viabilities were measured by counting the percent activated oncospheres and internal staining with 1% trypan blue. A semi-log plot showed the percent active oncospheres decreased at the rate of 3.7%/min ($R^2 = 0.84$) with increasing time of heat application at 40°C. No activity was found for any treatment beyond 50°C

for 5 minutes. A linear plateau model of percent internal staining vs. temperature indicated increased internal staining until 70°C with a slope of 1.12. Measures of percent activity indicated complete inactivation of oncospheres at temperature below the gelatinization temperature of potato starch. Additionally, trypan blue staining was not a good measure of viability of *Taenia* eggs.

Key Words: *Taenia hydatigena*, thermal inactivation, viability

Nonruminant Nutrition: Feed Ingredients

M177 Characterization of protein structure of the new co-products from bioethanol production in western Canada using DRIFT Spectroscopy: Comparison among blend DDGS, wheat DDGS and corn DDGS, between wheat and wheat DDGS, and corn and corn DDGS. P. Yu*, D. Damiran, and W. Nuez Ortin, *Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, SK, Canada*.

The objective of this study was to use DRIFT spectroscopy as a novel approach to identify differences in protein molecular structure in terms of amide profile between wheat and wheat DDGS, between corn and corn DDGS, between bioethanol plants, and among wheat DDGS, corn DDGS and blend DDGS. The items assessed included protein amide I, amide II and amide I-to-II ratio. The protein IR spectrum has two primary features, the protein amide I (ca. 1600-1700 cm-1) and amide II (ca. 1500-1560 cm-1) bands. The amide I and II profile depends on the protein molecular structural chemical make-up and they are usually affected by processing methods and condition. The hypothesis was that protein molecular structure (chemical make-up) was changed after bioethanol processing and these changes affected DDGS nutritive value. Results showed that using DRIFT spectroscopy, the protein molecular structural makeup was revealed and identified. Amide I peak area significantly differed between wheat and wheat DDGS (162.5 vs. 291.8 KM unit, P<0.05), corn and corn DDGS (64.4 vs. 261.8 KM unit, P<0.05), wheat and corn (P<0.05). No difference (P>0.05) among wheat DDGS, corn DDGS and blend DDGS was detected. The amide II peak area significantly differed between wheat and wheat DDGS (35.1 vs. 95.0 KM unit, P<0.05), and corn and corn DDGS (14.1 vs. 118.5 KM unit, P<0.05). No differences (P>0.05) between wheat and corn and among wheat DDGS, corn DDGS and blend DDGS were found. Amide I-to-II ratios significantly differred between wheat and wheat DDGS (4.61 vs. 3.08, P<0.05), corn and corn DDGS (4.56 vs. 2.21, P<0.05). No differences (P>0.05) between wheat and corn, between bioethanol plants but significant differences among wheat DDGS, blend DDGS and corn DDGS were detected. These results indicated that bioethanol processing changes the original protein molecular structure (chemical make-up), which may play a major role to determine nutritive value.

Key Words: protein structure and amide I to II ratio, DDGS, molecular spectra

M178 Effects of various cereals on nursery pigs: Gastrointestinal bacterial populations. Y. Liu*, M. Rossoni, J. Barnes, and J. E. Pettigrew, *University of Illinois*, *Urbana*.

A study was conducted to evaluate the influence of different cereal grains on the bacterial populations in the gastrointestinal tract of young weaned pigs. A total of 24 pigs (7.71 kg BW) were weaned at 21 days of age and randomly allotted to one of four treatments. Corn, barley, rolled oats, and rice were the only cereals contained in each treatment. Pigs were allowed *ad libitum* access to feed and water throughout the 14-day experimental period. At the end of the experiment, all pigs were euthanized and slaughtered to collect mucosal and digesta samples from ileum and distal colon. Denaturing gradient gel electrophoresis (DGGE) was used to estimate the species diversity of the bacterial population (the number of bands) and quantitatively measure the similarity of population structures (banding pattern) expressed by Sorenson's pairwise similarity coefficients (Cs) among pigs within (intratreatment) and between (intertreatment) treatments. Intratreatment Cs values varied according to the digestive tract site and sampling type. In ileal mucosa, the higher ($P < 0.05$) intratreatment Cs value in corn group (79, 68, 67% for corn, barley and rolled oats) indicated that feeding corn made pigs more similar to each other. However, in ileal digesta, barley had higher ($P < 0.05$) intratreatment Cs value compared with rolled oats and corn (71, 58, 49% for barley, rolled oats and corn). The intertreatment Cs values were lower ($P < 0.05$) than the intratreatment Cs values in the mucosa of distal colon, indicating that there were significant effects of different cereal grains on microbial populations in the distal colon mucosa of nursery pigs. Pigs fed rolled oats diet had more (22.25 vs. 12.25; $P < 0.05$) bands in ileal digesta than pigs fed corn diets. There was no difference in the number of bands in other sample sites. In a few cases, specific bands were present in most pigs fed one treatment, but absent from most pigs fed other treatments. In conclusion, feeding of different cereals as sources of energy altered microbial populations in the GI tract.

Key Words: cereals, microbial ecology, nursery pigs

M179 Effects of altering the syrup inclusion rate and the dryer recycling rate on DDGS composition and digestibility in pigs. K. A. Houin*, B. E. Aldridge, B. T. Richert, A. L. Sutton, and J. S. Radcliffe, *Purdue University*, *West Lafayette, IN*.

Ten crossbred barrows with an average initial BW of 27 kg were used in a replicated 5 x 5 Latin Square designed experiment to investigate the effects of syrup inclusion rate and dryer recycling rate on nutrient digestibility of DDGS. For this experiment the syrup inclusion level and the dryer recycling rate were altered in a commercial plant to produce the following DDGS batches: 1) normal syrup, normal recycle rate, 2) 0.5x syrup, normal recycle rate, 3) no syrup, normal recycle rate, and 4) 0.5x syrup, no recycling. Diets 1-4 consisted of 50% of each DDGS batch and 50% of a corn basal diet. Diet 5 was the corn basal diet. Each 2-week period consisted of a 7 d adjustment period, then a 7 d collection period comprised of a 3 d total collection, 12 h ileal collection, 3-day adjustment, and a second 12 h ileal collection. Feed was provided at 9% metabolic BW ($BW^{.75}$) in 2 daily feedings and water was provided ad libitum. Ileal samples were pooled by pig and freeze dried. During total collections, feces and urine were collected twice daily. Urine was collected in buckets containing HCl to prevent N loss. Feed, ileal digesta, and feces were analyzed for N, Cr, Ca, P, and DM. Amino acid concentrations of feed and ileal samples were determined by HPLC. As syrup inclusion in DDGS decreased, protein and amino acid concentration increased, while mineral content decreased. For example, CP protein concentration increased from 26.7% to 32.3% when syrup was reduced to 0%, while ash content decreased from 4.0

to 2.0%. Apparent ileal digestibility (AID) of amino acids was higher (P<0.05) for diets containing DDGS compared to the corn basal diet. However, no differences (P<0.10) were detected for AID of amino acids between DDGS batches. Overall, AID of amino acids was high, ranging from 82.6 to 86.6% for lysine. Phosphorus digestibility was higher for batch 1, indicating that the P in syrup is more available than in the DDG. Overall, nutrient digestibilities were higher in DDGS compared to corn. Altering the syrup inclusion rate or the dryer recycling rate had no affect on amino acid AID.

Key Words: pig, dried distillers grains with solubles, digestibility

M180 Combined usage of corn distillers solubles and corn steep water for liquid fed growing-finishing pigs. C. L. Zhu*, D. Wey, and C. F. M. de Lange, *University of Guelph, Guelph, ON, Canada*.

Liquid co-products, such as corn distillers solubles (CDS) and corn steep water (CSW), may serve as alternatives for conventional pig feed ingredients. In previous studies the optimum inclusion levels of CDS and CSW in growing-finishing pig diets have been established at about 15% of diet DM. The aim of this study was to establish the optimum dietary inclusion level of a 50:50 mix of CDS and CSW. Purebred Yorkshire pigs (n= 144; initial and final BW 31.9 and 116 kg, respectively; 4 gilts and 4 barrows per pen; 4 or 5 pens per treatment) were liquid-fed according to a 2-phase feeding program and exposed to one of four dietary treatments: (1) Control (standard corn and SBM based diets), (2) Low (5% CDS + 5% CSW; DM basis), (3) Moderate (10% CDS + 10% CSW), and (4) High co-products (15% CDS + 15% CSW). The DM contents of CDS and CSW were 31.5% and 49.0%, respectively. CSW was stored at source for at least 2 weeks prior to feeding to allow conversion of soluble sugars to lactic acid and incubation with phytase to release phytate phosphorus. Feed delivery (water to feed DM 2.6:1) was computer controlled using feed sensors in the troughs. Pigs had free access to additional water. Increasing dietary levels of co-products reduced ADG (1047, 1055, 966 and 933 g/d for treatments 1 to 4, respectively; SEM 27) and increased feed:gain (2.27, 2.26, 2.37, 2.43; SEM 0.03; DM basis) linearly (P < 0.01). Carcass back fat and estimated lean yield did not differ among treatments 2 to 4 (P > 0.10), but were least favorable (P < 0.05) for Control (backfat 22.4 for Control vs 18.2 to 19.2 mm for other treatments; SEM 0.8; lean yield 58.5 vs. 60.1 to 60.6%; SEM 0.4). Increasing dietary levels of co-products linearly increased lightness (Minolta L value; 48.2, 48.8, 51.0 and 50.9; n=8; SE 0.1; P = 0.03) and drip losses from loin samples (9.1, 8.4, 10.3 and 10.8%; n=8; SE 0.7; P = 0.04). Increasing levels of both CDS and CSW to 10% or more of diet DM compromised growth performance and some aspects of meat quality in growing-finishing pigs.

Key Words: pigs, co-products, liquid feeding

M181 Comparison of drying methods for whole frozen fish commonly fed to marine mammals. S. M. Langowski[1], A. W. White[1], K. L. West[1], K. S. Yamamoto[2], and J. R. Carpenter*[2], [1]*Hawaii Pacific University*, *Honolulu*, [2]*University of Hawaii at Manoa*, *Honolulu*.

Aquaria routinely determine the nutritional composition of the fish that are fed to captive marine mammals by sending samples to commercial laboratories. Establishing proximate composition is expensive and time consuming. However, previous work has demonstrated that dry matter values can be used to predict the proximate composition of fish commonly fed to marine mammals. The aims of this study were to compare different drying methods for whole fish. Six random samples for each fish type (capelin, high fat herring, low fat herring, pollock and squid) were each analyzed in duplicate using six different drying techniques. Fish were homogenized and wet weights obtained prior to drying. Dry weights were obtained using drying temperatures (50°C, 65°C, 100°C) with conventional ovens (CO), a 50°C Forced Air oven (FA), a freeze drier (FD) and a standard microwave (MW). The percent DM and percent error for duplicate analyses were then determined. An ANOVA was run to determine the statistical significance between the drying method and the species of fish dried. The interactions between species were significant (p =.002) which indicated that the degree of percent error in a particular species of fish is dependent on the method of drying. However interactions between drying methods were not significant (p=0.432) which indicated that there is no significant difference in dry matter values among the drying methods. It was concluded that the percent error among duplicate samples can be used to evaluate the repeatability of the various drying methods. Methods with the lowest to highest percent error among the samples were FD, MW, 50CO, 100CO, 65CO, and 50CFA. A standard microwave yields reliable results when used as a drying method for whole fish. It is feasible to obtain results using the microwave on site at zoos and aquaria. In conjunction with DM predictive equations, this could potentially save facilities time and money when interested in the nutritional composition of animal diets.

Key Words: drying methods, proximate analysis, microwave and freeze dried

M182 Effects of feeding soybean meal from high protein or low oligosaccharide varieties of soybeans to weanling pigs. K. M. Baker*, B. G. Kim, and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was conducted to determine the effect of using 5 different sources of soybean meal (SBM) on growth performance of weanling pigs. The 5 sources included hexane extracted SBM produced from high protein (SBM-HP) or conventional soybeans (SBM-CV), and mechanically extruded-expelled SBM produced from high protein soybeans (EE-SBM-HP), low oligosaccharide soybeans (EE-SBM-LO), or conventional soybeans (EE-SBM-CV). A total of 200 pigs were weaned at approximately 20 d of age and randomly allotted to treatment diets. Five phase 1 diets containing each source of SBM were fed during the initial 14 d post-weaning and 5 phase 2 diets were fed during the following 17 d. All diets within each phase were formulated to contain similar quantities of ME and standardized ileal digestible AA. Digestibility values for AA and ME in the 5 SBM were measured in previous experiments. The ADG, ADFI, and G/F were determined for each phase and for the entire experimental period. There were no differences observed for ADG, ADFI, and G/F, for phase 1, phase 2, or for the entire period. These data confirm that the values for ME and digestible AA that were previously measured in SBM produced from high protein or low oligosaccharide varieties of soybeans can be used to formulate diets for weanling pigs without compromising pig performance.

Table 1. Performance during a 31-d post-weaning period of weanling pigs fed diets containing soybean meal (SBM) from high protein (HP), low oligosaccharide (LO), or conventional (CV) varieties of soybeans that were hexane extracted (HE) or extruded-expelled (EE)

Item	HE-SBM-HP	HE-SBM-CV	EE-SBM-HP	EE-SBM-LO	EE-SBM-CV	SEM	P-value
Initial BW, kg	5.37	5.32	5.33	5.33	5.35	0.32	0.681
ADFI, g	373	387	378	403	378	20	0.644
ADG, g	258	264	248	273	256	12	0.532
G:F	0.695	0.687	0.656	0.679	0.678	0.01	0.067
Final BW, kg	13.37	13.52	13.02	13.78	13.28	0.60	0.55

N=9.

Key Words: high protein soybean meal, low oligosaccharide soybean meal, weanling pigs

M183 The granulated barley provided during the finishing period improves the production cost, intramuscular fat percentage and oleic acid content in muscle from heavy pigs. A. Daza[1], M. A. Latorre*[2], G. Cordero[3], A. Olivares[3], and C. J. López-Bote[3], [1]*Universidad Politécnica de Madrid, Madrid, Spain*, [2]*Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain*, [3]*Universidad Complutense de Madrid, Madrid, Spain*.

This trial was conducted to determine the growth performance, production cost, carcass traits, and intramuscular fat (IMF) quality of heavy pigs fed one of two different diets. Thirty-two Duroc × (Large White × Landrace) barrows (86.6 kg BW) were randomly allotted to sixteen pens (2 pigs per pen) and fed according to the following treatments: sixteen pigs were given a control diet (3200 kcal ME/kg, 13.6% CP, and 0.60% digestible lys) and the other sixteen pigs received granulated barley (3000 kcal ME/kg, 10.1% CP, and 0.26% digestible lys). Both groups of pigs were slaughtered at 129.8 kg BW. The dietary treatments did not affect growth rate, daily intake or carcass traits. Feed conversion ratio was higher (P<0.05) for pigs fed barley than for pigs fed the control diet (5.11 vs. 4.52 kg/kg, sem = 0.14). However, the cost of production of carcass weight/kilogram was lower (P<0.05) in pigs that consumed barley than for those given the control diet (1.30 vs. 1.73 euros/kg, sem =0.014). The IMF percentage in Longissimus dorsi muscle tended to be (P<0.07) higher in pigs fed granulated barley than in pigs fed the control diet (1.73 vs. 1.30%, sem = 0.15). The pigs fed granulated barley had higher (P<0.05) a*, b*, and c* values and a lower (P<0.05) H° value and thawing losses than the pigs fed the control diet, while no significant differences were observed for shear force, L* value, and cooking losses. The dietary treatments did not significantly effect the proportions of C16:0, C18:0, and SFA in IMF from the Longissimus dorsi muscle. However, the C18:1 n-9 and MUFA proportions were higher (P<0.05) in IMF from pigs fed granulated barley than in that from pigs fed the control diet (48.38 vs. 45.79%, sem = 0.56 and 52.49 vs. 49.82%, sem = 0.56, respectively). We can conclude that the granulated barley provided during the finishing period improved the cost of production, intramuscular fat proportion and oleic acid content in muscle from heavy pigs.

Key Words: barley, finishing period, heavy pigs

M184 Nutritive utilization of protein and amino acids from raw cowpea flour (*Vigna unguiculata*) in growing rats. G. Kapravelou[1], J. Martino*[1], E. Nebot[1], J. M. Porres[1], and I. Fernández-Fígares[2], [1]*University of Granada, Granada, Spain*, [2]*Spanish Research Council, CSIC, Granada, Spain*.

Cowpea (*Vigna unguiculata*) is a widely consumed legume with important nutritional and functional potential due to its high content of protein, complex carbohydrates, minerals, vitamins and antioxidants. The aim of this study was to compare raw cowpea and casein-methionine (control) in terms of nutritive utilization of protein and amino acids using the rat as a model. Two experimental diets in which casein or raw cowpea flour were the sole sources of protein, both supplemented with 0.5% methionine, were ad libitum fed for two weeks to growing rats (10 per group) individually housed in metabolic cages to allow for separate urine and feces collection. Prior to the experimental period, the animals were fed a low-protein (4%) diet for 6 days to estimate endogenous excretion of N and amino acids. Daily food intake was similar (P ≥0.05) between the two groups studied, whereas standardized digestibility of protein and most AA of the raw cowpea diet was significantly lower than control (79.4 *vs*. 91.5% for N, 83.1 *vs*. 93.6% for total AA; P ≤0.001) No differences (P ≥0.05) were found for metabolic utilization of protein. Weight gain (5.22 *vs*. 4.16 g/day; P ≤0.001) and growth efficiency coefficient (daily gain/ protein intake; 3.03 *vs*. 2.77; P ≤0.01) were significantly higher for the control fed rats when compared to the raw cowpea group. Liver and spleen weights were higher (P≤0.05) and cecal weight was lower (P ≤0.05) in the control group of rats when compared to the raw cowpea group, whereas no differences (P ≥0.05) were found in colon weight. In conclusion, nutritive utilization of cowpea protein ought to be significantly enhanced to achieve a nutritive utilization similar to casein. Heat treatment or fermentation are technological treatments that could potentially improve the protein quality of raw cowpeas. Further investigation is warranted to improve the nutritive value of this legume.

Key Words: cowpeas, protein and amino acids, nutritive utilization

M185 Influence of sunflower seed meal on histological alterations of broiler chickens. S. Salari*, H. Nassiri Moghaddam, J. Arshami, A. Golian, and M. Maleki, *Ferdowsi University of Mashhad, Mashhad, Iran*.

In this study, 176 day-old male broiler chickens (Ross strain) were allocated to four treatments in pens (120x100x90 cm) with four replicates (11 birds /pen) in a completely randomized design to evaluate the effect of sunflower seed meal (SFSM) on histological alterations of the small intestine in broiler chickens. Treatments were 0, 7, 14 and 21 percent of SFSM for 1-28 days and calculated to contain 20.86% CP and 2900 kcal of ME per kg of diet. At the end of the experiment (28 days of age) one bird from each treatment was killed by cervical dislocation, and segments were removed from the duodenum, jejunum, and ileum as follows: 1) intestine from the gizzard to pancreatic and bile ducts was referred to as the duodenum, 10 cm of first section of which was taken for microscopy; 2) 10 cm of first section, between the point of entry of the bile ducts and Meckel's diverticulum (jejunum), and 3) 10 cm of first section from Meckel's diverticulum to the ileocecal junction (ileum). The samples were flushed with physiological saline and fixed in 10% formalin. Cross sections for each intestinal sample were prepared after staining with hematoxylin and eosin using standard paraffin embedding procedures. Villus height was measured from the tip of the villus to the villus-crypt junction; crypt depth was defined as the depth of the invagination between adjacent villi. The villus width measured at the bottom of villi. The slides were evaluated

using Olympus (BX51, Japan) microscope coupled with camera and the computer image analysis software for the morphometrical research was used. The results showed that by increasing levels of SFSM in the diets, villus height and crypt depth of duodenum and jejunum were significantly ($p<0.05$) decreased and increased, respectively. But SFSM did not affect the villus of the ileum. Also, incorporation of SFSM had a significant effect on villus width ($p<0.05$). We concluded that the high fiber content of SFSM had a negative effect on histological parameters of the small intestine of broilers.

Key Words: histology, villus, broiler chicks

M186 Guar gum as a source of soluble non-starch polysaccharides for swine decreases nutrient digestibility and ammonia emission while increasing manure odor. W. Zhang[1], E. van Heugten*[1], T. van Kempen[1,2], and V. Fellner[1], [1]*North Carolina State University*, *Raleigh*, [2]*Provimi, RIC*, *Brussels, Belgium*.

This study was designed to determine the impact of soluble NSP (sNSP) on nutrient digestibility and emission of ammonia and odor from manure. Diets consisted of a low fiber control (degermed, dehulled corn and soy protein isolate) and the control with 2, 4, or 8% added guar gum (> 75% galactomannan). Pigs (n=28; BW = 26.8±1.4 kg) were fed diets for 4 wk. Subsequently, feces and urine were collected quantitatively for 3 d and pigs were then sacrificed for collection of digesta from the ileum, cecum, and colon. Fresh manure was obtained by mixing feces and urine for each pig at the ratios they were produced. Aged manure was obtained by anaerobically aging this mixture for 21 d. Guar gum did not affect fecal DM output, but linearly decreased ($P < 0.001$) ileal and fecal DM content and thus increased daily fecal output ($P < 0.02$). Apparent ileal N digestibility ($P < 0.01$), fecal N and GE digestibility ($P < 0.001$), ADFI, ADG, N intake, and N retention ($P \leq 0.03$) linearly decreased with increasing guar gum. pH of the colon content, but not ileum or cecum, decreased linearly with increasing guar gum. Fecal concentrations of acetic acid, propionic acid, butyric acid, valeric acid, and total SCFA increased linearly ($P < 0.05$) with increasing guar gum. Increasing guar gum had no effect on odorants and pH in fresh manure, but it linearly ($P < 0.05$) increased dimethyldisulfide ($\log_{10}$ peak area; 7.96, 8.32, 8.57, and 8.55), dimethyltrisulfide (7.03, 7.45, 7.76, and 7.92), and phenol (7.45, 7.67, 7.81, and 7.80) in head space and acidity of aged manure. Odor intensity tended ($P = 0.08$) to increase (2.96, 3.27, 3.40, and 3.35) with increasing guar gum in aged manure, but not fresh manure. Cumulative manure ammonia emission increased in fresh manure with increasing guar gum but only up to 24 h ($P < 0.05$). In aged manure, ammonia emission decreased linearly (up to 47% at 12 h and 7% at 96 h; $P < 0.05$) with increasing guar gum. In conclusion, the use of sNSP reduced ammonia emission in aged manure, but decreased nutrient digestibility and increased odor emission, thus limiting its environmental benefits.

Key Words: ammonia, NSP, odor

M187 The effect of dried distillers grains with solubles in the diet of the growing-finishing pig on performance and nitrogen and phosphorus excretion. P. McDonnell, J. J. Callan, and J. V. O'Doherty*, *Lyons Research Farm, University College Dublin*, *Newcastle, Co Dublin, Ireland*.

A completely randomised design experiment was performed to determine the optimum inclusion level of dried distillers grains with solubles (DDGS) on pig growth performance, carcass characteristics, apparent nutrient digestibility, nitrogen (N) balance, phosphorous (P) balance and ammonia emissions. Three hundred fifty two pigs (42.4 kgs, SD = 6.4 kgs) were blocked on the basis of initial live weight and assigned to one of the 4 dietary treatments: (T1) basal diet, (T2) basal diet with 100g/kg DDGS, (T3) basal diet with 200g/kg DDGS, (T4) basal diet with 300g/kg of DDGS. The DDGS directly replaced wheat in the diet. The diets were formulated to contain similar concentrations of ileal digestible amino acids, available P and net energy. There was no effect of increasing levels of DDGS on daily gain, feed intake, gain to feed ratio and carcass characteristics during the experimental period. There was a linear decrease ($P<0.01$) in DMD and gross energy digestibility with increasing levels of DDGS in the diet. There was a linear increase in N intake ($P<0.01$), urinary N excretion ($P < 0.001$) and total N excretion ($P < 0.001$) with increasing levels of DDGS in the diet. There was a linear decrease ($P < 0.01$) in P intake as the level of DDGS increased in the diet. There was no difference in ammonia emissions as the level of DDGS increased in the diet. Results from this study indicate that the inclusion levels of 300g/kg of DDGS in the diet of the growing-finishing pig do not affect performance or carcass characteristics. However, increasing the level of DDGS in the diet will increase total nitrogen excretion.

Key Words: pigs, DDGS

M188 Influence of sunflower seed meal (SFSM) on body organ weights and blood parameters of broiler chickens. S. Salari*, H. Nassiri Moghaddam, J. Arshami, and A. Golian, *Ferdowsi University of Mashhad*, *Mashhad, Iran*.

In this study, 176 day-old male broiler chickens (Ross strain) were allocated to four treatments with four replicates (11 in each replicate) in a completely randomized design to evaluate the effect of sunflower seed meal on body organ weight and blood parameters of broiler chicks for 7 weeks. Treatments were 0, 7, 14 and 21 percent of SFSM for starter (1-21 days) and grower phases (22-49 days). The starter phase diets were calculated to contain 20.86% CP and 2900 kcal of ME per kg of diet. They also contained 18.75% CP and 3000 kcal of ME per kg of diet for the grower phase. At 28 days of age, blood samples were collected from chicks. At the end of the experiment (49 days), one bird from each replicate was slaughtered to study the relative weights of liver, abdominal fat, gizzard, thigh, breast and gastrointestinal tract. The results of the present study indicated that triglyceride and LDL concentrations decreased significantly and HDL concentration increased ($P<0.05$) in the birds fed increasing levels of SFSM but the activity of alkaline phosphatase and the levels of calcium, phosphorus, glucose and protein in serum were not affected by the treatments employed. The relative weight of the breast, thigh, liver and abdominal fat were not affected by the SFSM. However, the relative weight of gizzard and gastrointestinal tract were increased significantly ($P < 0.05$) in birds fed SFSM diets compared to those fed control diet. It is concluded that SFSM can be used in broiler chick diets and its high fibre content had no significant effect on body organ weight and blood parameters.

Key Words: blood parameters, organ, broiler chicks

M189 The effects of increasing the level of rapeseed meal in the diet of the growing-finishing pig on the growth performance and nitrogen and phosphorus excretion. P. McDonnell, S. Figat, J. J. Callan, and J. V. O'Doherty*, *Lyons Research Farm, University College Dublin*, *Newcastle, Co. Dublin, Ireland*.

A completely randomized design experiment was performed to examine the effects of increasing the level of rapeseed meal (RSM) and reducing the level of soybean meal (SBM) on the growth performance, carcass characteristics, apparent nutrient digestibility, nitrogen (N) balance, phosphorous (P) balance and ammonia emissions in the diet of the growing-finishing pig. Three hundred thirty-six pigs (42.1 kgs S.D. = 3.0 kgs) were blocked on the basis of initial live weight and assigned to one of four dietary treatments. (T1) basal diet with 210g/kg SBM; (T2) basal diet with 140g/kg SBM and 70g/kg RSM; (T3) basal diet with 70g/kg SBM and 140g/kg RSM; (T4) basal diet with 210g/kg RSM. All diets were formulated on an ileal digestible amino acid, net energy and available phosphorous basis. There were no significant effects of increasing levels of RSM on average daily gain, feed intake, gain to feed ratio and carcass characteristics during the experimental period. There was a linear decrease in gross energy digestibility ($P<0.01$) with increasing levels of RSM in the diet. There was a linear decrease ($P<0.05$) in N intake ($P<0.05$), urinary N excretion ($P<0.01$), N digestibility ($P<0.05$), total N excretion ($P<0.05$) and N retention ($P<0.05$) with increasing levels of RSM. There was a quadratic response ($P<0.05$) in fecal P excretion and total P excretion with increasing levels of RSM in the diet. There was no further increase in fecal P excretion and total P excretion above 140 g/kg RSM inclusion. The results of this study indicate that RSM can be used as a direct replacement for soybean meal with no depression in performance when formulated on an ileal digestible amino acid and net energy basis. Increasing the level of RSM in the diet will reduce N intake, urinary N excretion and total N excretion.

Key Words: rapeseed, soybean, pigs

M190 Effect of hydrothermally processed corn on fecal digestibility of energy in cannulated roosters. L. Babinszky* and J. Tossenberger, *Kaposvár University*, *Kaposvár, Hungary*.

The trial aimed to determine how hydrothermal processing of corn in corn-soy based broiler diets affects fecal digestibility and availability [intake-feces-urine/intake] of dietary energy. Studies were conducted with 4 adult Hy-Line brown roosters (initial live weight: 3.4 ± 0.2 kg) per treatment (trt), in 2 replicates (n=8/trt). Before the studies a simple T-cannula was implanted in the terminal colon to allow separate and quantitative collection of feces and urine, and thus the determination of digestibility of energy. Diets [starter (S); grower (G); finisher (F)] contained 13.0;13.1;13.2 MJ AMEn (calculated), 226;213;182 g CP, 13.0;12.2;9.6 g LYS and 10.6;9.3;7.1 g M+C per kg. Proportion of corn in diets was 515;515;566 g/kg. Two trts per diet were formulated. Trts "A" were formulated with untreated corn (UTC); trts "B" with steam-flaked corn (100°C, 101.3 kPa, 30 min) (SFC). Nutrient content of the diets was determined according to AOAC (1989); energy content of diet, feces, urine was measured in an adiabatic bomb calorimeter. Data were analyzed by ANOVA (SAS, 2004). The digestibility of energy in diets with UTC was 87.0% (S), 88.5% (G) and 89.3% (F); energy availability was 83.7%, 85.2% and 86.1%. Steam flaking of the corn component increased energy digestibility to 88.6%, 90.1% and 90.9% ($P<0.05$) and improved availability to 86.0%, 87.3% and 88.4% ($P<0.05$). The difference between digestibility and availability in diets with UTC was 3.3% (S), 3.3% (G) and 3.2% (F) (3.3% on average); while in diets with SFC it was 2.6%, 2.8% and 2.5% (2.6% on average). Diets with SFC in contrast to diets with UTC had: DE 14.6 vs 14.4 (S); 15.3 vs 15.0 (G); 15.4 vs. 15.1 MJ/kg (F); AME 14.3 vs 13.8 (S); 14.9 vs 14.5 (G); 15.0 vs 14.5 (F) MJ/kg; AMEn 13.6 vs 13.3 (S); 14.4 vs 14.0 (G); 14.5 vs. 14.1 (F) MJ/kg. Lower differences in AMEn vs AME are attributable to higher N retention of birds fed SFC diets. It can be concluded that the higher energy level due to heat treatment of ingredients should be taken into account in the formulation of dietsl.

Key Words: rooster, digestibility, availability

M191 Evaluation of blue mussel shells as an alternative dietary calcium source for laying hens. J. L. MacIsaac*[1] and D. M. Anderson[2], [1]*Atlantic Poultry Research Institute*, *Truro, Nova Scotia, Canada*, [2]*Nova Scotia Agricultural College*, *Truro, Nova Scotia, Canada*.

In Atlantic Canada, over 5000 tonnes of blue mussel shells (BMS) are produced annually. A trial designed as a one-way analysis with calcium source as the main effect (30% oyster shell (OS): 70% ground limestone (GL), 30% large particle limestone (L): 70% GL, 30% large particle blue mussel shells (BMS): 70% ground blue mussel shells (GBMS), 100% GL, 100% GBMS) was conducted to evaluate BMS as a replacement for large particle sized commercial OS or L as well as ground L. A total of 480 White Leghorn (Lohmann Lite) hens were fed the experimental diets starting at 25 weeks of age for 52 weeks. A calcium balance study was conducted at 30 weeks of age. Calcium source did not have an effect ($P>0.05$) on hen-day production, feed consumption or body weights for the duration of the trial. Egg weights did not differ ($P>0.05$) among the treatments except at the end of the trial. Eggs produced from hens fed the GBMS treatment (62.3 g egg^{-1}) weighed less ($P\leq0.05$) than those produced from hens fed the OS/GL (66.3 g egg^{-1}) and BMS/GBMS (67.3 g egg^{-1}) treatments. Up to 77 weeks of age, there was no effect ($P>0.05$) of calcium source on egg specific gravity (SG) except at 45 weeks of age. Egg breaking strength was not affected ($P>0.05$) by calcium source except at 29 and 59 weeks of age. Birds fed the diet containing L/GL maintained a higher ($P\leq0.05$) calcium balance (1.91 g $bird^{-1}$ day^{-1}) than those fed the OS/GL (1.25 g $bird^{-1}$ day^{-1}) and GL (1.09 g $bird^{-1}$ day^{-1}) diets. Birds fed the GBMS diet maintained a higher ($P\leq0.05$) calcium balance (1.76 g $bird^{-1}$ day^{-1}) than those birds fed the GL diet. BMS and GBMS effectively replaced OS and GL as sources of large and fine particle calcium for layer hens.

Key Words: blue mussel shells, laying hen, production performance

M192 Feeding flax to late-pregnant and lactating sows: Effects on sow immunity and antibody transfer to their piglets. M. Lessard*, H. V. Petit, A. Giguère, and C. Farmer, *Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*.

The impact of feeding flax as seed, meal or oil to late-pregnant and lactating sows on sow immunity and transfer of antibody (Ab) against ovalbumin (OVA) to piglets was studied. Sixty gilts were fed one of four diets from d 68 of gestation until d 21 of lactation. Diets were: standard without flax, CTL (n=15); 10% flaxseed, FS (n=16); 6.5% flaxseed meal, FSM (n=14); and 3.5% flaxseed oil, FSO (n=15). On d 88 and 101 of gestation, sows were immunized against OVA. Jugular blood samples were obtained before the 1st injection and on d 110 of gestation and d 2 and 21 of lactation to measure Ab against OVA (anti-OVA), lymphocyte proliferation and lymphocyte production of γ-interferon (IFN-γ) after activation with concanavalin A. Milk samples were obtained on d 3 and 20 of lactation to measure anti-OVA. One piglet per litter was slaughtered on d 1 postpartum and a jugular blood sample obtained for anti-OVA analyses. In CTL sows, IFN-γ production by lymphocytes dropped between d 101 of gestation and d 2 of lactation, whereas in FS sows, it increased (P = 0.007). Anti-OVA response for

the whole experimental period was greater in FS than in FSO sows (P = 0.03) and there was no difference between CTL sows and sows from other groups. Anti-OVA concentration in milk on d 3 of lactation was not affected by treatments. Serum concentrations (laboratory arbitrary unit, AU) of anti-OVA in 2 d-old piglets were greater (P = 0.002) in FS (730 AU), FSM (782 AU) and FSO (1098 AU) litters than in CTL (233 AU) litters and percent mortality on d 2 postpartum was lower (P = 0.03) for FS (20.2%), FSM (20.2%) and FSO (20.1%) litters compared with CTL (24.5%) litters. The lymphocyte proliferative response was not affected by treatments. In conclusion, feeding flaxseed to pregnant and lactating sows altered their cellular and humoral immune responses, and feeding flax as seed, meal or oil increased the transfer of anti-OVA to their offspring and reduced piglet mortality. These results suggest that feeding flax to sows may have beneficial effects on piglet health. *Thanks to Shur-Gain and the Québec Federation of Swine Producers for financial support.*

Key Words: fatty acids, immunity, sow

M193 Changes in gut microbiota of broiler chicks fed distillers dried grains with solubles (DDGS) during a coccidial infection. V. Perez-Mendoza*[1], C. Jacobs[1], C. Parsons[1], J. Barnes[1], M. Kuhlenschmidt[1], M. Jenkins[2], and J. Pettigrew[1], [1]*University of Illinois, Urbana*, [2]*United States Department of Agriculture, Beltsville, MD*.

The effect of dietary DDGS and *Eimeria* infection on composition of the chick gut microbiota was evaluated using a CRD with a factorial arrangement of 3 diets (0, 10, and 20% DDGS) × 2 challenges [*Eimeria acervulina* (*Eimeria*) or non-infected (NoCh)]. The experimental unit was a cage with 5 chicks (8 replicates/treatment) for a total of 240 chicks (6 d old, 82.8±0.11 g BW). Experimental diets were fed at d 7 of age and inoculation was 3 d later: single oral dose of *Eimeria* at 1×10^6 sporulated oocysts/dose. Chicks' weight was recorded on inoculation day and 14 d after; feed intake was also recorded. Mucosal scrapings from the cecum were collected from all chicks and pooled per cage on d 14 post-inoculation. Microbial diversity was assessed as the number of bands by denaturing gradient gel electrophoresis using the V3 region of bacterial 16S ribosome, where each band represents at least 1 bacterial species. Sorenson's similarity percentages (Cs) were used to compare banding patterns between pairs of pens within treatments (homogeneity) and among treatments (inter-treatment Cs values). Feed intake was reduced only by *Eimeria* (40.9 vs. 37.3 g/d; SEM=0.38; P<0.001). Weight gain was reduced by *Eimeria* (30.1 vs. 26.7 g/d; SEM=0.22; P<0.001) and 20% DDGS (28.7, 28.7, 27.8 g/d; SEM=0.27; P=0.03); no interaction was detected. *Eimeria* reduced (P=0.02) microbial diversity, but 10% DDGS increased it in both *Eimeria* and NoCh (DDGS quadratic, P<0.001): 24.9, 31.1, 25.5, 27.8, 36.4, 27.4 bands (SEM=1.7) for 0, 10, and 20% DDGS with *Eimeria* and NoCh. Feeding 10% DDGS increased homogeneity in NoCh chicks, but feeding 20% DDGS reduced it in *Eimeria* chicks (*Eimeria* × DDGS quadratic, P=0.07). Analysis of inter-treatment Cs values indicated that microbiota was changed by each level of DDGS and *Eimeria*, as shown by lower inter-treatment Cs than corresponding intra-treatment values (P<0.05). In summary, dietary DDGS did not prevent *Eimeria* infection, but changed chick gut microbiota regardless of the infection. Additional studies are needed to determine if the observed changes on gut microbiota can be utilized to improve intestinal health.

Key Words: broilers, DDGS, microbiota

M194 Effects of feeding garbanzo beans and canola seed meal to finishing pigs on production, carcass quality and expression of key metabolic control genes. J. McNamara, A. Hutchins, A. Youngquist*, J. Busboom, J. Vierck, C. Schachtschneider, A. Whalen, J. Miller, and A. Lowe, *Washington State University*, *Pullman*.

The objective was to determine production, carcass traits and quality, and to explore gene expression in adipose tissue, liver and muscle of finishing pigs fed garbanzo beans or canola seed meal. Animals (n = 182;Yorkshire and Duroc crosses) were blocked by weight and allotted to diets: Control (C): 61.5% Corn, 31% Peas, 4% SBM; Garbanzo beans (GB): 62.5% Corn, 30% GB, 4% SBM; Canola Seed Meal (CS): 77.5% Corn, 19% CS or both (GBCS): 71% corn, 12.75% garbanzo beans, 12.75% CSM. Pigs were started at BW of 55.7 (SE .53) kg and were fed 9 weeks until the average BW was 110.9 (SE 0.97) kg. An initial slaughter group of 26 pigs was killed for comparison. Treatment groups did not differ in feed intake (2.98 kg/d), ADG (0.91 kg/d) or gain:feed (0.31). Ending BW of pigs killed for carcass analysis (n = 48, 117.4 kg); 10th rib back fat (2.50 cm); loin eye area (39.4 sq cm); and other slaughter and carcass quality traits were not affected by diet. Animals fed CS had numerically more backfat (2.5 and 2.6 cm for CSM and Both). Animals fed C or CS had numerically larger LEA (40.8 and 40.5 sq cm). The GB diet was 1.8% lower in protein, the GBCS diet had about 0.4% less, and animals on GB did eat numerically less feed; this would explain the difference in LEA. However, a diet with garbanzo beans at the same protein concentration would likely support high carcass quality. Adipose tissue (subcutaneous over 10th rib); muscle (semimembranosus) and liver samples were taken and RNA was extracted; RNA samples from 30 pigs showed high quality (A260:A280 = 2.10). Expression of several genes coding for lipogenic enzymes (acetyl CoA carboxylase, fatty acid synthetase); lipolysis control (beta-adrenergic receptors, hormone sensitive lipase) in adipose and liver were measured by RT-PCR. Gene transcripts for lipogenic enzymes mirrored fatness of the animals. There were no clear dietary effects on expression of these genes. These alternative crops can be used for quality pork production without negatively affecting performance or underlying metabolic controls.

Key Words: alternative feeds, carcass quality, gene expression

M195 Digestible and metabolizable energy of oils and lards for growing pigs. H. O. Silva, R. V. Sousa, E. T. Fialho*, J. A. F Lima, and L. F. Silva, *University Federal of Lavras*, *Lavras, MG, Brazil*.

The importance of accurate and reliable Digestible Energy (DE) and Metabolizable Energy (ME) values for oils and lards becomes evident when one considers the fact that energy is the most expensive component of swine diets. Therefore, the objective of this study was to determine the DE and ME values of five samples of different oil sources and two lard sources using a common control diet. The oils used included canola, soybean, linseed, PUFA (polyunsatured fatty acids) , and coconut oil, while the fats were tallow and choice yellow grease. A total of 40 barrows with an average BW of 40.2 ± 1.4 kg were used in the study. For each of the seven experimental diets, diets were formulated by substituting 15 g/kg of oil or lard to a basal corn-soybean meal diet that contained 190 g CP/kg of diet. The corn and soybean meal were adjusted at the same ratio to account for the substitution. Each diet was fed to five barrows in individual metabolism cages with a 5-d acclimation followed by a 5-d period of total, but separate, collection of feces and urine. The DE (kcal/kg) and ME (kcal/kg) results obtained were: canola oil (8630 ± 42 and 8340 ± 38); soybean oil (8670 ± 62 and 8410 ± 56); linseed oil (8380 ± 14 and 8220 ± 46); PUFA (8750 ± 34 and 8540 ± 43); coconut oil (8860 ± 87 and 8680 ± 82); tallow (8880 ± 76 and 8710 ± 58), and

choice yellow grease (8870 ± 67 and 8690 ± 74). There were differences in DE and ME among the oils studied (P<0.05), showing that choice yellow grease had higher energetic values than oils, possibly due to a higher concentration of saturated fatty acids. In conclusion, the variation in each of the oils and lards may be dependent on their fatty acid concentrations. The interaction among these components influences energy content in the ingredients used for swine feed.

Key Words: metabolism assay, energetic value, fatty acids

M196 Feeding flax to late-pregnant and lactating sows: Effects on fatty acid profiles, hormones and performances of sows and their litters. C. Farmer*, A. Giguère, M. Lessard, and H. V. Petit, *Agriculture and Agri-Food Canada, Dairy and Swine R & D Centre, Sherbrooke, QC, Canada*.

The impact of feeding flax as seed, meal or oil to late-pregnant and lactating sows on fatty acid (FA) profiles and sow and litter performances was studied. Sixty gilts were fed one of four diets from 68 d of gestation until 21 d of lactation. Diets were: standard without flax, CTL (n=15); 10% flaxseed supplementation, FS (n=16); 6.5% flaxseed meal supplementation, FSM (n=14); and 3.5% flaxseed oil supplementation, FSO (n=15). Jugular blood samples were obtained on d 62 and 110 of gestation and on d 2 and 21 of lactation to measure FA profiles and concentrations of estradiol, prolactin and progesterone. Milk samples were obtained on d 3 and 20 of lactation. One piglet per litter was slaughtered on d 1 for compositional analyses and piglets were weighed on d 2, 7, 14, 21 (weaning), 28, and 56. On d 110 of gestation and d 21 of lactation, sows fed FS and FSO had less SFA ($P < 0.05$), more PUFA ($P < 0.001$), more n-3 FA ($P < 0.001$) and a lower n-6/n-3 FA ratio ($P < 0.001$) in their serum than sows fed FSM. Milk from sows fed FS and FSO also showed increased n-3 FA ($P < 0.01$) and decreased n-6/n-3 FA ratio ($P < 0.001$) on both d 2 and 20 of lactation. Carcass from FS and FSO newborn piglets had increased n-3 FA ($P < 0.001$) and decreased n-6/n-3 FA ratio ($P < 0.01$) compared with FSM piglets. Circulating hormonal concentrations in sows were not affected overall ($P > 0.1$). On d 20 of lactation, milk from FS, FSM, and FSO sows had more protein than that from CTL sows ($P < 0.01$). FSM piglets tended to weigh more on d 28 ($P < 0.1$) and weighed more on d 56 (23.8 vs 22.6 kg, $P < 0.05$) than FS and FSO piglets. Carcasses of one day-old FSM piglets had greater glycogen (102.8 vs. 59.1 µmole/g, $P < 0.0001$) and DM ($P = 0.05$) contents than those of FS and FSO piglets but organ weights and circulating concentrations of glucose and IGF-I did not differ ($P > 0.1$). Feeding flax as seed or oil to sows altered their FA profiles and that of their offspring without affecting litter growth rate, whereas feeding FSM improved postweaning growth of piglets. *Thanks to Shur-Gain and the Québec Federation of Swine Producers for financial support.*

Key Words: flax, lactation, pigs

M197 Effect of the substitution of soybean meal and corn for cull chickpeas on the apparent digestibility of nutrients in growing diets for pigs. J. M. Uriarte*, J. F. Obregon, H. R. Guemez, R. Barajas, and P. A. Valdez, *Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México*.

The objective of this experiment was to determine the effect of the substitution of soybean meal and corn for cull chickpeas on apparent digestibility of nutrients in growing diets for pigs. Six pigs (BW = 42.25 ± 1.45 kg; Large White × Landrace × Large White × Pietrain) were used in a replicated Latin Square Design. Pigs were assigned to consume one of three diets: 1) Diet with 18.0% CP and 3.27 Mcal ME/kg, containing corn 69.9%, soybean meal 27.6%, and premix 2.5% (CONT); 2) Diet with 18.0% CP and 3.26 Mcal ME/kg with corn 51.7%, cull chickpeas 25%, soybean meal 18.5%, vegetable oil 2.3%, and premix 2.5% (CHP25), and 3) Diet with 18.0% CP and 3.26 Mcal ME/kg with corn 33.5%, cull chickpeas 50%, soybean meal 9.4%, vegetable oil 4.6%, and premix 2.5% (CHP50). Pigs were individually placed in metabolic crates (0.6 × 1.2 m). The adaptation period was 6 days and sample collection period was 4 days. From each diet and period, one kg of diet was taken as a sample and the total fecal production was collected. DM excreted in feces (216, 221, and 195 g/day) was not affected by treatments (P=0.64) for CONT, CHP25 and CHP50, respectively. Crude protein in feces was similar (P=0.51) between treatments (46, 51 and 44 g/day). Apparent digestibility of DM was equal (P = 0.81) across treatments (88.67, 88.28 and 89.33%). Apparent digestibility of crude protein was not altered (P=0.85) by CHP inclusion (86.30, 85.19 and 86.14%). These results suggest that cull chickpeas can be used up to 50% in growing pig diets without affecting nutrient digestibility.

Key Words: chickpeas, digestibility, pigs

M198 The effect of corn of different textures in dry grain or silage forms on digestibility and growth performance of piglets from 7 to 15 kg. E. T. Fialho*, J. V. Neto, V. S. Cantarelli, M. G. Zangeronimo, J. A. F. Lima, and P. B. Rodrigues, *University Federal of Lavras, Lavras, MG, Brazil*.

A study was conducted to evaluate corn with different textures and storage forms on digestibility of nutrients and growth performance in young piglets. A total of 24 barrows with initial BW 18.7 ± 1.5kg were blocked by weight and randomly allotted to one of four treatments. The treatments were in a 2 × 2 factorial arrangement with main effects of corn textures (flint and dentate) and ensilage process (dry grain and corn grain-70%DM-silage). The diets were formulated to meet the nutrient requirements of piglets according to NRC (1998). Each treatment was fed to six barrows in individual metabolism cages with a 5-d acclimation followed by a 5-d period of total, but separate, feces and urine collection. The results show significant differences (P<0.05) with the silage process, which shows increases (P>0.05) in the digestible coefficient of dry matter and digestible protein and on digestible energy of diets when compared to the results from dry grain. The textures of corn did not show (P>0.05) any influence on digestibility of nutrients on diets formulated with the corn that was tested. A total of 60 barrows (initial weight of 6.5 ± 1.5 kg) were used in a growth performance study for 28-d post-weaning, and were randomly allotted to one of the four treatments described in the metabolism assay. There were three pigs (two barrows and one gilt) per pen and five pens/treatment. Throughout the whole period of the experiment, there were no treatment effects (P>0.05) on body weight, ADG or daily feed intake for piglets fed diets with different flint or dentate corns textures. The dentate corn and the ensilage processes improved (P<0.05) F:G in comparison to the flint texture. In conclusion, the use of ensilage corn increases the digestibility of nutrients and improves the F:G of rations formulated with dentate corn in diets for piglets from 7 to 15 kg.

Key Words: performance, metabolism assay, piglets

M199 Changes in diversity and homogeneity of the gut microbiota of pigs fed distillers dried grains with solubles (DDGS) after an *E. coli* challenge. V. Perez-Mendoza*[1], J. Barnes[1], C. Maddox[1], J. Pluske[2], and J. Pettigrew[1], [1]*University of Illinois, Urbana*, [2]*Murdoch University, Murdoch, WA, Australia*.

To determine changes in pig gut microbiota due to dietary DDGS and *E. coli* infection post-weaning, 48 pigs (6.6±0.51 kg BW) were used in a CRD with a factorial arrangement of 4 diets (0, 5, 10, and 20% DDGS) × 2 challenges [β-hemolytic F18 SLT2 *E. coli* (EcCh), or distilled water (NoCh)]. Diets were fed at weaning (21 d old) and inoculation begun 3 d after (1 oral dose during 3 consecutive days, with 10^{10} cfu/dose in EcCh). Mucosal scrapings were collected from jejunum, ileum, cecum, and colon on post-inoculation d 11. Microbial diversity was assessed as the number of bands by denaturing gradient gel electrophoresis using the V3 region of bacterial 16S ribosome, where each band represents at least 1 bacterial species. Sorenson's similarity percentages (Cs) were used to compare banding patterns between pairs of pigs within treatments (homogeneity) and among treatments (inter-treatment Cs values). In jejunum, microbial diversity was greater (P<0.001) in EcCh; homogeneity increased in NoCh pigs fed 10 and 20% DDGS, but it was reduced with 10% DDGS in EcCh pigs (DDGS × Challenge quadratic, P<0.03). In ileum, microbial diversity and homogeneity did not change. In cecum, microbial diversity was greater in pigs fed 5 and 10% DDGS than in those fed 20% (DDGS quadratic, P<0.01); homogeneity was reduced in EcCh pigs fed 10 and 20% DDGS (DDGS × Challenge linear, P<0.01). In colon, homogeneity was reduced by feeding 10% DDGS in NoCh and by 20% DDGS in EcCh pigs (DDGS × Challenge, P<0.001). Analysis of inter-treatment Cs values indicated differences between most of the EcCh treatments and specific levels of DGGS in NoCh pigs across intestinal sites: microbiota of NoCh pigs fed 10 and 20% DDGS differed (lower inter-treatment Cs than corresponding intra-treatment values; P<0.05) from that of EcCh pigs fed 0 and 20% DDGS in jejunum, or fed 10 and 20% DDGS in cecum. Pig gut microbiota may be altered differently by the inclusion level of DDGS in the diet and the presence of enteropathogenic *E. coli*. It is not clear whether the observed changes in gut microbiota alter intestinal health.

Key Words: pigs, DDGS, microbiota

M200 Variation and relationships in nutrient and mineral composition for six species of whole fish commonly used as animal feeds. K. S. Yamamoto*[1], J. R. Carpenter[1], S. Atkinson[2], L. Polasek[2], and H. Zaleski[1], [1]*University of Hawaii at Manoa, Honolulu*, [2]*Alaska SeaLife Center, Seward, AK*.

Capelin (*Mallotus villotus*), herring (*Clupea harengus*), mackerel (*Scomber scombrus*), pollock (*Theragra chalcogramma*), smelt (*Allosmerus elongates* and *Hypomesus pretiosus*), and squid (*Loligo* spp.) are six species of whole fish commonly used as animal feeds, particularly as prey in captive marine mammal diets. Due to the great variation in nutrient composition between and within species, knowledge of the nutrient content of these prey items is essential when performing research and also in the daily management and husbandry of marine mammals where diet assessment is critical. The purpose of this study was to determine the variation and relationships of nutrient and mineral composition both on a DM and as-fed basis for a variety of whole fish species [capelin (n=70), herring (n=99), mackerel (n=25), pollock (n=45), smelt (n=37) and squid (n=52)]. Frozen samples had been collected from three different locations in Hawaii and Alaska and analyzed between 1982 and 2007. Proximate analysis to evaluate DM, CP, EE, ash was performed using standard methods of the Association of Official Analytical Chemists, and GE was determined by bomb calorimetry. Minerals were determined by inductively coupled plasma emission spectroscopy. Nutrient data for each species was sorted according to both %CP and %EE and correlations run to determine relationships. Percent DM and H_2O differed significantly (p<0.05) between all fish species analyzed in this study. On a DM basis, percent EE between herring and smelt, and between capelin and mackerel did not differ. Ash (%, DM basis) did not differ between pollock and mackerel, and between squid and smelt. Percent CP (DM basis) did not differ between capelin, pollock and mackerel, and between herring and smelt. Gross energy (kcal/g, DM basis) did not differ between capelin, squid, and pollock. Inverse relationships were observed both between EE and CP, and between GE and CP. It was also determined that mineral content tended to parallel CP content. Squid did not have the same nutrient trends observed in the other prey items and was the only non-fish species considered.

Key Words: whole fish, nutrient composition, nutrient-mineral relationships

M201 In vitro starch kinetics hydrolysis and fermentation of field peas (*Pisum sativum*). C. A. Montoya, P. Kish, and P. Leterme*, *Prairie Swine Centre Inc., Saskatoon, SK, Canada*.

The reason for the high variability in digestible energy content of field peas in pigs is unclear. No acceptable relationship between chemical composition and energy value has been established so far. Starch hydrolysis could partly be responsible for that variation. Therefore, the kinetics of starch hydrolysis of 15 pea samples of high and low quality was studied in vitro. The rate of fermentation in the large intestine was also studied. A sequential in vitro hydrolysis of starch was carried out (pepsin 120 min plus one mix of pancreatin, isomaltase and maltase enzymes for 240 min). Samples were taken at different times to analyse soluble glucose. The residues of hydrolysis were used to evaluate their rate of fermentation by the gas technique. Differences in starch hydrolysis were observed after 20 min of pancreatin mix hydrolysis (i.e. 140 min after pepsin addition). Camry and Cooper pea cultivars presented the highest rate of hydrolysis and Midas and Montero the lowest (P < 0.001). The trends remained until 360 min of hydrolysis (P < 0.001; 98.4, 91.3, 74.7 and 74.4%, respectively). A negative correlation was observed between the rate of starch hydrolysis at 360 min and the NDF content of peas (r= 0.55; P = 0.036). The residues of hydrolysis of the Midas and Montero cultivars presented the highest rates of fibre fermentation in the large intestine (252 and 254 ml, respectively; P < 0.001). This could partly be explained by their higher content in resistant starch. The Sage cultivar presented the lowest rate of fermentation (232 ml), explained by its higher NDF content (205 vs. 186 to 132 g/kg DM). In conclusion, differences in in vitro starch hydrolysis and fermentation were observed among the pea cultivars. The large differences in starch hydrolysis could possibly explain the variation in digestible energy content of field peas observed in pigs.

Key Words: pigs, peas, starch

M202 Ileal amino acid digestibility in dried distillers grains with solubles originating from wheat, corn or wheat-corn blend fed to growing pigs. Y. Yang*, E. Kiarie, B. A. Slominski, A. Brûlé-Babel, and C. M. Nyachoti, *University of Manitoba, Winnipeg, MB, Canada*.

The aim was to determine the apparent (AID) standardized (SID) ileal CP and AA digestibility in dried distiller′s grains with solubles

(DDGS) derived from wheat (wDDGS), a wheat-corn (70:30 wt/wt) blend (wcDDGS), or corn (cDDGS). Three diets, each containing one of the DDGS samples as the only protein source, and a low-casein diet were fed to 12 ileal cannulated pigs (20.3±1.3 kg BW) in a two-period cross-over design, giving six replicates per diet. The casein diet was used to estimate basal endogenous CP and AA losses for determining SID. All diets contained chromic oxide (0.3%) as an indigestible marker. Daily feed allowance was set at 4% BW at the beginning of each period and was offered in two equal amounts at 0800 and 1630 h in mash form. After 5 d of diet adaptation, digesta were collected for 12 h each on d 6 and 7. The AID and SID of CP were similar among the DDGS samples and averaged 69% and 80%, respectively. The wcDDGS had higher ($P < 0.05$) AID (%) of His (76 vs. 71), Ile (79 vs. 73), Leu (81 vs. 75), Val (76 vs. 70), and Met (83 vs. 76) than wDDGS. Among the indispensable AA, Lys and Thr had the lowest AID values in all DDGS samples and averaged 45% and 60%, respectively. The mean AID values for indispensable and dispensable AA were 68, 74, and 72 and 66, 69, and 68 for wDDGS, wcDDGS and cDDGS, respectively. The wcDDGS and cDDGS samples had higher ($P < 0.05$) SID (%) of Leu and Met compared with wDDGS. The SID of Ile was higher ($P < 0.05$) for wcDDGS than for cDDGS. The SID values for Lys and Thr were 56, 61, and 57 and 71, 74, and 74 for wDDGS, wcDDGS, and cDDGS, respectively, and were lower than for other AA. The mean SID values for indispensable and dispensable AA were 78, 82, and 83 and 80, 82, and 81 for wDDGS, wcDDGS and cDDGS, respectively. The results show that Lys and Thr were poorly digested compared to other AA, which may be indicative of damage to these AA during processing.

Key Words: DDGS, amino acid digestibility, pigs

M203 In vitro rabbit cecal fermentation patterns of four substrates: Glucose, cellobiose, microcrystalline cellulose and NDF separated from alfalfa hay. H. J. Yang*[1], Q. Yue[1], Y. C. Cao[1], D. F. Zhang[1], and J. Q. Wang[2], [1]*China Agricultural University, Beijing, P.R. China*, [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, China Academy of Agricultural Sciences, Beijing, P.R. China*.

The in vitro cecal fermentation patterns of glucose (GLU), cellobiose (CEB), microcrystalline cellulose (MCC) and neutral detergent fiber prepared from alfalfa hay (aNDF) were investigated with New Zealand hybrid mixed cecal microorganisms of broiler rabbits. At the end of 72 h incubation, Carboxymethyl cellulase activity was highest with GLU (436 umol sugar L^{-1} min^{-1}), while with MCC it was significantly lower than with GLU and CEB (P<0.05). Xylanase activity tended to be higher compared with aNDF (591 umol sugar L^{-1} min^{-1}), MCC and GLU as the substrate than those with CEB. Feruloyl esterase activities were highest with aNDF (8.7 umol Ferulic acid L^{-1} min^{-1}), which was at least twice that of MCC and CEB (P<0.05). Less volatile fatty acids were produced from aNDF than those from other substrates (P<0.05). Fermentation of aNDF and MCC produced significantly more propionate and less butyrate than fermentation of GLU. With aNDF as the substrate, the molar percentage of acetate was significantly lower than with the other substrates (P<0.05), while that of glucose was highest with 80.1% (mol/mol). As a molar proportion of the total gas production, more methane was produced from MCC and aNDF, while that of GLU and CEB was almost zero. Therefore, the presence of low molecular weight carbon source without ester bond linkage like glucose and cellobiose might stimulate rabbit cecal microbes to produce more carboxymethyl cellulase, whereas the presence of microcrystalline cellulose or more ester bond linked cell walls in alfalfa stimulate activities of the acetyl esterase and ferulic acid esterase. Methane can be produced by rabbit cecal microorganisms and methanogenesis increases gradually with an increasing fiber content in feeds.

Key Words: rabbit, in vitro cecal fermentation, methanogenesis

M204 Nutritional evaluation of fermented fish meal (*L. acidophilus* GB-LC2 and *B. licheniformis* GB-F2) based on nitrogen balance and nutrient digestibility in comparison with spray-dried plasma protein for weanling pigs. J. H. Cho*[1], J. S. Yoo[1], J. H. Ahn[2], I. B. Chung[2], and I. H. Kim[1], [1]*Dankook University, Cheonan, Choongnam, Korea*, [2]*National Institute of Animal Science, RDA, Korea*.

Fifteen crossbred [(Landrace × Yorkshire) × Duroc] barrows (8.58±0.32 kg) with simple T-cannulas were used to compare spray dried animal plasma with fermented (*L. acidophilus* GB-LC2 and *B. licheniformis* GB-F2) local fish meals on nitrogen balance and apparent ileal nutrient digestibility. Dietary treatments are as follows: 1) SDAP (3% Spray-dried animal plasma), 2) FFA (5% fermented domestic fish meal: *L. acidophilus* GB-LC2) and 3) FFL (5% fermented domestic fish meal: *B. licheniformis* GB-F2). After a 14 d recovery period, pigs were permitted a 7 d adjustment to the experimental diets and 2 d of ileal digesta collection. Nitrogen concentration and excretion in the urine were lower in SDAP group than FFA and FFL groups (P<0.05). SDAP group had lower N concentration and excretion in the feces than FFL group (P<0.05). Additionally, total N excretion of SDAP group was lower than that of the other groups (P<0.05). N retention and biological value were greater in SDAP group than FFL treatment (P<0.05), and N ileal digestibility was higher in SDAP group than FFA and FFL group (P<0.05). Moreover, calcium digestibility in SDAP group was found to be higher (P<0.05) than FFA group. Also, arginine, histidine, isoleucine, lysine, phenylalanine, aspartic acid, cysteine and glutamic acid digestibilities were higher in SDAP group than FFL group (P<0.05). Finally, the digestibilies of valine and tyrosine were greater in SDAP group than in the other groups (P<0.05).

Key Words: fermented fish meal, nitrogen balance, weanling pig

M205 Apparent metabolizable energy of hydrolyzed swine intestinal mucosa (Palbio RD50®) for broiler chickens. D. Solà-Oriol[1], R. Muns[1], D. Martínez-Puig*[2], and J. F. Pérez[1], [1]*Universitat Autònoma de Barcelona, Bellaterra, Spain*, [2]*Bioiberica, Palafolls, Spain*.

Palbio RD50® is a hydrolyzed intestinal mucosa ingredient which is commonly used as a highly digestible protein source for feed formulation. However, less information is available about its dietary metabolisable energy content for poultry. The objective of the present study was to determine the N corrected apparent metabolizable energy (AMEn) value of hydrolyzed intestinal mucosa of swine with 50%CP (HIM50) for broiler chickens. Twenty four female broiler chickens (BW 1610 g ± 64) were individually allocated and randomly distributed into three experimental groups. Three experimental treatments were formulated with corn, soybean meal 44%CP and HIM50 as the only energy sources. The T1 diet contained 69.9% corn and 26.41% soybean meal at a fixed ratio (control diet, AMEn=2685 kcal•kg^{-1}); T2 and T3 were prepared by the substitution of 5% and 10% of the corresponding amount of corn-soybean meal by HIM50. Feed was offered *ad libitum* in mash form. After a 5-d adaptation period, feed intake was individually controlled and animal excreta samples were collected for 3 consecutive days. Dry Matter (DM) and Gross Energy (GE) were determined in feed and in excreta samples after freeze drying. Nitrogen content was

also determined in order to obtain AMEn, assuming that the excreted N energy is 8.22 kcal•g^{-1} N. The estimated AMEn content of the control diet was 2685 kcal•kg^{-1}. It was estimated that an inclusion of 5 or 10% of HIM50 in the corn-soybean meal based diet for broilers, under the conditions of the present study, reduced the AMEn of the diet by 28 and 57 kcal•kg^{-1}, respectively. It is concluded that the calculated value of AMEn for hydrolyzed intestinal mucosa of swine with 50%CP for the animals used in the present study was 2227 kcal•kg^{-1}.

Key Words: AMEn, broiler, feedstuff evaluation

M206 Digestibilities of components in three sources of liquid mycelium feed products in growing pigs. W. C. Sauer[1,2], A. B. Araiza*[1], B. Schutte[3], M. Cervantes[1], A. Morales[1], R. Zijlstra[2], and J. L. Landero[1], [1]*ICA, Universidad Autónoma de Baja California, Mexicali, BC, México*, [2]*DAFNS, University of Alberta, Edmonton, AB, Canada*, [3]*S&P Consultancy, Bennekom, The Netherlands*.

The digestibilities of components in three different liquid mycelium feed products (LMP) were determined with pigs. The LMP are feed ingredients obtained from *Penicillium chrysogenum* cultivated for the production of penicillin G. The LMP were Vevocel®, Vevocid® and flocculated Vevocid. In Exp. 1, the apparent ileal digestibilities (AID) of CP and AA were determined with pigs fitted with post-valve T-cannulas. Four diets were fed. The basal was a corn-barley-soybean meal based diet. The other 3 diets consisted of 70% of the basal diet and 30% of each of the 3 preparations of LMP on a DM basis. The AID of CP and AA in the preparations of LMP were determined with the difference method. Eight barrows with an average initial BW of 42.2 kg, were assigned to the four dietary treatments. The barrows were fed twice daily, at 0800 and 2000, equal amounts each meal, at a rate of 2.4 times the daily maintenance requirement for ME (418 kJ/BW$^{0.75}$). Each experimental period comprised a 7 d adaptation period followed by a 5 d collection of ileal digesta from 0800 to 2000 on d 8, 9, 10, 11, and 12. The AID of CP and AA were usually highest (P<0.05) in flocculated Vevocid, intermediate in Vevocel® and lowest in Vevocid®. In the same order for the feed ingredients, the AID of CP were 64.7, 61.3 and 52.3%, respectively. For lysine, which is often limiting, the AID were 76.3, 67.7 and 61.4%, respectively. In Exp. 2, the total tract digestibilities (ATTD) of components including GE, CP and P were determined with intact pigs, with an average initial BW of 42.4 kg. This experiment was carried out exactly under the same conditions as described under Exp. 1. Feces were collected from 0800 on d 8 until 0800 on d 13. There were no differences (P>0.05) in the ATTD of GE, ranging from 77.9 to 82.8%; the ATTD of P was higher (P<0.05) in Vevocel® (70.2%) and flocculated Vevocid (67.8%) than in Vevocid® (61.5%). The ATTD of CP was higher (P<0.05) in flocculated Vevocid® (87.9%) than in Vevocel® (83.7%) and Vevocid® (82.6%). These data show significant differences in the AID and ATTD of components between the different liquid mycelium products

Key Words: swine, digestibility, mycelium

M207 A spreadsheet program for making a balanced Latin square design. B. G. Kim* and H. H. Stein, *University of Illinois, Urbana*.

The Latin square design is often employed in animal experiments to minimize the number of animals required to detect statistical differences. In this design, each treatment is assigned once to each row and each column, and the sequences of rows and columns are randomized. This procedure generally does not balance out potential carryover effects. For example, treatment A may immediately precede treatment B never or more than once. A systemic method is available for balancing the first order residual effects. Even though this is not overly complicated, it is time-consuming if an experiment requires a large size of square or multiple squares. Therefore, we have developed an Excel spreadsheet-based program, the Balanced Latin Square Designer, to facilitate the generation of Latin squares balanced for carryover effects. The source codes for the modules have been written in Visual Basic for Application as an Excel XP add-in. The program allows a user to input the number of treatments that is equal to the number of animals and periods in a square. A user may also input the number of squares. Then, the program will automatically generate Latin squares. For an even number of treatments, each treatment immediately precedes and follows every other treatment exactly once in the square. For Latin squares with an odd number of treatments, the first order residual effects can only be balanced if they are replicated an even number of times, and the spreadsheet program allows for that. The program also displays a table for an experimental schedule sorted by period and animal. The Balanced Latin Square Designer allows animal scientists to quickly and accurately generate Latin squares balanced for the first order carryover effects. This program reduces the amount of time required to prepare Latin square experiments.

Key Words: animal experiment, carryover effect, Latin square design

M208 Influence of phytase on the apparent ileal digestibility of amino acids in soybean meal diets in growing pigs. H. Silva, E. Fialho*, R. Sousa, N. Schoulten, W. Santos, L. Silva, and V. Cantarelli, *University Federal of Lavras-UFLA, Lavras-MG- Brazil*.

A total of eight barrows with an initial BW of 38.7 ± 2.1 kg were surgically equipped with a T-cannula in the distal ileum and used to evaluate the effect of phytase level supplementation on the apparent ileal digestibility of amino acids (AIDAA) in growing pig. The pigs were randomly allotted to four dietary treatments (0, 400, 800 and 1200 FTU/kg) during a 4-wk experiment in a Latin Square Design. Pigs were fed corn soybean meal based on diets formulated to meet the requirements for apparent ileal digestible lysine (0.61%) for growing pigs according to NRC (1998). Phytase (from Natuphos@5000) and 0.25% chromic oxide as an indicator were used in the diets. During wk 1, pigs were fed only a basal diet; during wk 2 to 4, treatment diets were provided, and ileal samples were collected on day 6 and 7 of each week. The supplementation of phytase improved the apparent ileal digestibility coefficient of Glu, Gly, Arg, Ala, Pro, Tyr, His and Lys. A linear increase (P = 0.009) was observed for phytase level on the apparent ileal digestibility coefficient of Thr and Ser, and a quadratic effect was observed (P = 0.006) for the apparent ileal digestibility coefficients of Val, Phe, total of non-essential amino acids and total of essential amino acids. Phytase additions between 440 and 900 FTU/kg in the diets maximized ileal AA digestibility values. In conclusion, phytase supplementation is beneficial by improving the apparent ileal digestibility of all essential and non-essential AA in growing pigs fed corn-soybean meal diets, and also reduces the environmental pollution impact due to higher ileal AA digestibility.

Key Words: ileal digestibility, phytase, growing pigs

M209 Effects of the gestation and farrowing housing system on physiology and performance of primiparous sows and piglets. W. S. Ju*, L. G. Piao, H. F. Long, Y. D. Jang, S. K. Jang, and Y. Y. Kim, *Seoul National University, Seoul, Korea*.

The objective of this experiment was to investigate the effects of different environments on gilts and their progeny during gestation, farrowing and lactation. A total of 41 gilts (Yorkshire x Landrace) were assigned to 2 treatments in a completely randomized design. Treatments were: 1) S - housed in gestation stall (2.15 × 0.6 m) and then farrowing crate (2.50 × 1.80 m), 2) P - housed in open pen (3.9 × 2.4 m) during gestation and lactation. During the whole gestating period, no significant differences were observed in the body weight and backfat thickness among all treatments. However, P gilts had higher backfat gain than S at d 110 of pregnancy($P<0.01$). Apart from the third week, the feed intake and body weight of the P group in the lactation period was greater than the S group ($P<0.05$). On the other hand, there were no differences in the weight and backfat thickness loss of lactating sows. The treatments had no effect on litter size, litter weight and litter weight gain. Although significant differences were not found, the mortality number and rate of piglets of treatment P were numerically higher than treatment S. The crushing rates (9.5% of P vs. 5.2% of S; $P=0.10$) and death rate (not crushed; 9.0% of P vs. 3.6% of S; $P=0.09$) also had a similar tendency. The colostrum and milk composition of lactating sows were not affected by treatments. These results indicated that the housing in open pen during gestation, farrowing and lactation increased not only the gestation backfat thickness, feed intake and body weight of lactating sows, but also preweaning mortality rate of piglets, but did not affect other reproductive performances and milk composition of primiparous sows compared with the housing in commercial environments of Korea.

Key Words: farrowing condition, gilt, reproductive performance

M210 The effect of different double choice feeding protocols on the measurement of feed preferences. D. Solà-Oriol[1], E. Roura[2], and D. Torrallardona*[1], [1]*IRTA, Mas de Bover, Constantí, Spain*, [2]*Lucta SA, Barcelona, Spain*.

Piglets are able to choose between two feeds depending on their preference. However, as pigs may associate the preferred feed with the position of the hopper containing it, a change in hopper position may affect preference evaluation. A trial was conducted to study the effect of changing hopper position on the measurement of relative preference between a CONTROL diet and the same diet supplemented with a FLAVOR (Luctarom, Lucta SA, Spain) and an acidifier (Luctacid, Lucta SA, Spain). One hundred and eight 35-d old pigs *(LD × Pi)* of mixed sexes, in 36 pens were used. Each pen (3 pigs) was offered one of four experimental treatments, and preference was measured for three consecutive periods of 3, 4 and 3 days. The four experimental treatments were as follows: T-1: CONTROL vs. FLAVOR without changing hopper location; T-2: CONTROL vs. FLAVOR changing the position of the hoppers at the start of the second and third periods; T-3: CONTROL vs. CONTROL without changing hopper location; and T-4: CONTROL vs. CONTROL changing hopper location at the beginning of periods 2 and 3. Preference (percentage contribution of the test diet to total intake) was measured for each pen. The preference values of each treatment at each experimental period were compared to the neutral value of 50% of preference by using the TTEST procedure of the statistical package SAS. The preference values obtained for the FLAVOR diet were: 81.6%, 72.2% and 72.8% for T-1 and 88.3%, 76.8% and 73.1% for T-2 for the 1st, 2nd and 3rd periods, respectively. For both treatments, all the values were significantly different from the neutral value of 50% ($P<0.05$). On the contrary, for treatments T-3 and T-4 the relative preference of one of the diets over the other one were only significantly different from the neutral value of 50% in period 1 but not for periods 2 and 3. The effects observed for period 1 could be explained by the previous position of a single hopper before the trial started. It is concluded that the addition of flavor and acidifier improved feed preference for the piglets, and that piglets were able to identify the preferred feed even if the hopper position was changed.

Key Words: double choice, palatability, piglet

M211 Influence of the type of diet on the growth performance of two genotypes of quails in a floor housing system. D. Cardoso-Jiménez[1], A. Z. M. Salem*[1,2], R. Rojo-Rubio[1], and A. Perez-Cháves[1], [1]*Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Toluca-Tejupilco, Estado de México, México*, [2]*Alexandria University, Alexandria, Egypt*.

Growth performance and carcass yield of two genotypes of quails *Coturnix coturnix japonica* variety Japanese (JAP) and *Coturnix coturnix japonica* variety Jumbo (JUM)) were compared by feeding three experimental diets in a factorial design (2 genotypes × 3 experimental diets). One hundred and twenty six birds (~58g) of each genotype (10 d of age of both sexes) were used for a 15 d experimental period. Quail chicks were randomly assigned in three groups of each genotype (42 birds of each). Each group received one of the three experimental diets; ground yellow corn-based diet (Diet I), ground rice-based diet (Diet II), or commercial concentrate (Diet III) in 6 experimental groups (2 genotypes × 3 diets) with 7 birds per pen. Diets were formulated to meet the requirements of quails and were fed ad libitum. Quails from both genotypes ate more (326.9 vs. 218.3 and 190.0g/d, respectively; $P=0.0012$) from Diet III versus Diets I and II. Overall, quails of both genotypes had optimal growth ($P=0.001$) consuming corn-based diets vs. the other diets. Feed conversion ratio (FCR) was improved when Diet II or Diet III was fed vs. Diet I. Final BW and ADG were improved in JAP fed Diet I and Diet III, while it was only improved in JUM when fed Diet I vs. the other diets. FCR had the highest value ($P=0.0016$) in JUM fed Diet I, while it was inferior in the same genotype fed Diet III. FCR in JAP was not affected by the three types of diets. Carcass yield was improved ($P<0.05$) in JAP fed Diet I or Diet III vs. Diet II. Our results suggested a better growth performance and carcass yield of quails fed a corn-based diet or a commercial concentrate compared with a rice-based diet and JAP had more efficient diet utilization than JUM.

Key Words: quails, diets types, growth performance

M212 Effects of a dietary complex enzyme in corn distillers dried grains with solubles (DDGS) on meat quality and pork fatty acid composition of loin muscle. J. S. Yoo*[1], H. D. Jang[1], T. X. Zhou[1], J. P. Wang[1], and C. Y. Lee[2], [1]*Dankook University, Cheonan, Choongnam, Korea*, [2]*Regional Animal Industry Center, Jinju National University, Jinju, Gyeongnam, Korea*.

This study was conducted to evaluate the effects of a dietary complex enzyme (β-mannanase 800 IU/kg and Xylanase 700 IU/kg) in a diet containing corn distillers dried grains with solubles (DDGS) on meat quality and pork fatty acid composition. 96 pigs ([(Landrace × Yorkshire) × Duroc], 68.77 kg average initial body weight) were used in an 8 week growth assay. Dietary treatments included 1) corn-soybean meal diet, 2) corn-soybean meal diet + 0.05% enzyme complex, 3)

corn-soybean meal diet with 5% DDGS and 4) corn- soybean meal diet with 5% DDGS + 0.05% enzyme complex. The pigs were allotted randomly into four pigs per pen with six replicate pens per treatment in a completely randomized design. Pigs were slaughtered at the end of experiment and the loin muscle was obtained for meat quality. Meat pH ($p<0.01$), firmness ($p<0.01$) and redness ($p<0.05$) were higher in DDGS treatment than corn-soybean meal treatment. However, color, marbling, lightness, yellowness, TBARS, water holding capacity, drip loss, cooking loss and loin muscle area were not significantly different among treatments ($p>0.05$). The pigs fed the diet containing DDGS had higher total UFA concentration and total UFA/SFA ratio of loin and backfat. In conclusion, DDGS can change pH, firmness, redness and total UFA concentration and total UFA/SFA ratio of meat and backfat, however, enzyme addition has no affect on meat quality.

Key Words: DDGS, fatty acid composition, finishing pigs

M213 Supplementation with phytase and xylanase can increase energy availability in swine diets containing corn distillers dried grains with solubles (DDGS). M. D. Lindemann*[1], G. A. Apgar[2], G. L. Cromwell[1], P. H. Simmins[3], and A. Owusu-Asiedu[3], [1]*University of Kentucky, Lexington*, [2]*Southern Illinois University, Carbondale*, [3]*Danisco Animal Nutrition, Marlborough, UK*.

One way of enhancing dietary energy at times of high feed prices is to use exogenous enzymes to improve diet digestibility and utilize more of the nutrients already present in a diet containing byproducts such as DDGS. To examine the potential for enzymes to enhance nutrient release, a study was conducted with 96 crossbred pigs (mean initial and final BW of 64 and 123 kg) allotted to pens of 4 pigs (2 barrows and 2 gilts). Treatments were: 1) a positive control [PC] corn-soybean meal diet with 20% DDGS and 3% choice white grease [CWG], and 2) a negative control [NC] similar to the PC but with 1% CWG and no inorganic P source. The NC was lower in ME [90 kcal/kg] and available P [about 0.02%]. The enzymes added were phytase (Phyzyme® 6-phytase, EC 3.1.3.26; PHY; 250 or 500 U/kg diet) and xylanase (Porzyme® 9300, endo 1,4-beta-xylanase; XYL; 2000 or 4000 U/kg diet). Diets 3-8 were the NC plus: 3) 250 PHY and 0 XYL, 4) 250 PHY and 2000 XYL, 5) 250 PHY and 4000 XYL, 6) 500 PHY and 0 XYL, 7) 500 PHY and 2000 XYL, and 8) 500 PHY and 4000 XYL. The ADG for the PC and NC (1.04 vs 1.05 kg), ADF (2.78 vs 2.93 kg), and F/G (2.68 vs 2.78) were as anticipated with higher F/G in the NC diet. Fecal digestibility for DM (77.1 vs 73.7%, P=0.02), energy (75.5 vs 71.4%, P=.006), and N (72.7 vs 68.8%, P=0.007) was consistently higher for PC compared to NC. For Trt 3-8 the ADG (1.04, 1.07, 1.03, 1.00, 0.95, and 1.01 kg) and F/G (2.77, 2.73, 2.66, 2.75, 2.75, and 2.68) illustrated an apparent release of energy with incremental PHY and XYL additions. For Trt 3-8 the DM (76.1, 76.7, 74.6, 76.2, 74.4, and 74.6%), energy (73.8, 74.4, 71.2, 73.7, 72.0, and 71.6%), and N (70.9, 71.7, 70.3, 71.1, 69.5, and 71.3%) digestibility confirmed an improved digestibility. The inclusion of PHY improved digestibility ($P<0.05$) of all 3 components. Further improvements in fecal digestibility were not observed with XYL but the recovery of F/G was observed only when the high level of XYL was included with the PHY. These data demonstrate that appropriate exogenous enzymes are a means of nutrient release in diets containing byproducts.

Key Words: phytase, pigs, xylanase

Physiology and Endocrinology: Endocrinology and Metabolism

M214 Methionine requirements for the preimplantation bovine embryo. L. Bonilla*[1], D. Luchini[2], E. Devillard[3], and P. J. Hansen[1], [1]*University of Florida, Gainesville*, [2]*Adisseo USA, Inc., Alpharetta, GA*, [3]*Adisseo France, SAS, Commentry, France*.

The objective was to determine the requirement of in vitro produced embryos for the essential amino acid methionine. Oocytes were matured for 20-22 h and fertilized for 6-8 h. Embryos were cultured in groups of 15 in 25 µL microdrops of potassium simplex optimized medium - bovine embryo modification 2 (KSOM-BE2) at 38.5°C in 5% (v/v) oxygen. In Experiment 1 (n=963 putative zygotes in 4 replicates), embryos were cultured with 0, 35, 50, 100, 200 or 400 µmol/L L-methionine for 8 d. The percent of oocytes that cleaved was observed at Day 3 after insemination and blastocyst development at Day 7 and 8. At Day 7, a group of blastocysts was stained with Hoescht 33258 to determine total cell number. There was no effect of methionine concentration on cleavage rate. The percent of oocytes that developed to blastocyst was lower for embryos without methionine at Day 7 ($P<0.05$) and 8 ($P<0.01$) than other groups but was similar for embryos cultured with 35-400 µmol/L. Least-squares means were 4.2, 23.2, 18.2, 21.5, 16.3, and 21.3 for 0, 35, 50, 100, 200, or 400 µmol/L for Day 7 (SEM=3.4%) and 13.5, 36.1, 30.9, 33.6, 29.8 and 33.0 for Day 8 (SEM=3.4%). Total cell number was not affected by methionine concentration. In Experiment 2 (n=1,204 putative zygotes in 4 replicates), embryos were cultured with 0, 7, 14, 21, 28 or 35 µmol/L methionine. There was no effect of methionine concentration on cleavage rate. The percent of oocytes that developed to blastocyst was lower for embryos without methionine at Day 7 ($P<0.005$) and 8 ($P=0.01$). At Day 7, least-squares means were 8.2, 20.3, 27.2, 27.7, 24.3, and 21.2 for 0, 7, 14, 21, 28, or 35 µmol/L (SEM=2.5%). There was a tendency for 7 µmol/L to be lower than 14 ($P=0.07$) and 21 µmol/L ($P=0.06$). At Day 8, least-squares means were 17.8, 35.2, 37.8, 43.0, 37.9, and 33.6 for 0, 7, 14, 21, 28, or 35 µmol/L (SEM=3.5%). Means were similar for 7-35 µmol/L. In conclusion, methionine requirements for optimal blastocyst yield are between 7 and 21 µmol/L. Further studies to further define optimal concentration and to examine competence of embryos for development after transfer are warranted. *Support: Adisseo.*

Key Words: methionine, embryos, development

M215 Effect of exogenous insulin and fasting on estradiol production and growth hormone receptor (GHR) and insulin-like growth factor I (IGF-I) genes expression by the pre-ovulatory follicle of ewes. A. Schneider[1], L. F. M. Pfeifer[1], E. Schmitt[1], J. W. Silva Neto[1], L. T. Hax[1], M. M. Antunes[1], F. A. B. Del Pino[1], G. R. Paludo[2], and M. N. Corrêa*[1], [1]*Federal University of Pelotas, Brazil*, [2]*University of Brasilia, Brazil*.

The aim of this study was to investigate the effect of fasting and insulin injections for 96 hours on estradiol concentrations and expression of GHR and IGF-I mRNA in the pre-ovulatory follicle of ewes. In the eleventh day of the estrous cycle 15 ewes received an injection of $PGF_2\alpha$, 36 hours after a GnRH injection and 24 hours after a CIDR® was inserted and removed 6 days later together with an injection of $PGF_2\alpha$ (Day 0). In Day -2 the ewes were divided in: 1) control group (CG, n = 5) that received a maintenance diet; 2) insulin group (IG, n = 5) that received insulin injections (s.c., 0.25 IU/kg) every 12 hours

from Day -2 to 2 and 3) fasting group (FG, n = 5), that was submitted to fasting from Day -2 to 2. Estradiol concentrations were evaluated on Day 2, when ovaries were also collected for evaluation of the follicular population and dissection of theca (TC) and granulosa (GC) cells of the pre-ovulatory follicle (> 4 mm). Expression of GHR and IGF-I mRNA was evaluated through real time RT-PCR. Data were compared among groups by one-way ANOVA using the Tukey-Kramer adjustment. The diameter of the pre-ovulatory follicle on Day 2 was not different among groups (7.60 ± 0.38 mm) neither the number of small (< 2 mm, 10.73 ± 2.19), medium (< 4 mm, 0.8 ± 0.2) and pre-ovulatory (1.13 ± 0.09) follicles per ewe was different. IG had higher (P<0.05) estradiol concentrations on Day 2 (53.70 ± 1.82 pg/mL) than FG (29.97 ± 6.96 pg/mL), but was not different from CG (35.92 ± 5.72 pg/mL). Although GHR or IGF-I mRNA expression was detected in GC and TC, no difference among groups was detected. For IG estradiol was positively correlated to follicular diameter (r=0.93, P<0.05), GC GHR (r=0.87, P<0.01) and IGF-I mRNA (r=0.79, P<0.1). In conclusion, insulin injection increased estradiol production without any change in the expression of GHR and IGF-I mRNA in the pre-ovulatory follicle.

Key Words: GHR, IGF, insulin

M216 TNFα and adipocyte-hepatic metabolism at drying off and during early lactation in dairy cows. H. A. van Dorland[1], H. Sadri[2], and R. M. Bruckmaier*[1], [1]*University of Bern, Vetsuisse Faculty, Veterinary Physiology, Bern, Switzerland*, [2]*Isfahan University of Technology, Department of Animal Science, Isfahan, Iran*.

Adipose tissue excretes components, such as TNFα, that play a role in the multifaceted regulation of lipolysis. This study investigated TNFα and other metabolic modulators in adipose tissue over time, and if TNFα is involved in interactions between adipose tissue and liver metabolism. Blood was sampled from 28 cows from week 10 ante partum (wk-10) up to week 4 post partum (wk4), and analyzed for concentrations of NEFA, glucose, insulin, and TNFα. Liver and adipose tissue biopsies were obtained in wk-10, on d1 post partum (d1), and in wk4. Adipose tissue was analyzed for mRNA levels by real-time RT-PCR of genes encoding for TNFα, peroxisome proliferator activated receptor γ (PPARγ), hormone-sensitive lipase (HSL), and fatty acid synthase (FASN). Liver was analyzed for mRNA levels of genes encoding enzymes of fatty acid β-oxidation (CPT1A CPT2, ACADVL), and of PPARγ. Data were evaluated by the Mixed procedure of SAS including biopsy time-point and parity as fixed effects with cow as repeated subject. Spearman Rank correlation coefficients were also calculated. Concentrations of NEFA were highest in wk-10, followed by d1, compared to wk4, suggesting adaptation to the reduction of nutrients at the start of the dry period. Plasma TNFα concentrations were very low (0.11±0.01 ng/ml) with no significant differences over time, suggesting that TNFα had a local effect. TNFα mRNA levels in adipose tissue were lowest (P<0.05) on d1 compared to the other time-points. HSL mRNA was highest (P<0.05) in wk-10, followed by d1, compared to wk4, which correspond to the high NEFA concentrations in wk-10. PPARγ mRNA levels were lowest in wk4 compared to the other time points. Levels of mRNA of FASN and liver parameters did not significantly change over time. Most significant correlations between adipose and liver tissue-related parameters were observed in wk4 compared to the other time-points. TNFα was not involved. In conclusion, TNFα is not a signaling factor that links adipose tissue and liver metabolism in healthy dairy cows. Other factors are responsible for the orchestrated regulation of adipose tissue and liver metabolism in wk4.

Key Words: dairy cow, adipose tissue, TNFα

M217 Early-weaning up-regulates the expression of sucrase-isomaltase in the jejunum of the piglet. D. Lackeyram*, T. Archbold, K. C. Swanson, and M. Z. Fan, *University of Guelph, Guelph, ON, Canada*.

Sucrase-isomaltase (SIM) is a small intestinal apical membrane disaccharidase that hydrolyses both sucrose and maltose. The objectives of this study were to examine the responses of SIM activity and protein abundances associated with the mucosal homogenate (H), intracellular soluble (S), and the apical membrane (M) fractions as well as SIM mRNA abundance and its regulation during early-weaning in comparison with suckling pigs. A total of 20 Yorkshire piglets, 10 suckling (SU) and 10 early-weaning (WN) with an average BW of 3 kg at the age of 10 d, were used in this study. Weanling piglets were fed a corn and SBM-based diet for 12 d. Proximal jejunal samples from both SU and WN groups were collected. Sucrose (0-25 mM) and maltose (0-60mM) were used in the enzymatic kinetic experiments. Abundances of SIM protein and mRNA were analyzed by Western blot and the real time RT-PCR using β-actin as the housekeeping gene. The jejunal SIM maximal specific activity (μmol/mg protein.min) for sucrose was increased (P<0.05) in weaning piglets (H: WN, 159.02±3.25 vs. SU, 76.72±2.89; S: WN, 16.42±1.28 vs. SU, 5.85±1.01; and M: WN, 141.39±3.84 vs. SU, 69.47±4.73). Similar increases (P<0.05) were observed for maltose (H: WN, 55.11±0.29 vs. SU, 40.79±0.81; S: WN, 17.81±0.24 vs. SU, 12.70±0.61; and M: WN, 516.51±1.05 vs. SU, 389.92±1.18). Corresponding increases (P<0.05) in the SIM protein abundance for the WN group was also observed in all of the jejunal fractions, H, 34%; S, 84%; M, 61%, respectively. Furthermore, early weaning increased (P<0.05) the relative abundance of SIM mRNA by 1.9 fold (WN, 0.306±0.03 vs. SU, 0.105±0.01). The increase in SIM mRNA could be accounted for by an increase (P<0.05) in the abundance (arbitrary units) of a key intestinal homeodomain transcription factor Cdx2 (WN, 2.365±0.01 vs. SU, 1.073±0.03). In conclusion, early-weaning increases small intestinal SIM activity at transcriptional, translational and post-translational levels.

Key Words: gene expression, sucrase-isomaltase, weanling pigs

M218 Effect of propionate infusion on hepatic PEPCK and glucose-6-phosphatase expression in neonatal Holstein calves. S. S. Donkin*, E. Cedeño, and S. L. Koser, *Purdue University, West Lafayette, IN*.

Cytosolic phosphoenolpyruvate carboxykinase (PEPCK), a rate-limiting enzyme for gluconeogenesis in liver, is sensitive to nutritional and hormonal cues. The objective of this experiment was to determine the effects of in vivo propionate supply on hepatic PEPCK mRNA expression. Sixteen male Holstein calves were blocked by birth date, and assigned to either: saline infusion (4 ml/min), propionate infusion (2 mmol/h/kg $BW^{.75}$), acetate infusion (3.5 mmol/h/kg $BW^{.75}$), or pre-treatment with phlorizin (100 mg at 8 h intervals for 24h) followed by propionate infusion. Blood samples were collected immediately prior to the initiation of infusion via indwelling jugular vein catheters and at hourly intervals during the 8 h infusion period. Liver biopsy samples were obtained immediately after the end of the 8 h infusion period and analyzed by real time PCR for pyruvate carboxylase (PC), PEPCK, glucose-6-phosphatase (G–6–Pase) and 18S mRNA. Abundance of PEPCK mRNA, relative to 18S was increased (P < 0.05) in response to propionate and acetate infusion (0.34 vs. 1.89 ± 0.24, arbitrary units). Propionate with phlorizin pretreatment did not alter PEPCK mRNA (0.34 vs. 0.69 ± 0.24, arbitrary units). Expression of PC mRNA was similar among all treatments. Abundance of G–6–Pase followed a pattern similar to PEPCK mRNA and was elevated (P < 0.05) for calves given acetate and propionate relative to saline control (0.82 vs. 2.70

and 2.32 ± 0.45, arbitrary units for control, acetate, and propionate, respectively). The data indicate that propionate modulates expression of PEPCK and G–6–Pase in vivo and extends our previous observations that propionate induces bovine PEPCK expression by direct activation of the PEPCK promoter. The action of propionate to induce PEPCK gene expression identifies a novel feed-forward response for gluconeogenesis in bovine that is modulated by substrate sensing to activate PEPCK and G-6-Pase expression and consequently enhance the capacity for hepatic gluconeogenesis and hepatic glucose release. *Supported by NRI Grant no. 2006–35206–16646 from the USDA CSREES.*

Key Words: propionate, liver, gene

M219 The Effects of supplemented diet with fish oil and canola oil during transition period to early lactation on follicular dynamics of Iranian Holstein dairy cows. T. S. Vafa, A. Heravi Mousavi*, A. Naserian, M. Danesh Mesgaran, R. Valizadeh, and A. Parand, *Excellent Center for Animal Science, Ferdowsi University of Mashhad*, *Iran*.

Increasing ration nutrient density is one of the strategies to improve nutrient intake in early lactation cows. For studying the effects of combination of fish oil and canola oil on follicular dynamics in early lactation, Holstein cows were randomly assigned in 1 of 2 treatments: 1) 0% oil (Control, n=9) and 2) 2% oil (FoCo, 1% fish oil plus 1% canola oil, n=9). Holstein cows were blocked in pairs based on their previous 305 d milk production, parity and expected calving. To monitor follicular parameters, ultrasound measurements of follicular activity were made on alternate days from days 10 – 45 postpartum (PP) to ascertain the characteristics and fate of the first follicular wave utilizing a 7.5-MHz rectal transducer. Dominant follicle development was characterized by follicular mapping of recorded ultrasound images. A dominant follicle was defined as a follicle that was >10 mm in diameter in the absence of other large (>9 mm) growing follicles. The data were analyzed using the General Linear Model procedure of SAS for a completely randomised design. Diameter of follicles (≥3.5 mm) on d 10 PP (p=0.007; 3.9 and 7.9 ± 0.88 mm, respectively) was significantly increased in the supplemented diet. Number of follicles (≥3.5 mm) on d 10 PP and 14 PP, diameter of follicles on d 14 PP, number of days until detection of a follicle ≥10 mm in diameter (p=0.13; 17.37 ± 2.27 and 12.44 ± 2.14 d, respectively), and diameter of first ovulatory follicle (p=0.13; 12.50 ± 0.13 and 14.37 ± 0.78 mm, respectively) were all similar between diets. Number of days to first ovulation (p=0.07; 28.83 ± 2.63 and 21.85 ± 2.44 d, respectively) was not affected by the dietary groups. Results of this study showed that the combination of fish oil and canola oil had no apparent effect on most follicular parameters and days postpartum to first ovulation.

Key Words: dairy cows, follicular dynamic, fish and canola oils

M220 The effects of supplemented diet with fish oil and canola oil during transition period to early lactation on complete blood count of Iranian Holstein dairy cows. T. S. Vafa, A. Heravi Mousavi*, A. Naserian, M. Danesh Mesgaran, and R. Valizadeh, *Excellent Center for Animal Science, Ferdowsi University of Mashhad*, *Iran*.

The study was designed to test the effect of including fish oil and canola oil from transition period to early lactation on immunology responses in Holstein dairy cows. Holstein cows were randomly assigned in 1 of 2 treatments: 1) 0% oil (control, n=9) and 2) 2% oil (supplemented, 1% fish oil-1% canola oil, n=9). Cows were blocked by parity, previous 305-2x milk production and expected calving time. Using vacutainer tubes, blood samples were collected weekly from -2 to 7 week relative to calving via venipuncture of coccygeal vessels before the morning feeding to monitor Complete Blood Count (CBC). The blood samples for CBC were kept in room temperature until analyzing for CBC. Complete blood counts were automatically determined with a hematology analyzer. The data repeated in time were analyzed by using a mixed model for a completely randomized design with repeated measures. The number of red blood cells (p=0.99; 5496900±133000 and 5495200 ± 132300 / µl, respectively), number of white blood cells (p=0.45; 6602±376.91 and 7008.68±373.07 /µl, respectively), hemoglobin (p=0.56; 8.15±0.20 and 7.98±0.20 g/dl, respectively), platelet (p=0.67; 349100±26010 and 333220±25720 /µl, respectively), hematocrit (p=0.65; 25.11±0.58 and 24.73±0.58%, respectively), number of lymphocyte (p=0.28; 3993±284 and 4448±302, respectively), number of monocytes (p=0.64; 1865±213 and 1718±130, respectively), number of neutrophil (p=0.067; 3944±180 and 3413±201, respectively), and number of eosinophil (p=0.32; 190±29 and 145±32, respectively) were similar between control and supplemented diets. The results of this study demonstrate that feeding a combination of fish oil and canola oil pre- and postpartum had no apparent effects on immunological parameter measured as total cell count.

Key Words: dairy cow, complete blood count, fish oil-canola oil

M221 Serum metabolomics of multiparous Holstein cows during the transition period. C. Chen, W. J. Weber, M. Carriquiry, S. C. Fahrenkrug, and B. A. Crooker*, *Department of Animal Science, University of Minnesota*, *St Paul*.

Transition from pregnancy to lactation is associated with dramatic alterations in metabolism that can significantly impact health, milk yield and reproductive performance. Advances in metabolomic techniques have improved the ability to monitor metabolic profiles and flux of small molecules in serum to define changes in metabolism on a global scale. Cows from control (stable milk yield since 1964; CL; n = 5) and select (contemporary; SL; n = 6) lines that differed in milk yield (6,200 and 11,100 kg milk/305 d) were fed ad libitum quantities of the same diets, milked 2X/d, and exposed to the same environment. Diets were fed as TMR composed primarily of legume-grass hay, corn silage, ground corn, and soybean meal, and were formulated to meet or exceed requirements. A dry cow diet (15.5% CP, 1.60 Mcal NEL/kg DM) was fed until calving and an early lactation diet (18.2% CP, 1.67 Mcal NEL/kg DM) was fed thereafter. Production results were analyzed by repeated measures analysis and means differed if $P < 0.05$. Deproteinized serum samples collected at -14, -7, 3, 14, 28 and 38 DIM were separated by ultra-performance liquid chromatography and ionized chemical components detected by a time-of-flight mass spectrometer. Mass, retention time, and intensity of serum ions was extracted from chromatograms and spectra and used to construct a multivariate model by principal components analysis. Chemical structures of serum ions were determined by accurate mass measurement and MS/MS fragmentation. The SL cows produced more FCM (29.5 vs. 45.6 ± 2.1 kg/d) during the first 42 DIM. Differences between pre- and postpartum serum samples were due mainly to dramatic postpartum increases in several lipid species, especially lysophosphatidylcholines. Differences between CL and SL cows were less striking. Overall, this study demonstrated that serum metabolomics can serve as a useful tool to investigate the underlying mechanisms of lactation-induced metabolic changes.

Key Words: metabolomics, serum

M222 Effects of heat stress on ghrelin secretion in lactating dairy cattle. S. E. Cossel*, M. E. Field, M. V. Skrzypek, S. R. Sanders, S. L. Marion, J. B. Wheelock, S. R. Hartman, Y. Yuxi, P. B. Hoyer, R. J. Collier, R. P. Rhoads, L. H. Baumgard, and M. L. Rhoads, *University of Arizona*, *Tucson*.

The effects of heat stress on ghrelin, a potent regulator of feed intake and whole-body metabolism, was evaluated in two studies using lactating dairy cattle. In experiment 1, eight lactating Holstein dairy cows (90.0 ± 1.7 DIM; 566.48 ± 19.55 kg BW) were housed in environmentally controlled chambers and subjected to a thermal neutral (TN; 20.22 °C and 51.23% humidity) period for 2 days followed by a heat stress (HS; 35.34°C and 21.99% humidity) period for 3 days. On the final day of each period, blood samples were taken peri-prandially every 20 minutes beginning 2 hours prior to the morning feeding and ending 4 hours after the morning feeding. Plasma was harvested and stored at -20°C for assay of ghrelin concentrations. Vaginal temperatures, taken by intra-vaginal thermal dataloggers, increased during the HS period (38.61 ± 0.17 vs. 37.81 ± 0.17°C; $P<0.05$) while feed intake was lower on the HS sampling date (35.1 ± 1.7 vs. 39.6 ± 1.7 kg; $P<0.01$). Plasma ghrelin concentrations were affected by treatment ($P<0.05$) and time ($P<0.01$). Compared to TN, HS increased plasma ghrelin concentrations (234.97 ± 26.31 vs. 259.05 ± 26.32 pg/ml, respectively) and plasma ghrelin concentrations were greater during the pre-prandial period than the post-prandial period. In experiment 2, three lactating Holstein dairy cows were housed in environmentally controlled chambers and subjected to a TN period for 11 days followed by a HS period for 9 days. Plasma ghrelin concentrations were measured on day 8 of each period beginning 5 hours prior to the afternoon feeding and ending 1.5 hours prior to the afternoon feeding. Plasma ghrelin concentrations did not differ between treatments and were not affected by time. These results indicate that heat stress increases plasma ghrelin concentrations, but that measurable changes in ghrelin secretion are limited to the peri-prandial period.

Key Words: ghrelin, heat stress, dairy

M223 Plant oil supplementation in dietary concentrate improves milk yield, ovarian function and uterine health of postpartum dairy cows in a tropical environment. C. Navanukraw*, A. Boonsom, S. Guntaprom, S. Uriyapongson, and C. Wachirapakorn, *Khon Kaen University*, *Khon Kaen, Thailand*.

Thirty, Holstein Friesian, prepartum multiparous cows were randomly allocated to one of 3 treatments according to RCBD as follows; control (no supplement), 4% palm oil supplement, and 4% sunflower oil supplement. All cows were fed ad libitum of roughage and dietary concentrate 4 wk prior to parturition and 4 wk postpartum to meet requirements for lactating cows. Following parturition, milk yields, ovarian follicular dynamics and uterine health were monitored along with plasma concentrations of progesterone. Milk yields of cows fed palm and sunflower oil supplements were greater than that of control cows (23.8, 22.8 and 18.1 kg/d respectively, $P<0.05$). Numbers of small (3-5 mm) and large (≥10 mm) follicles of cows fed oil supplements were greater than those of control cows ($P<0.05$). Cows supplemented with sunflower oil had a lesser uterine score than control and cows supplemented with palm oil (1.4, 2.0 and 2.0; $P<0.05$). Uterine involution time and the first estrus postpartum of cows fed oil supplements occurred sooner ($P<0.01$) than control cows (42.0 and 56.4 days for cows fed palm oil; 32.2 and 50.2 days for cows fed sunflower oil; and 50.4 and 91.8 days for control cows). Cows fed oil supplements also had increased ($P<0.05$) progesterone concentrations since 3 wk after parturition. This study highlights the strategy of nutritional management of reproduction in pre- and postpartum dairy cows. *Supported by NRCT-50 to CN.*

Key Words: plant oil, ovarian follicular dynamics, uterine health

M224 Hematological profile of confined ewes fed corn silage. J. P. F. Silveira[1], J. L. C. B. Reis*[2], M. A. Factori[1], D. H. Vieira[3], V. L. Tierzo[1], L. F. D. Medeiros[1], and C. Costa[4], [1]*São Paulo State University*, *Botucatu, SP, Brazil*, [2]*University of Agrarian Sciences - University of Marília*, *Marília, SP, Brazil*, [3]*Center of Creation of Animals of Laboratory*, *Rio de Janeiro, RJ, Brazil*, [4]*Rural Federal university of Rio de Janeiro*, *Seropedica, RJ, Brazil*.

Hematological evaluation is considered an important tool for animal health analysis. This work was carried out to determine the hematological profile of animals confined in metabolic chambers. Twenty-four Santa Inês lambs having an average age of three months and an average initial weight of 25 kg were used. The experimental design was completely randomized, in a 2 x 2 factorial scheme (two corn hybrid, dent and flint; and two corn mass ensilage processing, present and absentee). Blood samples were collected after 27 days of confinement. Data were analysed by a two-way analysis of variance. Tukey's multiple test was used to determine differences due to corn hybrid and process. Differences were considered significant at the 0.05 probability level. Erythrocyte number (ERIT), hematocrit percentage (HTC) and hemoglobin rate (HB) were determined. Mean corpuscular volume (MCV) and mean corpuscular hemoglobin concentration (MCHC) were calculated. ERIT and MCV were significantly different among treatments. The highest ERIT and the lowest MCV were determined for animals fed flint no process diet. The lowest ERIT number and the highest MCV were determined for animals fed process dent diet. The animals fed process dent diet showed also the highest EPG. HTC, HB and MCHC did not differ among treatments. Confinement may have determined ERIT statistics difference since diets were formulated to reach the species nutritional requirement. The 27-day confinement determined alterations on sheep hematological profile.

Key Words: hematology, nutrition, physiological evaluation

M225 Effects of lactation and pregnancy on metabolic and hormonal responses of Holstein dairy cattle. I. M. Thompson*[1], R. L. Cerri[1], I. H. Kim[2], A. D. Ealy[1], P. J. Hansen[1], C. R. Staples[1], and W. W. Thatcher[1], [1]*University of Florida*, *Gainesville*, [2]*Chungbuk National University*, *South Korea*.

Objectives were to develop and characterize an experimental platform to evaluate lactation and pregnancy effects for subsequent analyses of the endometrial trancriptome in dairy cattle. Pregnant heifers (n=34) were assigned randomly after calving to a lactating group (LG, n=17) and a non-lactating group (NLG, n=17). The LG was fed a TMR (1.65Mcal NEL/kg, 16.5% CP) ad libitum. The NLG was fed a maintenance ration (1.45 Mcal NEL/kg, 12.2% CP) once per day. Rectal temperatures and blood, for analyses of progesterone and metabolites, were collected thrice weekly. Ovarian ultrasonography and BW measurements were performed weekly. BCS was measured every 14 d. All cows were pre-synchronized and enrolled in a timed(T)-AI protocol (Presynch/5 d CIDRSynch), but only 10 in the LG and 12 in the NLG were TAI. On d 17 after GnRH/TAI, all cows were slaughtered and endometrial, conceptus, oviductal and ovarian tissues collected. Temporal changes in BCS, BW, and rectal temperature did not differ between LG and NLG.

NLG cycled earlier than LG (26.3<34.7d postpartum; P<0.04) Mean plasma concentrations of NEFA postpartum did not differ between NLG and LG (236 vs 204 mEq/L); although NLG>LG in week one (573>276 mEq/L; P<0.01). Cows in LG had greater (P<0.01) plasma concentrations of BHBA (4.98>2.94 μg/mL) and BUN (11.65>6.5 mg/dL) than NLG. Glucose in plasma was lower (P < 0.01) for LG (74<80 mg/dL). Plasma progesterone from GnRH or TAI (d 0) until d 17 was lower for LG due to a lower progesterone concentration in pregnant than cyclic cows versus no difference between cyclic and pregnant of NLG (LactationxPregnantxDay; P<0.05). In conclusion, lactation\diet altered metabolic status even though BW and BCS were the same between LG and NLG. Lactation delayed initiation of cyclicity and tended to lower concentrations of progesterone in pregnant cows during a programmed period following an induced ovulation.

Key Words: lactation, metabolites, progesterone

M226 Does a low feeding level enhance estradiol synthesis in preovulatory follicles of Holstein × Normande dairy cows? E. Cutullic*[1], A. Benhaim[2], S. Barbey[3], H. Mitre[2], S. Carreau[2], and C. Disenhaus[1], [1]*UMR1080 INRA Dairy Production, Rennes, France*, [2]*INRA USC2006, Estrogen and Reproduction, Caen, France*, [3]*INRA UE326 Le Pin-au-Haras, Exmes, France*.

Enhanced estrus expression has been reported for feeding strategies which limit milk yield. The objective of this study was to evaluate 17β-estradiol (E2) in preovulatory follicles of cows submitted to 2 feeding levels. Holstein x Normande crossbred dairy cows were fed a total mixed ration composed either of 55% maize silage, 15% alfalfa hay and 30% concentrate (Control: C-group, N=7) or of 60% grass silage and 40% hay (L-group, N=8). Milk progesterone profiles were used to follow cyclic activity from calving to slaughter (85±6 days postpartum). Cows were synchronized by two prostaglandin-F2α analogue injections and slaughtered 40 hours after the 2nd one. Ovaries were collected. Follicular fluid (FF) from dominant follicles (DF, diameter>12 mm) was separated from granulosa cells (GC) by centrifugation. E2 concentration was measured in FF by RIA. In GC, aromatase activity (AA) was determined by the tritiated-water method and aromatase mRNAs (A-mRNA) were quantified by RT-PCR. L-group cows produced less 11-week average daily milk yield (MY) even though they lost more body condition (BC) from calving to slaughter than C-group (20.5 vs. 34.5kg/day; -0.66 vs. -0.20 unit; P<0.001). Seven cows were well synchronized. E2 concentration in FF was highly correlated to ln(AA) (r=0.98; P<0.001) and A-mRNA (r=0.92; P<0.05). L-group tended to have higher FF E2 concentration and AA than C-group (5699 vs. 960 ng/mL, 3106 vs. 295 fmol/h/mg protein, N=4 and 3, P<0.10). In regard to the literature and to some preliminary results (N=8, 33.4 kg/day MY, -0.33 unit BC loss, 524 ng/mL FF E2), FF E2 of the L-group appeared very high. More investigations are needed both to confirm this feeding level effect and to determine if it could be due to production or to nutritional restrictions.

Key Words: estradiol, aromatase, dairy cows

M227 Serum and anterior pituitary gland (AP) concentrations of IGF-I during an estradiol induced LH surge in gilts. N. M. Rasmussen*, C. E. Hostetler, and J. A. Clapper, *South Dakota State University*, *Brookings*.

Increasing serum concentrations of estradiol are known to trigger the LH surge in gilts. Administration of estradiol has been shown to increase serum and anterior pituitary gland (AP) concentrations of IGF-I in barrows. However, whether this occurs in gilts during the preovulatory LH surge has not been determined. Therefore, the objective of this experiment was to determine if serum and AP concentrations of IGF-I increase in response to an estradiol induced LH surge in ovariectomized gilts. Twelve crossbred gilts of similar weight (123 kg) were ovariectomized and assigned to either control (C; n=6) or estradiol (E; n=6) groups. E pigs received 2.5 mg estradiol in corn oil i.m. while C pigs received an equal volume of corn oil i.m. on d 0. Blood samples were obtained by jugular venipuncture on d 0, 1, and 2. Pigs were slaughtered on d 3 when blood and AP were collected. Serum and AP concentrations of LH and IGF-I were determined in duplicate by RIA. Differences in serum and AP concentrations of LH and IGF-I were determined using the Proc Mixed procedure of SAS. Serum concentrations of LH were not different (P>.05) in C and E pigs on d 0. Serum concentrations of LH decreased (P<.05) in E pigs compared to C pigs on d 1, but were not different (P>.05) than C pigs on d 2 and 3. Serum concentrations of LH in C pigs were not different (P>.05) from d 0 through d 3. Serum concentrations of IGF-I were not different (P>.05) between C and E pigs on d 0, but by d 3 serum concentrations of IGF-I were greater (P<.05) in E pigs than C pigs. AP concentrations of LH did not differ (P>.05) between C and E pigs, however, AP concentrations of IGF-I tended (P=.09) to be greater in E pigs than C pigs. These preliminary data suggest that serum and AP concentrations of IGF-I may increase during the preovulatory LH surge in gilts.

Key Words: pigs, IGF-I, LH

M228 Influence of heifer development method on post-AI blood metabolites. B. L. Perry*, J. A. Walker, C. L. Wright, K. C. Olson, and G. A. Perry, *Dept. Anim. and Range Sci., South Dakota State University*, *Brookings*.

Method of heifer development has been reported to have influenced pregnancy success. Therefore, the objective of the current study was to evaluate differences in plasma glucose and urea nitrogen (PUN) concentrations following AI between heifers developed in a feedlot or on grass and turned to grass immediately following AI. Weaned heifers were developed from weaning to breeding either in a feedlot (n=52; LOT) or on grass (n=53; GRASS). Immediately following fixed-time AI all heifers were moved to the same pasture. Blood samples were collected from all heifers on d -23, -9, the day of AI (d 0), and d 11. Pregnancy success was determined 42 d following AI. There tended (*P*=0.10) to be more LOT heifers cycling prior to the breeding season (94% vs 84%), but no difference (*P*=0.20) between GRASS and LOT in pregnancy success (57% vs. 44%). There were effects of development (*P*<0.01), time (*P*<0.01), and development by time (*P*=0.02) on glucose concentrations. Glucose concentrations decreased from d 0 to d 11 in both groups. Glucose was greater (*P*<0.01) in GRASS compared to LOT heifers (*P*<0.01; 87.3 ± 1.24 and 80.2 ± 1.25 mg/dL) on d 0 but similar (*P*=0.43; 76.29 ± 1.24 and 74.9 ± 1.24 mg/dL) on d 11. Pregnant heifers had greater glucose than open heifers on d 11 (*P*= 0.04; 77.4 ± 1.24 and 73.8 ± 1.24 mg/dL) but not on d 0 (*P*=0.88). Concentrations of PUN were influenced by development (*P*<0.01) and time (*P*<0.01). Concentrations increased from d 0 to 11, and were greater in GRASS (12.9 ± 0.22 and 15.1 ± 0.22 mg/dL) compared to LOT (11.8 ± 0.22 and 13.6 ± 0.22 mg/dL) heifers. There tended (*P*=0.07) to be a development by pregnancy interaction with similar (*P*=0.54) PUN concentrations between LOT pregnant and open heifers, but greater (*P*=0.04) concentrations in GRASS open compared to GRASS pregnant heifers. Method of heifer development (LOT or GRASS) influenced both glucose and

PUN concentrations with GRASS heifer having greater glucose and PUN concentrations compared to LOT heifers, and pregnant heifers tended to have greater glucose than open heifers.

Key Words: glucose, PUN, heifer development

M229 Relationships between dry matter intake (DMI), plasma progesterone (P4), and liver catabolic enzymes in lactating dairy cows. O. G. Sa Filho*[1,3], C. O. Lemley[2], M. E. Wilson[2], J. Hillegass[3], J. L. M. Vasconcelos[1], and W. R. Butler[3], [1]*FMVZ/UNESP, Botucatu, SP, Brazil*, [2]*West Virginia University, Morgantown*, [3]*Cornell University, Ithaca, NY*.

Increased liver blood flow in response to high DMI has been reported to increase steroid metabolism in lactating dairy cows, but little information exists on the regulation of steroid catabolic enzymes. The aim of this study was to evaluate the relationships between DMI, milk production, P4, ovarian structures, and hepatic catabolic enzymes. Day of ovulation was synchronized in lactating Holstein cows with the Ovsynch protocol and only cows that ovulated in response to GnRH treatment (d 0) were used (n=18). We evaluated the relationships between DMI (range 16-31 Kg/d), milk production (MP), follicle diameter (FD) on d 0, corpus luteum volume (CLV) and P4 on d 7, and progesterone catabolic enzymes cytochrome P450 2C (CYP2C) and 3A (CYP3A) activity (measured as the isoform specific substrate dependant oxidation of NADPH) from liver biopsy samples collected on d 7. Total enzyme activity (TEA) was calculated as sum of the activities of CYP2C and CYP3A. The ratio P4/CLV was used as a relative measure of P4 production and liver catabolic activity. Data were analyzed by PROC GLM of SAS. The DMI positively affected (P<0.05) MP (MP=2.6+1.9•DMI; r2=0.47), FD (FD=3.1+0.4•DMI; r2=0.34), and CLV (CLV=913.7+366.5•DMI; r2=0.33). Despite the positive effect on CLV, DMI had negative effects (P<0.05) on P4 (P4=7.2-0.1•DMI; r2=0.27) and on the ratio P4/CLV (P4/CLV=0.0015-0.000042•DMI; r2=0.5). Plasma P4 was negatively affected by CYP2C (P4=2.7-0.3•CYP2C; r2=0.4; P<0.05) and tended to be negatively affected by CYP3A (P4=2.0-0.04•CYP3A; r2=0.24; P=0.1) and TEA (P4=2.0-0.02•TEA; r2=0.29; P<0.1). The P4/CLV ratio was negatively affected by CYP2C (P4/CLV=0.0008-0.00043•CYP2C; r2=0.36; P<0.05) and tended to be negatively affected by TEA (P4/CLV=0.00059-0.000012•TEA; r2=0.29; P<0.1), whereas no effects of CYP3A or mRNA for the enzymes were found. In conclusion, higher DMI and liver catabolic enzymes in lactating dairy cows were related to decreased plasma P4 concentration.

Key Words: DMI, progesterone, catabolic enzymes

M230 Method development and preliminary evaluation of the potential for using erythrocyte membranes in the assessment of long-chain polyunsaturated fatty acid status in dairy cows. C. L. Preseault*[1,2], J. Kraft[1], H. M. Dann[2], and A. L. Lock[1], [1]*University of Vermont, Burlington, VT*, [2]*William H. Miner Agricultural Research Institute, Chazy, NY*.

Due to the limited availability of long-chain polyunsaturated fatty acids (LCPUFA) leaving the rumen, recent observations suggest that the modern high producing dairy cow may, under certain situations, be deficient in these fatty acids (FA). Erythrocyte membrane (EM) FA profile has been used previously in human studies to assess long term FA intakes, and can therefore possibly be used as a marker for LCPUFA status. The objectives of this work were to develop methods and undertake a preliminary examination of the potential for using EM-FA profile in the evaluation of LCPUFA status of dairy cows. Whole blood was collected from 53 Holstein cows at 5 stages of the lactation cycle (far-off dry, close-up dry, early lactation, mid lactation, and late lactation). After isolation and purification of the EM, total lipids were extracted and FA methyl esters prepared and purified by thin-layer chromatography. FA composition was determined by gas-liquid chromatography. Significant differences in the concentration (g/100g FA) of all reported FA was observed across the 5 stages. Late lactation cows were highest in C18:2 n-6 (31.29; *P*<0.01) whereas far-off dry cows were highest in C18:3 n-3 (0.81; *P*<0.01). C20:4 n-6 and C20:5 n-3 were highest in the close-up group (4.17 and 0.21; *P*<0.001 and P<0.05, respectively). Both dry cow groups had higher levels of C22:5 n-3 (*P*<0.001) than lactating cows. This preliminary evaluation highlights potential differences in LCPUFA status of cows at different stages of the lactation cycle and may help determine the efficacy of nutritional strategies aimed at improving LCPUFA status.

Table 1. Selected LCPUFA of EM in dairy cows at defined stages of the lactation cycle.

FA (g/100g)	Far-Off Dry Cows (n=10)	Close-Up Dry Cows (n=6)	Early Lactation Cows (n=12)	Mid Lactation Cows (n=12)	Late Lactation Cows (n=13)	SEM	*P*-value
C18:2 n-6	27.03^{b}	27.88^{ab}	24.80^{b}	27.88^{b}	31.29^{a}	1.73	<0.01
C20:4 n-6	3.86^{a}	4.17^{a}	2.52^{bc}	2.24^{c}	3.00^{b}	0.37	<0.001
C18:3 n-3	0.81^{a}	0.74^{ab}	0.58^{bc}	0.56^{c}	0.57^{bc}	0.07	<0.01
C20:5 n-3	0.10^{b}	0.21^{a}	0.13^{b}	0.09^{b}	0.11^{b}	0.03	<0.05
C22:5 n-3	0.36^{a}	0.46^{a}	0.09^{b}	0.09^{b}	0.18^{b}	0.06	<0.001

^{a,b,c} *P*<0.05.

Key Words: dairy cows, long-chain polyunsaturated fatty acids, erythrocyte membrane

M231 Effects of BCS and level of concentrate feeding during early lactation on plasma concentrations of blood metabolites in pasture–fed dairy cows. F. Y. Obese*[1,2], T. E. Stirling[3], C. R. Stockdale[4], K. L. Macmillan[3], A. R. Egan[2], and S. Humphrys[5], [1]*CSIR-Animal Research Institute, Accra, Ghana*, [2]*School of Agriculture and Food Systems, the University of Melbourne, Melbourne, Victoria, Australia*, [3]*School of Veterinary Science, the University of Melbourne, Werribee, Victoria, Australia*, [4]*Department of Primary Industries, Kyabram, Victoria, Australia*, [5]*Primegro Pty Ltd, Thebarton, South Australia, Australia*.

The objective of this research was to assess the effects of body condition score (BCS) at calving and level of supplementation on insulin-like growth factor-I (IGF–I), betahydroxybutyrate (BHB), non-esterified fatty acids (NEFA) and urea concentrations in Holstein cows in a pasture-based system. Concentrations of IGF-I in cows that had commenced estrous cycle were compared with that of cows that were anestrus at the start of the breeding program. Cows (n=72) were managed over a period of 5 months to calve in BCS of 4, 5 or 6 using a scale from 1 (thin) to 8 (obese). They grazed pasture and were supplemented in early lactation with either 1 or 6 kg of grain per day. Calving BCS affected NEFA and BHB concentrations at Week 0 (calving). The concentrations were higher in cows with BCS 6 than BCS 4 with respect to NEFA (1.23 ± 0.11 vs 0.84 ± 0.11 mmol/L; P=0.022) and BHB (0.61 ± 0.04 vs 0.38 ± 0.04 mmol/L; P<0.001). These effects had diminished by Week 10 postcalving. Plasma concentrations of IGF-I at Week 10 were increased with the higher level (6 kg) of grain feeding (87.8 ±

4.7 vs 72.1 ± 4.7 ng/mL; P = 0.022) whereas urea concentrations were decreased (5.16 ± 0.21 vs 4.11 ± 0.21 mmol/L; P = 0.001). Cows that had commenced estrous cycles by the start of the AI program had higher plasma concentrations of IGF-I than anestrous cows at Week 0 (56.5 ± 3.8 vs 39.8 ± 4.1 ng/mL; P=0.009) and Week 10 (87.3 ± 4.2 vs 64.5 ± 4.3 ng/ml; P=0.001). These results suggest an association between plasma concentrations of IGF–I and resumption of ovarian function in pasture-fed Holstein-Friesian cows.

Key Words: anestrus, blood metabolite, body condition

M232 Metabolic profile of the hypocalcemic dairy cows in an intensive grazing system in south of Brazil. E. Schmitt*[1,2], D. A. C. Hoffmann[1], M. E. Lima[1], T. dos S. Farofa[1], M. A. Goulart[1], M. S. Lopes[1], P. Montagner[1], R. T. França[1], F. A. B Del Pino[1], J. J. Loor[2], and M. N. Corrêa[1], [1]*Federal University of Pelotas, Pelotas, RS, Brazil*, [2]*University of Illinois, Urbana*.

Some dairy farms in the south of Brazil rely on intensive grazing due to low cost of this practice. This nutritional management system without supplementation of grain could increase the risk of periparturient clinical and subclinical problems. We used 13 crossbred Jersey cows grazing tropical pastures to research blood metabolic profiles during the transition period emphasizing subclinical hypocalcemia. During -22 and 22 DIM, every 2 d blood was collected from the coccygeal vein to measure concentrations of calcium, magnesium, phosphorus, chlorides, glucose, insulin, glucagon, NEFA, aspartate aminotransferase (AST), and gamma-glutamyl-transferase. Cows were retrospectively divided into a hypocalcemic (HYP, n = 5) and normocalcemic (NOR, n = 8) group (total calcium < 8 mg/dL >) prior to statistical analysis. Average milk yield for the first 3-wk postpartum was higher (P <0.01) for HYP cows (14.4 vs. 10.7 L/d). These cows had higher (interaction P <0.05) calcium at -12 and lower calcium at 4 DIM. Glucose concentration also was higher (interaction P < 0.05) prepartum (-14 DIM) and lower postpartum (16 DIM) than NOR cows. The HYP cows had higher levels (interaction P < 0.05) of AST (6 DMI), NEFA (0, 4 and 10 DIM), glucagon (6, 10, 18, 20 and 22 DIM) and glucagon:insulin (6 and 20 DIM). Other variables were not different between groups. Results indicate that high milk production potential, in particular, is related to the incidence of subclinical hypocalcemia in cows grazing tropical pastures. These animals might be at higher risk of development other disorders in the transition period due to the more sever negative energy balance.

Key Words: hypocalcemia, energy balance, transition period

M233 A comparison of physiological and endocrine parameters during the periestrual period in lactating dairy cows that did and did not conceive. A. K. Sanders*[1], D. Ray[1], C. H. Hamilton[1], C. Tritsch[1], M. E. Risley[2], M. F. Smith[2], and W. J. Silvia[1], [1]*University of Kentucky, Lexington*, [2]*University of Missouri, Columbia*.

Reproductive physiological and endocrine parameters during the first periestrual period postpartum were compared in lactating dairy cows that conceived versus those that did not. Holstein (n=48) and Holstein X Jersey crossbred (n=7) cows were used in the experiment. A modified Ovsynch protocol was initiated 52 to 94 days postpartum (100 ug GnRH, i.m., Factrel, Fort Dodge Animal Health). Seven days later (day 0), two injections of prostaglandin (PG) F2a (25 mg, i.m., Lutalyse, Pfizer Animal Health) were administered, 12 h apart, to induce luteolysis. The ovaries were examined ultrasonographically 2x daily beginning on day 0. Blood samples were collected at 6-h intervals for quantification of estradiol-17b. On day 2, the frequency of sample collection was increased to every 2 h for quantification of LH. Beginning on day 2, cows were observed for estrus behavior at 4-h intervals. For each cow, 27 variables were calculated from the data collected. These included the timing and magnitude of estradiol-17b and LH secretion, time of onset, intensity and duration of estrus, maximum follicle diameter, time of ovulation and intervals from onset of estrus to peak of LH and ovulation. Preovulatory surges of LH and ovulation were observed in 31 cows. Differences between cows that conceived (n=13) and those that did not (n=18) for each variable were examined by t-test. Estrus began at 74.4 h after PGF2a and lasted for 12.6 h. Peak LH occurred at 77.3 h. Ovulation occurred at 104.1 h, 25.7 h after peak LH. Peak concentration of estradiol-17b occurred at 75.8 h and averaged 2.6 pg/ml. The diameter of the preovulatory follicle was 15.4 mm. None of these variables were different between cows that conceived and those that did not (p > 0.2). The interval from onset of estrus to peak LH tended to be different between groups (p = 0.08) (4.7 h in cows that conceived, 1.6 h in cows that did not). The impact of this asynchrony in time of estrus relative to peak LH on fertility remains to be determined. *Supported by the KY Agr Expt Stn and USDA NRI-CGP 2006-35203-17133.*

Key Words: dairy cow, conception, estrus

M234 Plant-based diets enriched with linseed oil or marine algae and organic selenium alter reproductive performances of broiler breeder hens over the reproductive season. C. Brèque*[1,2], C. Coss[1,2], C. Lessard[1,2], R. Gervais[2], D. Venne[3], M. R. Lefrançois[2], P. Y. Chouinard[2], G. Vandenberg[2], and J. L. Bailey[1,2], [1]*Centre de recherche en biologie de la reproduction, Québec, QC, Canada*, [2]*Département des Sciences Animales, Québec, QC, Canada*, [3]*Couvoir Scott Ltée, Scott Jonction, QC, Canada*.

There are indications that plant-based diets and organic (org) Se alter fertility in broiler breeders. We hypothesised that supplementing plant-based diets with n-3 fatty acids and org Se may improve female reproductive parameters. Individually caged, 23-week (wk) old female broiler breeders were fed 8 diets (n=50/diet). The control diet contained meat meal + 50 IU/kg vit E (MM50), while the others were plant-based: 2.3% soya oil + 50 IU/kg vit E (SO50), 2.3% soya oil + 100 IU/kg vit E (SO100), 2.3% soya oil + 100 IU/kg vit E + 0.3 ppm org Se (SO100Se), 2.3% linseed oil + 100 IU/kg vit E (LO100), 2.3% linseed oil + 100 IU/kg vit E + 0.3 ppm org Se (LO100Se), 1% marine algae (42% oil) + 100 IU/kg vit E (MA100), and 1% marine algae + 100 IU/kg vit E + 0.3 ppm org Se (MA100Se). Hens were inseminated at 41-46 wk and 55-60 wk of age at 3 wk intervals. Insemination doses from pooled ejaculates from males fed the same diets were standardized to $100x10^6$ spz/hen and repeated on 2 consecutive days. Overall fertility rates (F), hatchability (H) and embryo mortality (early: EEM, intermediate: IEM and late: LEM) were estimated. Data were analysed as a completely randomized design. Regardless of the insemination period, LO diets had the best overall F (P<0.05). However, after the first inseminations, H was higher in SO50 and SO100, whereas F was highest after the second inseminations for SO100Se (P<0.05). Dietary MA increased EM and reduced F and H at both periods (P<0.05). Org Se as replacement for inorganic Se in plant-based diets decreased EEM (wk 41-46) and IEM (wk 55-60) but had adverse effects on LEM (both periods) (P<0.05). Supplementing plant-based diets with LO provides insight towards improving the reproductive performances of broiler breeder hens but research is needed to elucidate the role of org Se.

Key Words: broiler breeder, fertility, hatchability

M235 Temporal changes in hepatic gene expression during the periparturient period of spring-calving beef cows on grazing conditions. A. L. Astessiano*[1], R. Perez-Clariget[1], G. Quintans[2], P. Soca[1], B. A. Crooker[3], and M. Carriquiry[1], [1]*School of Agronomy, UDELAR, Uruguay*, [2]*INIA, Treinta y Tres, Uruguay*, [3]*Department of Animal Science, University of Minnesota, St. Paul*.

Primiparous crossbred (Hereford/Angus; n=10) were used in a randomized block design, to study effects of day postpartum (DPP) on hepatic gene expression during the periparturient period. Cows grazed together on a native pasture paddock (60 ha) with an average forage mass available of 453 kg DM/ha (13.2% CP and 24.4% ADF). Milk yield was measured at 14 and 35±4 DPP and liver biopsies obtained at -11, 7, 31, and 52 DPP. The amount of mRNA for growth hormone receptor (GHR), GHR-1A, insulin-like growth factor-I (IGF-I), IGF binding proteins-2 (BP2),-3 (BP3), and an endogenous control (hypoxanthine phosphori bosyltransferase;(HPRT) were measured by real time RT-PCR. Means from a repeated measures analysis differed when P<0.05. Cows lost 1.25 units of body condition score (BCS,scale 1-8) during the last 60 d of gestation, calved with a BCS of 3.7 ±0.08 units, and lost only 0.25 units during the first 60 DPP. Milk yield tended (*P=0.07*) to decrease from 6.3 to 5.5±0.4 kg/d from 14 to 35 DPP, but this decrease was evident only in cows that calved with BCS≤3.5. Abundance of HPRT mRNA was not affected by DPP or BCS at calving. Relative amounts of GHR mRNA reached nadir at 7 DPP, and increased thereafter until 52 DPP, but there was no effect of DPP on amounts GHR-1A pr IGF-I mRNA amounts. However, when BCS at calving was considered in the analysis, mRNA expression of GHR1A and IGF-I tended (*P<0.10*) to increase for cows with BCS≤3.5 but tended to decrease for cows with BCS>3.5 from -11 to 52 DPP. Although BP2 and BP3 mRNA relative amounts were not affected by DPP, BP2/BP3 mRNA ratio tended (*P=0.11*) to decrease from -11 to 52 DPP and BP2 mRNA was greater for cows with BCS≤3.5 at calving. Hepatic expression of genes associated with GH-IGF the axis were affected during the periparturient period in spring-calving beef cows under grazing conditions and tended to be modulated by BCS at calving.

Key Words: liver, somatotropic axis

M236 Effect of short-term prepartum supplementation on reproduction of multiparous beef cows on grazing conditions. G. Quintans*[1], G. Banchero[1], G. Roig[1], and M. Carriquiry[2], [1]*INIA, Treinta y Tres, Uruguay*, [2]*School of Agronomy, UDELAR, Uruguay*.

Multiparous Aberdeen Angus x Hereford crossbred cows were used to evaluate the effect of supplementation during the last month of gestation on reproductive performance. Cows were ranked by body weight (BW) and body condition score (BCS, scale 1-8) and assigned randomly to supplement (SUP; n=18) or control (CON; n=17) treatments. Supplemented cows were offered (1 kg/100 kg BW) a mix (67:33% as-fed basis; 16% CP, 11% ADF) of sorghum grain and protein concentrated from 33±1.4 d prepartum until calving. Before, during, and after the supplementation period, cows grazed together a native pasture paddock with an average forage mass available of 1345 kg DM/ha (10.4% CP, 45.2% ADF). The breeding season (BS) started at 60 d postpartum (DPP) and lasted 60 d. Means were considered to differed when *P*<0.05. Cow BCS at calving and at the onset of the BS were, respectively, 0.25 and 0.5 units greater for SUP than CON cows. Plasma NEFA concentrations during the last month of gestation were reduced for SUP cows (0.81 vs 0.66±0.05 mEq/L for CON and SUP cows, respectively) but there were no differences between treatments in plasma NEFA during the postpartum. The maximum follicle diameter at the beginning of the BS did not differ between treatments (10.8±0.7 mm); however, the probability of cows presenting follicles with diameter≥10 mm was greater for SUP than CON cows (77 vs 55%). Days to first ovulation did not differ between treatments and averaged 80±1.4 DPP. The incidence of anovulation at the beginning of the BS did not differ between treatments but the probability of cows cycling during the first 90 DPP tended (*P*=0.084) to be greater for SUP than CON cows (83 vs 65%). The interval beginning of BS-conception did not differ between treatments but final pregnancy rate tended (*P*=0.082) to be greater in SUP than CON cows (100 vs 88%). Supplementation during the last month of gestation could benefit reproductive performance of spring calving-beef cows on grazing conditions.

Key Words: prepartum supplementation, reproduction

M237 Endocrine and reproductive parameters of North American Holstein × New Zealand Holstein-Friesian crossbred cows on grazing conditions. A. Fernandez-Foren*[1], M. Carriquiry[2], V. Artegoitia[1], D. Laborde[3], and A. Meikle[1], [1]*Veterinary School, UDELAR, Uruguay*, [2]*School of Agronomy, UDELAR, Uruguay*, [3]*Private consultant, Uruguay*.

The aim of this work was to study endocrine and reproductive parameters in North American Holstein (NAH) and NAH x New Zealand Holstein-Friesian crossbred (NAxNZ) multiparous cows on grazing conditions. Cows (n=50) were blocked by calving date, body condition score (BCS) at calving, lactation number (3 or 4), and economic value of milk (New Zealand selection index). All cows grazed on the same implanted pasture (legume-grass mix; 14.5 kg DM/cow/d of assigned forage) and were supplemented with 5.1 kg DM/d of corn whole-plant silage, 3.8 kg DM/d of high moisture sorghum silage and 6.3 kg DM/d of concentrate (corn grain, wheat middling, barley grain and sunflower meal). Days to first ovulation were determined as days to plasma progesterone concentrations >1 ng/ml). Means from repeated measure analysis differed when *P*<0.05. Body weight (BW) for NAH was 33 ± 6 kg greater than for NAxNZ cows along the period evaluated (calving to 140 days postpartum, DPP). Cow BCS tended (*P*=0.10) to be greater for NAH cows, but this was due to a greater BCS at calving. Both groups lost 0.7 ± 0.06 units, reached BCS nadir at 35 DPP, and at 140 DPP had not returned to BCS at calving. Plasma insulin and insulin-like growth factor-I (IGF-I) concentrations along the period evaluated did not differ between genetic origins. The incidence of anovulation at 30 (62%) and at 60 DPP (28%) and days to first ovulation (42.1 and 42.8 ± 4 d for NAH and NAxNZ, respectively) were not different between genetic origins. The reproductive performance in terms of reinitiation of ovarian cyclicity was similar among NAH and NAxNZ origins and this is consistent with insulin and IGF-I profiles after calving in cows on grazing conditions.

Key Words: dairy, genetic origin, reproduction

M238 Effect of short-term prepartum supplementation on milk production and calf performance of multiparous beef cows on grazing conditions. M. Carriquiry*[1], G. Roig[2], G. Banchero[2], and G. Quintans[2], [1]*School of Agronomy, UDELAR, Uruguay*, [2]*INIA, Treinta y Tres, Uruguay*.

Multiparous Aberdeen Angus x Hereford crossbred cows were used to evaluate the effect of supplementation during the last month of gestation on milk production and composition, and calf performance. Two month

prior to calving, cows were ranked by body weight (BW) and body condition score and assigned randomly to supplement (SUP; n=18) or control (CON; n=17) treatments. Supplemented cows were offered (1 kg/100 kg BW/d) a mix (67:33% as-fed basis; 16% CP, 11% ADF) of sorghum grain and protein concentrate from 33±1.4 d prepartum until calving. Before, during, and after the supplementation period, cows were grazed together in a native pasture paddock with an average forage mass available of 1345 kg DM/ha (10.4% CP, 45.2% ADF). Means from a repeated measures analysis differed when $P<0.05$. Cow BW did not differ between treatments (470±3 kg) but there was an interaction of treatment by d postpartum (DPP). During the last month of gestation, BW decreased 3.2% for CON but was maintained for SUP cows. Milk production decreased from 6.9 to 3.9±0.42 kg/d from 30 to 180 d DPP. Although there was no difference in milk production between treatments (5.0 vs 4.8±0.22 for CON and SUP cows, respectively), milk yield tended ($P=0.11$) to be 1 kg/d greater at 30 DPP for CON than for SUP cows. No differences were detected for milk fat, protein, and lactose contents between treatments (2.0±0.13, 3.3±0.04, 4.9±0.05%, respectively). Milk energy output (4.9 Mcal EN/d) represented approximately 50% of energy requirements. Calf weight at birth did not differ between treatments (42.5 kg), but at weaning, calf weight was greater for CON than SUP cows (182 vs 172±4.2 kg). This was associated with greater average daily gain during the first 30 DPP in calves from CON cows (0.97 vs 0.83±0.04 kg/d for CON and SUP cows, respectively). Short-term supplementation during the last month of gestation could modify postpartum nutrient partitioning between body reserves and milk production in beef cows.

Key Words: prepartum supplementation, milk yield

M239 Effect of bovine somatotropin (bST), dietary fat, and day in milk (DIM) on hepatic mineral concentrations in Holstein cows. M. Carriquiry*[1], W. J. Weber[2], W. A. House[3], and B. A. Crooker[2], [1]*School of Agronomy, UDELAR, Uruguay*, [2]*Department Animal Science, University of Minnesota, St. Paul*, [3]*SDA-ARS, Ithaca, NY*.

Multiparous cows (n=59) were blocked by expected calving date and previous milk yield and assigned randomly to treatments to determine effects of bST, dietary fat, and DIM on hepatic minerals (Ca, P, Mg, Na, K, Fe, Mn, Zn, Cu, Cd, Mo). Dietary n-6 or n-3 fatty acids were provided from calving as whole, high-oil sunflower seeds (SS; 10% of diet DM) or as a mixture of Alifet-High Energy® and Alifet-Repro® (AF; 3.4 and 1.5% of diet DM). Cows received 0 (N) or 500 (Y) mg bST (POSILAC®) every 10 d from 12 to 70 DIM and at 14-d intervals thereafter. Treatments from the factorial combination were designated SSN, SSY, AFN, and AFY. Biopsies were collected at -12, 10, 24, and 136 DIM and mineral content (μg/g DM) determined by inductively coupled plasma atomic emission spectrometry. Means from a repeated measures analysis differed when $P< 0.05$. Liver DM decreased from -12 to 136 DIM (27.6 ± 1.1% vs. 23.9 ± 1.3%) and was not affected by bST or diet. Hepatic P, K, Zn, Cu, Mo, and Cd decreased and Ca tended ($P < 0.09$) to decrease after calving, reached nadir at 10 or 24 DIM, and returned to or exceeded prepartum values by 136 DIM. The Mg values at -14 DIM were intermediate and values at 10 and 24 DIM less than at 136 DIM. Hepatic Fe increased from -12 to 10 DIM and decreased from 10 to 136 DIM. Hepatic Mn increased 50% from -12 to 136 DIM but Na was not affected by DIM. Hepatic Zn (100 vs. 90 ± 3.3 μ/g) and Fe (213 vs. 188 ± 7 μ/g) were reduced in bST treated cows. Hepatic Zn (101 vs. 89 ± 3.3 μ/g), Mn (7.6 vs. 6.7 ± 0.3 μ/g), and Fe (210 vs. 192 ± 7 μ/g) decreased in cows fed AF. There was an interaction of bST, diet, and DIM on K and Mo as their concentrations were less at 24 and 136 DIM in AFY cows than in SSN, SSY, and AFN cows. Hepatic concentration of several minerals decreased with initiation of lactation, bST and AF but no signs of deficiency were detected.

Key Words: minerals, liver, dairy

M240 Responses of physiological parameters in cattle to a short period of induced heat load. Y. Aharoni[1], A. Brosh*[2], E. Tahar[1], and A. Abud[1], [1]*VETERIX Ltd, Or Aqiva, Israel*, [2]*Agricultural Research Organization, Ramat Yishai, Israel*.

Changes in the physiological status of an animal are reflected in changes in the levels of some of its physiological parameters, such as temperature, heart rate, etc. Therefore, detection of events such as illness, parturition, estrus or stress conditions that affect the physiological status will be possible if these parameters are monitored continuously and interpreted in real time. The basic physiological parameters in cattle are now monitored continuously by a system that was developed by Veterix®, Israel. The system comprises capsules, which are inserted through the mouth to the reticulum of the cows and record at 5-min intervals the following physiological parameters: heart rate (HR), respiratory rate (RR), interval between rumen contractions and rumen temperature (Tr). These data are transmitted by RF communication to a central computer unit that stores and interprets the data to produce a set of alerts for the herd manager. According to this system, Tr was about 0.6°C greater than vaginal temperature. This higher level sharply dropped for a short while after the animal had drunk water. This higher level of Tr, was probably due in part to heat produced by rumen fermentation. The sequence of changes in parameter levels following exposure to a short period of heat load was compared to that during natural estrus: during estrus a simultaneous rise of HR, RR and Tr was evident, but when a cow was exposed to heat load, its first response was to increase its HR considerably; later the HR decreased to a level lower than the initial one, simultaneously with a sharp increase of RR and a moderate increase of Tr, which was interrupted by Tr drops due to more frequent drinking. We suggest that the first response of a cow to heat load is to increase blood flow to the skin in order to increase heat dissipation. When this cooling was not sufficient, HR was decreased as a result of the animals' effort to reduce intrinsic heat production, and RR is increased to enhance evaporative heat dissipation from the lungs.

Key Words: cow, heat load, heart rate

M241 Differential propionate effects on the mRNA expression of a putative beta-hydroxybutyrate sensitive receptor GPR109A in two adipose depots of goats. M. Mielenz* and H. Sauerwein, *University of Bonn, Bonn, Germany*.

The short chain fatty acid (SCFA) propionate is the main energy substrate in ruminants. We have demonstrated that propionate which is a ligand for the fatty acid binding receptors GPR41/43, increases the expression of a putative GPR41 mRNA in subcutaneous (SC) but not in perirenal (PR) adipose tissue (AT) of goats. The concentrations of beta-hydroxybutyrate (BHB) increase during negative energy balance. Stimulation of the BHB sensitive receptor GPR109A with nicotinic acid results in a reduction of lipolysis in monogastrics. We herein tested the effects of a propionate infusion on the mRNA expression of a putative GPR109A in SC and PR AT of goats in short-term. In addition, the mRNAs of PPARγ and PGC-1α were analyzed. Castrated male goats (Deutsche-Edelziege, 10 to 12 months old) were allocated to infusions

through jugular catheters after an over-night fast. They received propionate infusions (96 µmol/kg/min, pH 7.4; n=4) or NaCl-solution of the equivalent Na-concentration (n=5). Infusions were carried out for 260 minutes. The mRNAs were quantified by real-time RT-PCR after euthanasia in PR and SC AT and were evaluated using independent samples t-test. The abundance of putative GPR109A mRNA was decreased by propionate infusion in PR AT (P=0.037), but not in SC AT (P=0.782). In PR AT the mRNA for PPARγ and PGC-1α was numerically increased (P=0.142 and 0.117, respectively) but could only be considered as trend when using a relatively high P-value in defining a trend, e.g. P<0.15. This might be attributable to the limited number of animals. In conclusion, the responsiveness towards BHB which will increase in situations of lipid mobilization seems to be maintained in situations of energy surplus solely in the SC depot but will be decreased in PR AT. PPARγ / PGC-1α seem to be involved in down-regulating the putative GPR109A in short-term; however, it remains to be elucidated what changes might be induced during short and long term energy deficits.

Key Words: GPR109A, beta-hydroxybutyrate, goat

M242 Effect of maternal nutrition and selenium (Se) supply on growth and thyroxine (T4) and triiodothyronine (T3) concentrations in female lambs. L. A. Lekatz*, J. J. Reed, T. L. Neville, D. A. Redmer, L. P. Reynolds, J. S. Caton, and K. A. Vonnahme, *Department of Animal Sciences, North Dakota State University, Fargo*.

To examine the effects of maternal dietary Se and nutrient restriction or excess on postnatal growth and T4 and T3 concentration in female lambs, 82 pregnant ewe lambs (52.2 ± 0.8 kg) were allotted randomly to one of six treatments in a 2 x 3 factorial. Factors were dietary Se from Se enriched yeast [adequate Se (ASe, 9.5 µg/kg BW) vs. high Se (HSe, 81.8 µg/kg BW], initiated at breeding and maternal nutrition [control (CON, 100% of requirements) vs. restricted (RES, 60% of controls) vs. excess (EXC, 140% of controls], initiated at d 50 of gestation. At parturition lambs were removed from ewes and fed artificial colostrum for the first 20 h followed by milk replacer until weaning (d 57). Lambs were maintained on common diets until necropsy (d 180). The RES female lambs had a smaller ($P < 0.01$) girth at birth compared to the CON lambs (38.3 vs. 40.6 ± 0.53 cm) with EXC lambs being intermediate (39.6 cm). The RES female lambs were lighter ($P < 0.01$) at birth and d 7 compared to the CON and EXC lambs (birth: 3.77 vs. 4.46 and 4.35 ± 0.17 kg; d 7: 4.95 vs. 5.70 and 5.71 ± 0.19 kg); however, after this time all female lambs were similar ($P \geq 0.08$) in wt. Female lambs had similar ($P \geq 0.12$) ADG. Diet did not affect ($P \geq 0.08$) T4 or T3 concentration; however, there was a day effect ($P = 0.01$) for both T4 and T3. Concentrations of T4 were similar ($P = 0.54$) at birth and d 7 (106.2 and 109.4 ± 5.23 ng/ml), increasing on d 21 and 35 (126.9 and 122.2 ± 4.17 ng/ml), and falling sharply by weaning (79.5 ± 2.65 ng/ml). Concentration of T4 remained similar ($P = 0.73$) from post weaning (d 78) until d 180 (70.8 and 71.8 ± 2.43 ng/ml). Concentration of T3 was similar ($P = 0.56$) at birth and d 7 (3.38 and 3.49 ± 0.17 ng/ml) and significantly decreased ($P < 0.01$) until d 57 (2.99, 2.19, 1.79, and 1.22 ± 0.09 ng/ml for d 21, 35, 49, and 57, respectively). The T3 concentrations at d 57 and d 78 were similar ($P = 0.52$) and were greater ($P = 0.01$) than the T3 at d 180 (1.22 and 1.18 vs. 1.02 ± 0.06 ng/ml). Postpartum female lamb T3 and T4 concentrations are not affected by gestational maternal diet.

Key Words: thyroxine, triiodothyronine, sheep

M243 Stearoyl-CoA desaturase gene expression and its fatty acid products in bovine tissues. P. Rezamand, J. Watts, D. Pfeifer, K. M. Hunt*, S. Zaman, and M. A. McGuire, *University of Idaho, Moscow*.

Stearoyl-CoA desaturase (SCD) contributes greatly to the fatty acids present in milk and meat of cattle. The SCD enzyme introduces a double bond into some saturated fatty acyl-CoAs producing monounsaturated fatty acids (MUFA) as well as converts 18:1 t11 (vaccenic acid) to c9, t11 conjugated linoleic acid (CLA). The objective of this study was to determine any association between the gene expression of SCD and occurrence of its products (14:1 c9, 16:1 c9, 18:1 c9, and 18:2 c9 t11) in various bovine tissues. Tissue samples were obtained from lactating Holstein cows (n=28) at slaughter, frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted and converted to cDNA for quantitative real time PCR analysis of the *SCD* gene. Extracted lipid was converted to fatty acid methyl esters and analyzed by gas chromatography. Tissues varied in expression of SCD gene with mammary ≈ intestinal adipose ≈ skeletal muscle > liver (384, 328, 284, and 21 copies/ng RNA, respectively). Across tissues, the desaturase indices for 18:1 c9 (r=0.45), all SCD products (r=0.36), and overall index (all products/(all substrates + all products); r=0.43) were positively correlated with SCD gene expression (P<0.001 for all) whereas a negative correlation was detected for the desaturase index of 14:1 c9 (r=- 0.26; P=0.05). Within each tissue, the relationship between *SCD* gene expression and the desaturase indices varied. No correlation was detected between *SCD* expression and desaturase indices in the liver or skeletal muscle. Positive correlations, however, were detected between *SCD* expression and all of the desaturase indices in intestinal adipose tissue (P<0.02 for all) whereas only 18:1 c9, CLA, and all SCD products desaturase indices were positively correlated with SCD expression in mammary tissue ($P \leq 0.03$). Overall, the relationship between *SCD* gene expression and occurrence of its products seems to be tissue specific. A greater understanding of the regulation of tissue fatty acids is necessary because the activity of SCD has clear benefits to human health.

Key Words: bovine tissue, fatty acid, stearoyl-CoA desaturase

M244 Effects of heat stress on glucose homeostasis and metabolic response to an endotoxin challenge in Holstein steers. R. P. Rhoads*[1], S. R. Sanders[1], L. Cole[1], M. V. Skrzypek[1], T. H. Elsasser[2], G. C. Duff[1], R. J. Collier[1], and L. H. Baumgard[1], [1]*University of Arizona, Tucson*, [2]*USDA-ARS, Beltsville, MD*.

Twelve steers (318 ± 49 kg BW) housed in climate chambers were subjected to either a thermoneutral (TN: constant 19°C) environment or heat stress (HS) conditions (cyclical temperatures; 32.2 to 40.0°C) for 9d. On d 4 and 7 steers received an endotoxin challenge (LPS, 0.2 µg/kg BW, i.v.) and blood samples collected at 0, 1, 2, 4, 7 and 24h relative to LPS administration. A 4-h hyperinsulinemic-euglycemic clamp (HEC) was preformed on 3 steers during TN conditions and again during HS. Insulin was infused at 10 µg/kg BW/h and euglycemia maintained by varying intrajugular glucose infusion rates. All body temperature indices were increased in HS steers. Rectal temperatures increased (0.78°C) at 1h post LPS and the maximum difference (1.19°C) occurred at 7h and there were no differences between the 1st and 2nd LPS challenge. During each LPS challenge, steers exhibited hyperglycemia within 1h but the glucose response was larger in HS (53%) compared to TN steers (10%). Both HS and TN steers were hypoglycemic (19%) at 4 and 7h post LPS and had normal glucose values 24h later. Plasma insulin levels increased (>10-fold) 2h but returned to basal levels by 4h post LPS in each challenge and was not affected by environment. NEFA levels decreased (26%) 2h then increased (42%) 7h post LPS and was similar between

challenges and environments. During the HEC, plasma insulin levels increased (>20-fold) and stabilized after 1h. The rate of glucose infusion was similar between TN and HS steers during the first 3 h of the HEC, but increased (152 vs 119 g/h) in HS steers during the 4th h of the HEC. Overall, these data indicate that glucose utilization appears to increase during HS. Moreover, combined environmental stresses (HS and LPS challenge) alter glucose homeostasis to a greater extent than LPS challenge alone. Taken together, this suggests the contribution of glucose in support of whole-body energetics increases when steers experience a thermal load alone or when coupled with an LPS challenge.

Key Words: heat stress, endotoxin, insulin

M245 Impact of unsaturated fatty acid supply on the regulation of CLA-induced milk fat depression in lactating cows. M. J. de Veth[1], J. M. Griinari[2], V. Toivonen[3], and K. J. Shingfield*[3], [1]*BASF-AG, Offenbach/Queich, Germany*, [2]*University of Helsinki*, *Helsinki, Finland*, [3]*MTT Agrifood Research Finland*, *Jokionen, Finland*.

Trans-10, *cis*-12 conjugated linoleic acid (CLA) reduces milk fat synthesis in a predictable and dose dependent manner in the lactating cow. In some situations the decrease in milk fat to CLA supplements is less than predicted, with evidence that the supply of fatty acids to the mammary gland may be an important determinant of the overall response. In this experiment, the impact of unsaturated fatty acid (oleic and linoleic acid) supply on milk fat responses to *trans*-10, *cis*-12 CLA was examined. Four rumen-fistulated cows in mid-lactation were used in a 4 x 4 Latin square design. Treatments were 1) control, 2) 3.65 g/d of *trans*-10, *cis*-12 CLA alone (CA), 3) 3.65 g/d of *trans*-10, *cis*-12 CLA and a mixture of methyl esters supplying 239 g/d of *cis*-9 18:1 (CO), and 4) 3.65 g/d of *trans*-10, *cis*-12 CLA and a mixture of ethyl esters supplying 247 g/d of 18:2n-6 (CL). All treatments were abomasally infused four-times/d over a 7 d period with a 7 d interval between infusions. All CLA treatments reduced ($P < 0.01$) milk fat yield compared to the control, with CA reducing milk fat yield by 26.4%. The decrease in milk fat yield was less with treatments CO and CL (13.5 and 13.3%, respectively). Reductions in the synthesis of fatty acids de novo were comparable across CLA treatments; whilst the incorporation of preformed fatty acids was lower ($P < 0.05$) for CA compared to CO and CL and accounted for the differences in the extent of the milk fat depression. Milk fatty acid content of *trans*-10, *cis*-12 CLA (g/100g fatty acids) increased ($P < 0.01$) from < 0.01 for the control to 0.11, 0.10, and 0.11 for CA, CO, and CL respectively. Results indicate that despite the comparable transfer and incorporation of *trans*-10, *cis*-12 CLA into milk fat, the extent of reductions in milk fat synthesis may, at least in part, be regulated by the availability of unsaturated fatty acids at the mammary gland. In conclusion, altering either oleic acid or linoleic acid supply available for absorption at the small intestine may alter the magnitude of decreases in milk fat synthesis to *trans*-10, *cis*-12 CLA in the lactating cow.

Key Words: conjugated linoleic acid, unsaturated fatty acids, mammary lipogenesis

Production, Management and the Environment: Beef and Dairy

M246 Sexed-biased semen for nulliparous heifers: Effects on reproductive and lactational performances. F. Guagnini[1], J. E. P. Santos[2], J. R. Lima[1], J. Fetrow[3], and R. C. Chebel*[1], [1]*Veterinary Medicine Cooperative Extension, University of California Davis*, *Tulare*, [2]*Department of Animal Science, University of Florida*, *Gainesville*, [3]*Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*.

Objectives were to evaluate the effects of using sexed-biased semen for first AI of heifers on reproductive and economic performances during first lactation. Holstein heifers (herd A=227 and herd B=1,144) received first AI with sexed-biased semen (SS, n=343) or conventional semen (CS=1,028). Heifers that displayed estrus following first AI were re-inseminated with conventional semen. In herd AI, age at first AI were SS=13.1±0.1 and CS=13.8±0.1 mo ($P<0.01$), and, in herd B, 12.9±0.1 mo for both groups ($P=0.44$). Pregnancy per AI after first AI was greater for CS heifers (51.8 vs. 40.2%; $P<0.01$), but risk of pregnancy was not different. From heifers initially enrolled, 70.2% calved in herds A (n=188) and B (n=774) and first lactation data were collected. Interval from first AI to calving was not different in herd A (10.1±0.1 mo), but, in herd B, SS heifers had longer ($P < 0.01$) interval than CS heifers (10.3±0.1 vs. 9.8±0.1 mo). In herd A, SS heifers were younger ($P<0.01$) at calving (22.8±0.1 vs. 23.5±0.2 mo), but in herd B there was no difference (22.8±0.1 mo). Among heifers conceiving to first AI, SS heifers were ($P<0.01$) more likely to have a female calf (85.7 vs. 47.7%) and, overall, 64.6% of SS heifers and 51.0% of CS heifers had a female calf ($P<0.01$). More SS heifers conceiving to first AI had stillbirths (8.8 vs. 3.4%; $P<0.01$), but among heifers conceiving to later AI there was no difference. Among heifers conceiving to first AI, gestation length of SS heifers delivering female calves was ($P<0.01$) longer than those delivering males (277.3±0.8 vs. 267.8±1.7 d), but CS heifers delivering females had ($P=0.02$) shorter gestation than those delivering males (275.2±0.6 vs. 276.6±0.6 d). No differences in incidence of disease, risk of pregnancy, and risk of culling were observed. In herd A there was no difference in rearing cost from first AI to calving ($764.9±7.5), but, in herd B, rearing cost of SS heifers was ($P<0.01$) greater ($778.8±8.7 vs. 740.8±4.3). Calf revenue ($288.0±7.5), milk yield (9,245.5±84.7 Kg), income over feed cost ($832.1±7.6), and overall economic return ($78.1±34.1) did not differ between SS and CS heifers.

Key Words: sexed-biased semen, dairy heifer, economics

M247 Use of sex-sorted semen in superovulated Holstein cows and heifers: A case study. S. R. Potter[1], B. J. Paus[1], J. M. DeJarnette[2], and R. L. Nebel*[2], [1]*Spruce Haven Farm, LLC*, *Union Springs, NY*, [2]*Select Sires, Inc.*, *Plain City, OH*.

Data from use of commercially available, flow-cytometrically sex-sorted semen (SS) in superovulated (SO) Holstein cows (n=10) and heifers (n=34) were compared to SO results using conventional semen (CS) in cows (n=255) and heifers (n=104) in the same herd. Procedures for AI were identical for SS and CS with 1 straw administered at 36, 48, and 60 h after SO treatment. Preferential use of SS in females responding to SO resulted in more ($P<0.05$) total embryos/ova recovered per flush than CS (14.2±1.6 vs. 10.4±0.4). Across all ova, the percentage fertilized was lower ($P<0.05$) in cows (73%, n=2963) than in heifers (86%, n=1471) but was not influenced ($P>0.05$) by semen type. Across all flushes, the distribution of embryo quality was influence ($P<0.05$) by semen source in both cows and heifers. The embryo quality distribution of cows for SS (n=148) and CS (n=2815) was: Grade 1, 17 vs. 36%; Grade 2, 17 vs. 16%; Grade 3, 6 vs. 10%; fertile-dead (FD), 27 vs. 15%; and unfertilized ova (UFO), 33 vs. 23%, respectively. The embryo quality distribution within heifers for SS (n=464) and CS (n=1007) was: Grade 1, 33 vs. 42%; Grade 2, 22 vs. 24%; Grade 3, 10 vs. 9%; FD, 21

vs. 15%; and UFO, 14 vs. 10%, respectively. In each case, SS resulted in a shift towards a greater percentage of FD and UFO at the expense of Grade 1 embryos. Among Grade 1 & 2 embryos, conception rates were greater (P<0.05) for fresh (65%, n=855) than for frozen-thawed (43%, n=148) transfers. Among fresh embryo transfers, conception rates of Grade 1 & 2 embryos (66%, n=855) were greater (P<0.05) than those of Grade 3 (33%, n=147) embryos. Within embryo quality grade, semen type had no affect (P>0.05) on conception rates of fresh or frozen-thawed transfers. In conclusion, although these data tend to imply SS may possess a disproportionate percentage of uncompensable sperm defects as reflected by altered embryo quality distributions, it is not possible to determine if this observation is a direct effect of the sorting procedure per se or perhaps an indirect effect as a function of lower sperm dosages for SS and thereby reduced sperm competition at the time of fertilization.

Key Words: sexed semen, superovulation, embryo transfer

M248 What percentage of Nellore *(Bos indicus)* bulls exhibit fertility-associated antigen on sperm membranes? J. C. Dalton*[1], L. Deragon[2], and J. L. M. Vasconcelos[3], [1]*University of Idaho, Caldwell*, [2]*Alta Genetics Brazil, Uberaba, MG, Brazil*, [3]*FMVZ-UNESP, Botucatu, SP, Brazil*.

During ejaculation, the seminal vesicles, prostate, and Cowper's glands secrete heparin-binding proteins (HBP) which coat the sperm (Miller et al., 1990, Biol. Reprod. 42:899−915). Bulls with sperm that exhibited a 31-kDa molecular weight HBP, called fertility-associated antigen (FAA), were 7 to 9 percentage points more fertile following AI than bulls producing sperm lacking FAA (Sprott et al., 2006, Prof. Anim. Sci., 22:353-357). Unfortunately, on average, 12% of bulls tested (predominantly *Bos taurus* or *Bos taurus* × *Bos indicus*) have been reported to be FAA-negative (Bellin et al., 1998, J. Anim. Sci. 76:2032−2039), while the percentage of Nellore *(Bos indicus)* bulls with or without FAA on sperm is not currently known. Consequently, the objective was to determine the percentage of FAA-positive and FAA-negative Nellore bulls. Ejaculates from Nellore bulls (n = 49; range in age: 2 yr 8 mo to 11 yr) housed at Alta Genetics Brazil were collected by artificial vagina. Immediately following semen collection, 2.0 mL of neat semen was removed from the collection vial for use in a lateral flow cassette which facilitated rapid on-site determination of FAA in semen. Presence of FAA in the sample was shown by binding of FAA and labeled antibody to immobilized antibody, resulting in a visible colored band at the test position. Visualization of a colored control band verified that the cassette performed correctly, regardless of the presence or absence of FAA in the sample. Fifty tests were conducted on ejaculates from 49 bulls. Forty-seven tests (on ejaculates from 47 bulls) provided a distinct determination of FAA status, while three tests on ejaculates from two bulls were inconclusive (due to failure of the test, as evidenced by lack of a visible control band on the cassette). Five bulls (10.6%; 5/47) were FAA-negative, while 42 bulls (89.4%; 42/47) were FAA-positive. The FAA status of Nellore *(Bos indicus)* bulls is similar to *Bos taurus* and *Bos taurus* × *Bos indicus* bulls.

Key Words: bulls, proteins, sperm

M249 Effect of dry period length on productive and reproductive parameters at subsequent lactation period of Holstein cows. D. R. Lozano[1] and C. F. Aréchiga*[2], [1]*Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Aguascalientes, Aguascalientes, México*, [2]*Universidad Autónoma de Zacatecas, Zacatecas, Zacatecas, México*.

The objective of present study was to evaluate effect of dry periods length on productive and reproductive parameters at subsequent lactation period of Holstein cows. During the first replicate, Holstein cows (n=30) were assigned at random to different dry-period length treatments: 1) 60 d (n=10; 58.8 ± 3.8 d); 2) 45 d (n=10; 43.9 ± 5.32 d), and 3) 30 d (n=10; 29.2 ± 2.6). Secondly, Holstein cows (n=74) were randomly assigned to different dry-period length treatments: 1) 60 d (n=40; 61.8 ± 1.07 d) and 2) 40 d (n=10; 38.5 ± 1.16 d). During the first experimental period, blood samples were collected weekly from d 0 - 42 postpartum (PP) to evaluate serum concentrations of glucose (mg/DL), nonesterified fatty acids (NEFA; mmol/L), urea (mmol/L) and beta-hydroxybutyrate (mmol/L). Weekly milk production was registered. Differences in body condition score (BCS) of the cow and the interval calving to conception were registered and analyzed by covariance. Metabolites concentrations and milk production were analyzed by nested models with repeated measurements. By the time of calving, serum concentration of glucose was greater for cows having a dry period length of 60 days (91.7 ± 3.4; P<0.05), compared to 45 d (77.0 ± 3.5) and 30 d (65.7 ± 3.7). However, from 7 to 42 d PP, glucose concentration was similar among treatments (P>0.05). At the day of calving, cows with a dry-period length of 30 days had an increased concentration of NEFA (99.1 ± 0.06; P<0.05) compared to cows having a dry-period length of 45 d (75.2 ± 0.06) and 60 d (76.0 ± 0.06). Serum concentrations of urea and beta-hydroxybutyrate during the period of study, BCS losses at 30 d PP, milk production and interval from calving to conception were similar among treatments (P>0.05). In conclusion, a short dry-period length did not compromise productive and reproductive parameters during the subsequent lactation period of Holstein cows.

Key Words: dry period length, milk yield, reproduction

M250 Effect of total dissolved solids and sulfates in drinking water on growing heifers fed sorghum silage. J. I. Arroquy*[1,2], M. Avila[1], J. Saravia[1], R. Ibañez[1], and P. Fisolo[1], [1]*INTA Santiago del Estero, Santiago del Estero, Argentina*, [2]*Univ. Nacional de Santiago del Estero - Fac. Agronomía y Agroindustrias, Santiago del Estero, Argentina*, [3]*CONICET, Santiago del Estero, Argentina*.

In north-western Argentina drinking water for cattle often exhibit high levels of total dissolved solids (TDS) and sulfates. Sorghum silage has more than 65% of water, thus in this study was speculated that cattle could get enough volume of water from silage reducing the problems of saline water. The objective was to evaluate the effect of increasing levels of TDS and sulfates in drinking water on weight gain, dry matter intake, and feed efficiency on growing heifers fed sorghum silage. Seventy five heifers (Bradford, and Braford × Criollo; initial BW = 156 ± 20 kg) without previous adaptation to saline water were blocked by weight and randomly assigned to one of 10 pens (7 or 8 heifers/pen). Each pen was randomly assigned to five water treatments based on TDS-sulfates concentrations (g/L): 1) 2 (0.65 sulfates); 2) 5 (1.70 sulfates); 3) 8 (3.00 sulfates); 4) 11 (3.70 sulfates); 5) 14 (4.70 sulfates). Heifers were fed once daily. Ration had on DM basis: 88% sorghum silage and 12% supplement (cottonseed, mineral mix, and vitamins). Average daily gain (ADG; P < 0.05), DM intake (DMI; P < 0.05), total water intake (water from feed plus drinking water; P < 0.05) lineally decrease in response to increasing levels of TDS and sulfates in water. However ADG and DMI for treatment 1 (2 g/L) was only statically different from treatment 5 (14 g/L of TDS). ADG were 411, 330, 339, 306, and 263 g/d (SEM = 38) for treatments 1, 2, 3, 4, and 5 respectively. DMI means were

25.00, 21.85, 21.90, 19.25, and 17.40 g/kg BW (SEM = 2.65) for 1, 2, 3, 4, and 5 respectively. In contrast feed efficiency did not differ among treatments. On average feed efficiencies were 11.0 kg of feed to weight gain (SEM = 1.8). Total water intake to DMI ratio (TWI: DMI ratio) was similar among treatments. Overall TWI: DMI ratio was 5.12 kg of water intake per kg of DMI (SEM = 0.67). In conclusion, within the range of TDS and sulfates evaluated in this experiment liveweight gain lineally decreased in response to increasing levels of salt and sulphur, whereas feed efficiency was not affected all across levels of TDS and sulfates in drinking water.

Key Words: water quality, liveweight gain, sorghum silage

M251 Non genetics effects on reproductive traits in Nellore female: I. Gestation length. D. H. Vieira[1], V. C. Rodrigues[2], L. F. D. Medeiros[2], C. G. Barbosa[2], J. P. F. Silveira[3], V. L. Tierzo[3], J. L. C. B. Reis*[4], and R. S. B. Pinheiro[3], [1]*Center of Creation of A, Rio de Janeiro, RJ, Brazil*, [2]*Rural Federal university of Rio de Janeiro*, *Seropedica, RJ, Brazil*, [3]*São Paulo State University*, *Botucatu, SP, Brazil*, [4]*University of Agrarian Sciences - University of Marília*, *Marília, SP, Brazil*.

This study was aimed at evaluating the reproductive performance of Nellore cattle herd, raised in pasture, with no supplementation in dry season, in Baixada Litorânea region, Rio de Janeiro state, between 1980 and 2004. The gestation length (GL) average was 293.30 ± 0.13 days. The GL varied from 275 to 305 days, with a higher concentration (67.08%) between 287 and 299 days. The GL was significantly influenced by year (P<0.05), month (P<0.01) and sex of calf (P<0.05). The parturition order was not significant (P>0.05). The average for GL is considered normal for the species and breed.

Key Words: beef cattle, extensive system, Nellore

M252 Effects of differing levels of rumen degradable protein on nitrogen metabolism in dairy cows and environmental pollution. H. Rafiee*, *University of Tehran*, *Tehran, Iran*.

Nine midlactation Holstein cows averaging 171±17 days in milk and 24.1±3.2 Kg of milk/d were assigned to a replicated 3×3 Latin square design to study the effects of three levels of rumen degradable protein (RDP) on nitrogen metabolism. RDP and Crude protein (CP) contents were 9.8 and 14.3, 10.8 and 15.3, and 11.8 and 16.3% DM respectively. Diets consisted of 45% forage DM including 25% alfalfa hay and 20% corn silage. The concentrate contained cottonseed meal and urea as protein sources. Each period lasted 21 days with the last 7 days for sampling. Results were analyzed by MIXED models with effect of cow(square) as a random and days of sampling in each period as repeated measures. Differences declared as significant where P<0.05. Increasing dietary RDP resulted in linearly increased nitrogen (N) intake (P < 0.01), N apparently absorbed (P < 0.01), and urine N (P < 0.05). Pollution N tended to be significant between treatments (P = 0.05), and increased linearly from diet 1 to 3. Results indicate that as nitrogen (N) intake increases, excretion of N in urine increases and it becomes the principal route of N excretion from ruminants. Balancing rations to further improve the nitrogen utilization efficiency may be of higher priority value. Decreasing dietary CP from 16.3 to 15.3% of DM did not affect cow production but reduced estimated excretion of the environmentally labile urinary N, and increased estimated N efficiency. Therefore, the recommended level of dietary CP will depend on the criteria used to define optimum N use.

Table 1. Effect of dietary RDP on nitrogen balance measurements

	RDP level					linear
Items	9.8	10.8	11.8	SEM	P <	contrast
N intake, g/d	432.2	466.3	489.3	16.55	0.003	0.008
Fecal N	104.3	102.3	104.1	6.28	0.96	0.98
Absorbed N	318.8	363.9	385.1	13.59	0.005	0.002
Urine N	200.6	227.2	245.6	9.96	0.01	0.004
Milk N	109.8	114.5	117.4	4.37	0.14	0.21
Pollution N	305.0	329.6	349.7	12.39	0.05	0.01
N efficiency, %	25.9	24.8	24.1	0.87	0.36	0.16

N: nitrogen

Key Words: rumen degradable protein, nitrogen, environment

M253 PGF2α analog on uterine health and reproductive performance of dairy cattle. R. M. Santos*[1], D. G. B. Demétrio[2], C. C. Dias[2], and J. L. M. Vasconcelos[2], [1]*FAMEV-UFU*, *Uberlandia, MG, Brazil*, [2]*FMVZ-UNESP*, *Botucatu, SP, Brazil*.

Cows with a normal or abnormal puerperium treated with PGF2α early postpartum had improved fertility, and these effects were independent of plasma P4 at the time of treatment (Bonnet et al., 1990). Prostaglandins and other arachidonic acid metabolites might be important mediators of resistance or susceptibility to uterine infections (Lewis, 1997). The objective was to evaluate the effect of two injections of different PGF2α analogs at 2nd and 4th week postpartum (WPP) on uterine health and reproductive performance. Holstein cows (n=106), calving at summer and maintained in free-stall barn, were divided into three treatment groups: G1=0.530mg Cloprostenol sodium, G2=25mg Dinoprost tromethamine, or G3=control (no treatment). The injections were given at 2nd and 4th WPP. Samples for endometrial cytology (low-volume uterine lavage) were obtained at 6th and 8th WPP. Endometritis was defined as presence of 5% of neutrophilis on endometrial cytology, 40 to 60 DIM (Gilbert et al., 2005). The variables endometritis, conception at first AI and pregnancy by 200 DIM were analyzed by the binary logistic regression and the calving to conception interval was evaluated by GLM. Treatment, BCS, retained placenta, milk yield, body temperature, cyclicity (P4≥1ng/ml) recorded at 2nd; 4th; 6th and 8th WPP, and all possible interactions were included in the model. Treatment had no effect on endometritis (65.7% at 6th WPP; 62% at 8th WPP) and reproductive performance (8.4% conception at first AI; 189.4 d calving to conception; 29.2% pregnancy by 200 DIM). Cycling cows at 8th WPP had lower endometritis at this time (P<0.05; 72 vs. 50%). The endometritis at 6th WPP had no effect on reproductive performance, however at 8th WPP had a negative effect on pregnancy by 200 DIM (P<0.05; 42.1 vs. 20.9%) and calving to conception interval (P<0.05; 168.3 vs. 210.4d). The endometritis at 8th WPP had a negative impact on reproductive performance, and this time is probably the best for endometritis diagnosis and treatment. Some spontaneous recovery may occur before 8th WPP.

Key Words: endometritis, prostaglandin, dairy cattle

M254 Effects of GnRH treatment 7 days prior to resynchronization on conception rates to previous and repeat inseminations. R. L. Nebel*[1], J. M. DeJarnette[1], and B. A. Meek[2], [1]*Select Sires, Inc.*, *Plain City, OH*, [2]*Cache Valley/Select Sires*, *Logan, UT*.

Lactating Holstein (n=1870) in 3 herds were used to determine the effects GnRH administered 7 days prior to resynchronization on conception rates to previous and repeat AI. Cows that had not been detected in estrus by 25 to 32 d post AI (Mean = 29±0.08 d) were assigned by odd and even ID number to receive either no further treatment (Control, n=912) or GnRH (100 μg, im; n=958). Cows not detected in estrus in the next 7 d were presented for pregnancy diagnosis (32 to 39 d post-AI) and open cows in the Control (n=408) and GnRH groups (n=435) were submitted for resynchronization (100 μg GnRH, 7d, 25 mg $PGF_{2\alpha}$, 72 h, 100 μg GnRH and fixed-time AI). Data were analyzed for the effects of treatment on the percentage of cows detected in estrus within 16 d post treatment, and on conception rate at both previous and repeat inseminations. Repeat inseminations were analyzed separately for estrus-based and fixed-timed AI. Treatment had no effect (P>0.05) on conception rate at previous AI (52%, n=912 vs. 51%, n=958 for Control vs. GnRH, respectively). The percentage of open cows detected in estrus from treatment d 0 to 16 was greater (P<0.05) for Control (31%, n=408) than in GnRH treated cows (21%, n=435), however conception rate at estrus (23%, n=128 vs. 21%, n=90) and fixed-time inseminations (21%, n=280 vs. 25%, n=345) were not influenced (P>0.05) by treatment for Control vs. GnRH-treated cows, respectively. The cumulative percent pregnant after initial and repeat AI was not influenced by treatment (65%, n=912 vs. 66%, n=958 for Control vs. GnRH-treated respectively). Conception rates at initial AI were influenced (P<0.05) by herd and by postpartum interval. Cows <100 d postpartum at first AI had greater (P>0.05) conception rates those ≥100 d postpartum. In conclusion, GnRH administered 7 d prior to resynchronization had no affect on reproductive performance in these herds wherein both estrus detection and resynchronization are used to manage intervals to re-insemination. These results may not apply in herds that rely more exclusively on resynchronization to manage repeat insemination interval.

Key Words: resynchronization, GnRH, fixed-time AI

M255 Tasco alleviation of heat stress in dairy cows. L. B. Pompeu*[1], J. E. Williams[1], D. E. Spiers[1], R. L. Weaber[1], M. R. Ellersieck[1], K. M. Sargent[1], N. P. Feyerabend[1], H. L. Vellios[1], and F. Evans[2], [1]*University of Missouri*, *Columbia*, [2]*Acadian Seaplants*, *Dartmouth, NS, Canada*.

The present study determined if Tasco-14, *Ascophyllum nodosum*, supplementation reduces heat stress in cows. Cows (n=32) were assigned to treatments (trt) using a randomized complete block design, with 8 cows per trt. The study was divided into 3 periods. In Period 1 (7 d), cows adapted to the Calan gate system. In Period 2 (28 d) the following trt began: Control-1 (C-1); Control-2 (C-2); .25% Tasco (.25T); .50% Tasco (.5T). In Period 3 (28 d), C-2 was changed to 0.50% Tasco (C-.5T) in order to evaluate duration of feeding Tasco. Ambient temperature (T_a) and humidity were continuously recorded using Onset "Hobo" dataloggers. Respiration rate (RR), rump (T_{rump}) and ear (T_{ear}) skin temperatures were measured daily at 0700, 1600, and 1900 h. Milk production and composition data were collected. In Period 2, no differences (P > .10) were found between C-1 and C-2 for any parameter, so they were combined for this period (C). The average daily values for max and mean T_a were 28.0 and 23.2°C, respectively, and the mean RH was 77%. A trt x d interaction (P < .05) revealed DM intake (DMI) of .25T was lower than C for 3 d and lower than .5T for 1 d. For DMI per body weight, .25T was lower than C for 4 d and lower than .5T for 1 d (P < .05). A trt x h interaction (P < .10 and P < .01, respectively) revealed lower T_{ear} for .25T vs. .5T and lower T_{rump} for .25T vs. other trt, at 1600 and 1900 h. In Period 3, the average daily values for max and mean T_a were 31.0 and 26.2°C, respectively, and the mean RH was 81%. No differences in DMI or DMI per body weight were noted (P > .10). A trt x d interaction (P < .05) revealed higher T_{rump} for C-1 than .25T (4 d), than .5T (2 d) and than C-.5T (1 d). T_{rump} was higher (P < .06) for C-.5T vs. .25T (7 d) and vs. .5T (2 d). For 1 d, .5T had higher (P < .05) T_{rump} than C-1 and C-.5T. No differences (P > .10) were observed for RR, milk production, milk fat, and milk protein yield among trt. From the results, it suggests the inclusion of 0.25% Tasco may reduce heat strain of cows and maintain milk production, even with a reduction in DMI; however, no progressive benefit was seen with Tasco. The length of feeding Tasco did not have an effect.

Key Words: Tasco, heat stress, dairy cows

M256 Evaluation of the nitrogen balance module of the AminoCow ration evaluator. R. A. Patton*[1], W. Heimbeck[2], and J. R. Patton[1], [1]*Nittany Dairy Nutrition, Inc.*, *Mifflinburg, PA*, [2]*Evonik Degussa GmbH, Health & Nutrition*, *Hanau, Germany*.

AminoCow (AC) is a semi-mechanistic, nutritional model used to evaluate and balance rations for all classes of dairy cattle. Version 3.5.2 has added an environmental module to track the effect of ration changes on the loss of nutrients into the environment. A major part of this module predicts the movement of nitrogen (N) through the cow in response to amino acid balance and provides a prediction of milk urea nitrogen (MUN). In order to determine the accuracy of this model, 37 papers representing 45 separate studies and 155 individual diets that reported N intake, N in milk, N retention, N excreted in manure, N excreted in urine, urine volume, manure dry matter, and MUN were compared against predictions by the AC model. Not all studies reported all variables. Accuracy of prediction was judged by simple regression and by use of the mean square predicted error (MSPE) technique. With the exception of N retained, N in urine and urine volume, predictions were reasonably close to observed. AC predicted a mean of 8.9 g of N retained while the reported mean was 41.1 g. This observed retention would equate to a growth rate of approximately 1 kg/day, a rate not observed in practice. This suggests that there were large inaccuracies in measuring urine N. We conclude that with the exception of N retained and N lost in urine, the model generally predicts the magnitude and direction of N partitioning. Prediction of MUN also appears reasonable; however, prediction of urine volume lacks accuracy.

Table 1.

Item	Number of diets	Predicted Mean	Observed Mean	RMSPE* % of Mean	R^2	% Error due to Central Tendency	% Error due to Regression
N intake, g	155	590.0	592.0	30.4	0.90	0.3	1.9
N milk, g	155	149.6	153.5	8.3	0.89	9.2	0.7
N retained, g	108	8.9	41.1	169.2	0.03	21.5	36.4
N manure, g	147	222.3	209.0	56.5	0.42	5.6	0.3
N urine, g	133	232.6	205.0	88.9	0.06	9.63	42.1
Urine vol, L	50	28.5	28.0	35.9	0.02	0.0	41.0
Manure DM, kg	98	8.0	7.8	23.8	0.40	0.0	38.4
MUN, mg/dl	108	13.3	13.4	16.3	0.53	0.0	0.0

*Root Mean Square Predicted Error = square root of MSPE

Key Words: model, N loss, MUN

M257 Validation of right ruminal artery and vein as models of bovine foregut vasculature. J. L. Klotz*[1], L. P. Bush[2], and J. R. Strickland[1], [1]*USDA-ARS, FAPRU, Lexington, KY*, [2]*University of Kentucky, Lexington*.

Endophyte-infected (*Neotyphodium coenophialum*) tall fescue (*Lolium arundinaceum*) produces alkaloids that have been associated with peripheral vasoconstriction in grazing animals and ingestion of these alkaloids may effect splanchnic vasculature. Because of significant differences in morphological and functional characteristics between vasculature supporting digestive and peripheral tissues, the implementation of a bovine foregut vascular model required validation. Experiments were conducted, using dose-responses to norepinephrine (NE) and serotonin (5HT), to evaluate the responses of vessels equilibrated at different tensions and determination of a reference compound. Segments of a branch of right ruminal artery and vein were collected from the ventral coronary groove of healthy mixed breed and gender cattle (n=7) at local abattoirs. Tissues were placed in Krebs-Henseleit buffer and kept on ice until they were trimmed of excess fat and connective tissue, sliced into 2-3 mm sections and suspended on luminal supports in a chamber of a multi-myograph containing continuously oxygenated Krebs-Henseleit buffer (95% O_2/5% CO_2; pH=7.4; 37°C). Vessels were allowed to equilibrate at either 0.5 or 1.0 g of tension for 1.5 h prior to additions of either NE or 5HT. Increasing doses of each compound were administered in 15-min intervals following buffer replacement. Data were normalized as a percent of contractile response induced by the maximal dose (1×10^{-4} M) of NE or 5HT for each tension. Ruminal artery and vein both contracted in a dose-dependent manner ($P<0.05$) to both NE and 5HT treatments. Tension did not affect contractile response of the vein, but 0.5 g tension resulted in a greater arterial response ($P<0.05$) than 1.0 g. Contractile response to NE was greater than 5HT for both the artery and the vein ($P<0.05$). These results enable future experiments to separate the effects tall fescue alkaloids have on both the right ruminal artery and vein as representative vessels that support tissues functioning in nutrient absorption.

Key Words: bovine, ruminal artery and vein, tall fescue

M258 Effects of a commercial product containing *Morinda citrifolia* extract on growth performance and health of calves with a high risk of developing bovine respiratory disease. M. S. Brown*[1], R. Godbee[2], B. Coufal[1], C. L. Maxwell[1], J. O. Wallace[1], and C. H. Ponce[1], [1]*Feedlot Research Group, West Texas A&M University, Canyon*, [2]*Morinda Agriculture, Provo, UT*.

Continuing development of technologies to improve health and performance of high-risk calves are needed to improve beef production efficiency. Crossbred male calves (n = 139, initial weight = 222 kg) were purchased at auction barns in the Southeast US and used in a 45-day pilot receiving study to evaluate the influence of a product containing *Morinda citrifolia* extract (MorindaMax, Morinda Agriculture, Provo, UT) on growth performance and health. Treatments included a basal 65% concentrate diet based on steam-flaked corn that was supplemented with a top dress of 0 or 0.55 g of MorindaMax/kg of BW from days 1 through 10 and days 28 through 32. Calves were processed on arrival, including metaphylaxis with ceftiofur crystalline free acid and castration by knife (91% bulls on arrival), and randomized to pens (5 pens/treatment, 13 to 14 cattle/pen). Calves fed *Morinda citrifolia* extract consumed more feed (P = 0.01; 10.2%) and gained weight more rapidly (P = 0.09; 22.9%) during the first 28 d than calves fed the control treatment, but feed efficiency did not differ (P = 0.32). The improvement in performance was associated with a tendency (P = 0.14) for fewer calves to be treated for respiratory disease during the first 28 d (20.5% and 10.0% for 0 and 0.55 g/kg). Overall DMI was also greater (P = 0.03; 6.1%) for calves fed *Morinda citrifolia* extract than for calves fed the control treatment. However, overall ADG and feed efficiency were not influenced by treatment (P > 0.31). Over the entire trial, the number of calves treated once and the total number treated for respiratory disease did not differ (P > 0.66) among treatments. Feeding *Morinda citrifolia* extract tended (P = 0.17) to reduce mortality over the entire trial (7.4% and 1.4% for 0 and 0.55 g/kg), perhaps due to the numeric reduction in the number of cattle retreated for respiratory disease during the first 28 d. *Morinda citrifolia* extract fed at 0.55 g/kg of BW for days 1 through 10 and days 28 through 32 increased feed intake and tended to reduce death loss in high-risk calves.

Key Words: morbidity, growth performance, plant extract

Ruminant Nutrition: By-product Feeds

M259 Nature of fermentation in stored wet distillers grains. A. R. Geis*, P. J. Kononoff, A. M. Gehman, and C. S. Heine, *University of Nebraska, Lincoln*.

Wet distillers grains are commonly stored in polyethylene silo bags until needed for feeding. The preservation of this feed is different from traditional methods of forage preservation through ensiling because the amount of fermentable carbohydrate is limited. The objective of this experiment was to evaluate the nature of ensiling wet distillers grains (WDGS) alone or in combination with other feeds. A 3 x 3 x 4 factorial experiment was conducted in which three loads of distillers grains were co-ensiled with three feeds (corn silage, ground corn, and brome hay) at four levels (0, 50, 75, 100% DM). Approximately 2.4 L of each mix was vacuum-sealed in plastic bags measuring 35 x 40cm. Following a 60-d storage period, a water extraction was used to determine pH, lactic acid, butyrate, and ammonia levels as potential indicators of fermentation. The addition of feeds to WDGS increased ($P < 0.01$) the pH of stored material. Specifically, when mixed with WDGS at 0, 50, 75 and 100% DM, the pH of corn was 3.78, 4.58, 4.99, 6.29 ± 0.19, 3.86, 4.0, 4.31, 6.42 ± 0.19 for hay, and 3.80, 3.75, 3.93, 4.13 ± 0.19 for corn silage. Small but significant ($P < 0.01$) reductions in both butyrate and ammonia were observed when the proportion of ground corn and hay increased. As corn inclusion increased, butyrate decreased from 0.62 to 0.05 ± 0.12% DM and ammonia decreased from 0.15 to 0.002 ± 0.03% DM. As hay inclusion increased, butyrate was reduced from 0.58 to 0.07 ± 0.12% DM and ammonia was reduced from 0.14 to 0.008 ± 0.03% DM. Mixes with corn silage resulted in a reduction ($P < 0.01$) in butyrate from 0.6 to 0.14 ± 0.12% DM when the percent of silage increased. The addition of corn silage did not decrease ammonia, which averaged 0.20 ± 0.03% DM across levels. These results suggest the low pH of WDGS limits fermentation activity in stored WDGS, but the inclusion of other feeds increases pH. In addition, the low pH, butyrate, and ammonia suggest fermentation by clostridia was limited.

Key Words: wet distillers grains, fermentation, pH

M260 The effect of ensilage storage duration and proportion of wet distillers grains and straw on in situ dry matter disappearance. K.

L. Neuhold*, J. J. Wagner, T. E. Engle, S. L. Archibeque, and K. S. Sellins, *Colorado State University*, *Fort Collins*.

The objective of this study was to investigate the effect of the proportion of wet distillers grains (WDG) and wheat straw (WS) and ensilage storage duration on in situ DM disappearance. WDG and WS were mixed at five different ratios of WDG to WS 100:00, 90:10, 80:20, 70:30, and 0:100. The three combination treatments were packed into experimental silos. Silos were made out of PVC pipe (3.8 cm x 15.0 cm) caped on one end and sealed with a removable rubber cap on the other end. Mixtures were ensiled for 0, 4, 8, 12, and 24 d. Samples were prepared for in situ evaluation by drying the entire silo contents for each time point for 48 hr at 60°C and then grinding the sample through a 2 mm screen. A mass to area ratio of 10 mg sample/cm2 was utilized for each in situ bag. Bags were incubated in two fistulated steers for 0, 4, 8, 12, 24, 48, and 72 h. Steers were fed a high concentrate diet (70% steam flaked corn) for 21 d, then in situ fermentation was initiated. After the 72 h time point, steers were switched to a high roughage diet (50% corn silage and 50% alfalfa) for 21 d and then in situ fermentation was initiated. After the 72 h incubation, in situ bags were washed, dried for 48 hr at 60°C, and DM disappearance calculated. Polynomial curves were generated over incubation time within each ensiling time by diet. The area under each curve was calculated and analyzed using the Proc Mix procedure of SAS. Days ensiled had no impact on DM disappearance. The straw to WDG ratio was a significant ($P < 0.0001$) source of variation for DM disappearance. One hundred percent WDG had the greatest disappearance, followed by 90:10, 80:20, 70:30, and WS (56.17, 46.92, 42.07, 36.07, 27.12%, LSM respectively). Diet (high concentrate or high roughage diet) was also a significant ($P < 0.0001$) source of variation for DM disappearance (36.7 and 46.9% LSM, respectively). Samples across all time points had greater DM disappearance when incubated in steers consuming a high roughage diet compared to steers consuming a high concentrate diet. Using WS to facilitate storage of WDG did not improve in situ disappearance of WS.

Key Words: wet distillers grain, wheat straw, storage

M261 In situ ruminal protein degradation of whole corn or corn endosperm distiller grains. W. Z. Yang*[1], L. E. Armentano[2], and Y. L. Li[1], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [2]*University of Wisconsin*, *Madison*.

The grain-based ethanol industry is heading toward a fractionation process by physically separating dry shelled corn into a high fiber bran, germ and endosperm prior to fermentation of endosperm. This process increases fermentation efficiency and market opportunities for by-products. However, ruminal protein degradability of distiller grains (DG) derived from the fractionation process would be different from that of the traditional dry-grind process because the fractions of bran and germ are not subjected to the fermentation. The objective was to determine in situ ruminal protein degradability of traditional and fractional DG. Eight samples with 6 traditional DG with solubles (TraDGS), 1 fractional with solubles (endosperm DGS) and 1 fractional without solubles (endosperm DG) were tested. Five grams of ground (2-mm) sample were incubated in situ in the rumen of 3 lactating dairy cows for 0, 2, 4, 8, 13, 18, 24 and 48 hours. The model $y=a+b(1-e^{-kd(t-t0)})$ was fitted to determine the kinetics of protein degradation, where y is protein degraded, a is soluble fraction, b is slowly degradable fraction, kd is degradation rate constant, t is incubation time, and t0 is lag time. Protein content of endosperm DGS (52%) and endosperm DG (51%) was higher ($P<0.01$) than that of TraDGS (32%). The soluble fraction and degradation rate constant (a, kd) were the highest for endosperm DGS (25%, 5.1%/h), the lowest for endosperm DG (2%, 1.6%/h) and the medium for TraDGS (12%, 2.9%/h). However, the slowly degradable fraction was higher ($P<0.01$) for endosperm DG (95%) than for TraDGS (74%) and endosperm DGS (72%). Thus, as observed for a and kd, effective degradability of protein was the highest for endosperm DGS (56%), the lowest for endosperm DG (22%) and the medium for TraDGS (33%). The results indicate that protein content and ruminal degradability of DG vary considerably with milling process and whether the soluble fraction is included in the endosperm DG products.

Key Words: distiller grain, protein degradability, dairy cow

M262 In situ ruminal degradability and intestinal digestibility of protein in soybean and dried distillers grains with solubles products. K. Mjoun*, K. F. Kalscheur, A. R. Hippen, and D. J. Schingoethe, *South Dakota State University*, *Brookings*.

New fractionation and fermentation technologies in the ethanol industry have resulted in the production of different distillers grains with solubles (DGS). Such products are low fat, high protein, and modified wet DGS. Characterization of the protein fractions of these coproducts is important for formulation of these feedstuffs in dairy cattle diets. In situ and in vitro techniques were conducted to estimate protein availability in four soybean feedstuffs, solvent-extracted soybean meal (SBM), expeller soybean meal (ESBM), extruded soybeans (ES), and soyhulls (SH), and four DGS, regular dried DGS (rDGS), de-oiled dried DGS (dDGS), high protein dried DGS (HPDGS), and modified wet DGS (mWDG). Nylon bags containing 5g of each feed were incubated in the rumen of three cannulated lactating cows for 2, 4, 8, 12, 18, 24, and 48 h. The rapidly degradable CP fraction (A) varied from 8.1 and 36.3%, respectively for SBM and mWDG. The slowly degradable CP fraction (B) was highest for SBM, ES, HPDGS (88.0 ±3.7%), followed by ESBM, rDGS, and dDGS (76.8 ± 4.1%), SH and mWDG had the lowest B fraction (63.8%). The rate of degradation of B fraction, Kd (%/h) ranged from 11.8 for SBM to 2.7 for dDGS. Rumen undegradable protein (RUP) varied widely (32.2-60.4%) with dDGS having the highest and SBM having the lowest. Intestinal digestible protein (IDP) was estimated by pepsin-pancreatin digestion of rumen preincubated (16h) samples. The IDP was highest for soybean products (97.7 ± 0.75) with the exception of SH while DGS products were 92.0 ± 0.5%. Similarly total digestible protein (TDP) was highest (99%) for soybean products while DGS grains products had a TDP of 96%. These results suggest that the protein availability in DGS products is relatively comparable to soybean products.

Table 1.

Item/ Feed	SBM	ESBM	ES	SH	rDGS	dDGS	HPDGS	mWDG	SEM
A, %	8.1^{e}	11.4^{d}	12.6^{d}	27.1^{b}	18.4^{c}	17.2^{c}	11.1^{d}	36.3^{a}	0.92
B, %	91.9^{a}	81.5^{bc}	87.4^{ab}	64.1^{d}	75.2^{c}	73.7^{c}	84.6^{ab}	63.6^{d}	3.80
C, %	0.0	7.1	0.0	8.9	6.4	9.0	4.2	0.0	3.52
Kd, %/h	11.8^{a}	7.5^{cd}	5.3^{bc}	7.5^{b}	3.9^{cd}	2.7^{d}	4.3^{cd}	3.8^{cd}	0.9
RUP, %	32.2^{e}	53.7^{b}	48.0^{c}	38.0^{d}	52.3^{b}	60.4^{a}	54.5^{b}	39.4^{d}	2.48
IDP, %	97.0^{a}	98.5^{a}	97.7^{a}	42.3^{d}	92.4^{bc}	91.4^{c}	93.5^{b}	92.1^{bc}	0.53
TDP, %	99.0^{a}	99.2^{a}	98.9^{a}	78.0^{d}	96.0^{bc}	94.8^{c}	96.5^{b}	96.9^{b}	0.44

$^{a–e}$Means in rows with different superscripts differ ($P < 0.05$).

Key Words: crude protein, rumen, intestine

M263 Effects of feeding different combinations of stored wet corn distillers grains plus soluble (WDGS) on performance of lactating dairy cows. H. A. Ramirez Ramirez*, P. J. Kononoff, and A. M. Gehman, *University of Nebraska Lincoln, Lincoln*.

The objectives of this experiment were to evaluate the effects of feeding wet distillers grains plus solubles (WDGS) on milk production and also to investigate the potential of storing WDGS mixed with other feeds. Twenty Holstein cows (8 primiparous and 12 multiparous) averaging (mean ± SD) 620 ± 61 kg BW and 103 ± 13 DIM were used in a 4 X 5 Latin rectangle. Prior to initiation of the study WDGS were stored alone or co-ensiled with either 12% ground corn (DM basis), 15% brome hay (DM basis) or 15% corn silage (DM basis) in polyethylene silo bags. Animals were assigned to one of five treatments during each 21-d period. A diet not containing WDGS was formulated (CONT), along with one containing 30% WDGS (DM basis) (WDGS). Three additional diets, similar to the WDGS treatment, were formulated to include one of the three co-ensiled blends. These diets were WDGS+C, WDGS+H, WDGS+S for WDGS co-ensiled with corn, brome hay and corn silage respectively. Dry matter intake (DMI) was affected by diet (P < 0.01) and compared to CONT was greater for WDGS (23.5 ± 0.70 kg) and WDGS+C (24.2 ± 0.70 kg). Compared to CONT DMI was not different when cows consumed WDGS+H and WDHS+S. Milk yield, 3.5% FCM, and fat yield were not affected by treatment, averaging 27.9 ± 0.91 kg/d, 29.0 ± 1.03 kg/d, and 1.03 ± 0.04 kg/d across treatments. The percentage of milk protein was affected (P = 0.03) and yield of protein tended to (P = 0.12) be affected by dietary treatment; compared to CONT milk protein percent was higher for cows consuming WDGS and WDGS+C (2.96, 3.01, and 3.03 ± 0.06% for CONT, WDGS and WDGS+C respectively). Similarly, compared to CONT milk protein yield was higher for animals consuming WDGS and WDGS+C (0.83, 0.87, and 0.89 ± 0.03 kg/d for CONT, WDGS and WDGS+C). Compared to CONT milk urea N increased (P = 0.04) when the diets included WDGS (14.4, 15.3, 15.5, 15.8 and 15.5 ± 0.42 mg/dL for CONT, WDGS, WDGS+C and WDGS+S). These results suggest that dairy rations can be formulated to include stored WDGS at 30% DM without negative effects on milk production and composition.

Key Words: wet distillers grains plus solubles, feed storage, dairy cow

M264 The effect of feeding dried distillers grains plus solubles on the performance of Chinese Holstein cows. Z. Yan, J. Wang*, D. Bu, M. Wang, and H. Wei, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

The objective of this study was to evaluate the effects of dried distillers grains with solubles (DDGS) on the lactational performance of Chinese Holstein cows. 48 multiparous Chinese Holstein cows average 99±58.56d in milk were randomly assigned to one of 4 treatments. During the 8-wk periods, cows were fed total mixed diets containing 20.9% soybean meal (control), 11.8% soybean meal and 14.1% DDGS (DDGS1), 4.8% soybean meal and 26.4% DDGS (DDGS2), or 36.9% DDGS (DDGS3) as the major protein source. All diets had a 55:45 forage-to-concentrate ratio, and were formulated to be isonitrogenous at 15.15% CP. Results showed that dry matter intake did not differ among control, DDGS1 and DDGS2 (16.54,16.47 and 16.54kg/d), but was lower for DDGS3 (16.27kg/d). Milk yield (16.36, 16.45, 16.83 and 16.67kg/d) tended to increase linearly when DDGS replaced soybean meal and corn until when the percentage of DDGS reached 36.7% DM. Milk SNF, TS, Fat and protein percentages decreased for DDGS3 compared with other groups, but only the percentage of milk SNF and protein reached significant level. Milk fat yield was higher for DDGS2 and DDGS3 compared with control and DDGS1. Milk protein yield were lower for DDGS1, DDGS2 and DDGS3 compared with control. The percentage of milk lactose was higher for DDGS1 compared with the other three treatments, whereas the milk lactose yields of DDGS2 and DDGS3 were higher than control and DDGS1. Results of this study showed that maximum economic payback could be obtained when the dairy ration was formulated to contain about 26% DDGS(DM basis).

Key Words: dried distillers grains with solubles (DDGS), performance, Chinese Holstein cow

M265 The effects of replacing barley silage or barley grain with dried distillers grains plus solubles on productivity of lactating dairy cows. S. Z. Zhang*, G. B. Penner, and M. Oba, *University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to determine the effects of partially replacing barley silage or barley grain with dried distillers grain plus soluble (DDGS) on dry matter intake (DMI), chewing activity, rumen fermentation, and milk yield and composition. Six ruminally cannulated lactating Holstein cows (160 ± 97 days in milk) were used in a replicated 3×3 Latin square design with 21-d periods. Cows were fed a control diet (CON: 45% barley silage, 5% alfalfa hay, and 50% concentrate mix), a low forage (LF) diet or a low grain (LG) diet in which barley silage or barley grain was replaced by DDGS at 20% of dietary DM, respectively. All diets were formulated to contain 18% crude protein by partially replacing beet pulp in the LF and LG with canola meal, corn gluten meal and urea in the CON. Compared to the CON, feeding the LG diet did not affect any response variables measured in this study. The LF diet had higher DMI (26.0 vs. 22.4 kg/d, $P = 0.004$) than CON, but no difference in the passage rates of solid and liquid, averaging at 2.94 and 22.8%/h. The LF diet increased milk yield (36.4 vs. 33.0 kg/d, $P = 0.03$), and milk protein yield (1.18 vs. 1.05 kg/d, $P = 0.01$) without affecting milk fat yield (1.14 vs. 1.14 kg/d, $P = 0.23$). Chewing time was decreased with the LF diet (29.7 vs. 39.1 min/kg DMI, $P = 0.01$), which was likely due to reduced intake of large particles (particles retained on 19- or 8-mm screens of the Penn State Particle Separator) compared to cows fed the CON diet (2.70 vs. 3.61 kg/d, $P = 0.0001$). However, mean ruminal pH was not decreased and the duration that ruminal pH below 5.8 was not increased by feeding the LF diet, averaging at 6.19 and 258 min/d, respectively. These results indicate that DDGS can be effectively used as a partial replacement of barley grain without negatively affecting milk production, and that partial replacement of barley silage with DDGS can increase DMI and milk yield without affecting milk fat production providing ruminal pH is not depressed.

Key Words: barley silage, barley grain, DDGS

M266 In vitro intestinal digestion of ruminal undegraded protein of distiller grain. Y. L. Li*[1], W. Z. Yang[1], and L. E. Armentano[2], [1]*Agriculture and Agri-Food Canada, Research Center, Lethbridge, AB, Canada*, [2]*University of Wisconsin, Madison*.

Corn-based distiller grains (DG) from ethanol plant are derived either from fermentation of whole kernel (traditional) or only endosperm (fractional). The objective of this study was to investigate whether intestinal digestibility of ruminal undegraded protein (RUP) varies with source of DG and duration of incubation in the rumen. Eleven samples with 7 traditional DG with solubles (TraDGS), 1 fractional DG with solubles (endosperm DGS), 2 fractional DG without solubles (endosperm DG) and 1 mixture of bran and syrup (MBS) were tested using the original

three-step in vitro procedure. The 7 TraDGS were collected from 4 plants; the endosperm DGS was from 5th plant; and endosperm DG and MBS were from 6th plant. Rumen residues were produced by incubating nylon bags in the rumen of three lactating dairy cows for 8 h, 13 h and 18 h. The bag residues were pooled by animal and by ruminal incubation time. Samples were exposed to a shaking incubator and a pepsin (1 hr, 38°C, pH=1.9)-pancreatin (24 hr, 38°C, pH=7.8) enzymatic solutions to mimic digestion in the small intestine. There was no interaction (P>0.05) of DG with ruminal incubation time. The ruminal incubation time did not affect in vitro intestinal digestibility of RUP which was 80%, 81% and 81% for 8 h, 13 h and 18 h, respectively. The RUP digestibility of TraDGS from the 1st plant (86%) was similar to that the 2nd plant (83%), but was higher (P<0.05) than that from the 3rd (79% and 81%) and the 4th plant (76% and 77%). The RUP digestibilities of endosperm DGS (84%) and endosperm DG (84%) were the same, but different (P<0.05) from that of TraDGS from the 4th plant. The lowest digestibility of RUP was observed for the MBS (66%) due to likely the low digestion of corn bran. The results indicate that RUP digestibility of DG is variable depending on source of sample (i.e., plant) rather than the kernel processing prior to ethanol fermentation. In addition, ruminal retention time between 8 h and 18 h have little effect on measurement of the intestinal digestibility of RUP.

Key Words: distiller grains, intestinal digestion, in vitro

M267 Effects of diets containing elevated levels of modified wet corn distillers grains with solubles (DGS) on performance and carcass characteristics of beef steers. J. M. Carmack*[1], P. M. Walker[1], R. L. Atkinson[2], S. W. Reader[2], and B. R. Wiegand[3], [1]*Department of Agriculture, Illinois State University*, *Normal*, [2]*Animal Science, Food and Nutrition, Southern Illinois University*, *Carbondale*, [3]*Division of Animal Science, University of Missouri*, *Columbia*.

Little data is available regarding the effects of DGS inclusion rates above 50% in feedlot diets. The objectives of this study were to: 1) determine the effects of diets containing 70% DGS on feedlot performance and carcass characteristics of beef steers, 2) compare isocaloric and isonitrogenous diets to diets containing 40% DGS to clarify DGS effects as protein or energy. The treatments (DM %) were: 80 shelled corn/5 soybean meal/15 corn silage (CON), 40 DGS/45 shelled corn/15 corn silage (40 DGS), 40 DGS fed 56 d switched to 70 DGS/15 shelled corn/15 corn silage (40-70), 70 DGS/15 shelled corn/15 corn silage fed 56 d switched to 40 DGS (70-40), CON + soybean meal iso-nitrogenous to 40 DGS (N40) and CON + corn oil isocaloric to 40 DGS (E40). Angus cross steers (n=208; 425 ± 5.0 kg BW) were stratified by weight to 32 pens, with unequal replication. Three steers in each pen were harvested on d 106 when estimated low choice or higher quality grade. All remaining steers were harvested on d 142 when 80% were estimated low choice or higher quality grade. Significant differences were observed: N40 steers had lower harvest wt and DMI, and CON and E40 steers had higher G:F. No significant differences in carcass wt, ribeye area, marbling score, yield grade and KPH % were observed. Liver abscess scores were higher (p= 0.05) for CON than 40 DGS, 70-40 and N40. No significant differences in rib fat thickness were observed between CON, 40-70 and E40 but 40 DGS and 70-40 had less (p=0.02) rib fat than CON, 40-70 and E40 while 40 DGS and N40 were similar (p=0.08). The results of this study suggest DGS can be included in feedlot diets up to 70% of DMI and the energy contribution of DGS may have more impact than the protein contribution.

Key Words: carcass characteristics, feedlot performance, elevated levels of wet distillers grains

M268 Effects of high levels of distillers grains and composition of distillers grains on performance and carcass characteristics in steers. J. M. Carmack*[1], P. M. Walker[1], R. L. Atkinson[2], S. W. Reader[2], and B. R. Wiegand[3], [1]*Department of Agriculture, Illinois State University*, *Normal*, [2]*Animal Science, Food and Nutrition, Southern Illinois University*, *Carbondale*, [3]*Division of Animal Science, University of Missouri*, *Columbia*.

Few studies have been conducted comparing modified wet corn distillers with solubles (DGS) and dried distillers grains with solubles (DDGS) on feedlot performance and carcass characteristics when fed at greater than 50% of diet DM. Data of two companion studies were pooled and analyzed as one study. Dietary treatment pen and their interactions were independent variables. Steer performance data were dependent variables. The objective of the studies were to: 1) determine the effects of diets containing 70% DGS or DDGS on feedlot performance and carcass characteristics of beef steers, 2) compare isocaloric and isonitrogenous diets to diets containing 40% DGS or DDGS to evaluate protein and energy effects of distillers grains. The dietary treatments (DM%) were: 80 shelled corn/5 soybean/15 corn silage (CON), 40 DGS or DDGS/45 shelled corn/15 corn silage (40), 40 fed in tandom with 70 DGS or DDGS/15 shelled corn/15 corn silage (40-70), 70 DGS or DDGS/15 shelled corn/15 corn silage fed in tandom with 40 (70-40), CON + soybean meal isonitrogenous to 40 (N40) and CON + corn oil isocaloric to 40 (E40). Harvest weights were lower (p=0.001) for N40 steers compared to 40 and compared to all other treatments (p=0.02). No differences (p=0.22) in ADG were observed between treatments. Steers fed CON and E40 had greater (p=0.01) G:F compared to 40-70 and 70-40 but were similar to 40 and N40. No significant differences in carcass measurements between treatments were observed but CON, N40 and E40 tended to result in greater rib fat (p=0.06) and higher yield grades (p=0.08) than DGS/DDGS. Analyses of these data found little difference in performance for steers fed either wet or dry distillers grains and similar performance for steers fed up to 70% distillers grains.

Key Words: high levels distillers grains, steer performance

M269 Effect of varying ratios of corn to wheat grain in ethanol production on fermentation of ethanol by-product in batch culture. W. Z. Yang*[1], J. J. Mckinnon[2], T. A. McAllister[1], K. A. Beauchemin[1], and D. J. Gibb[1], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [2]*University of Saskatchewan*, *Saskatoon, SK, Canada*.

The blend of corn and wheat with variable ratios of both grains are often used to be cost effective for ethanol production in western Canada. Feed value may be different between corn- and wheat-based dried distiller grains with solubles (DDGS) derived from ethanol production. The objective of this study was to determine the effects of the ratio of corn to wheat in the blend grain on nutrient composition and fermentation characteristics of DDGS. Forty-one DDGS samples varied with ratio of corn to wheat (corn:wheat; 100:0, 70:30, 30:70 or 0:100) were measured in batch culture during 0, 4, 8, 14, 24 and 48 h of incubation. The mean content of OM (95%), NDF (33%) and ADF (11%) were similar among the 4 categories samples. However, variation of individual sample within category could be large and ranged from 28 to 41% for NDF, and 8 to 14% for ADF. Concentrations of total VFA (117 to 127 m*M*), acetate (65 to 69 m*M*) and propionate (23 to 26 m*M*) at 24 h of incubation were not affected (P > 0.05) by the ratio of corn to wheat, whereas, variation of individual samples was substantial and ranged from 91 to 160 m*M* for total VFA. Dry matter disappearance (DMD) linearly (P < 0.01) increased from 20 to 54% with increasing incubation time from 0 to 48 h without having reached a plateau. Mean DMD (average of 0 to 48h)

were similar with values of 37, 40, 38 and 38% for the 100:0, 70:30, 30:70 or 0:100 of corn to wheat DDGS, respectively. The NDF content of original DDGS was moderately correlated (r=0.53, P < 0.01) with fermentation pH, but was not correlated with DMD. The results indicate that the ratio of corn to wheat in the blend of grain had minimal effects on fiber content, fermentation and DMD of DDGS in batch culture. However, nutrient content and digestibility of individual DDGS sample could vary substantially and thus need to be individually considered for formulating ration.

Key Words: distiller grain, fermentation, batch culture

M270 Effects of feeding glycerol on fermentation kinetics of alfalfa hay. N. A. Krueger*[1], R. C. Anderson[1], L. O. Tedeschi[2], W. K. Krueger[2], and D. J. Nisbet[1], [1]*USDA-ARS-Food Feed Safety Research Unit, College Station, TX*, [2]*Texas A&M University, College Station*.

This study aimed to determine the effect of feeding various levels of glycerol on neutral detergent fiber (NDF) digestibility and volatile fatty acid (VFA) profile using the in vitro gas production technique. This experiment was set up as a completely randomized design with 5 treatment (TRT) levels of glycerol (0, 5, 10, 20, 40% as fed) and 4 replicates (125 ml Wheaton bottles). Each bottle received 0.2 g of substrate, which consisted of ground (2 mm) alfalfa hay plus glycerol. Substrates were inoculated with rumen fluid, from a ruminally cannulated cow consuming bermudagrass hay, and incubated for 48 h. Gas production was measured using a computerized gas monitoring apparatus. A logistic 2-pool model was used to fit the gas production. Treatment differences were analyzed using the PROC GLIMMIX of SAS. Orthogonal contrasts were used to evaluate the effects of glycerol levels on the parameters. Gas fermentation in the first (fast) pool (glycerol fraction) increased linearly (P < 0.001; from 8.87 to 18.4 ± 0.81 ml) as the amount of glycerol increased. Additionally, higher levels of glycerol resulted in a quadratic decrease (P = 0.012; from 0.18 to 0.12 ± 0.02 1/h) of the first pool fractional rate of fermentation (kd). Even though gas production in the second (slow) pool (NDF fraction) decreased quadratically (P = 0.009; from 9.03 to 4.27 ± 0.46 ml), there was no clear relationship when glycerol levels were between 0 and 20%. Glycerol consistently decreased (from 0.06 to 0.03 ± 0.004 1/h) the kd in a linear fashion (P = 0.002). The NDF digestibility did not differ (P = 0.53) among TRT which is consistent with the lack of change in gas production in the fiber fraction for glycerol levels up to 20%. Increasing amounts of glycerol had a linear effect on acetate (P = 0.002) and quadratic effect on propionate (P = 0.011) concentrations as well as a quadratic effect on the acetate to propionate ratio (P < 0.0001) but did not affect butyrate (P = 0.06) and iso-butyrate (P = 0.32) concentrations. These results indicated that glycerol supplementation greater than 20% may negatively affect fiber digestion and alter the VFA profile.

Key Words: glycerol, ruminant, digestion

M271 Performance of post-weaned Holstein heifer calves fed grain mixes with glycerin as an energy source. G. Golombeski*[1], M. Raeth-Knight[1], B. Ziegler[2], R. Larson[2], D. Ziegler[3], H. Chester-Jones[3], and J. Linn[1], [1]*University of Minnesota, St. Paul*, [2]*Hubbard Feeds, Mankato, MN*, [3]*University of Minnesota, Southern Research and Outreach Center, Waseca*.

Ninety dairy heifers (86.1 ± 0.86 kg BW) were used in a 112-d study to evaluate feed intake and performance from 9 to 25 weeks of-age. Heifers were housed in 9.14 x 4.57 m pens (6 heifers/pen) within a naturally ventilated bedded-pack pole barn and randomly assigned to 1 of 3 grower diets among 5 replicated pens/treatment. Treatments were 1) 18.6% CP (DM) pelleted grain mix fed at 2.72 kg/d (CON); 2) 18.8% CP pelleted grain mix with 3.0% glycerin fed at 2.72 kg/d (3%GLY); 3) 19.2% CP pelleted grain mix including 6.0% glycerin fed at 2.72 kg/d (6%GLY). From d 85-112 all heifers were fed (2.27 kg/d) a common whole corn and pellet grain mix (18.7% CP). All heifers had access to a 16.5% CP hay free choice for the duration of the trial. Data were analyzed as repeated measures using the PROC MIXED procedure of SAS and contrasts were used to compare treatment affects. Under the conditions of this study, heifers fed 6%GLY had improved daily gain through d 84, compared to heifers fed CON or 3%GLY. Feeding 3%GLY or 6%GLY improved feed efficiency compared to those heifers fed CON. The study suggested that up to 6% glycerin can effectively replace corn in grain mixes fed to post-weaned heifers.

Table 1.

	Treatments				Contrasts	
Item	CON	3%GLY	6%GLY	SEM	linear	quadratic
Day 1 to 84						
ADG, kg/d	0.96	0.97	1.00	0.01	0.05	NS
Grain DMI, kg/d	2.46[a]	2.41[b]	2.43[c]	0.01	0.01	<0.001
Total DMI, kg/d	3.80	3.75	3.73	0.04	NS	NS
Feed/gain, kg	3.92[a]	3.86[b]	3.71[c]	0.04	0.001	NS
Day 1 to 112						
ADG, kg/d	0.96	0.97	0.99	0.02	NS	NS
Grain DMI, kg/d	2.36[a]	2.32[b]	2.34[c]	0.01	0.03	0.001
Total DMI, kg/d	4.14	4.10	4.12	0.04	NS	NS
Feed/gain, kg	4.36	4.27	4.12	0.09	0.08	NS

[a,b]Means within a row without common superscripts are different at P < 0.05.

Key Words: dairy heifers, glycerin, performance

M272 Effects of replacing starch or sugar with glycerin in diets for dairy cows on production and blood metabolites. D. E. Rico*, Y.-H. Chung, C. M. Martinez, T. Cassidy, K. S. Heyler, and G. A. Varga, *Department of Dairy and Animal Science, The Pennsylvania State University*, *University Park*.

The objectives of this experiment were to evaluate the effects of glycerin as a feed ingredient replacing starch or sugar in the diet of dairy cows on dry matter intake (DMI), milk yield and blood metabolites. Nine multiparous Holstein cows (DIM = 112 ± 8.6) were used in a 3 x 3 replicated Latin square design. Glycerin (42.5% food grade glycerol) was fed at 4% of ration DM replacing equivalent amounts of pure corn starch or sugar (sugar cane molasses) in the diet. The trial had 3 experimental periods 14 d each and d 1 through 9 were used for adaptation. Daily DMI and milk yield were measured and milk samples were taken on d 13 of each period. Blood samples were drawn from the jugular vein post-feeding for 4h on the last day of each period. Dry matter intake did not differ among treatments and averaged 27.7 kg/d. There was a numerical trend (P = 0.08) for higher milk yield for cows provided the molasses vs. glycerin (43.1 vs. 40.8 kg/d). Milk yield for cows provided the starch treatment (41.4 kg/d) did not differ from those fed glycerin. Milk protein was lower for glycerin (P < 0.01) than for molasses or starch and the values were 2.94, 3.03, 3.02%, respectively. Other milk components were not different among treatments. Blood concentrations

of glucose and β-hydroxybutyrate were not affected by treatment and averaged 69 mg/dL and 747 µmol/L, respectively. Blood concentration of insulin was greater (P < 0.05) for cows fed glycerin than those cows fed molasses (0.72 vs. 0.4 ng/ml), however this did not differ from cows fed starch. At the level of inclusion used in this experiment, glycerin did not affect DMI or milk yield. β-hydroxybutyrate values do not suggest significantly increased butyric acid in the rumen due to glycerin fermentation. These results indicate that glycerin can replace starch or molasses in the diet without negative effects on performance and can be considered in dairy rations when prices are favorable.

Key Words: glycerin, milk production, blood metabolites

M273 Effects of increasing concentrations of dietary glycerol on ruminal environment and digestibility in lactating dairy cows. J. Boyd*, J. W. West, and J. K. Bernard, *University of Georgia*, *Tifton*.

A study was conducted to evaluate effects of increasing concentrations of dietary glycerol on rumen environment, blood metabolites, and nutrient digestibility. Six rumen cannulated Holstein cows averaging 70 DIM and 37.9 kg/d of milk were used in the study. The study was conducted from May to July 2008. Experimental design was a 3x3 Latin square with a 3wk adjustment period followed by a 1wk collection period. Cows were blocked into groups of 2 and progressed through the three 4wk periods until exposed to all treatments. Diets were corn silage based and balanced to be iso-caloric and iso-nitrogenous. Treatments were control (C), 200g glycerol h/d (G2), and 400g glycerol h/d (G4). DMI was higher for C (24.17 ± 0.29) compared with G2 (22.99 ± 0.29) versus G4 (22.96 ± 0.29) at (P<0.01). Milk yield was greater (P<0.01) for C (37.8 ± 0.47) than G4 (35.83 ± 0.47), but G2 (37.2 ± 0.47) was not significantly different. Milk protein percentage was lower (P<0.001) for C and G2 than for G4 (2.75%, 2.75%, and 2.8%). Milk fat percentage was lower (P<0.01) for G2 (3.31 ± 0.03) and G4 (3.35 ± 0.03) compared with C (3.46 ± 0.03). A significant effect (P<0.04) for ECM was noted between C (40.0 ± 0.34) and G4 (38.8 ± 0.34), but G2 (39.4 ± 0.34) was not effected. A trend (P<0.18) for improved efficiency (ECM/DMI) was noted for G2 and G4 (1.73 ± 0.02) versus C (1.68 ± 0.02). No effect on ruminal pH and ammonia (mean 6.06 and 11.19 mg/dl) was observed. No effect on DM, NDF, ADF, or CP digestion or on blood glucose (63 mg/dl) was noted. A trend for lower plasma urea N (P<0.09) was seen for G4 (20.5 mg/dl) versus C and G2 (21.7 and 21.8 mg/dl). Molar proportions of propionate tended to increase whereas acetate tended to decrease with G4 versus C. The decrease in milk fat percentage between G2 and G4 versus C and the increase in milk protein percentage with G4 versus C supports the ruminal data. The addition of glycerol to the diet may alter ruminal VFA profile and improve efficiency in dairy cows.

Key Words: dietary glycerol, ruminal environment, efficiency

M274 Response of dairy cows to the complete substitution of corn by crude glycerin. O. F. Zacaroni[1], N. M. Lopes[1], S. Siécola Júnior[1], G. S. Dias Júnior[1], L. L. Bitencourt[1], B. F. Carvalho[1], J. R. M. Silva[2], R. A. N. Pereira[3], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, MG, Brazil*, [2]*Centro Federal de Educação Tecnológica*, *Januária, MG, Brazil*, [3]*Better Nature Research Center*, *Ijaci, MG, Brazil*.

This trial evaluated the complete replacement of finelly ground mature corn by the biodiesel byproduct crude glycerin. Eighteen Holsteins (227±88 DIM, five primiparous) received a sequence of three treatments, in six 3x3 Latin Squares, with 28-day periods and 21 days of adaptation. Only the contrast Control *vs.* Glycerin will be presented. Diets contained (% of DM): Corn silage (27.7), tifton hay (6.1), citrus pulp (19.4), whole cottonseed (8.6), Megalac (1.2) and a mineral-bicarbonate premix (3.5). The Control TMR contained 14.8% of corn and 18.6% of soybean meal, replaced in Glycerin by 12.3% of crude glycerin and 21.3% of soybean meal. The substitution of corn by glycerin tended to increase the total tract apparent digestibility of DM (DM D) and had no effect on rumen pH 12 hours post feeding. Daily ingestion time was reduced by glycerin, but the intake rate was increased. Crude glycerin reduced milk secretion without affecting feed intake, resulting in lower ratio of milk yield to DMI. *Funded by Nutron/Provimi.*

Table 1.

	Glycerin	Control	SEM	P
Milk yield	21.3	23.4	.58	.02
DMI	16.7	16.8	.37	.85
Fat yield	.750	.797	.027	.24
Protein yield	.680	.736	.024	.13
Lactose yield	.942	1.050	.028	.01
Fat %	3.53	3.43	.097	.48
Protein %	3.24	3.15	.063	.32
Lactose %	4.42	4.46	.070	.63
Milk energy (Mcal/d)	14.41	15.58	.435	.07
Milk yield/DMI	1.30	1.40	.037	.05
Rumen pH	6.53	6.41	.074	.29
DM D (%)	73.8	70.1	.47	.10
Ingestion time (min/d)	228	254	9.0	.05
Ingestion time (min/DMI)	12.6	14.2	.49	.03

Key Words: glycerol, glycerin, starch

M275 Glycerol supplementation to corn silage- or cottonseed hull-based diets for lactating dairy cows. J. H. Shin*[1], S. C. Kim[1,2], D. Wang[1], A. T. Adesogan[1], and C. R. Staples[1], [1]*Department of Animal Sciences, University of Florida*, *Gainesville*, [2]*Department of Animal Science, Gyeongsang National University*, *Jinju, Gyeongsangnam, South Korea*.

Objective was to evaluate the effect of glycerol supplementation to corn silage (CS)– or cottonseed hull (CSH)–based diets on DMI, milk yield (MY), blood metabolites, and ruminal fermentation of lactating cows. Cows (n=24; days in milk 116 ± 13) were assigned to 6 dietary treatments for 3 consecutive 27–d periods (14 d adaptation and 13 d collection). Treatments were arranged in a 2 by 3 factorial design: 2 forage sources (CS at 37% and alfalfa hay at10% of dietary DM vs. CSH at 25% and bermudagrass hay at 10% of dietary DM) and 3 concentrations of glycerol (0, 5, and 10% of dietary DM). Additionally, 4 ruminally canulated cows arranged in a 4 by 4 Latin square design were assigned to 4 treatments (CS vs. CSH and 0 vs. 10% glycerol) in a 2 by 2 factorial design (20–d periods of 14 d adaptation and 6 d collection). Glycerol (90% DM; donated by West Central) replaced ground corn in the diet. Cows were milked twice daily and milk sampled at a.m. and p.m. on d 19, 20, 26, and 27 of each period. Blood was taken via coccygeal vessels on 16 d of each period. Ruminal fluid from canulated cows was collected hourly for 12 h on d 16 and measured for pH. Body weight (BW) was measured for 2 consecutive days at the start and end of each period. Cows fed CSH had greater DMI (29.7 vs. 24.4 kg/d; 4.26 vs. 3.58% of BW), MY (36.9 vs. 35.2 kg/d), milk fat (1.2 vs. 1.1

kg/d), milk protein (1.1vs. 1.0 kg/d and 2.99 vs. 2.87%), BW change (0.68 vs. 0.06 kg/d), blood urea nitrogen (16.5 vs. 13.8 mg/dl), runimal fluid pH (6.5 vs. 6.1), ruminal solids (8.7 vs. 12.3 kg DM), and liquid passage rate from rumen (0.16 vs. 0.13/h) than those fed CS, but lower milk efficiency (FCM/DMI; 1.10 vs. 1.24). Milk fat concentrations and DMI were greatest whereas feed efficiency (MY/DMI) was lowest for cows fed 5% glycerol diets. Concentration of blood urea nitrogen decreased linearly as intake of glylcerol increased (16.1, 15.5, and 13.8 mg/100 ml). Glycerol supplementation did not affect blood glucose, ruminal fluid pH, or rumen solids volume. Feeding glycerol tended to increase MY of cows fed CS but tended to decrease MY of cows fed CSH (forage by glycerol interaction).

Key Words: glycerol, dairy

M276 The effects of feeding glycerol on rumen fermentation and bacteria. R. B. Potu*[1], A. A. AbuGhazaleh[1], D. Hastings[1], S. Abo El-Nor[2], and S. Ibrahim[3], [1]*Southern Illinois University, Carbondale*, [2]*Egyptian National Research Center, Cairo, Egypt*, [3]*North Carolina A&T State University, Greensboro*.

The effects of substituting corn with glycerol with respect to feed digestibility, fermentation, bacterial DNA concentration and rumen fatty acids (FA) were investigated using continuous fermenters. Four fermenters were used in a 4 x 4 Latin Square design with four 10 d consecutive periods. Four (T1, T2, T3, T4) treatment diets (60:40 forage to concentrate) were fed at 45 g/d dry matter (DM) in three equal portions. The forage consisted of alfalfa pellets. The grain mix contained corn, SBM, soy hulls, minerals and vitamins. Glycerol replaced corn in the grain mix at proportions of 0% (T1; control), 15% (T2), 30% (T3) and 45% (T4). On days 8, 9, and 10 of each diet processing period, 25% of the overflow was collected from each fermenter and analyzed for chemical composition. On day 10 of each period, additional rumen samples were collected from each fermenter at 3 and 6 hr after the morning feeding and analyzed for VFA, NH3, FA, and microbial DNA concentration. Results showed that NDF digestibility was lower ($P < 0.05$) for T3 and T4 compared to T1 and T2. Glycerol had no effects on rumen pH, NH3 concentration, and DM and ADF digestibility. Acetate levels were lower ($P < 0.05$), while butyrate, valerate and isovalerate levels were higher ($P < 0.05$) for the T3 and T4 compared to T1 and T2. DNA concentrations for *Selenomones ruminantium* were lower ($P < 0.05$) with the T3 and T4 compared to the T1 and T2. In addition, the DNA concentrations for *Butyrivibrio fibrisolvens* and total bacteria were lower ($P < 0.05$) with T4 compared to the other diets. No significance differences for the DNA concentrations for *Ruminoccocus albus* were observed. The concentrations of C18:1 and C18:2 were higher ($P < 0.05$) with T1 compared to the other diets. Concentrations of C18:1 trans also were higher ($P < 0.05$) with T1 compared to T3 and T4. In conclusion, these results suggest that glycerol at proportions of up to 15% could be used to replace corn in ruminant animals′ diet without adversely affecting fermentation or ruminal bacteria. Higher levels may adversely affect fiber digestion and bacterial population and negatively impact acetate production.

Key Words: glycerol, fermentation, microbial

M277 Effects of replacing corn starch or sugar with glycerin on ruminal fermentation during continuous culture. D. E. Rico*, Y.-H. Chung, C. M. Martinez, T. Cassidy, K. S. Heyler, and G. A. Varga, *Department of Dairy and Animal Science, The Pennsylvania State University, University Park*.

The objective of this experiment was to evaluate the effects of glycerin as a feed ingredient replacing starch or sugar in the diet on ruminal fermentation using a single effluent continuous culture system. A 3 x 3 Latin square design was used with glycerin as the treatment and pure corn starch and sugar as 2 separate controls such that glycerin (42.5% food grade glycerol) was fed at 4% of ration DM replacing equivalent amounts of pure corn starch or sugar (sugar cane molasses) in the diet. The trial had 3 experimental periods of 9 d each, using the first 6 d for adaptation and the last 3 d for sampling. Fermenter effluent were collected daily and subsampled for analysis of volatile fatty acids (VFA), ammonia and dry matter (DM) content. Fermenters (1015 to 1040 ml in volume) were incubated with ruminal fluid (1 L) and ruminal digesta (25 g) from a cow receiving a diet with a 55:45 forage to concentrate ratio. Fermenters were fed 25 g DM of the experimental diets three times per day and the solids retention time was set at 24 h. Replacing starch or molasses with glycerin, did not affect total VFA concentration (90.8 mmol/L) however, there was a numerical trend ($P = 0.07$) for higher acetate to propionate ratio when fermenters were provided glycerin vs. molasses (2.8 vs. 2.5). Butyrate molar proportion was lower ($P < 0.01$) for glycerin compared to starch or molasses (13, 16, and 18% of total VFA, respectively). Ammonia was highest ($P < 0.01$) for glycerin compared to molasses or starch and concentrations were 24.9, 8.8 and 11.8 mg/L, respectively. Dry matter digestibility was lower ($P < 0.05$) for glycerin than for starch (39 vs. 42%) but was not different from the molasses treatment (39%). These results suggest that diet digestibility is reduced by replacing some of the dietary starch with glycerin under the present experimental conditions. In addition, higher ammonia concentrations and lower butyrate in fermenters fed glycerin perhaps reflect changes in bacterial populations and inefficient use of nitrogen as ammonia compared to sources of starch or sugar; however, this requires further verification.

Key Words: glycerin, continuous culture, ruminal fermentation

M278 Effect of glycerol level in feedlot diets on animal performance. B. R. Ilse* and V. L. Anderson, *Carrington Research Extension Center, North Dakota State University, Carrington*.

Two separate feedlot trials were conducted (receiving and finishing) to evaluate the effects of increasing levels of glycerol on animal performance. Receiving trial steers (n = 198) were allotted by BW (283 ± 15.6 kg) in a randomized complete block design and sorted into 16 identical pens (four pens per treatment). Treatments were 0, 6, 12, and 18 percent glycerol (70% DM; water was added to reach 70% DM to increase the viscosity and decrease freezing temperature) on a DM basis replacing dry-rolled corn and co-products in the diet (25 Mcal NEg). Dry matter intake was quadratically affected during the 30 d feeding period ($P = 0.05$) with 9.24; 9.56; 9.58; 8.83 kg consumed for 0, 6, 12, and 18 percent glycerol, respectively. Gains were not affected by glycerol level ($P = 0.78$) and feed efficiency was similar ($P > 0.92$) among treatments. Finishing trial heifers (n = 132; BW = 414.3 ± 15.1 kg) were blocked by weight and allotted to one of 16 pens, assigned to 0, 6, 12, 18 percent glycerol (85% DM) dietary treatments (28 Mcal NEg). Dry matter intake linearly decreased during the 102 d feeding period ($P = 0.05$; 12.75; 12.68; 12.56; 11.86 kg for 0, 6, 12, and 18 percent glycerol, respectively). Gains were not affected by glycerol level ($P = 0.26$) during any of the four individual 28 d weigh periods or overall. Feed efficiency was also similar ($P > 0.22$) among treatments. If the availability of feed grade glycerol increases with the increase in biodiesel production, glycerol could be a viable alternative to corn in feedlot diets.

Key Words: glycerol, beef, feedlot

M279 Kinetics of fermentation of apple residues. Y. Castillo-Castillo[1], O. Ruiz-Barrera*[1], A. Elias-Iglesias[2], C. Arzola-Alvarez[1], C. Rodriguez-Muela[1], J. A. Ortega-Gutierrez[1], O. LaO-Leon[2], C. Holguin-Licon[1], and Y. Ricardo-Olive[3], [1]*Facultad de Zootecnia y Ecologia, Universidad Autonoma de Chihuahua*, *Chihuahua, Chihuahua, Mexico*, [2]*Instituto de Ciencia Animal*, *La Habana, Cuba*, [3]*Instituto de Investigaciones Agropecuarias Jorge Dimitrov*, *Bayamo,Granma, Cuba*.

Several data indicate that nutritive value of agro-industrial residues may be improved by using solid state fermentation, by the way of promoting growth of beneficial microorganisms and enhancing amount of crude and true protein, linked to degradation of lignocellulosic compounds. Most solid state fermentation (SSF) studies are conducted under aerobic environments, but knowledge concerning the effects of non- aerobic conditions is limited. The objective of this study was to evaluate fermentative pattern, microbial growth, and chemical composition of apple waste under partial aerobic conditions using four times of incubation (0, 24, 48, 72 h) and a complete random design with four repetitions in every time of incubation. Apple waste was added with urea (1.5%), ammonium sulphate (0.2%) and mineral and vitamin salts (0.5%) and fermented in serum flasks at 32º C during three days. A significant reduction on pH (P≤0.007) was shown (4.13, 3.85, 3.86 and 3.81) during time of incubation; meanwhile, lactic acid concentration increased (P ≤0.0001) (22.24, 22.50, 22.87 and 23.75 µg/g DM) as well as ammonium nitrogen (N-NH3) (1.92, 1.95, 1.98 and 2.00 mmol/g DM) (P≤0.0001). Total bacteria, lactobacilli and yeast counts (expressed in log10) was drastically reduced (P≤0.0001) during time (7.14, 5.96, 4.73 and 4.55 ufc/ml-1; 8.60, 8.14, 8.73 and 8.53 ufc/ml-1; 7.42, 7.35, 6.0 and 4.80 ufc/ml-1, respectively). Crude protein was not affected by time of incubation (36.19, 36.02, 35.57 and 35.47) (P≥0.05), however, true protein (16.89, 21.15, 19.5 and 18.12) showed statistical difference, decreasing after the 24 h (P≤0.03). Neutral detergent fiber (%) was not affected by time of incubation, but acid detergent fiber concentration (%) was significantly decreased (41.57, 41.45, 38.8 and 39.42) (P≤0.0001). We conclude that pH had a big impact on SSF, affecting total counts of microorganisms, probably due to the metabolic activity produced during growth of lactic bacteria. On the other hand, SSF was efficient on the improvement of chemical composition parameters.

Key Words: apple waste, fermentation, microorganisms

M280 Feeding behavior of yearling bulls fed a finishing diet containing low pectin wet citrus pulp silage. J. O. Sarturi*[2], L. G. Nussio[1], M. Zopollatto[1], J. T. Vasconcelos[2], and J. G. M. Munoz[1], [1]*University of São Paulo*, *São Paulo, SP, Brazil*, [2]*University of Nebraska*, *Scottsbluff*.

The objective of this study was to evaluate the feeding behavior of animals fed finishing rations containing low pectin wet citrus pulp silages (LPWCPS). Fifty-four yearling bulls (Nelore/Angus or Nelore/Santa Gertrudis x Braunvieh crosses; BW = 389 ± 32kg) were assigned to a complete randomized block design (18 pens, 3 bulls per pen). Cattle were fed the following diets: C (control diet, without LPWCPS); A (diet with LPWCPS and which received the additive Sodium benzoate during ensiling); B (diet with LPWCPS without additive). Diets were composed of (DM basis) sugar cane bagasse fine chopped (15.04%), pelleted citrus pulp (75.35 or 52.75%), cottonseed meal (5.18%), urea (2.05%), sodium bicarbonate (0.96%), mineral-vitamin mix (1.68%) and LPWCPS (0 or 22.6%). Diets were formulated to be isoproteic (13.5%) and with a positive balance of DIP and MP (NRC, 1996; level 1). Evaluations were carried out at intervals of 10 min., during 24 h, consecutively, at approximately d 60. Data were analyzed using the PROC MIXED procedure of SAS. Means were compared using the Tukey test, with 5% significance. Cattle fed C spent more time (P<0.05) ruminating and chewing per NDF unit when compared to other treatments (36, 25, and 23; 54, 44, and 41 min/kg of NDF, for C, A and B, respectively). Diet C had lower (P<0.05) NDF content (38.9, 47.9, and 47.2%, for C, A, and B, respectively). There were no differences (P>0.05) between treatments for rumination time/d, rumination time/kg of DM, intake/d, intake/kg of NDF, intake/kg of DM, chewing time/d, chewing time/kg of DM, water intake/d and resting time/d (321, 282 and 247; 14, 12 and 11; 160, 201 and 202; 18, 18 and 19; 7, 9 and 9; 481, 483 and 449; 21, 21 and 19; 10, 9 and 13; 948, 948 and 977 min, for C, A and B, respectively). The lower time spent ruminating and chewing per unit of NDF of cattle fed the diet with LPWCPS (with or without additive during the ensilage process) is a good indicator of the low physical effectiveness of the fiber present in this byproduct.

Key Words: byproduct, benzoate, additive

M281 Feeding behavior of yearling bulls fed a finishing diet containing low pectin wet citrus pulp. J. O. Sarturi*[2], L. G. Nussio[1], M. Zopollatto[1], J. T. Vasconcelos[2], and L. J. Mari[1], [1]*University of São Paulo*, *São Paulo, SP, Brazil*, [2]*University of Nebraska*, *Scottsbluff*.

The aim of this trial was to evaluate the feeding behavior of animals fed finishing diets containing low pectin wet citrus pulp (LPWCP) or not. Forty-eight bulls (24 Nelore and 24 Canchin; BW = 448 ± 45kg) were randomized by blocks in a 2 x 2 factorial (breed and diet) arrangement with 16 pens (3 bulls per pen). Cattle were fed the following diets: C (control diet without LPWCP) and B (diet with LPWCP). Diets were composed of (DM basis) sugar cane bagasse fine chopped (15%), pelleted citrus pulp (75.2 or 52.6%), soybean meal (5%), urea (2.1%), sodium bicarbonate (1%), mineral-vitamin mix (1.7%), and LPWCP (0 or 22.6%). Diets were formulated to be isoproteic (13.5%) and with a positive balance of DIP and MP (NRC, 1996; level 1). Behavioral evaluations were carried out at intervals of 10 min., during 24 h, consecutively, at approximately d 60. Data were analyzed using the PROC MIXED procedure of SAS. No interactions (P>0.05) were observed for breeds and diets. Means were compared with LSMEANS, using 5% level of significance. Cattle on diet C spent more time (P<0.05) ruminating per NDF unit (66 vs. 46 min/kg of NDF) and had greater (P<0.05) chewing activity per NDF unit (125 vs. 99 min/kg of NDF) when compared to cattle fed diet B. The diet C, however, had lower (P<0.05) NDF content when compared to diet B (36.1 vs. 45.3%). There were no differences (P>0.05) between dietary treatments for rumination time/d, rumination time/kg of DM, intake/d, intake/kg of NDF, intake/kg of DM, chewing time/d, chewing time/kg of DM, water intake/d and resting time/d (187 vs. 163; 24 vs. 20; 168 vs. 180; 60 vs. 53; 21 vs. 23; 355 vs. 343; 45 vs. 43; 22 vs. 26; 1061 vs. 1070 min, for C and B, respectively). The lower time spent ruminating and chewing per unit of NDF for the diet with LPWCP can be a strong indicator of the low physical effectiveness of the fiber present in this byproduct. The addition of LPWCP increased of the NDF level of the diet B, but animals had shorter rumination and chewing time per unit of NDF.

Key Words: rumination, byproduct, chew

M282 Dry matter and nutrient intake of sheep fed with different levels of cashew nut in the diet. E. S. Pereira*, P. G. Pimentel, J. G. L. Regadas Filho, M. S. S. Carneiro, and I. S. G. Maia, *Universidade Federal do Ceará*, *Fortaleza, Ceará, Brasil*.

The objective of this study was to evaluate the effect of different levels of cashew nut on the dry matter and nutrient intake of sheep. Eight Santa Ines wethers, averaging 25 kg BW, were allotted in a replicated X 4 Latin square, and maintained in metabolic cages. Cashew nut was fed in the concentrate at the levels of 0; 10; 20 and 30%; the forage portion of the diet was Tifton hay. The diets were offered once daily in 60:40 forage:concentrate ration. Periods were 16 d long; the first 10 d of each period were for dietary adaptation, with weight and samples of diets and refusals taken during day 11 to 16 of each period to determine the consumption of dry matter and nutrients. Meals were offered to allow 10% refusals according to the calculated diet consumed on the previous day. The samples were analyzed for dry matter (DM), organic matter (OM), crude protein (CP), ether extract (EE), ash (Ash), neutral detergent fiber (NDF), acid detergent fiber (ADF) and total carbohydrates (TC). The ether extract content of the experimental diets was, respectively, 2.97; 4.35; 5.95 and 7.78%, to the levels 0; 10; 20 and 30% of cashew nut inclusion. The intake of the diets without cashew nut and at the level of 30% varied of 1004.29 to 794.24; 929.04 to 730.39; 152.68 to 120.30; 75.25 to 63.85; 453.77 to 340.99; 246.69 to 193.00 and 745.65 to 489.48 g/day, respectively, for DM, OM, CP, Ash, NDF, ADF and TC, showing quadratic behavior (p=0.05). Dry matter intake as percentage of live weigh was not affected by the treatments. Ether extract intake, as expected, increased linearly (30.72; 47.50; 60.85 and 69.18 g/day) with the addition of the byproduct. The high content of lipids in cashew nut possibly altered the dry matter and nutrient intake of sheep diets.

Key Words: byproducts, lipids, ruminants

M283 Antioxidant activity of plasma and carcass characteristics of mature cows fed diets with manzarina. C. Rodríguez-Muela[1], S. Romero-Villalobos*[1], H. E. Rodríguez-Ramírez[2,1], A. C. Arzola-Alvarez[1], A. Flores-Mariñelarena[1], G. Corral[1], O. La O-León[3], and J. A. Grado-Ahuir[1], [1]*Universidad Autónoma de Chihuahua*, *Chihuahua, Chihuahua, México*, [2]*Instituto Nacional de Investigaciones Agrícolas Forestales y Pecuarias*, *Delicias, Chihuahua, México*, [3]*Instituto de Ciencia Animal*, *La Habana, Cuba*.

The objective of the present study was to evaluate the effect of the inclusion of a fermented feed of apple pomace (manzarina) upon the antioxidant activity of blood plasma and carcass characteristics of mature feedlot cows. Manzarina has a high content of phenolic compounds and yeasts. It is known that some phenolic compounds have antioxidant properties. Twenty-five Angus x Charolais mature cows with an average initial body weight of 407.1±9.3 kg were fed for 75 d. Diets had the same level of CP (9.3%) and energy (NEm 1.7, NEg 1.09 Mcal kg^{-1}) on dry matter basis. Control diet (CT) was prepared with corn silage (40.0%), oat hay (14%), steam rolled corn (34.2%), cotton seed (8%), sugar cane molasses (3.0%), salt (0.3%), mineral supplement (0.3%) and calcium carbonate (0.2%)(as fed basis). Manzarina treatment diet had 15% of manzarina in the whole ration (MT). Manzarina replace to the steam corn rolled (7%) and the oat hay (8%) in MT. Variables evaluated were antioxidant activity (AA) of blood plasma (FRAP technique) at the beginning and at the end of the feeding period. Carcass yield (CY), rib eye area (RA) and fat thickness (FT) were measured at slaughter. A complete random design was used for carcass variables using treatment as main effect. AA was analyzed with a mixed model. Treatment (T), sampling moment (SM at the begining and at the end of the trial) and their interaction were the fixed effects. The cow nested on T*SM interaction was the random effect. AA of MT cows (4.775±0.08 mM Fe_2 eq.) was higher ($P<0.05$) than AA of CT cows (4.546±0.08). AA of cows plasma at the beginning of feeding period (4.03±0.07) was lower ($P<0.01$) than AA after feeding period (5.29±0.07 mM Fe_2 eq.). There was no effect of diet on the carcass characteristics ($P>0.05$). CY values were 51.4±0.9% and 49.4±0.9% for MT and CT. RA values were 9.5±0.5 in^2 and 9.1±0.5 in^2 for MT and CT. FT value was 0.6±0.1 cm for MT and CT. We conclude that the inclusion of 15% of manzarina in mature cow feedlot diets improves the antioxidant activity of plasma, indicating better animal health without affecting carcass characteristics.

Key Words: phenol compounds, antioxidant activity, apple pomace

M284 Effects of tomato pomace on feed intake and milk production of lactating dairy cows. R. Safari, R. Valkizadeh*, A. A. Naserian, and A. M. Tahmasbi, *Department of Animal Science (Excellent Center of Animal Nutrition), Faculty of Agriculture, Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The aim of this study was to evaluate the effects of dried and ensiled tomato pomace on feed intake and milk production. Nine primiparous and multiparous Holstein cows within 76 ± 12 (mean ±SD) days in milk were evaluated in a 3 x 3 change over design. The dietary treatments were 1) ordinary diet without dried or ensiled tomato pomace, 2) ordinary diet consisting 40% forage (barley silage and alfalfa hay) and 60% concentrate including 8% dried tomato pomace (DTP), 3) ordinary diet including 8% ensiled tomato pomace (ETP). Tomato pomace was replaced with whole barley silage and protein modified with cotton seed meal. Throughout the experiment, cows were housed in a tie stall and fed three times daily after milking (6:00 h, 14:00 h and 22:00 h). Amounts of feed offered and orts were weighed for each cow separately. Cows were milked three times a day. Milk was sampled at each milking time from day d 14 to 20. Ruminal samples were collected through mouth by a vacuum pomp, at 10:00 h on day 21. Ruminal fluid pH was measured immediately after sampling and then mixed with the same amount of HCl 0.2N. Rumen NH3-N samples was determined by micro-Kjeldahl analysis. Inclusion of tomato pomace in dried and ensiled forms did not alter ($p\geq0.05$) DMI of the cow significantly (25.71, 26.39 and 24.36 kg/d for control, DTP and ETP respectively; SEM = 0.92). Ruminal pH was significantly affected by treatments and was lower($p\leq0.05$) for the diets containing dried and ensiled tomato pomace (6.67, 6.41 and 6.20 for control, DTP and ETP respectively; SEM = 0.1) possibly due to the low pH of this by-product. Ruminal NH3-N% was not significantly ($p\geq0.05$) affected by dried tomato pomace or ensiled tomato addition. Milk production was significantly increased ($p\leq0.05$) by tomato pomace addition (40.31, 41.35 and 41.16 kg/d for control, DTP and ETP respectively; SEM = 0.11). The milk fat content (2.76%; SEM = 0.11) was similar ($p\geq0.05$) for cows fed control diet and those fed dried or ensiled tomato pomace. Milk protein yields were higher for experimental treatments than control (1.24, 1.28 and 1.27 kg/d for control, DTP and ETP respectively; SEM = 0.009).

Key Words: tomato pomace, dairy cow, milk yield

M285 The effect of allocation frequency in rotational grazing systems on the fatty acid (FA) profile in milk fat of dairy cows. B. Vlaeminck*[1], P. A. Abrahamse[2], V. Fievez[1], J. Dijkstra[2], and S. Tamminga[2], [1]*Laboratory for Animal Nutrition and Animal Product Quality, Ghent University, Melle, Belgium*, [2]*Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands*.

Eight Holstein cows were blocked in 2 groups according to milk yield, parity and DIM to evaluate the effect of frequency of allocation to new grazing plots on profiles of FA in milk fat. The 2 treatments were daily allocation to 0.125-ha plots (1D) or allocation every 4 d to 0.5-ha plots (4D) of Lolium perenne L. and were tested in a randomized block design (2 rotations with 2 measuring periods of 4 d each). The model included the effect of treatment, day within treatment, rotation, cow, the interaction between treatment and rotation and the covariate value. Significance was declared at $P<0.05$. There were no differences in the FA composition of the offered and residual pasture between 1D and 4D. Within days in the 4D treatment, the proportion of 16:0, 18:0 and 18:2n-6 increased, and that of 18:3n-3 as well as total FA content of grass decreased linearly. Treatment effects on milk FA composition and secretion were small. In contrast, milk FA composition was largely affected by day within the 4D treatment. Secretion of de novo synthesised and C16-FA decreased linearly during the 4 d whereas secretion of odd- and branched and C18-FA were not affected by day in the 4D treatment. Proportions of trans-11-18:1 in milk fat increased on d 2 (4.60 g/100 g FA) and decreased thereafter (3.86 g/100 g FA on d 4). Proportions of cis-9, trans-11-18:2 (2.34 and 1.83 g/100 g fatty FA on day 2 and 4, respectively), trans-11, cis-15-18:2 (0.81 and 0.63 g/100 g FA on day 2 and 4, respectively) and 18:3n-3 (0.87 and 0.83 g/100 g FA on day 2 and 4, respectively) in milk fat followed the same pattern. Results from this study suggests that increasing pasture allocation frequency from once every 4 d to every day has no effect on profiles of FA in milk. In addition, short term variation in pasture quality during the 4 days affected milk FA composition with a greater effect on biohydrogenation intermediates in milk fat compared with its major precursor, 18:3n-3.

Key Words: dairy cow, rotational grazing, milk fatty acids

M286 Economic analysis of alfalfa hay inclusion in wet corn gluten feed based diets for lactating dairy cattle. C. R. Mullins* and B. J. Bradford, *Kansas State University, Manhattan*.

A breakeven analysis was conducted to determine if including alfalfa in a ration containing 31% wet corn gluten feed increases production enough to justify feeding it to lactating dairy cattle. Data was gathered from a pen study where alfalfa hay (AH) was shown to linearly increase ECM production and DMI in 80 Holstein cows. Changes in milk income, feed consumed, and feed costs were incorporated in a partial budget model to determine the relative difference in AH vs. corn silage (CS) value (DM basis) at different milk:feed cost ratios. For the economic model, the value of AH was fixed at $250/ton DM ($0.27/kg), and milk value was fixed at $0.20/lb ($0.44/kg), whereas the value of CS and TMR cost varied with the AH price differential and the milk:feed cost ratio, respectively. Changes to the fixed values had little effect on the results, although the model was somewhat sensitive to the soybean meal to corn grain price differential. To account for this, the model was evaluated using maximum ($188/ton), mean ($120/ton), and minimum ($80/ton) price differentials between soybean meal and corn from 2003 to 2008. The additional value of AH relative to CS ranged from less than $5/ton DM to as much as $60/ton DM. Alfalfa's relative value increased as milk:feed cost ratio increased and also increased with increased soybean meal - corn grain price differential. The mean breakeven price differential was $30/ton DM, substantially less than typical differences in on-farm prices for these feedstuffs. The model was also evaluated using data from a study with 0% and 25% AH diets including 15% distillers grains (Kleinschmit et al. 2007 JDS 90:5587). The effect of milk:feed cost ratio on breakeven AH - CS price differential was far greater with this data (range -$20 to $100/ton DM) due to more dramatic treatment effects on DMI and production, and the mean breakeven differential was slightly greater ($60/ton DM). Based on data from these studies, adding AH to diets with large proportions of non-forage fiber may not be profitable, especially when milk:feed cost ratios are low.

Key Words: partial budget, alfalfa, dairy

M287 Effect of alfalfa hay particle size and source of neutral detergent soluble carbohydrates on intake, chewing activity, ruminal fermentation and nutrient digestibility of midlactation cows. A. Asadi*, G. R. Ghorbani, M. Alikhani, and M. Bagheri, *Department of Animal Sciences, Isfahan University of Technology, Isfahan, Iran*.

The effects on cows′ intake, performance, and digestibility of partial replacement of neutral detergent soluble fiber (NDSF) for starch were studied in diets with two sizes of alfalfa hay. Eight multiparous Holsteins averaging 146 ± 6 DIM and 36.7 ± 2.6 kg/d of milk were used in a double 4 × 4 Latin square design with a 2 ×2 factorial arrangement. Treatments included short (SH) or long (LN) alfalfa each combined with high starch concentrate (HiSt); and SH or LN alfalfa each combined with high NDSF concentrate (HiSF). The HiSt and HiSF treatments contained 28.5% and 24% starch and 8.5% and 13% NDSF, respectively and diet NDF content was 33%. Periods were 21 d in length with last 7d for sampling and analysis. The DM, OM, and CP intakes were unchanged by particle size (PS), while it was greater for HiSt vs. HiSF treatments ($P < 0.05$). The NDF intake was higher in SH vs. LN and in HiSt vs. HiSF treatments ($P < 0.05$). Interestingly, apparent digestibility of DM, OM, NDF and CP were significantly higher for cows fed HiSF diet than cows fed HiSt diet ($P < 0.05$). Total chewing, eating and ruminating times were not affected by treatments, however, eating time per kg NDF intake was longer in LN vs. SH and tended to be longer in HiSF vs. HiSt diets. Sorting behavior was apparent in LN diets in this study; cows sorted against particles > 19 mm and in favor of particles < 8 mm with majority of sorting occurred after 8 h postfeeding. Rumen pH, total VFA and proportion of individual VFA were unaffected by treatments ($P > 0.05$), however, butyrate was significantly higher with HiSF diets. No interaction between PS and carbohydrate form was found for nutrient digestibility and ruminal fermentation variables. In conclusion, results suggested that in diets exceeding minimum NDF recommendations and containing no more than 30% starch, alfalfa PS may not interact with form of carbohydrates to affect rumen metabolism and nutrient digestibility.

Key Words: dairy cow, neutral detergent soluble carbohydrates, chewing activity

M288 Differentiating effects of effective fiber sources on performance of lactating dairy cows. R. A. Starkey*, P. N. Gott, M. L. Eastridge, E. R. Oelker, A. R. Sewell, B. Mathew, and J. L. Firkins, *The Ohio State University, Columbus*.

Because of high feed costs and limited availability of some forage sources, alternative effective fiber sources are being considered. The objective of this study was to compare the feeding of corn silage as the sole forage versus feeding corn silage with alfalfa hay, wheat straw, and corn stover to lactating dairy cows. A 5x5 Latin square design was used with 5 multiparous cannulated Holstein cows (122 ± 62 DIM). Diets were: 1) CS = corn silage as sole forage source, 2) ALF = corn silage and 11.5% alfalfa hay, 3) STW-5 = corn silage and 5% straw, 4) STW-10 = corn silage and 10% straw, and 5) STV = corn silage and 5.5% corn stover (without cobs). Diets were formulated for similar concentrations of CP, NFC, and 18% forage NDF, except for STW-10 with 23% forage NDF. Diets were fed for 3 wk, and samples were collected during the last week of each period. Period 4 was extended 9 d because one cow had a displaced abomasum at the beginning of the period. The DMI was lowest for STW-10 (28.6, 28.9, 30.5, 26.7, and 28.6 kg/d for CS, ALF, STW-5, STW-10 and STV, respectively; $P < 0.05$). The BW (734 kg) and BCS (3.18; 1 to 5 scale) were similar. Milk (35.6 kg/d), milk fat (3.56%), milk protein (2.87%), and MUN (17.4 mg/dl) also were similar. The different forage sources resulted in similar total tract digestibilities of OM (76.9%) and NDF (63.5%). Rumen pH (6.12), acetate:propionate (3.10), and ruminal concentrations of total VFA, acetate, propionate, butyrate, and valerate were similar. Concentrations of isovalerate ($P < 0.01$) and isobutyrate ($P < 0.10$) were highest for STW-10 compared to the other diets, and isovalerate was also lower ($P < 0.10$) for ALF than for STW-5 and STV. Feeding the higher level of straw may have caused more rumen fill and thus reduced DMI, which would likely lower milk yield in a longer study. Feeding similar forage NDF concentrations using corn, alfalfa hay, and wheat straw can result in similar animal performance and ruminal fermentation with adequate formulation of NFC and total NDF.

Key Words: corn stover, straw, effective fiber

M289 Effect of roughage to concentrate ratio on ruminal parameters and protein degradability in dairy cows. L. J. Erasmus*[1], W. A. van Niekerk[1], H. Nienaber[1], and P. H. Robinson[2], [1]*University of Pretoria, Department of Animal and Wildlife Siences, Pretoria, South Africa*, [2]*University of California, Department of Animal Science, Davis*.

Published research suggest it might be feasible to decrease ruminal protein degradability by lowering rumen pH through dietary manipulation of rumen fermentation. Three ruminally cannulated Holstein cows were used in a 3 x 3 Latin square design experiment and fed three total mixed rations differing in roughage : concentrate ratio (60 : 40; 45 : 55 and 30 : 70). The roughage portion consisted of equal parts of Lucerne hay and *Eragrostis curvula* hay with maize the primary energy component and the three feedstuffs to be evaluated the primary dietary CP components.The CP (%DM) content of the three diets were 14.7%,15.4% and 16.2%,the NDF content 38.6%,32.6% and 26.4%, and the NFC content 36.1%,41.4% and 46.7% respectively. Protein degradability of three feedstuffs differing in potential degradability (sunflower oilcake meal, cottonseed oilcake meal, roasted soya) was estimated using the in situ technique. Incubation times were 0,2,4,8,16,24,48 and 72h.Rumen fluid samples were taken every 6 hours for three consecutive days during each 16 day experimental period.Repeated variables were analysed with the GLM Repeated Measures Procedure (SAS,2006). Mean ruminal pH over 24 h differed and was 6.44, 6.27 and 6.00 respectively for the 3 diets ($P < 0.05$). Time below a rumen pH of 5.8 was 2.5 h, only for the high concentrate (70%) diet. Mean ruminal NH3-N and VFA concentrations did not differ among treatments although the high concentrate diet resulted in a lower acetic : propionic acid ratio ($P < 0.05$). Dietary treatment did not affect protein degradability within feedstuff ($P > 0.05$) suggesting that roughage : concentrate ratios ranging from 60 : 40 to 30 : 70 and pH ranging from 6.0 to 6.4 are still within the physiological boundaries where rumen pH do not affect ruminal protein degradability. Alternatives such as chemical or heat treatment would be more feasible than dietary manipulation of pH to increase dietary RUP content when formulating practical dairy cattle diets.

Key Words: ruminal protein degradability, roughage to concentrate ratio, dairy cows

M290 Effect of decreasing forage fiber in close-up cows diets on rumination time, DMI and subsequent lactation performance. A. Nikkhah*[1], V. Keshavarz[2], H. Amanloo[2], M. Dehghan[1], and M. Kazemi Bonchenari[1], [1]*Department of Animal Sciences, University of Tehran, Karaj, Iran*, [2]*Department of Animal Sciences, University of Zanjan, Zanjan, Iran*.

One of the main goals of the close-up diets is to maximize DMI in the subsequent lactation period to support high energy demand for early lactation. Previous studies clearly demonstrated that decreasing fiber concentration in dairy cows diets increased DMI of the cows. From the other hand decreasing the fiber in diets reduced the rumination time. The objective of this study was to improve DMI with decrease forage fiber but still provide required eNDF without effect on rumination time and milk fat content. 18 multiparous close-up dairy cows in 31d (SD=6) before expected calving date fed different levels of forage fiber and also effective fiber (the forage fiber and effective fiber were 30.5-30.4, 26.7-27.38 and 22.9-24.61 for diets 1, 2 and 3 respectively) were assigned in to a completely randomized design to investigate the effect of experimental diets on rumination activity and also on DMI and production traits in the subsequent lactation. The different diets were fed to dairy cows in close-up period and a similar diet was fed to all cows in lactation period and data collection period was lasted until 20d after parturition. The Data were analyzed with SAS (SAS institute 1999). As it is given in table 1, the highest DMI in both close-up and early lactation periods were for diet 2. The results showed that decreased forage fiber in close-up period increase DMI but severe decreasing the forage decreased rumination time (P<0.03). It could be concluded that it is recommendable to decrease forage fiber in close-up diets but this decrease should not as much as to address rumination time.

Table 1. Effect of different forage fiber in close-up diets on rumination time, DMI and production traits

	Treatments				
Item	1	2	3	SE	P<F
Close-up period					
Rumination time (min/d)	473[b]	443[ab]	408[a]	40.15	0.03
DMI (kg/d)	12.07[b]	14.29[a]	12.89[b]	0.32	0.0007
Lactation period					
Milk Yield (kg/d)	28.40	31.1	29.83	0.85	0.09
DMI (kg/d)	17.41[c]	19.03[a]	18.72[b]	0.43	0.001
Milk Fat (kg/d)	1	1.02	0.93	0.06	0.23
Milk Protein (kg/d)	0.83	0.97	0.95	0.04	0.07

[a,b,c] Least squares means within the same row without a common superscript differ ($P < 0.05$)

Key Words: forage fiber, rumination time

M291 Feed sorting of dairy cows receiving diets different in dietary fiber level. O. AlZahal*, M. S. Douglas, S. L. Greenwood, and B. W. McBride, *University of Guelph, Guelph, ON, Canada*.

The objectives of this study were to nutritionally induce subacute ruminal acidosis (SARA) in lactating dairy cows by feeding a low-fiber diet and examine the cows' feed sorting responses in comparison with cows consuming a higher-fiber diet. Six rumen-fistulated Holstein dairy cows (639 ± 51 kg of body weight) were used in the study. Cows were randomly assigned to 1 of 2 dietary treatments, a high-fiber (HF; % of dry matter, 40% corn silage, 27% alfalfa silage, 7% alfalfa hay, 18% protein supplement, 4% ground corn, and 4% wheat bran) or a low-fiber (LF; % of dry matter, 31% corn silage, 20% alfalfa silage, 5% alfalfa hay, 15% protein supplement, 19% ground wheat, and 10% ground barley) total mixed ration. Ruminal pH was continuously recorded 3 d a week and feed sorting was assessed on d 19. The rumen fluid in cows receiving the LF diet on average was below pH 5.6 for a longer duration than in cows receiving the HF diet (357 vs. 103 min/d), indicating that the LF cow were suffering from SARA. Results showed that cows sorted fine particles (< 1.18 mm) differently across treatments ($P < 0.05$), cows receiving the HF diet sorted for fine particles, whereas cows receiving the LF diet sorted against those particles, likely in an attempt to attenuate their rumen condition (105.5 ± 2.7% and 93.9 ± 2.7% of predicted intake of fine particles, respectively). Additionally, sorting of the fine particles was positively correlated with mean pH ($R^2 = 0.77$, $P = 0.02$) and was negatively correlated with durations (min/d) ruminal fluid was below pH 5.8 ($R^2 = 0.73$, $P = 0.03$). In summary, the study demonstrated that cows undergoing SARA sorted their feed to avoid fine particles in attempt to attenuate their condition. The extent of this alteration was related to the magnitude of ruminal pH depression.

Key Words: dairy cow, subacute ruminal acidosis, feed sorting

M292 Corn bran vs. corn grain at two levels of forage: Intake and production responses by lactating dairy cows. C. Arndt*[1], L. E. Armentano[1], and M. B. Hall[2], [1]*Department of Dairy Science, University of Wisconsin, Madison*, [2]*U.S. Dairy Forage Research Center, University of Wisconsin, Madison*.

A cow performance trial was conducted to estimate the effect of substituting corn bran (CB) for corn grain and to determine if the impact was affected by the level of forage in the diet. Twelve multiparous and 12 primiparous Holsteins were assigned to a 2x2 factorial (CB vs. corn, and high vs. low forage) using 6 4x4 randomized complete block Latin square design with 3 week periods. Cows were blocked by parity and three levels of production within parity. Feed samples were collected every second day over the last 8 days of each period. Dry matter intake and milk weights were recorded over the last 5 days of each period. Milk samples were collected over the last 5 days of each period at am and pm milking. Intake and milk data were averaged across days for each cow in each period. The forage was 64.2 or 38.4% of TMR DM. The high forage corn diet (HFC, 29.7% NDF, 25.6% starch by analysis) had 20% corn, the low forage corn diet (LFC, 23.1% NDF, 34.0% starch) had 39.3% corn, the high forage CB diet (HFCB, 42.6% NDF, 14.8% starch) had 19.3% CB and the low forage CB diet (LFCB, 48.4% NDF, 12.9% starch) had 37.9% CB (DM basis). The LFC diet supported maximum milk and milk protein yield. Milk fat yield on the LFC diet did not differ from HFC or LFCB but milk fat % was lowest for the LFC diet. Loss in milk yield due to substitution of CB for corn was greater on the lower forage diets, but this also corresponded to a larger substitution of CB for corn. Intake was depressed by forage and CB, but lower intake does not appear large compared to reduction in milk yield. Lower milk protein and higher MUN suggests that lack of starch in the CB diets may have interfered with rumen microbial protein synthesis. The effect of substituting CB for both forage and corn grain can be estimated by comparing LFCB to HFC. This way of using CB significantly reduced milk fat yield, but numerical reductions in milk and milk protein yield were not statistically significant.

Table 1.

Item	HFC	HFCB	LFC	LFCB	SE	Forage	Corn	Forage × Corn
DMI kg/d	24.8^{ab}	24.3^{a}	26.7^{c}	25.9^{bc}	0.44	**	*	
Milk kg/d	42.0^{b}	38.7^{a}	46.7^{c}	40.5^{ab}	0.79	**	**	**
Fat kg/d	1.70^{c}	1.51^{a}	1.61^{bc}	1.58^{b}	0.04		**	**
Protein kg/d	1.25^{b}	1.12^{a}	1.47^{c}	1.19^{ab}	0.02	**	**	**
Fat %	4.04^{b}	3.91^{b}	3.47^{a}	3.90^{b}	0.10	**	*	**
Protein %	3.00^{b}	2.91^{a}	3.18^{c}	2.95^{ab}	0.04	**	**	**
MUN mg/dl	13.38^{b}	17.54^{c}	10.70^{a}	18.37^{c}	0.66	*	**	**

^{a,b,c} Means in a row not sharing a common superscript differ (P<0.05). **<0.01, *<0.05, blank>0.05.

Key Words: corn bran, milk

M293 Corn bran vs. corn grain at two levels of forage: Apparent digestibilities by lactating dairy cows. C. Arndt*[1], L. E. Armentano[1], and M. B. Hall[2], [1]*Department of Dairy Science, University of Wisconsin, Madison*, [2]*U.S. Dairy Forage Research Center, University of Wisconsin, Madison*.

A digestibility trial was conducted to estimate the effect of corn bran (CB) for corn grain and to determine if the impact was affected by the level of forage in the diet. Apparent digestibility was determined with Yb as an external marker in conjunction with a lactation performance trial using 24 Holsteins in 6 4x4 Latin squares with 3 week periods. Ort, TMR and fecal samples were taken over the last 5 days of each period. Individual feed samples were taken every second day over the last 8 days of each period. Apparent digestibilities and intakes were averaged across days for each cow in each period. The forage (55% corn silage DM, 45% wilted alfalfa silage DM) was 64.2 or 38.4% of TMR DM. The concentrate consisted of either primarily corn or CB (75.1% NDF, 14.6% starch) with added whole cottonseeds, distillers dried grains with solubles, blood meal, soybean meal and a mineral mix. The high forage corn (HFC, 29.7% NDF, 25.6% starch) diet contained 20% corn, the low forage corn (LFC, 23.1% NDF, 34.0% starch) diet contained 39.3% corn, the high forage CB (HFCB, 42.6% NDF, 14.8% starch) diet contained 19.3% CB and the low forage CB (LFCB, 48.4% NDF, 12.9% starch) diet contained 37.9% CB (DM basis). Observed digestible organic matter intake (DOMI) was not significantly different between the two CB diets, as increasing CB based concentrate in place of forage actually reduced organic matter digestibility (OMD) while increasing intake. Corn based diets had greater OMD, and LFC provided the greatest OMD, OM intake (OMI) and DOMI of all diets. No significant difference was found for starch digestibility (StarchD) among the diets, but it was higher than non-starch NFC digestibility (NSNFCD) and NDF digestibility (NDFD), resulting in the greater OMD for corn diets. The greater DOMI of the corn diets results from greater OMI and starch content resulting in greater digestible starch intakes (DStarchI) and digestible NSNFC intakes (DNSNFCI) which compensate their lower digestible NDF intake (DNFDI).

Table 1.

Item	HFC	HFCB	LFC	LFCB	SE	Forage	Corn	Forage × Corn
OMI kg/d	22.9[a]	22.4[a]	24.7[b]	24.1[b]	0.41	**	*	
DOMI kg/d	15.2[b]	13.7[a]	16.8[c]	14.0[a]	0.31	**	**	**
OMD %	66.3[c]	61.2[b]	67.7[c]	58.3[a]	0.68		**	**
NDFD %	38.9[b]	42.0[b]	29.1[a]	41.2[b]	1.62	**	**	**
StarchD %	96.7[a]	97.0[a]	96.1[a]	96.8[a]	0.31			
NSNFCD %	75.3[ab]	77.4[b]	71.7[a]	76.4[b]	1.36		**	
DNDFI kg/d	4.5[b]	6.8[c]	4.1[a]	8.2[d]	0.12	**	**	**
DStarchI kg/d	6.1[b]	3.5[a]	8.6[c]	3.2[a]	0.13	**	**	**
DNSNFCI kg/d	1.1[b]	0.9[a]	1.1[b]	0.8[a]	0.06		**	

[a,b,c,d]Means in a row not sharing a common superscript differ (P<0.05). **<0.01, *<0.05, blank>0.05.

Key Words: corn bran, digestibility

M294 Effects of increasing levels of concentrate supplementation on milk production of grazing dairy cows. G. A. Gagliostro*, L. Antonacci, P. Barbera, D. A. Garciarena, and C. A. Cangiano, *Instituto Nacional de Tecnología Agropecuaria*, *Balcarce, Buenos Aires, Argentina*.

The effect of supplemental energy was evaluated in twelve Holstein cows grazing spring pastures (alfalfa 70% and orchardgrass 30%) with an herbage allowance of 27 kg DM/cow/d. Cows were blocked by DIM and randomly assigned to three treatments in a replicated Latin square. At the start of the experiment the six cows from square 1 (514 kg LW) were producing 28.2 kg milk/d and averaged 35 DIM. In Square 2, LW, milk yield and DIM were 554 kg, 31.3 kg/d and 197 d respectively. Treatment periods were 19 d., the first 14 d as adaptation and the last 5 d as the sampling period. Treatments (C3, C6, and C9) were three levels (3, 6, and 9 kg/d) of concentrate (90.4% DM) containing (g/kg DM) CP (160), starch (351), soluble carbohydrates (149), ether extract (39.7) and NDF (248). Supplements were thoroughly consumed by cows. Pasture (30.78% DM) contained (g/kg DM) CP (183), NDF (368), ADF (217), soluble carbohydrates (94.6), starch (33.5) and digestible DM (709). Data were analyzed with effect of square, period, cow within square; treatment, interaction between period and treatment (NS) and residual error. Pasture intake averaged 11.94 kg DM/cow/d (P<0.69). Substitution rate of pasture was low either in C6 (0.10) or in C9 (0.19). Total DM (kg/d) and ME (Mcal/d) intake was higher (P<0.05) in C9 (19.38 and 51.4) compared to C3 (15.12 and 39.3) but not to C6 (17.62 and 46). Milk yield (27.5 kg/d) and FCM (23 kg/d) resulted higher (P<0.05) in C9 compared to C6 (25 and 21 kg) and to C3 (23.6 and 20.3 kg). No differences were detected between C3 and C6. Milk fat content (29.9 g/kg) or yield (754 g/d) and milk protein content (31.6 g/kg) did not differ. Protein yield (g/d) resulted higher (P<0.05) in C9 (885) compared to C3 (735) but not to C6 (789). Lactose (48.6 g/kg) and milk urea (39.98 mg/dl) content did not differ. BW gain (kg/d) tended (P<0.15) to increase with intake of concentrate (C3 = 0 .246, C6 = 0,364 and C9 = 0,772). In high quality spring pastures increasing the amount of concentrate in the diet up to 9 kg/d increased total DM and ME intakes, milk and protein yields without depressing mil fat content or pasture DMI.

Key Words: grazing dairy cows, concentrate levels, milk production

M295 Effect of dietary concentrate level on rumen fermentation, digestibility, and nitrogen losses in dairy cows. M. Agle*[1], A. N. Hristov[2], S. Zaman[1], and C. Schneider[1], [1]*University of Idaho*, *Moscow*, [2]*Pennsylvania State University*, *University Park*.

The objective of this experiment was to investigate the effect of level of concentrate in the diet on rumen fermentation, digestibility, and N losses in lactating dairy cows. The experiment was a replicated Latin square design with 2-wk adaptation periods. Ruminal contents were exchanged between cows at the beginning of each adaptation period. The diets contained (DM basis): 52 (LowC; control), 61 (MedC), and 72% (HighC) concentrate. Crude protein content of the diets was 16.5, 14.8, and 16.4%. Dry matter intake was not affected by diet ($P = 0.76$). Milk yield was increased ($P = 0.046$) by HighC compared with LowC and MedC (36.0, 33.2, and 32.3 kg/d, respectively). Concentration of milk true protein was not different ($P = 0.23$) among diets, but milk fat percentage (and yield) was decreased ($P = 0.019$) by MedC and HighC compared with LowC. Urinary N excretion and MUN concentration were decreased ($P = 0.003$ and < 0.001) and plasma urea N tended to be decreased ($P = 0.09$) by MedC compared with the other diets. Both MedC and HighC decreased ($P = 0.013$) rumen pH compared with the control (6.00, 6.04, and 6.14, respectively). Rumen ammonia concentration was lowered ($P < 0.001$) by HighC and MedC compared with LowC. Propionate concentration was increased ($P = 0.006$) by HighC and tended to be increased ($P = 0.07$) by MedC compared with LowC. Acetate:propionate ratio was similar for LowC and MedC and lower for HighC ($P = 0.008$). Rumen methane production, polysaccharide-degrading activities, and microbial protein synthesis (estimated based on urinary purine derivatives excretion) were not affected ($P = 0.30$ to 0.86) by diet. Apparent total tract digestibility of DM, OM, N, and starch were not affected ($P = 0.08$ to 0.41) by diet, but NDF digestibility was decreased ($P = 0.007$) by MedC and HighC. Increasing concentrate level of the diet increased milk yield and decreased rumen ammonia concentration, but decreased NDF digestibility. The MedC diet decreased urinary N losses.

Key Words: dietary energy, rumen fermentation, dairy cow

M296 Feeding dairy cows rolled barley grain treated with lactic acid and heat delays *in situ* DM disappearance and prevents development of sub-acute ruminal acidosis. Q. Zebeli*, A. Mazzolari, S. M. Dunn, and B. N. Ametaj, *University of Alberta*, *Edmonton, AB, Canada*.

Due to the high content in readily degradable carbohydrates, inclusion of barley grain in the diet of dairy cows is associated with high risk of sub-acute ruminal acidosis (SARA). The aim of this study was to evaluate the effects of feeding barley grain treated with lactic acid (LA) and heat on *in situ* DM degradation and diurnal rumen pH patterns. Eight rumen-fistulated Holstein cows (170 DIM) were fed once daily (at 0800) a TMR containing rolled barley grain (32.8%, DM basis) steeped for 48h in equal quantity of water (CTR) or 1% LA solution (v/v) and oven-heated at 55°C (TRT). A crossover design with two 21-d periods (first 11d of adaptation diet) was used. Duplicate samples of rolled barley grain were incubated *in situ* (Dacron-bag technique) for 72-h in the rumen of cows fed the CTR- or TRT-diet, and the DM disappearance rate was measured at 0, 2, 4, 8, 16, 24, 48, and 72h post-incubation. Rumen fluid pH was measured on d10 of the measurements period on samples collected at 0h (pre-feeding) and at 2, 4, 6, 8, 10, and 12h post-feeding. The in situ data showed that cows fed the TRT diet had lower DM disappearance rate of barley grain substrate from 0h (19.4 vs. 36.5%; P<0.001) up to 24h (73.4 vs. 80.7%; P=0.02) post-incubation. However, DM disappearance rates were equal in both treatments starting

at 48h (86.5 and 87.2% for TRT- and CTR-diet, respectively; P=0.59) until 72h (P=0.47) post-incubation. Moreover, cows fed the TRT diet showed greater *in situ* lag time than controls (9.2 vs. 4.2h; P<0.001). Additionally, results showed higher (P=0.01) rumen pH for cows fed the TRT diet. Thus, cows fed the TRT diet maintained higher rumen pH (5.92 vs. 5.67) at the nadir (8h post-feeding), as well as at 10h (6.02 vs. 5.75) and 12h (6.10 vs. 5.78) post-feeding. In conclusion, feeding dairy cows 32.8% rolled barley grain treated with 1% LA and heat delayed *in situ* DM disappearance and prevented the decline of rumen pH at SARA levels post-feeding.

Key Words: barley grain, dairy cow, lactic acid processing

M297 Dietary energy source in primiparous dairy cows during the transition period: Blood metabolites, metabolic hormones and milk production. M. A. T. Artunduaga*[1], S. G. Coelho[1], B. G. Campos[1], A. M. Borges[1], A. M. Q. Lana[1], R. B. Reis[1], H. M. Saturnino[1], H. N. Da Costa[2], and R. V. Sá Fortes[2], [1]*Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brazil*, [2]*Human Resources on Agribusiness, ReHAgro*, *Belo Horizonte, Minas Gerais, Brazil*.

Increasing the availability of glucogenic and lipogenic nutrients during the transition period has been hypothesized to improve energy balance and to decrease the incidence and severity of metabolic and reproductive disorders in early lactation. Therefore, the objectives of this study were to compare the effects of a glucogenic or a lipogenic diet on blood metabolites, metabolic hormones and milk production in primiparous dairy cows during the transition period. Cows (n= 40) were fed on a standard diet from wk 3 prepartum to wk 6 postpartum. Cows received either a lipogenic or glucogenic supplement during the transition period and were randomly assigned to 1 of 4 treatments as follows: control, calcium salts of soybean fatty acids - Megalac-E (100g prepartum and 250g postpartum), toasted soybean (400g prepartum and 800g postpartum) and propylene glycol (300 ml pre and postpartum). Diets were isocaloric (net energy basis). Blood samples were taken from each animal 10 and 5 days prior to the expected calving date and at days 7, 14, 21, 28, 35 and 42 postpartum. Milk production was recorded on days 10, 20, 30 and 40 postpartum. Data was analysed using a completely randomized split-plot design. Milk yield did not differ among treatments (P=0.067). Fat corrected milk (FCM 3.5%) was higher for cows supplemented with Megalac-E and propylene glycol (P = 0.047) (24.90±4.85 and 24.58±5.32, respectively). Insulin and glucose concentrations were significantly higher in the Megalac-E treatment (P<0.05). The lowest insulin and glucose concentrations were observed on cows supplemented with propylene glycol. Non esterified fatty acid concentration (NEFA) were lower for all treatments compared to control group (0.24±0.16 mmol/l) (P<0.05). Plasma IGF-I concentration was higher for treatments receiving the lipogenic supplements (P<0.05). Overall, results suggest that calcium salts of soybean fatty acids reduced the dramatic metabolic and endocrine changes characteristic of the transition period, reflected in improved energy balance which could be associated with better reproductive and productive performance.

Key Words: insulin, glucose, IGF-I

M298 Corn endosperm type influences nutrient digestibility in lactating dairy cows. J. C. Lopes*[1], R. D. Shaver[1], P. C. Hoffman[1], M. S. Akins[1], S. J. Bertics[1], H. Gencoglu[2], and J. G. Coors[3], [1]*Department of Dairy Science, University of Wisconsin*, *Madison*, [2]*Department of Animal & Nutritional Sciences, Faculty of Veterinary Medicine, Uludag University*, *Bursa, Turkey*, [3]*Department of Agronomy, University of Wisconsin*, *Madison*.

The objective of this study was to evaluate the effect of corn endosperm type on ruminal fermentation parameters and total-tract nutrient digestibility in lactating dairy cows. Near-isogenic variants of an Oh43xW64A normal dent endosperm hybrid carrying floury-2 or opaque-2 alleles were grown in spatial isolation in field plots and harvested as dry shelled corn. Six ruminally-cannulated multiparous Holstein cows (67 ± 9 DIM and 638 ± 5 kg BW at trial initiation) were randomly assigned to a replicated 3 x 3 Latin Square design with 14-d periods; the first 11 d of each period were for diet adaptation followed by 3 d of sampling and data collection. Treatment diets that contained dry rolled vitreous-, floury-, or opaque-endosperm corn (33% of DM), alfalfa silage (55% of DM) and protein-mineral-vitamin supplement (12% of DM) were fed as TMR. The percentage vitreous endosperm was zero for the modified corn endosperm types and 64 ± 7% for the vitreous corn. The prolamin protein content of the modified corn endosperm types was only 30% of the content found in vitreous corn. Degree of starch access and in vitro ruminal starch digestibility measurements were 32% and 42% greater on average, respectively, for the modified corn endosperm types than vitreous corn. Dry matter intake and milk yield averaged 25.6 kg/d and 45.2 kg/d, respectively, for the trial and were unaffected (P > 0.10) by treatment. Dry matter and starch disappearances after 8-hr ruminal in situ incubations were 24 and 32%-units on average greater (P < 0.001), respectively, for the modified corn endosperm types than vitreous corn. Ruminal pH and acetate molar % were lesser (P < 0.01), propionate molar % was greater (P < 0.01), and acetate:propionate ratio was lesser (P < 0.01) for the modified corn endosperm types. Total-tract starch digestibility was 6.3%-units, on average, greater (P < 0.001) for diets containing modified corn endosperm types than the vitreous corn. Apparent total-tract NDF digestibility was lesser (P < 0.001) for diets containing the modified corn endosperm types. Corn endosperm type influenced starch and fiber digestibility in lactating dairy cows.

Key Words: corn, digestibility, starch

M299 Performance of dairy cows fed extruded or hydrated and ensiled mature corn grain. L. L. Bitencourt[1], S. Siécola Júnior[1], L. Q. Melo[1], N. M. Lopes[1], V. A. Silveira[1], I. R. Rios[1], J. R. M. Silva[2], R. A. N. Pereira[3], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, MG, Brazil*, [2]*Centro Federal de Educação Tecnológica*, *Januária, MG, Brazil*, [3]*Better Nature Research Center*, *Ijaci, MG, Brazil*.

In Brazil, all the corn used in concentrate feedstuffs has low digestibility, flint type endosperm. We evaluated the response to corn extrusion or to proteolysis and fermentation induced by ensiling. A mature flint hybrid (AG 2040) was ground and had its moisture content reconstituted to 43.7% at ensiling, for 358 days. Other treatments were the same hybrid ground in the same feed mill (11.8% moisture) or extruded (9.7% moisture). Fifteen Holsteins (160±84 DIM, three primiparous) received the treatments in five, 3x3 Latin Squares, with 21-day periods. Diet composition averaged (% of DM): Corn silage (41.5); soybean meal (21.5), citrus pulp (17.5), CP (17.3), NDF (30.9), and NFC (39.1). The content of corn was 16.7% of DM for ensiled, 17.4 for ground, and 17.7 for extruded. Two contrasts were evaluated: 1) Ensiled *vs.* Ground. 2) Extruded *vs.* Ground. Extruded corn depressed the secretions of milk energy and fat and DMI. Eating behavior was not as responsive as DMI. The content of MUN, the daily secretion of urinary allantoin, and the total tract apparent digestibility of the non-NDF OM (Non-NDF OM D) were not a supportive reasoning for the tendency of increased milk protein content with extruded corn. There was a tendency for increased OM

digestibility (OM D) with ensiled corn. Extrusion or ensiling of mature flint corn resulted in a slight increase in the conversion of feed into milk. *Funded by Fapemig and D'Vita Rações.*

Table 1.

	Ensiled	Ground	Extruded	Contrast 1	Contrast 2
DMI	21.6	22.1	21.1	.30	.05
Milk yield	33.4	33.0	33.5	.46	.20
Fat yield	.767	.785	.704	.53	.01
Protein yield	.795	.782	.783	.36	.94
Fat %	2.99	3.11	2.82	.25	.01
Protein %	3.15	3.11	3.17	.29	.09
Milk energy (Mcal/d)	21.05	21.02	19.92	.95	.03
MUN (mg/d)	15.2	16.2	17.1	.06	.06
Milk yield/DMI	1.55	1.49	1.55	.12	.15
Ingestion time (min/d)	287	284	277	.81	.43
First meal time (min)	29.5	33.2	30.0	.92	.51
Non-NDF OM D (%)	86.1	85.7	86.4	.66	.48
OM D (%)	76.6	74.4	76.1	.10	.19
Urinary allantoin (mmoles/d)	76.1	66.6	67.6	.23	.89

Key Words: corn processing, feed efficiency, flint corn

M300 Effect of starch infusion site on glucose rate of appearance (Ra) and digestibility of starch and nitrogen in dairy cows. F. Hassanat*, H. Lapierre, and D. R. Ouellet, *Dairy and Swine R&D Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*.

The objective of this study was to determine the impact of changing the site of starch infusion on whole body glucose Ra and digestibility of starch and N in dairy cows. Four mid-lactation cows fitted with ruminal, duodenal, and ileal cannulae were used in a Youden square design with 3 periods of 28 d. Starch was infused at a total continuous rate of 1.80 kg d-1 either in the Rumen, the Omasum, or equally partitioned in both sites (Mix), with dietary starch intake averaging 2.59±0.21 kg d^{-1}. On d 20, cows were infused in a jugular vein with D[6,6-d_2]glucose (12.0 mmol h^{-1}) for 180 min. Blood samples were obtained from the contralateral jugular vein every 20 min from 100 to 180 min of the infusion to determine glucose enrichment. Duodenal, ileal, and fecal samples were collected on days 27 and 28 (n=4 per d) to determine starch and N disappearance from the different digestive tract segments. Milk yield (29.1±5.7 kg d^{-1}) and composition were not affected by treatment. Similarly, plasma glucose concentration (3.99±0.23) was unaffected by treatments, although glucose Ra numerically increased with Mix treatment. Total tract starch digestibility was lowest when starch was infused only in the omasum as a result of decreased absolute disappearance in the rumen. This led to an increase in small intestine and hindgut disappearance, resulting in a reduced fecal pH. Infusing starch in the omasum decreased N total tract and hindgut digestibility. Indeed, negative N digestibility indicates N release across the hindgut with Omasum treatment. These results indicate that supplying additional starch in the small intestine did not increase plasma glucose concentration or Ra but that undigested starch was highly fermented in the hindgut. This will impact true N digestibility and endogenous N secretions lost by lactating cows.

Table 1. Impact of starch infusion on glucose Ra and digestibility of starch and nitrogen

	Rumen	Mix	Omasum	SEM	*P* value
Total tract starch digestibility, %	99.5^{a}	99.1^{a}	94.1^{b}	1.1	0.04
Starch disappearance g day^{-1}					
- rumen	3735^{a}	2895^{b}	2395^{c}	152	0.01
- small intestine	380^{b}	984^{ab}	1213^{a}	146	0.02
- hindgut	157^{b}	369^{ab}	813^{a}	120	0.02
Nitrogen digestibility, %					
- total tract	73.4^{a}	69.5^{ab}	67.4^{b}	1.4	0.05
- hindgut	15.9^{a}	0.5^{b}	-7.0^{b}	2.9	0.04
Glucose Ra, mmol hr^{-1}	666	732	700	35	0.43
Fecal pH	6.72^{a}	6.72^{a}	5.32^{b}	0.11	0.01

^{LS}means with different letters differ significantly

Key Words: starch infusion, glucose kinetics, digestibility

M301 The effects of different sources of nonstructural carbohydrates and addition of full fat roasted canola seed on milk production and composition in lactating cows. M. Sari, A. A. Naserian*, R. Valizadeh, and S. Salari, *Ferdowsi Universuty of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

The objective of this study was to examine the effects of modifying the dietary sources of neutral detergent-soluble carbohydrate (NDSC), addition of full fat roasted canola seed (RCS), and possible interactions on milk production and composition in lactating cows. Twelve lactating Holstein cows (BW=596±29 kg, DIM=85±14) were used in a 4×4 Latin squares design. Treatments were in a 2×2 factorial arrangement, and periods were 21 d. The first 15 d were used for diet adaptation. The cows were fed individually four experimental diets as TMR ad libitum. The diets, which contain 15% barley (S), 5% barley and 10% dried citrus pulp (NDSF), with or without addition of 6% ground RCS at the expense of corn and canola meal, were formulated to meet NRC (2001) recommendations. Diets contained 17.5% CP and constant forage to concentrate ratio (45:55). Cows were milked three times a day and samples were collected at each milking over the last three d of each period. Data were analyzed using the GLM procedure of SAS (2001). Daily DMI of cows fed S diets was higher than cows fed NDSF diets (24 vs 22.9 kg/d). Cows receiving diet S produced more milk (33.8 vs 32 kg/d) and animals fed NDSF diet produced milk with greater concentration of milk fat (3.20 vs 2.95%). Consequently, NFC source did not affect 3.5% FCM yield. An interaction (P<0.05) between NDSC sources and RCS was observed for ECM because of higher production with NDSF than S diet when RCS was added (P<0.05). Cows fed the S diet had an increased milk protein content than when fed the NDSF diet (P<0.05), and the inclusion of RCS reduced the protein content (P<0.01). Milk lactose was similar among treatments. Production efficiency was not affected by NDSC sources, but was higher for cows fed RCS diets. Results indicated that citrus pulp and barley differed in the type and quantity of metabolizable nutrients they provided. Adding RCS had positive effects on milk production and production efficiency using citrus pulp.

Key Words: dairy cows, nonstructural carbohydrates, roasted canola seed

M302 Supplemental starch in postpartum dairy cow diets 1. Effect on productivity. B. L. Dyck*[1], L. Doepel[1], and M. G. Colazo[2], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*Alberta Agriculture and Rural Development, Edmonton, AB, Canada*.

The objective of this study was to determine if increasing the level of dietary starch in postpartum Holstein cows would improve their productivity and metabolic status. One of 3 diets was fed from calving until 70 DIM. The diets contained 45% concentrate and 10% alfalfa hay. In addition, the low starch diet (n=14) contained 45% barley silage, the medium starch diet (n=13) contained 45% alfalfa silage, and the high starch diet (n=13) contained 41% barley silage plus 4% corn starch. Resulting starch levels were 23.5%, 25.3% and 26.9%, respectively. Body weight and BCS were measured biweekly, and DMI and milk yield recorded daily. Milk samples were obtained weekly; blood samples were taken at calving and then biweekly until 70 DIM for analysis of glucose, insulin, IGF-1, BHBA and NEFA. Data were statistically analyzed using the repeated measures option in Proc Mixed of SAS. Treatment had no effect on DMI, milk yield, milk fat or protein content (P>0.10) but cows fed the low starch diet had significantly higher levels of milk urea nitrogen compared to the other diets (P=0.001). Cows fed the high starch diet had higher BW than the other two treatments (P=0.04) but BCS was not different among treatments. Blood metabolite concentrations were unaffected by treatment. These results indicate that starch supplementation to well-balanced diets has little impact on productivity or metabolic status of postpartum cows.

Table 1. Effect of dietary starch level on production and metabolic parameters

	Starch level			
	Low	Medium	High	SEM
DMI, kg/d	18.0	19.3	18.5	0.8
Milk yield, kg/d	34.9	34.4	35.5	1.6
Milk fat, %	3.81	3.67	3.6	0.2
Milk protein, %	3.01	2.94	3.06	0.1
MUN, mg/dl	16.25[a]	13.56[b]	13.35[b]	0.7
Glucose, mg/dl	59.4	60.0	60.2	1.1
Insulin, µIU/ml	6.33	6.61	7.77	0.7
IGF-1, ng/ml	55.7	52.1	56.0	3.2
NEFA, mEq/L	294.2	349.8	268.0	30.4
BHBA, mg/dl	8.38	7.84	8.54	0.3
BW, kg	560[b]	557[b]	594[a]	14

Means within a row with different superscripts differ significantly (P<0.05)

Key Words: starch supplementation, postpartum cows, metabolic status

M303 Effect of dietary protein level on rumen fermentation, digestibility, and nitrogen losses in dairy cows. M. Agle*[1], A. N. Hristov[2], S. Zaman[1], and C. Schneider[1], [1]*University of Idaho, Moscow*, [2]*Pennsylvania State University, University Park*.

The objective of this experiment was to investigate the effect of dietary CP level on rumen fermentation, digestibility, and performance of lactating dairy cows. The experiment was a replicated Latin square design with 2-wk adaptation periods. Three diets varying in CP concentration were tested (CP, % of DM): 15.3 (HighCP), 13.3 (LowCP), and 12.8% (ExLowCP). RDP and RUP concentrations (estimated based on NRC, 2001) were: 10.2 and 5.1, 8.3 and 5.0, and 7.0 and 5.8% of DM, respectively. Estimated RDP supply exceeded requirements in HighCP and was deficient in LowCP and ExLowCP. In all diets, metabolizable protein intake met or exceeded the requirements of the cows. Concentration of NE_L was similar among diets (1.51 Mcal/kg). Dry matter intake was numerically lower (P = 0.15) for LowCP and ExLowCP, compared with HighCP. Milk (30 to 32 kg/d), 4% FCM, and energy-corrected milk yields and milk fat and protein concentrations and yields were not affected by treatment (P = 0.16 to 0.88). Rumen pH and ammonia concentration were decreased (P = 0.02 and <0.001, respectively) by both LowCP and ExLowCP, compared with HighCP. Ruminal VFA concentrations were not affected (P = 0.53 to 0.89) by diet. Plasma urea and MUN concentrations and absolute and relative (as proportion of N intake) urinary N losses were lower (P < 0.001 to 0.02) for LowCP and ExLowCP, compared with HighCP. Compared with HighCP, total urinary and fecal N losses were reduced (P = 0.05) by ExLowCP, but not by LowCP. As proportion of N intake, urinary and fecal N losses were not different (P = 0.97) among diets. Urinary allantoin excretion and estimated microbial protein outflow from the rumen were numerically reduced (P = 0.15) by LowCP and ExLowCP, compared with HighCP. Total tract apparent digestibility of DM, OM, N, and NDF was not affected (P = 0.07 to 0.35) by diet. Decreasing dietary CP within the range tested in this experiment did not affect cow productivity, but resulted in decreased urinary N losses.

Key Words: dietary protein, nitrogen losses, dairy cow

M304 Effect of dietary crude protein concentration on production and nitrogen balance of lactating dairy cows. T. Sun, Z.-J. Cao*, Y.-X. Dong, H.-T. Zhang, and S.-L. Li, *College of Animal Science and Technology, China Agricultural University, Beijing, China*.

Four ruminally cannulated multiparous cows averaging 73±13 days in milk (DIM) were used in a 4 × 4 Latin square design to determine the effects of different dietary crude protein levels on ruminal fermentation and production performance . Each experimental period was 21-d. The diets contained [dry matter (DM) basis] 20% alfalfa hay, 20% corn silage, 10% Chinese wildrye, and 50% concentrate mainly from corn, bran, rapeseed meal and soybean meal. Four experimental diets were formulated to contain similar concentrations of ADF, NDF, net energy of lactation (NEL), but with different crude protein (CP), rumen-degradable protein (RDP) and rumen-undegradable protein (RUP) levels: 12.8%CP, 7.5% RDP, 5.3% RUP (LD-LU diet); 14.6% CP, 9.2% RDP, 5.4% RUP (HD-LU diet); 14.0% CP, 7.6% RDP, 6.4% RUP (LD-HU diet) and 15.6% CP, 9.2% RDP, 6.4% RUP (HD-HU diet). Diets were fed as a total mixed ration. Results showed that milk yield tended to be increased in the cows given the HD-LU, LD-HU and HD-HU diets compared with that in the cows fed on the LD-LU diet. Higher DM intake (DMI) and milk yield/DMI were also detected in the cows fed the HD-HU diet and HD-LU diet compared with that for the LD-LU diet. Milk fat content was higher for the HD diets than the LD diets. Milk protein percentages and yields were not significantly affected by the level of RUP or RDP. Ruminal NH3 concentration was higher for the HD diets than the LD diets, and isovalerate concentration tended to be increased by increasing dietary CP level. Apparent nutrient digestibility and estimated bacterial CP synthesis were similar for all treatments. Blood and milk urea-N were increased by feeding higher dietary CP; Increasing dietary CP from 12.8% (diet LD-LU) to 15.6% (diet HD-HU) increased urinary N excretion by 37g/d and reduced apparent N efficiency (milk protein N/N intake) by 4.4 percentage units. Under the conditions of this trial, milk production and composition were improved by feeding higher

CP diets. But higher CP diets depressed N efficiency and increased N loss in urine.

Key Words: nitrogen metabolism, nitrogen excretion

M305 Use of milk urea nitrogen (MUN) to improve dairy farm management. M. Nourozi*[1,2], A. Heravi Moussavi[1], and M. Abazari[2], [1]*Department of Animal Science , Ferdowsi University of Mashhad, Mashhad, Iran*, [2]*Department of Animal Science, Khorasan Razavi Agricultural and Natural Resources Research Center, Torogh, Mashhad, Iran*.

The hypothesis of this study was that providing farmers with information regarding their herd′s milk urea nitrogen (MUN) would result in more accurate feed management, lower feed cost and a change in MUN toward target values. Milk samples of high (38 ±3 kg/d) and low (24 ±3 kg/d) yield dairy cows' and bulk tanks in thirty dairy milk producers were tested for MUN and crude protein each month for six months from the last month of spring until the last month of fall. Farms were divided into two equal groups. The first group of dairy Farms (n=15) was provided with the results of their MUN analysis each month along with interpretive information. Nitrogen intake, urinary and fecal N and efficiency of feed N utilization were estimated from survey data and milk analysis for each herd. Data were analyzed by using a mixed model (PROC MIXED, SAS Inst. Inc., Cary, NC) for a completely randomized design with repeated measures. For milk samples of high yielding dairy cows and bulk tanks, average MUN and efficiency of feed N utilization for the first group of farms (13.29±0.58, 12.31±0.59 mg/dl and 30.37±0.78, 27.10±0.58 percent; respectively) were lower and higher respectively than second group (18.52±0.66, 16.09±0.67 mg/dl and 27.30±0.92, 24.47±0.66 percent; respectively)($p<0.05$). The average MUN across all farms in the study increased in late summer, but the increase was significantly lower for farms receiving MUN results than other farms ($p<0.05$). Conversely, the average feed N utilization was decreased for all farms in late summer. Again, average feed N utilization calculated from high-producing cow or bulk tank samples for that time period was significantly higher for the informed group than the second ($p<0.05$). The farms which received MUN results were able to improve their management and significantly lower feed cost (45$/cow/305DIM, $p<0.05$) compared to farms without that information.

Key Words: dairy farms, milk urea nitrogen, fecal N

M306 Varying ruminally degradable protein concentrations in the lactating dairy cow diets maintains rumen fiber digestion and outflow of nutrients. J. Cyriac*[1], A. G. Rius[1], J. A. D. R. N. Appuhamy[1], R. E. Pearson[1], J. H. Herbein[1], K. F. Knowlton[1], J. L. Firkins[2], and M. D. Hanigan[1], [1]*Virginia Polytechnic Institute and State University, Blacksburg*, [2]*The Ohio State University, Columbus*.

This study investigated the effects of feeding diets containing varying concentrations of ruminally degradable protein (RDP) on ruminal metabolism and outflow of nutrients in lactating dairy cows. Seven ruminally cannulated, Holstein cows were used in a replicated Latin square design with 4 periods and 4 treatments. Period length was 21 d. Cows were randomly assigned to one of four diets formulated to contain 11.3, 10.1, 8.8 or 7.6% RDP with constant ruminally undegradable protein (7.1% of DM). All diets contained 47.5% forage and 52.5% concentrate on a DM basis. Ruminal outflow of nutrients was determined from omasal samples using a double marker system with Co-EDTA and Yb-labeled forage as markers. Data were analyzed using the Proc Mixed procedure of SAS. The varying levels of RDP in the diet did not significantly alter DM (17.8, 18.7, 17.4 and 17.0 kg/d) or fiber intakes. Protein intake decreased linearly (3.19 to 2.56 kg/d; $P<.05$) with decreasing concentrations of RDP in the diet. Milk yield (32.7, 34.5, 34.1 and 29.8 kg/d) and milk composition were similar across treatments excepting milk urea-N which decreased linearly with decreasing dietary RDP ($P<.05$). Ruminal NH_3 concentrations also decreased linearly with decreasing concentrations of RDP in the diet (from 10.8 to 3.96 mg/dL; $P<0.0001$). Ruminal outflow of DM declined from 14.9 to 13.3 kg/d for the high and low RDP diets, respectively indicating a trend for a linear reduction in flow ($P=0.08$). Ruminal outflow of acid detergent and neutral detergent fiber was not significantly affected by treatment. Ruminal digestibility coefficients for acid detergent and neutral detergent fiber were not significantly affected by treatment. However ruminal outflow of N decreased linearly with decreasing concentrations of RDP in the diet ($P<.01$). Feeding dietary RDP below NRC requirements did not appear to compromise fiber digestion, but it did result in a reduction in total N leaving the rumen. Reduced N availability to the animal could compromise milk production if maintained for longer periods of time.

Key Words: ruminally degradable protein, fiber digestion, nutrient flow

M307 Effect of NPN source and dietary fermentable carbohydrate composition on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech Biotechnology, Nicholasville, KY*.

Replacing corn with byproducts in dairy diets can improve feeding economics but lower fermentable carbohydrate (fCHO) could negatively impact ruminal function. Effects on ruminal performance of total replacement of corn grain with byproducts while holding fCHO constant were investigated in single-flow rumen-simulating fermenter cultures. Cultures were fed diets formulated in CPM (version 3.08) based on either corn and byproducts with equal fCHO. In addition, three NPN sources (urea-U, Optigen®-O, urea-Optigen) were utilized with each providing equal NPN (equivalent of 114 g NPN at 22.7 kg DM intake). Six cultures were used in a 2 X 3 factorial design with 6 dietary treatments and 4 experimental runs. Cultures were fed 12.5 g as fed of experimental diets twice daily for 6 days. Samples were collected from all cultures prior to morning feeding during the last 3 days of the experiment for fermentation analysis. Effluent composite samples from each fermenter were used for DM and NDF disappearance determination. Nitrogen flow measures were estimated by using purine to N ratios for effluent DM and bacteria. Data were analyzed for effects of dietary treatment using GLM procedure of SAS. Orthogonal contrasts were used to determine effects of NPN and fCHO. NPN source had no effect on culture pH, digestion, or N flow ($P>0.10$). Bacterial N% was greater ($P<0.05$) in cultures fed the U-O combination. Corn-fed cultures had higher molar proportions of butyrate ($P<0.001$) and isoacids ($P<0.0001$) and lower acetate ($P<0.0001$). Bacterial N yield was similar between cultures fed different fCHO formulations ($P>0.10$). Under dietary conditions utilized in this experiment, no effects of source were noted when NPN was provided by urea, Optigen, or a combination of the two. When diets were balanced for equivalent fCHO, total replacement of corn grain with byproducts resulted in differences in fermentation patterns but did not affect digestibility or nitrogen partitioning.

Key Words: non-protein nitrogen, Optigen, fermentable carbohydrate

M308 Effects of different levels of rumen degradable protein on rumen and plasma parameters in midlactation Holstein cows. H. Rafiee*, *Aboureihan Campus, Tehran University*, *Tehran, Iran*.

To evaluate the effect of different level of rumen degradable protein (RDP) on rumen and blood parameters, nine multiparous mid-lactation Holstein cows averaging 171 ± 17 days in milk and 24.1 ± 3.3 Kg of milk/d were assigned into a triplicate 3 × 3 Latin square design. Each period was 21-d (14 d of adaptation and 7 d for sampling). Diets were iso-energetic and based on a barley concentrate and 45:55 forage:concentrate ratio. Forage part consists of corn silage and alfalfa hay. The RDP % and crude protein level of diets were respectively: 1) 9.8 and 14.3 2) 10.8 and 15.3 3) 11.8 and 16.3. Urea was supplemented to increase of RDP. Rumen fluid was taken from each cow approximately 3 h after morning feeding and Blood samples were collected from the coccygeal vein of cows at approximately 2 h post feeding. Data were analyzed using PROC MIXED of SAS. Cow within square was the term of the RANDOM statement. Values reported as least squares means. Treatments had no effect on ruminal pH. However, increasing RDP from 9.8 to 11.8% resulted in significant linear increases ($P < 0.01$) in rumen concentration of ammonia (9.95, 12.50, and 14.11 mg/dL, respectively; SEM = 0.70). Treatments had no effect on glucose and total protein of plasma. But, increasing protein from 14.3 to 16.3% resulted in significant linear increases ($P < 0.01$) in plasma urea nitrogen (15.20, 16.86, and 17.76 mg/dL, respectively; SEM = 0.41). With increasing dietary RDP both plasma urea nitrogen (PUN) and rumen ammonia concentration increased significantly. The rumen ammonia not incorporated into microbial protein, is absorbed across the rumen wall and converted to urea in the liver and diffused in blood for secretion in milk, excretion in urine or recycling to the rumen through saliva. Because of the rumen fluid collection was difficult and harmful for animal, this result suggested that we can use form PUN for prediction rumen ammonia level.

Key Words: rumen degradable protein, rumen ammonia, plasma urea nitrogen

M309 Partial replacement of soybean meal by protected urea effects on milk yield and composition. V. L. Souza[1], D. F. F. Silva[1], P. R. B. Piekarski[1], C. P. Jesus[2], M. N. Pereira[3], and R. Almeida*[1], [1]*Universidade Federal do Paraná*, *Curitiba, PR, Brazil*, [2]*Colégio Agrícola Olegário Macedo*, *Castro, PR, Brazil*, [3]*Universidade Federal de Lavras*, *Lavras, MG, Brazil*.

The objective of this trial was to evaluate the effects of partial replacement of soybean meal by protected urea - Optigen® II (Alltech Inc., Nicholasville, USA) on milk yield and composition. Thirty-four lactating Holstein cows with 128 ± 60 days in milk and yield of 41.6 ± 6.7 kg/day at the beginning of the trial, were blocked by milk production, lactation number and days in milk. Variables measured before the application of treatments were used as covariate in the statistical model. Response variables were measured on days 30 and 60 of the comparison period. Data was analyzed with the mixed procedure of SAS with a model containing the continuous effect of the covariate and the fixed effects of block, period, treatment, day and the interaction of day and treatment. The mean square of cow nested within treatment was used as the error term to test the treatment effect. Treatments were isoenergetic and isonitrogenous diets with 1.66 ELL and 18.4% of CP (dry matter basis), described as: T1= 0.0% Optigen + 11.4% soybean meal; T2= 0.4% Optigen + 9.0% soybean meal, respectively. The composition of the control TMR was (% of DM): corn silage (30.2), grass haylage (11.7), concentrate mix (30.3), whole cottonseed (5.4), soybean meal (11.4), soybean hulls (8.4), Megalac-E® (0.8) and mineral mix (2.0). There was no detectable treatment effect on the daily production of milk and solids, MUN and SCC, although milk yield was numerically greater with Optigen® II. The slow release urea diet reduced milk fat and total solids content. The partial replacement of soybean meal by protected urea did not induce lower performance of lactating cows.

Table 1.

	Soybean meal		Optigen® II			
	Day-30	Day-60	Day-30	Day-60	SEM	*P* Treat
Milk yield (kg/d)	36.9	36.4	39.4	38.1	1.11	0.16
Fat content (%)	3.16	2.99	2.87	2.71	0.07	<0.01
Fat yield (kg/d)	1.14	1.13	1.12	1.04	0.04	0.24
Protein content (%)	3.12	2.82	3.03	2.79	0.04	0.21
Protein yield (kg/d)	1.14	1.07	1.19	1.08	0.03	0.51
Lactose content (%)	4.58	4.72	4.64	4.80	0.03	0.08
Lactose yield (kg/d)	1.70	1.73	1.83	1.84	0.06	0.13
Total solids content (%)	11.74	11.43	11.43	11.21	0.10	0.04
Total solids yield (kg/d)	4.31	4.19	4.47	4.25	0.12	0.46
Milk energy (Mcal/d)	23.6	22.6	24.1	22.5	0.62	0.77

Key Words: non-protein nitrogen, Optigen® II, slow-release urea

M310 Effect of different ratios of ammonia nitrogen to peptide nitrogen on microbial nitrogen synthesis in dairy cows. A. Nikkhah*, M. Kazemi Bonchenari, K. Rezayazdi, M. Dehghan, and H. Kohram, *Department of animal Sciences, Faculty of agronomy and animal sciences, University of Tehran*, *Karaj, Iran*.

Some of the studies showed that peptide nitrogen (PN) improves ruminal fermentation and also some studies reported that the minimum ammonia nitrogen (AN) concentration (5 mg/dl) is necessary for optimal microbial nitrogen synthesis (MNS). There is limited document related to the optimum ratio of AN/PN for microbial nitrogen synthesis (MNS). Three ruminally fistulated dairy cows assigned in a Latin square design (21d periods; 14d for adaptation and 7d for sample collection) and fed a similar basal diet. Sodium Caseinate was infused directly in to rumen before morning diet portion as peptide nitrogen source (PNS) (0, 50 and 100 gr/d as treatments 1, 2 and 3 respectively). Ruminal fluid samples were collected at 0, 1.5, 3, 4.5 and 6 hours after feeding. Separated aliquots were preserved for later analyses of PN and AN. Daily urinary output was measured by urine collection bag and total purine derivatives (uric acid + allantoin) were measured. MNS was estimated from total purine derivatives. Data were analyzed using Proc Mixed in SAS with the following model; $Y_{jklm} = \mu + P_j + C_k + T_l + \varepsilon_{jkl} + Z_m + ZT_{ml} + \alpha_{jklm}$ in which components respectively are; dependent variable, overall mean, effect of period j, effect of cow k, effect of treatments l, whole plot error, effect of time m, interaction between time m and treatment l, subplot error. The results are given in table 1. This study confirmed that rumen microbes need some of their N requirements as PN and the highest amount of MNS was for AN/PN ratio of 0.82. It could be concluded that it is necessary to fractionating and identification of rumen microbial requirements to different nitrogen sources (AN, amino acid N and PN).

Table 1. Effect of PNS infusion in to rumen on microbial nitrogen synthesis

	Treatments				P<F
Item	1	2	3	SE	Treatments
NH3-N (mM/L)	8.11^{c}	10.6^{bc}	12.96^{a}	2.11	<0.01
Pep-N (mM/L)	13.93^{c}	15.12^{ab}	15.74^{a}	1.23	<0.01
AN/PN	0.58^{c}	0.70^{ab}	0.82^{a}	0.04	<0.05
Total purine derivatives (mM/d)	334.4^{c}	351.3^{b}	378.4^{a}	39.1	<0.01
Microbial nitrogen (g/d)	222.8^{c}	238.7^{b}	257.5^{a}	25.9	<0.01

^{a,b,c} Least squares means within the same row without a common superscript differ (P < 0.05).

Key Words: peptide nitrogen, microbial nitrogen synthesis

Table 1. Effect of Sodium Caseinate on fiber digestibility and nitrogen efficiency

	Treatments				
Item	1	2	3	SE	P
NH_3-N mM	8.11^{c}	10.6^{bc}	12.96^{a}	1.16	<0.01
Pep-N mM	13.93^{c}	15.12^{ab}	15.74^{a}	1.2	<0.01
NH_3-N/Pep-N	0.58^{c}	0.70^{ab}	0.82^{a}	0.04	<0.01
BUN mg/dl	12.6^{bc}	12.9^{b}	14.3^{a}	2.1	<0.01
NDF digestibility %	45.2^{b}	46.2^{ab}	47.3^{a}	5.12	<0.05
ADF digestibility %	48.6^{bc}	50.1^{b}	52.5^{a}	5.8	<0.01

^{a,b,c} Least squares means within the same row without a common superscript differ (P < 0.05)

Key Words: peptide nitrogen, fiber digestibility

M311 Optimum ratio of ammonia nitrogen to peptide nitrogen in ruminal fluid for fiber digestibility and nitrogen utilization efficiency in dairy cows. M. Kazemi Bonchenari[1], K. Rezayazdi[1], M. Dehghan[1], A. Nikkhah*[1], H. Khalilvandi[1], V. Keshavarz[2], and F. Ghaziani[1], [1]*Department of Animal Sciencs, Faculty of Agronomy and Animal Sciences, University of Tehran, Karaj, Iran*, [2]*Department of Animal Sciences, University of Zanjan, Zanjan, Iran*.

Previous studies showed that increasing peptide nitrogen (Pep-N) concentration in ruminal fluid improve fiber digestibility. Some other studies showed that increased peptide nitrogen concentration decreased ammonia nitrogen (NH_3-N) concentration (under 5mg/dl that considered minimum requirement for optimum rumen fermentation) in rumen and therefore fiber digestibility negatively affected by high peptide nitrogen concentration. The optimum ratio of ammonia nitrogen to peptide nitrogen (NH_3-N/Pep-N) is not well documented. In this study three ruminally dairy cows was assigned to a Latin square design (21d periods; 14d for adaptation period and 7d for sample collection period) to investigate the optimum ratio of NH_3-N/Pep-N for fiber digestibility and nitrogen utilization efficiency. The basal diet was similar and Sodium Caseinate was infused in to rumen as peptide nitrogen source before morning diet (0, 50 and 100 gr/d which considered as treatments 1, 2 and 3 respectively). Pep-N and NH_3-N concentrations were measured in ruminal fluid in different hours. Blood urinary nitrogen (BUN) was measured and considered as nitrogen utilization efficiency indicator. Data were analyzed using Proc Mixed in SAS (SAS institute 1999). The results showed that NDF and ADF digestibility significantly increased by Sodium Caseinate infusion and also BUN was increased dramatically by Sodium Caseinate infusion (table 1). Both of the highest fiber digestibility and also the lowest nitrogen utilization efficiency was for the ratio of 0.82. It could be concluded that based on the present study the ratio of 0.70 is the optimum ratio of NH_3-N/Pep-N for both traits.

M312 Effect of whole cottonseed levels on ruminal parameters of dairy cows grazing elephant grass. J. Cesar Martinez*[1], F. Auguto Portela Santos[2], T. Vinhas Voltolini[2], A. Vaz Pires[2], and C. Maris Machado Brittar[2], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*São Paulo University*, *Piracicaba, São Paulo, Brazil*.

The trial evaluated whole cottonseed (WCS) inclusion on concentrate supplements offered to lactating cows grazing Elephant Grass during the rainy season. Trial was conducted at Animal Sciences Department, USP/ESALQ, Piracicaba/SP-Brazil. 12 multiparous Holstein (543kg LW, 142 DIM at trial beginning) were used on a replicated 4x4 Latin Square design. Data were analyzed by MANOVA and GLM procedures of SAS (2002). Animals were kept on a 4.6ha pasture area divided in 25 0.2ha paddocks fertilized with 80 kg N ha/month. All concentrates had 19% crude protein (CP) and were soybean and ground corn based. WCS was included at 7, 14 and 21% total DM, based on NRC (2001) DMI prediction. The microbial N was analyzed by HPLC, and VFA by photometry. Treatments did not affect ruminal VFA (131.17mM) and ammonia (34.86 mg/dl) concentrations and ruminal pH (6.13). Microbial N flux was affected by WCS14 and WCS21% treatments (P<0.05). Results indicate that WCS can be utilized as a replacement for corn and part of soybean meal on lactating cows rations with no effects on rumen fermentation parameters when used up to 14% of estimated DMI.

Table 1. Ruminal parameters of dairy cows supplied with differents levels of WCS

		Treatments				
	Corn	7%WCS	14%WCS	21%WCS	Mean	Pr(t)
C2[1]	67	69	67	66	68	0.8
C3[1]	41.7	43.8	37.5	35.9	40.5	0.4
C4[1]	16.3	17.1	15.4	14.9	16.1	0.34
iso-C4[1]	1.3	1.4	1.4	1.4	1.4	0.59
C5[1]	2.0	2.1	2.0	1.8	2.0	0.87
Total VFA[1]	131	136	127	123	131	0.35
NH_3 , mg/dL	33.0b	30.4b	35.4ab	40.7a	34.8	0.01
pH	6.1	6.1	6.1	6.3	6.1	0.32
Microbial N, gN/day	201.7a	191.0a	175.5b	169.8b	182.2	0.01

Within rows, means followed by different superscripts are significantly different (P < 0.05); [1]mM/mL

Key Words: volatile fatty acids, ruminal metabolism, tropical Pastures

M313 Effect of whole cottonseed levels on performance of dairy cows grazing elephant grass. J. Cesar Martinez*[1], F. Auguto Portela Santos[2], T. Vinhas Voltolini[2], M. Antonio Penati[2], and A. Mendonça Pedroso[2], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*São Paulo University*, *Piracicaba, São Paulo, Brazil*.

The trial evaluated whole cottonseed (WCS) inclusion on concentrate supplements offered to lactating cows grazing Elephant Grass during the rainy season. Trial was conducted at Animal Sciences Department, USP/ESALQ, Piracicaba/SP-Brazil. Twelve multiparous Holstein (543kg LW, 142 DIM at trial beginning) were used on a replicated 4x4 Latin Square design. Data were analyzed by GLM procedures of SAS (2002). Animals were kept on a 4,6ha pasture area divided in 25 0,2ha paddocks fertilized with 80 kg N ha/month. All concentrates had 19% crude protein (CP) and were soybean and ground corn based. WCS was included at 7, 14 and 21% total DM, based on NRC (2001) DMI prediction. Cows received concentrate according to milk production on a 1:3 basis, fixed at trial beginning, twice daily after each milking. Milk and 3,5% fat corrected milk (FCM) production were lower for WCS21% treatment (P<0,05). Treatments did not affect milk fat, protein, lactose, total solids and urea concentrations (P>0,05) (Table 1). As complement, the live weight (LW) (530 kg), body condition score (BCS) (2,3), plasma urea (49,7mg/dL) and non esterified fatty acids (NEFA) (366,0 meq/L) concentrations were not affected by treatments (P>0,05). Results indicate that WCS can be utilized as a replacement for corn and part of soybean meal on lactating cows rations with no effects on milk production and composition, LBW and blood composition when used up to 14% of estimated DMI.

Table 1. Milk yield and composition of dairy cows feed with different levels of WCS

		Treatments				
	Corn	7%WCS	14%WCS	21%WCS	Mean	Pr>(t)
Milk, kg/day	17.6a	17.4a	16.9a	15.3b	16.8	0.01
FCM, kg/day	17.8a	17.8a	17.8a	16.2b	17.4	0.01
Fat, %	3.5	3.6	3.8	3.8	3.7	0.27
Fat, kg/day	0.62	0.63	0.65	0.59	0.6	0.18
Protein, %	2.9	2.8	2.8	2.8	2.8	0.06
Protein, kg/day	0.51a	0.49a	0.47a	0.43b	0.48	0.01
Urea, mg/dL	13.4b	15.0a	15.9a	15.8a	15.05	0.01

Within rows, means followed by different superscripts are significantly different (P < 0.05)

Key Words: supplementation, tropical pastures, milk yield and composition

M314 Effect of whole cottonseed processing on ruminal degradability of dairy cow grazing elephant grass. J. Cesar Martinez*[1], F. Auguto Portela Santos[2], T. Vinhas Voltolini[2], and A. Dias Pacheco Júnior[2], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*São Paulo University*, *Piracicaba, São Paulo, Brazil*.

The objective of this trial was to evaluate the degradability of different processing of whole cottonseed (WCS) included on concentrate supplements offered to lactating cows grazing Elephant Grass during the rainy season. The trial was conducted at the Department of Animal Sciences, USP/ESALQ, Piracicaba/SP. Four multiparous Holstein cows (513kg LW, 103 DIM at trial beginning) were used on a 4x4 Latin Square design. Data were analyzed by Ørskov and McDonald (1979) model and GLM procedure of SAS (2002). Animals were kept on a pasture of 4.6ha divided in 25 0.2ha paddocks fertilized with 80 kg N ha/month. All concentrates had 19% crude protein (CP) and were soybean and ground corn based. WCS was included at 7, 14 and 21% total DM, based on NRC (2001) DMI prediction. After each milking, cows were fed concentrate twice daily according to milk production on a 1:3 ratio fixed at the beginning of the trial. The incubation time was 0, 2, 4, 6, 8, 12, 18, 24, 36, 48, 62, 84, 96 and 120 hours. When compared with corn grain concentrate, WCS incubated with linter altered significantly (P<0.05) the ruminal degradation kinetic parameters, lowering both the soluble (22.3 vs 2.38%) and the degradable (76.2 vs 28.63%) fractions. On the other hand, undegradable fraction was higher (66.14 vs 1.56 in corn grain). Degradation rate (4.88 vs 1.6%/h) and effective degradation (63.65 vs 11.93%) were lower for WCS. Ruminal and total retention time were only different for WCS7% treatment and byproduct inclusion did not affect forage ruminal passage. WCS ground at 5 mm had a similar degradation to non processed WCS. However, when it was ground at 2 mm the degradation was similar to that related to corn grain. Thereby, the WCS ground at 2 mm is a source of free lipids, as well as the WCS ground at 5 mm is a source of effective fiber.

Table 1. Ruminal degradability of dry matter of WCS incubated with different processing

			Treatments			
	Corn	WCS	2mm	5mm	Mean	Pr(t)
a, %	22.4a	2.4c	2.2c	30.3a	13.7	0.01
b, %	76.1a	31.3c	68.4cb	43.2b	47.4	0.01
c, %	1.5d	66.1a	59.3b	25.8c	38.7	0.01
C, %/h	4.9a	1.6c	1.2c	3.5b	2.8	0.01
Lag Time, h	1.5d	48.3a	44.4b	22.7c	29.5	0.01
Kp, %/h	4.1a	3.6b	3.5b	3.6b	3.7	0.05
Effective Deg.., %	63.6a	11.9c	11.2c	52.7b	34.1	0.01
Potential Deg., %	98.1a	28.9c	29.4c	73.4b	56.7	0.01

Within rows, means followed by different superscripts are significantly different (P < 0.05)

Key Words: ruminal metabolism, tropical pastures, linted whole cottonseed

M315 Effect of dietary protein on urea concentrations and preovulatory follicle characteristics in dairy cattle. U. Moallem*[1], R. Blank[2], M. Zachut[1,2], and A. Arieli[2], [1]*ARO*, *Bet Dagan, Israel*, [2]*Faculty of Agriculture*, *Rehovot, Israel*.

The objectives of this study were to determine the effects of dietary crude protein (CP) on metabolic parameters and preovulatory follicle characteristics in dairy cattle. Four intact and 4 rumen cannulated Holstein non-lactating cows were assigned to 3 treatments in 4 periods (39 d each). Diets consisted of 66% wheat straw with different mixtures of corn grain and soybean meal resulted with 6% (LP), 13% (MP) and 20% (HP) of CP. Individual intake was recorded daily, blood samples were taken twice a week and rumen fluids from the cannulated cows were taken twice in each period. Ten d after commencement of treatments the estrus cycle was synchronized with two $PGF_{2\alpha}$ (PG) injections 13d apart. Fourteen d after observed behavior estrus cows received PG injection and 40 h afterward follicular fluid (FF) from follicles ≥ 7 mm were aspirated. The feed intake of the LP group was lower than in other groups. Rumen ammonia concentrations were lower in the LP than in other groups. Blood urea concentrations were higher in the HP and lower

in the LP as compared to other groups. Similarly, the urea concentrations in FF were higher in HP and lower in the LP group than in other groups (17.1, 33.3 and 50.5 mg/dL for LP, MP and HP, respectively). The estradiol (E_2) concentrations in FF tended to be higher in the HP than in the MP and the progesterone (P_4) concentrations were higher in the HP than in both other groups. No differences in the E_2/P_4 ratio or in E_2 and P_4 contents in FF were observed among groups. The correlation between FF urea concentrations and P_4 content in follicles was significant (r=0.45). In conclusion, high dietary protein increased the urea concentrations in plasma and in a very similar manner in FF. However, the higher urea concentrations in FF as a consequence of high dietary CP was not detrimental to steroidogenesis as reflected by E_2 concentration and content, and E_2/P_4 ratio in preovulatory follicles.

Key Words: dietary protein, follicular fluid

M316 Relationship between milk odd and branched-chain fatty acids and duodenal flow of microbial protein. L. Wang, J. Q. Wang*, D. P. Bu, Khas-Erdene, and S. Y. Luan, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing , P. R. China*.

Effects of refined docosahexaenoic acid (DHA) and refined free linoleic acid (LA) or their combination on odd and branched-chain fatty acids (OBCFA) profiles of milk was studied. A correlation was developed between OBCFA secretion and duodenal flow of microbial protein in lactating dairy cows. Four multiparous Holstein-Friesian dairy cows with ruminal and duodenal cannulas averaging 139±10 DIM were used in a 4 × 4 Latin square design experiment. There were 4 periods of 3 wk each. Cows were fed 65% forage and 35% concentrate diet. In addition to the basal diet cows received either 0 (Control) or 0.5% DHA, 2.73% LA, and 0.5% DHA + 2.3% LA in combination. Fat was added by replacing grain in the diet. Milk and duodenal digesta samples were collected on 17, 18, 19 d and 16, 17, 18 d, respectively. Data were analyzed statistically by using PROC MIXED of SAS. Feed intake was not affected by fat supplement compared to control. Milk yields were 18.6, 17.2, 18.4, and 17.0 kg/d for control, DHA, LA, and DHA+LA treatments, respectively and were not affected by fat supplementation P > 0.05. Milk fat and protein percentages were the same in fat supplemented and control treatment. Compared with control, the concentrations of linear odd-chain fatty acids (C15:0 and C17:0) in milk were reduced by LA+DHA treatment, however, fat supplements had no significant (P>0.05) effects on the concentrations of *iso*-fatty acids or *anteiso*-fatty acids. No strong linear relationship (R=0.166) between milk secretion OBCFA and duodenal flow of cytosine were observed in this study, suggesting that milk OBCFA could not be used as a marker for duodenal flow of microbial protein when cows offered diets with fat supplements.

Key Words: odd and branched-chain fatty acids, microbial protein, dairy cows

M317 Comparison of optimal lysine and methionine concentrations in metabolizable protein estimated by the NRC (2001), CPM-Dairy (v.3.0.10) and AMTS.Cattle (v.2.1.1) models. N. Whitehouse*[1], C. Schwab[1], T. Tylutki[2], D. Luchini[3], and B. Sloan[3], [1]*University of New Hampshire, Durham*, [2]*Integrated Solutions for Sustainable Agriculture, Cortland, NY*, [3]*Adisseo, Atlanta, GA*.

Optimizing concentrations of lysine (Lys) and methionine (Met) in metabolizable protein (MP) is considered to be the first step to maximizing milk and milk component production and efficiency of use of MP by the dairy cow (NRC, 2001). Three commonly used programs to balance for amino acids (AA) are NRC (2001), CPM (v.3.0.10) and AMTS (v.2.1.1). Each program differs in the approach and assumptions taken to estimate AA supply. However, the indirect dose-response approach proposed by Rulquin et al. (1993) for identifying the optimal concentrations of Lys and Met in MP, and subsequently adopted by NRC (2001), can be extended to all models that predict passage of AA to the small intestine. In NRC (2001), this approach showed that maximal content of protein in milk was attained with 7.24% Lys and 2.38% Met in total MP; corresponding values for maximal yield of milk protein were 7.08 and 2.35%. However, a reevaluation of the requirement values for Lys and Met in MP using the NRC (2001) model (see companion abstract) yielded the requirements shown in the table. The objective of this work was to use the same trial dataset used to elaborate the NRC (2001) Lys and Met recommendations to estimate the comparable requirement values for Lys and Met in MP for both CPM (v.3.0.10) and AMTS (v.2.1.1). The dose-response plots were generated as described in NRC (2001). The resulting breakpoint estimates for the required concentrations of Lys and Met in MP for maximal content and yield of milk protein for the two models are shown in the table.

Table 1. Breakpoint estimates for required concentrations of Lys and Met in MP for maximal content and yield of milk protein

		Requirement for maximal milk protein content	Lys:Met ratio	Requirement for maximal milk protein yield	Lys:Met ratio
NRC	Lys	6.80	2.97:1	7.10	2.82:1
	Met	2.29		2.52	
CPM	Lys	7.46	2.90:1	7.51	3.00:1
	Met	2.57		2.50	
AMTS	Lys	6.68	2.78:1	6.74	2.92:1
	Met	2.40		2.31	

Key Words: lactating cows, lysine, methionine

M318 Reevaluation of the breakpoint estimates for the NRC (2001) required concentrations of lysine and methionine in metabolizable protein for maximal content and yield of milk protein. C. Schwab*[1], N. Whitehouse[1], D. Luchini[2], and B. Sloan[2], [1]*University of New Hampshire, Durham*, [2]*Adisseo, Atlanta, GA*.

The 7th Revised Edition of the Nutrient Requirements of Dairy Cattle (NRC, 2001) presents dose-response plots that relate changes in milk protein content (Figure 5-12) and yield (Figure 5-13) to predicted concentrations of Met and Lys in metabolizable protein (MP). A rectilinear model was used to describe the dose-response relationships. The breakpoint estimates for the required concentrations of Lys and Met in MP for maximal content of milk protein were 7.24 and 2.38%, respectively; corresponding values for maximal yield of milk protein were 7.08 and 2.35%. Because the amino acid submodel had to be developed before the final version of the NRC model was available, a beta version of the model was used to predict the concentrations of Lys and Met in MP in the studies that were used in developing the dose-response plots. The objective of this study was to repeat all of the steps, as cited in NRC (2001) (p. 82-85), to generate new dose-response plots, using the final version of the model to predict concentrations of Lys and Met in MP. The resulting breakpoint estimates for the required concentrations of Lys and Met in MP for maximal content of milk protein were 6.80 and 2.29%, respectively. Both values are lower than the corresponding values

of 7.24 and 2.38% reported in NRC (2001). The breakpoint estimates for the required concentrations of Lys and Met in MP for maximal yield of milk protein were 7.10 and 2.52%, respectively. The breakpoint estimate for optimal Lys concentration in MP for maximal protein yield (7.10%) is similar to that reported in NRC (2001) (7.08%), whereas the estimate for optimal Met concentration in MP for maximal protein yield (2.52%) is higher than that reported in NRC (2001) (2.35%). The reasons for these differences in required concentrations of Lys and Met in MP for maximal milk protein production are not clear. However, it is suggested that these new values be used as the reference values when using the NRC (2001) model to optimize Lys and Met concentrations in MP for lactating cows.

Key Words: lactating cows, lysine, methionine

M319 Rumen microbial population shifts in dairy cattle experimentally induced with subacute ruminal acidosis (SARA). E. Khafipour*, S. Li, J. C. Plaizier, and D. O. Krause, *Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada*.

We analyzed rumen microbial composition using terminal restriction fragment length polymorphism (T-RFLP) and real-time PCR in dairy cows experimentally induced with SARA. Our objective was to examine the relationships between microbial population shifts and free lipopolysaccharide (LPS) in the rumen, and the inflammatory response that occur during SARA. SARA was induced by addition of grain pellets or alfalfa pellets into diets in two separate experiments. Cows were clustered based on the severity of SARA with a discriminant multivariate analysis using animals as independent variable and duration of rumen pH < 5.6, LPS, and serum haptoglobin as the dependent variables. SARA cows were separated into mild and severe grain-induced, and alfalfa pellet-induced groups. Severe grain-induced SARA was separated from the mild group based on the greater content of LPS (179,762 vs. 100,175 EU/mL, $P < 0.05$) and inflammatory markers (608 vs. 343.3 μg/mL, $P < 0.05$). The alfalfa pellet-induced SARA was clustered separately ($P < 0.05$) for its high content of LPS (169,266 EU/mL) but no inflammatory response (21 μg/mL). Differences in microbial populations were detected using LSD multiple comparison test ($P < 0.05$). T-RFLP analysis indicated that the predominant shift during SARA was the decline in gram-negative *Bacteroidetes*. However, the proportion of *Bacteroidetes* was greater in alfalfa pellet-induced SARA compared to mild or severe grain-induced SARA (35.4% vs. 26.0% and 16.6% respectively). This shift was also evident from the real-time data for *Prevotella albensis*, *Prevotella brevis*, and *Prevotella ruminicola*, which are members of the *Bacteroidetes*. The real-time data also indicated that severe grain-induced SARA was dominated by *Streptococcus bovis* and *Escherichia coli*, whereas mild grain-induced SARA was dominated by *Megasphaera elsdenii*, and alfalfa pellet-induced SARA was dominated by *P. albensis*. Using discriminant analysis, the severity of SARA and inflammation was correlated with the abundance of *E. coli* and not with LPS in the rumen. We thus suspect that a subset of *E. coli* might be the putative pathogenic trigger for SARA.

Key Words: SARA, T-RFLP, real-time PCR

M320 Molecular population analysis of *Escherichia coli* associated with subacute ruminal acidosis (SARA) in dairy cattle. E. Khafipour*, J. C. Plaizier, and D. O. Krause, *Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada*.

Grain-induced SARA in dairy cattle is associated with increase in inflammatory markers in peripheral blood, such as haptoglobin and serum amyloid-A. However, induction of SARA with alfalfa pellets does not activate an inflammatory response. We hypothesize that diet induced changes to gut *Escherichia coli* populations may be partially responsible for the difference in inflammatory response. To test this hypothesis, low pH conditions were induced by addition of grain pellets or alfalfa pellets into diets in two separate experiments. Rumen fluid samples were collected before and 6 h after feeding and were cultured on chromogenic medium with or without acid shock for *E. coli* and total coliform numeration. Acid shock was performed by reducing the pH of rumen fluid samples to 5.2 with acetate for 2 h, or 2 with HCl for 1 h. From each non-shocked sample, five *E. coli* strains were isolated, typed with repetitive sequence-based PCR DNA fingerprinting, and genotyped using the A, B1, B2, and D phylotypes. Fingerprints were assessed for presence or absence of 23 bands ranging from 420 to 3,300 bp and were subjected to discriminant and cluster analysis using JMP and MEGA software, respectively. The numbers of *E. coli* in alfalfa pellet-induced SARA were extremely lower than in grain-induced SARA so that acid shock could not perform on these samples. The quantity of acid resistant populations remained stable during grain-induced SARA, while a higher degree of variation occurred in the control animals. Cluster analysis indicated that isolates from controls, and alfalfa pellet-induced SARA tended to cluster together. In contrast, grain-induced SARA *E. coli* were members of distinctly separate *E. coli* populations. There was also a shift from A to B1 type *E. coli* during grain-induced SARA. However, no significant difference was observed among *E. coli* when alfalfa-pellet induced SARA was compared to controls. These results suggest that only grain-induced SARA alters *E. coli* population in the rumen and suggests that *E. coli* from high grain diets may possess virulence factors that could be involved in the inflammatory responses observed with SARA.

Key Words: SARA, fingerprinting, *E. coli*

M321 Factors affecting lipopolysaccharide (LPS) in the feces of dairy cows and its relationship to sub-acute ruminal acidosis (SARA). J. C. Plaizier*, D. O. Krause, and S. Li, *University of Manitoba, Winnipeg, MB, Canada*.

The concentration of LPS in feces may be an indictor of SARA in dairy cows. We conducted a survey of 10 dairy farms in Manitoba to investigate factors that could affect this concentration. Each farm was visited once to collect blood samples, milk samples and fecal grab samples of 15 early and peak lactation Holstein cows with an average of 62 ± 38 days in milk (DIM, mean ± SD) and 15 late lactation Holstein cows with an average of 272 ± 67 DIM. Daily milk yield, days in milk, and parity were recorded. Blood was analyzed for the acute phase proteins serum amyloid A (SAA) and haptoglobin (Hp). Milk was analyzed for fat, protein, and somatic cell counts (SCC). Feces were analyzed for free LPS. Diets were analyzed for NDF. Farms were divided into 5 farms with low dietary NDF (< 34% DM) and 5 farms high dietary NDF (> 34% of DM) Data were analyzed in SAS PROC Mixed with a model consisting of the fecal LPS concentration as a dependent variable, level of dietary NDF as a fixed factor, farm within NDF level as a random factor, and parity, days in milk, SCC, and the concentrations on milk fat, milk protein, HP and SAA as independent variables. Farm within level of NDF affected fecal LPS. Days in milk, milk protein, milk fat, SAA and Hp did not affect fecal LPS. An increase in parity was associated with a reduction in fecal LPS ($P = 0.04$), whereas as an increase in daily milk yield was associated with an increase fecal LPS ($P = 0.05$).

Farms with low dietary NDF had higher fecal LPS than farms with a high dietary NDF (27,087 vs. 14,672 EU/ml). Fecal LPS tended to increase with increasing SCC (P=0.09). Results suggest that low dietary NDF, which is a risk factor for subacute ruminal acidosis (SARA), is associated with an increase in LPS in the feces. This could be due to increased fermentation and lysis of gram negative bacteria in the large intestine that accompany SARA. Hence, the measurement of LPS in feces could aid in the diagnosis of SARA. The relationship between SCC and fecal LPS suggests a relationship between SARA and mastitis, the mechanism of which warrants future investigation.

Key Words: LPS endotoxin, acute phase proteins, ruminal acidosis

M322 Estimation of herd level risk of subacute ruminal acidosis on four commercial dairies on the Priority P-One Program. K. Schneider*[1], D. Mertz[2], K. Mertz[2], and R. Breunig[1], [1]*Prority IAC, Manitowoc, WI*, [2]*Agtech Products, Inc., Waukesha, WI*.

Subacute ruminal acidosis (SARA) can often be found in well-managed dairy herds. To estimate herd risk for SARA on dairy farms, Oetzel (2004) recommended testing rumen fluid from 12 cows per group for incidence of ruminal acidosis (pH≤5.5). Priority IAC has developed a program (the P-One Program) which combines ration balancing with feeding Direct-fed microbials containing a lactate and a glucose utilizer to optimize ruminal function and manage risk of SARA. The objective of this study was to estimate risk of SARA in herds on the P-One Program. Four independent dairy herds with 1000 to 4800 lactating cows on the P-One Program were selected for this study. On average, the rations contained 29.4% starch (SD=3.8), 43.5% NFC (SD=2.6), and 16.0% CP (SD=0.4) on a DM basis, and fed to achieve 25.5 kg (SD=3.11) DMI. Rumen fluid samples were collected at 4, 7 and 10 hours post-feeding via oro-ruminal probe from two groups of cows in each herd, 12 cows in early lactation (ELAC, 27 DIM) and 12 cows in peak lactation (PLAC, 92 DIM). Rumen fluid pH was measured on farm using a portable pH probe. Group risk was calculated as the proportion of the sample population with a threshold pH≤5.5. Groups with ≤ 8.3% of the sample population at or below the threshold were not considered at risk. Groups with 16.6% to 33.3% of population at or below the threshold were considered borderline risk, and groups with sample populations >33.3% were positive for SARA. Analysis of variance was performed comparing sample times to determine significant rumen pH fluctuations. Mean pH across all groups for all herds at times 4, 7, and 10 hours was 6.7 (SD=0.3) and not found to be significantly different (P=0.9371). The proportion of cows declining to the threshold limit in both the ELAC and PLAC sample populations in all herds was 0 of 12 cows. The herds on the P-One Program in this study showed no clinical signs of ruminal acidosis and based upon the sample populations, not at risk for SARA.

Key Words: acidosis, direct-fed microbials, P-one program

M323 Use of magnesium exchanged natural zeolite as a source of ruminal buffer additive for lactating dairy cows. C. M. Dschaak*[1], J.-S. Eun[1], A. J. Young[1], and S. Peterson[2], [1]*Utah State University, Logan*, [2]*Zeotech Corporation, Fort Worth, TX*.

A lactating dairy trial was conducted in a completely randomized design to determine the influence of a developmental ruminal buffer product containing magnesium exchanged zeolite (Zeotech Corporation, Fort Worth, TX) on ruminal fermentation and lactational performance in dairy cows over 12 wk. Experimental TMR diet consisted of 37% alfalfa hay, 19% corn silage, 14% of corn grain, and 30% concentrate mix, and it was fed ad libitum. Thirty primiparous and multiparous lactating Holstein cows (52 ± 23 DIM) were assigned to one of 3 dietary treatments with 10 cows in each treatment: control (TMR diet without ruminal buffer), TMR diet with 1.4% sodium bicarbonate (SBD), and TMR diet with 1.4% zeolite product (ZLD). Ruminal fluid was collected from all animals using an oro-ruminal (Geishauser) probe. Intake of DM, milk yield, and milk composition values were reduced to weekly means before data analysis. Data were analyzed using the MIXED procedure of SAS with repeated measures. Intake of DM (average 26.5 kg/d) did not differ across treatments, and milk yield was similar among the 3 treatments (average 40.7 kg/d). Dairy efficiency (4% FCM/DMI) was not affected by dietary treatments. Milk fat concentration did not differ among treatments, whereas milk protein concentration tended to be higher for the ZLD than the control and the SBD (P = 0.15). Although feeding the ZLD resulted in the tendency of increased milk protein concentration, feed N efficiency for milk N did not differ among the 3 treatments. In addition, milk urea N concentration was not influenced by feeding the ZLD. Ruminal pH increased (P = 0.04) by feeding the ZLD compared to the control (6.42 vs. 6.61), but it resulted in a similar pH from cows fed the SBD. Concentration of ammonia-N did not differ among treatments. Feeding ZLD tended to decrease (P = 0.14) total VFA production compared to the control and the SBD, whereas molar proportions of acetate and propionate were not affected by the treatments. The zeolite product used in this study would replace sodium bicarbonate as a ruminal buffer additive cost-effectively in lactating dairy diet.

Key Words: zeolite, sodium bicarbonate, lactating dairy cows

M324 Dietary cation-anion difference with calcium supplementation: Effects on metabolites and health of Holstein periparturient cows. W. X. Wu*[1] and J.-X. Liu[2], [1]*College of Animal Science, Guizhou University, Guiyang, China*, [2]*Institue of Dairy Science, Zhejiang University, Hangzhou, China*.

Dietary cation-anion difference (DCAD) have been drawing much attention in dairy cow nutrition. In this study the effects of varying DCAD with calcium (Ca) supplementation on fluid acid-base balance, blood mineral profiles, health status, and subsequent lactational performance were evaluated in 3 blocks of 12 Holstein cows d 20 prepartum. Animals were randomly allocated to 1 of 3 treatments with DCAD levels at +150 (HD), -100 (LD), and -100 plus Ca (30g/d, LDCA). Urine was sampled 3 d prior ot calving, and blood at d-14, -7 and -3. Feeding of the two LD diets induced lower (P < 0.05) urinary and blood pH compared with the diet HD, with no significant difference (P > 0.05) for the two LD diets. There was a significant correlation between DCAD and urinary pH (P < 0.0001) and blood pH (P < 0.01). Serum Ca level was higher (P < 0.05) in cows fed diet LD than those on diets HD and LDCA, with little difference between diets HD and LDCA (P > 0.05). Cows fed diet LDCA had greater (P < 0.05) serum Mg concentration relative to those on diet LD. Diet LD resulted in higher (P < 0.05) serum P value relative to diet HD. The lowest serum Ca levels were observed for all cows near calving. No milk fever and displaced abomasum occurred within all cows. Hypocalcemia cases were higher (P < 0.05) for cows fed diet HD (33%) compared with those on diet LD (0%). Diet LDCA reduced (P < 0.05) retained placenta incidence (8%) over diet HD (50%). The DMI, milk yield and compositions were unaffected (P > 0.05) by dietary treatments. It may be suggested from the above-mentioned results that dietary inclusion of Ca (30 g/d) into DCAD -100 induced metabolic

acidosis. However, it did not improve blood calcium homeostasis as expected.

Key Words: dietary cation-anion difference, calcium supplementation, dairy cows

M325 Influence of subclinical hypocalcemia on post-partum disease incidence in dairy cows. W. G. Chamberlin*, J. R. Middleton, and J. N. Spain, *University of Missouri*, *Columbia*.

The purpose of this study was to evaluate the effects of calcium status at calving on incidence of common post-partum diseases in Holstein cows. It was hypothesized that cows with subclinical hypocalcemia at calving would have greater frequency of several common post-partum diseases. Forty-four multiparous Holstein cows were assigned to one of two groups 1) hypocalcemic (n=37; ionized calcium [iCa] ï‚£ 1.0 mmol/L) or 2) normocalcemic (n=7; iCa > 1.0 mmol/L) based on whole blood iCa concentrations on the day of calving. Milk samples were collected from all cattle for measurement of somatic cell count (SCC), solid-not-fat, protein, and fat concentration on the third day after calving, and again on 7d, 14d, 21d, 28d, and 35d postpartum. Occurrence of common post-partum diseases such as retained fetal membranes, clinical mastitis, post-partum metritis, clinical ketosis, and displacement of the abomasum were recorded by farm personnel in consultation with herd health veterinarians. On day 21, LSMean (± SE) linear SCC differed between groups with hypocalcemic cows having a linear SCC score (3.52 ± 0.24) that was higher than normocalcemic cows (2.12 ± 0.6; P=0.03). Milk protein concentration also differed between groups on day 7. Hypocalcemic cows had a lower LSMeans (± SE) concentration of milk protein (3.46 ± 0.03) compared to normocalcemic cows (3.65 ± 0.09; P=0.04). Between day 0 and day 14, there was a significant difference in body condition score (BCS) loss between groups. Hypocalcemic cows had a greater loss of BCS (mean ± SD BCS loss of 0.47 ± 0.16) than normocalcemic cows (mean ± SD BCS loss of 0.25 ± 0.0; Pï€¼0.001). Similarly, there was a trend toward greater incidence of clinical ketosis for hypocalcemic cows versus normocalcemic cows. Hypocalcemic cows had an incidence of 49% clinical ketosis, whereas normocalcemic cows had an occurrence of 14% (P=0.08). The results show a relationship between hypocalcemia at calving and increased linear SCC, BCS loss, and increased incidence of clinical ketosis.

Key Words: hypocalcemia, periparturient cows, diseases

M326 Effect of β-carotene supply during close-up dry period on ovulation at the first follicular wave postpartum in dairy cows. C. Kawashima*[1], S. Nagashima[1], Y. Fujihara[1], F. J. Schweigert[2], K. Sawada[3], A. Miyamoto[1], and K. Kida[1], [1]*Obihiro University of Agriculture and Veterinary Medicine*, *Obihiro, Hokkaido, Japan*, [2]*University of Potsdam*, *Potsdam-Rehbrüke, Germany*, [3]*DSM Nutrition Japan K.K.*, *Tokyo, Japan*.

β-Carotene functions in reproductive performance of dairy cows. Our previous study showed that lower plasma β-carotene level during close-up dry period related to anovulation at the first follicular wave postpartum (pp). The aim of our study was to examine the effect of β-carotene supply during close-up dry period on the ovulation at the first follicular wave pp in dairy cows. Two experiments of β-carotene supply at different levels (Exp.1; recommendation, Exp.2; pasture equivalent) were carried out using 10 and 22 cows, respectively. In both experiment, cows were fed a TMR consisting of grass, corn silage and concentrate. During close-up dry period, 5 cows (24.6±2.6 d) in Exp.1 and 12 cows (24.3±1.5 d) in Exp.2 were supplied daily 500mg and 2000mg of β-carotene, respectively. Blood samples were obtained once a week from 4 wk prepartum to 3 wk pp. Data was analyzed by repeated measures ANOVA. In Exp.1, plasma β-carotene levels in control group decreased and reached nadir at 1 d pp (1.5±0.2 mg/l), whereas it did not change in treated group (2.5±0.2 mg/l). Number of ovular cows at the first follicular wave was 4/5 in treated group and 1/5 in control group. In Exp.2, plasma β-carotene levels during close-up dry period was higher in treated group than control group ($p<0.05$, 5.9±0.3 vs. 5.1±0.0 mg/l), and the level of control group in Exp.2 was higher than treated group in Exp.1 ($p<0.001$, 5.1±0.0 vs. 2.8±0.4 mg/l). Number of ovular cows at the first follicular wave pp was 9/12 in treated group and 5/10 in control group. In Exp.1 and 2, plasma retinol levels and metabolic status from glucose, NEFA and metabolic hormones levels in plasma did not differ between both groups. In conclusion, β-carotene supply during close-up dry period may have an effect on the ovulation at the first follicular wave pp in dairy cows. Both doses of β-carotene supply used in the present study appear to stimulate an effect on the occurrence of the first ovulation pp.

Key Words: β-carotene, dairy cow, first ovulation

M327 Effect of prepartum diet on rumen bacterial adaptation to a lactation diet fed to dairy cattle. S. E. Stebulis*[1], D. M. Stevenson[2], G. J. M Rosa[1], P. J. Weimer[2,1], and R. R. Grummer[1], [1]*University of Wisconsin*, *Madison*, [2]*USDA-ARS US Dairy Forage Research Center*, *Madison, WI*.

The objective was to analyze changes in rumen bacterial populations during the transition period using automated ribosomal intergenic spacer analysis (ARISA) and rumen fermentation parameters. Fourteen ruminally cannulated, pregnant, nonlactating Holstein cows (n=8) and 3/4 Holstein x 1/4 Jersey cows (n=6) were used in a completely randomized design. Each cow was assigned to one of two dietary treatments, moderate grain (MG; NDF=37.6%) or high forage (HF; NDF=45.5%). Starting 45 d prior to expected calving date, all cows (n=14) were fed HF. At 21 d prior to expected calving date, 7 cows were switched to MG and remained on this diet until calving. The remaining cows continued to receive HF until calving. At calving, all cows were fed the same lactation diet. Rumen pH was not different ($P > 0.05$) prepartum (6.72 vs. 6.81 ± 0.06) or postpartum (6.21 vs. 6.15 ± 0.63) between the two groups. Rumen ammonia-nitrogen concentration was significantly increased ($P < 0.05$; 6.5 vs. 5.2 ± 0.28 mg/dL) in cows fed MG compared to cows fed HF prepartum, but was not affected ($P > 0.05$) postpartum. Total ruminal VFA, acetate, propionate, and butyrate concentrations were not different ($P > 0.05$) during prepartum or postpartum periods. Within Domain Bacteria, there were 293 total operational taxonomic units (OTU) detected using ARISA across the three time periods considered: prepartum (wk -4 relative to expected calving), transition (wk -1 and wk 0 relative to expected calving), and postpartum (wk 2 and wk 3 postpartum). Prepartum, 6.8% of OTU were significantly ($P < 0.05$) affected by diet (MG or HF). During the transition period, 9.9% of OTU were significantly ($P < 0.05$) affected by diet. Postpartum, 8.5% of OTU were significantly ($P < 0.05$) affected by prepartum diet. Principal component analysis showed clear separation between prepartum and postpartum ruminal bacterial communities across treatments, but no distinction between MG and HF diets. Overall, the prepartum diet did not affect the postpartum rumen bacterial population based on rumen fermentation patterns and microbial communities characterized by ARISA.

Key Words: rumen bacteria, periparturient

M328 Effect of feeding level on the sorting behavior of lactating dairy cows. E. K. Miller-Cushon and T. J. DeVries*, *Department of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, Ontario, Canada*.

It has been suggested that dairy cows sort their TMR more extensively when overfed. The objective of this study was to examine the effects of feeding level on the feed sorting behavior of lactating dairy cows fed a high-production TMR. Six lactating Holstein cows, individually-fed a TMR once daily, were exposed to 2 treatments in a crossover design with 7-d periods. The treatments were: 1) lower feeding level (LFL; target 10% orts), and 2) higher feeding level (HFL; target 20% orts). Dry matter intake (DMI) was monitored daily for each animal. For the final 4 d of each treatment period, fresh feed and orts were sampled for chemical (NDF and starch) and particle size analysis. The particle size separator had three screens (19, 8, 1.18 mm) and a bottom pan, resulting in 4 fractions (long, medium, short, fine). Sorting was calculated as the actual intake of each particle size fraction expressed as a percentage of the predicted intake of that fraction based on TMR particle size distribution and DMI. Sorting values > 100% indicate selection for, while values < 100% indicate sorting against. Analysis revealed no effect of day within treatment period; therefore, data were averaged across each treatment period. Treatment was tested using a general linear mixed model. Actual orts % averaged 11.5% for the LFL and 18.0% for the HFL treatments (SE=0.8; $P<0.001$). When on the HFL, cows sorted for the medium particles to a greater extent than on the LFL (103.0 vs. 101.1%; SE=0.6; $P=0.05$). Further, when on the HFL cows sorted against short particles to a greater extent than on the LFL (95.2 vs. 98.6%; SE=0.9; $P=0.03$). Despite greater sorting on the HFL, the concentration of NDF (29.6%) and starch (27.1%) in the feed consumed was similar between treatments. Given this, and that DMI was greater on the HFL compared to the LFL treatment (29.7 vs. 26.5 kg/d; SE=1.6; $P=0.02$), greater intakes of NDF (8.7 vs. 7.8 kg/d; SE=0.5, $P=0.02$) and starch (8.0 vs. 7.2 kg/d; SE=0.4, $P=0.02$) were also observed on the HFL treatment. The results suggest that, despite increased sorting, increasing the feeding level of lactating dairy cows promotes higher DMI and a balanced intake of nutrients.

Key Words: dairy cow, sorting, feeding level

M329 Relationship of dairy cattle chewing behavior with forage fragility and fiber digestibility. K. W. Cotanch*[1], H. M. Dann[1], C. S. Ballard[1], C. S. Mooney[1], R. J. Grant[1], T. Eguchi[2], and K. Yagi[2], [1]*William H. Miner Agricultural Research Institute, Chazy, NY*, [2]*Zen-Noh National Federation of Agricultural Cooperative Associations, Tokyo, Japan*.

The physically effective neutral detergent fiber (peNDF) system predicts chewing response of dairy cattle based on feed particle size, but does not consider forage fragility or NDF digestibility. Fragility is defined as change in physical effectiveness factor (pef) following 15 min of ball milling. Four chopped grass hays that differed in 24-h in vitro NDF digestibility and fragility were fed for ad libitum consumption to 16 Holstein dairy heifers (18.5 mo of age; average body weight of 570 kg) in replicated 4×4 Latin squares with 1-wk periods to measure intake and chewing responses. The 4 grasses were: 1) low NDF digestibility (31.4% of NDF), low fragility (46.2%; LL), 2) medium NDF digestibility (43.7%), low fragility (30.0%; ML), 3) high NDF digestibility (54.8%), high fragility (80.7%; HH), and 4) medium NDF digestibility (47.3%), high fragility (63.9%; MH). Forages were processed to similar particle size (average pef of 0.44). Data for intake (measured d 4 to 7) and chewing (measured d 6 to 7) were analyzed with model effects for diet, period, and replicate using MIXED procedure of SAS with heifer within replicate as random effect. The dry matter intake (% of body weight/d) for heifers fed LL, LM, HH, and HM, respectively, was 1.73, 1.81, 2.04, and 1.96 and differed for each grass (SEM = 0.04; $P < 0.05$). The NDF intake (% of body weight/d) was lower ($P < 0.01$) for heifers fed LL compared with those fed ML, HH, and MH (0.98, 1.08, 1.05, 1.05, respectively, SEM = 0.03). When heifers were fed ML versus MH, rumination and eating were similar (84 and 48 min/kg NDF intake, respectively; SEM = 2.0; $P > 0.05$) indicating a greater influence of NDF digestibility than fragility on chewing. However, rumination and eating were greater ($P < 0.01$) for heifers fed LL versus HH (99 and 85; 50 and 45 min/kg NDF intake, respectively; SEM = 2.0). For grasses within the range of NDF digestibility and fragility that we evaluated, fragility was less important than digestibility in eliciting chewing response to similarly sized grass particles.

Key Words: physically effective fiber, chewing, dairy cattle

M330 Parity and its effect on conjugated linoleic acid (CLA) content in confined Holstein cows milk, in the northwest of México. A. Martínez-Borraz, H. González-Rios, S. Y. Moya-Camarena, J. Hernández, and A. Pinelli-Saavedra*, *Centro de Investigación en Alimentación y Desarrollo, A.C., Hermosillo, Sonora, México*.

Studies in experimental animals with conjugated linoleic acid (CLA) have demonstrated beneficial properties such as anticarcenogenic, antiobesity and immune stimulatory. Milk and dairy products are a significant source of CLA, predominantly *cis*-9, *trans*-11-CLA. Most of the efforts to increase CLA content in milk fat have been focused in manipulation of diet; however, there are other less studied factors that may affect the CLA milk content such as parity. To date, the studies related to this factor are scarce. The aim of this study was to evaluate the effect of parity on the CLA content in confined Holstein cow´s milk in a commercial dairy farm in Northwest México. A total of 120 Holstein dairy cows were divided into groups of parity, including: primiparous (P, 1 parity, n = 42); earlier multiparous (EM, from 2 to 3 parities, n = 48); and late multiparous (LM, from 4 to 6 parities; n = 30). All cows were fed ration (as DM) based on 30.2% alfalfa, 27.6% maize silage and 42.2% concentrate. This ration met the requirements of dairy cows of 505 kg, 120 DIM and milk yield 30 L/d (CP: 15.7% DM; ENI: 1.55 Mcal /kg DM). The final forage-to-concentrate ratio was 58:42. Milk samples were collected from December to February. Pooled milk samples were analyzed for chemical composition and *cis*-9, *trans*-11-CLA content. Quantification of *cis*-9, *trans*-11-CLA was achieved by gas chromatography. All data were analyzed using the PROC MIXED of SAS. The model included Parity as fixed effect, and animal and DIM as covariates. The average CLA content in milk fat was 6.65 mg/g fatty acid. Milk from P cows had higher CLA content (6.43 ± 0.3 mg/g fatty acid, $P < 0.05$) compared to milk from LM cows (5.54 ± 0.3 mg/g fatty acid), but not significantly higher than milk from EM cows (6.17 ± 0.2 mg/g fatty acid, $P > 0.05$). These data shows that parity has an effect on *cis*-9, *trans*-11-CLA content in milk.

Key Words: conjugated linoleic acid, milk, parity

M331 Concentration of mammalian lignan enterolactone in milk of dairy cows fed different levels of flaxseed hulls. N. Gagnon*, C. Côrtes, C. Benchaar, and H. V. Petit, *Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*.

Flax lignans are concentrated in the outer fibre-containing layers, resulting in higher concentration of secoisolariciresinol diglucoside (precursor

of enterolactone: EL) in hulls than seeds. The objective of this study was to determine the effect of feeding different levels of flaxseed hulls (FH), a rich source of flax lignans, on milk concentration of the mammalian lignan EL, which has been linked to have potential human health benefits. Twenty lactating Holstein cows were assigned randomly to five different levels of FH in the diet: 0, 5, 10, 15, and 20% (DM basis). The experiment was carried out from wk 18 to 24 of lactation. Feed consumption was recorded daily. Milk samples were obtained weekly from wk 20 to 24 from each cow for two consecutive milkings and pooled separately (AM and PM) on a 5-wk basis for EL analysis using enzyme immunoassay. Concentrations of EL in AM and PM milkings increased (P=0.03) linearly with greater concentrations of FH, but there was no difference (P=0.84) between consecutive milkings. The CV of milk EL concentration for cows fed 0, 5, 10, 15, and 20% of FH was 20.4, 23.5, 36.2, 43.9, and 50.4%, respectively. The inter-variation of cow within the same diet increased with feeding concentration of flax lignan while there was no difference for the level of EL among consecutive milkings. Increasing dietary intake of flax hulls contributes to improving dairy milk composition through increased concentration of the mammalian lignan EL.

Key Words: enterolactone, flax hulls, milk

M332 Weekly excretion of the mammalian lignan enterolactone in milk of dairy cows fed flaxseed meal. N. Gagnon*, C. Côrtes, and H. V. Petit, *Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*.

Flaxseed meal (FM) is rich in the plant lignan secoisolariciresinol diglucoside (SDG), which is converted to the mammalian lignans enterodiol (ED) and enterolactone (EL) by ruminal microbiota. Feeding FM to dairy cows increases EL concentration linearly in milk but ED is not detected. The objectives of the study were to determine the time required to reach optimal concentrations of EL in the milk of dairy cows fed FM and the time required to return to the baseline level of EL when cows were switched from high to low intake of SDG. A total of 12 multiparous lactating Holstein cows used in a completely randomized design were assigned to one of two dietary treatments: control (CO) diet with no FM and a diet with 20% FM (DM basis). The control group was fed the CO diet for 6 weeks while the other group was fed the FM diet from wk 0 to 3 and was switched to the CO diet from wk 3 to 6. The concentration of SDG was determined in the total mixed diets. Milk samples were taken weekly for EL analysis. Concentrations of SDG and EL were determined by HPLC and enzyme immunoassay, respectively. The percentages of SDG averaged 0.048% and 0.357% (DM basis) in the CO and FM diets, respectively. Milk EL concentration from cows on the CO diet was similar over time and ranged from 116.27 to 179.30 nmol/l. Milk EL concentration increased significantly from wk 0 to 1 for cows on the FM diet (225.05 to 2312.47 nmol/l, P=0.03 according to a Wilcoxon signed rank test). Concentrations of milk EL remained at high levels from wk 1 to 3 (P=0.002 according to Wilcoxon rank-sum test comparing CO to FM cows for each week) before decreasing when the CO diet was reintroduced (from wk 3 to 4; 2167.37 to 264.47 nmol/l, P=0.03 and no statistical difference between the two groups on wk 4 to 6). This study shows that the metabolism of SDG to EL and the transfer of EL to the mammary gland of dairy cows were well established after one week of FM intake and that the baseline level of EL is recovered after one week of FM privation.

Key Words: milk, excretion, enterolactone

M333 Effect of dietary plant antioxidant on milk fatty acids oxidation. D. Tedesco*, L. Garavaglia, and L. Chiesa, *University of Milan, VSA Dep.*, *Milan, Italy*.

Milk fat with high level of UFA and PUFA has been shown to have several potential health benefits. The aim of the present study was to evaluate the effect of a plant post-processing derivative waste product (SAFEWASTES, EU project n. 513949), administered to dairy cows in preventing/minimizing lipid oxidation in milk. Thirty Holstein cows selected according to parity, milk production (32,57±1.98 kg/d), DIM (115±25) and SCC (<100,000), were divided into two groups. The treated group received 300 g/d of SAFEWASTE products and the control group 300g/d of placebo, mixed with 1 kg of total mixed diet, for 14 d. Milk production was daily recorded and samples collected on 0 and 14 d. Composition (protein, fat, lactose and urea) was assessed on milk samples. Milk samples collected on day 14 were stored at 4°C for four days and analyzed for hexanal accumulated by Head-Space solid-phase microextraction (HS-SPME) in combination with gas chromatography flame ionization detection using a Trace GC Ultra (Thermo-Fisher Scientific; Waltham, MA) Gas Chromatograph coupled to a quadruple Mass Spectrometer Trace DSQ (Thermo-Fisher Scientific; Waltham, MA) and equipped with a RT-wax column. Concentration of hexanal was determined in duplicate as relative area (analyte/I.S.ratio) using the calibration curve. Peak identification was based upon MS spectra in comparison with spectra and retention time of standards. Statistical analysis was performed using PROC MIXED of SAS. Treatment did not affect milk production and composition (P>0.05). Milk was assessed for the antioxidant quality by milk hexanal content, a secondary lipid peroxidation product from the oxidation of milk fatty acids. A significative lower level was observed in milk stored at 4°C for 4 days after milking, in the treated group. The exanal concentration was 14.27 ng/mL in the control group and 7.92 ng/mL in the treated group (SEM 1.097; P < 0.01). This result suggests an antioxidant effect on milk fatty acids oxidation and an extension of milk shelf life.

Key Words: milk, fatty acids oxidation, exanal

M334 Performance and ruminal fermentation parameters of lactating dairy cows during hot environment. J. P. Wang[1,2], J. Q. Wang*[2], D. P. Bu[2], F. D. Li[1], X. K. Huo[2], T. J. Guo[2], H. Y. Wei[2], and L. Y. Zhou[2], [1]*Gansu Agricultural University*, *Lanzhou, Gansu, China*, [2]*Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Influence of temperature and heat index (THI) on milk yield and rumen parameters was studied in high and medium producing dairy cows during mid- and late-lactation. Forty eight cows were assigned to high production (40.4 ± 4.7 kg/d), mid production (30.5 ± 1.7 kg/d), primiparous, multiparous, mid-stage (136 ± 17 DIM) or late-stage (205 ± 3.4 DIM) groups with a factorial design. There were 6 cows in each group. The experiment was conducted for 11 weeks from June 15 to September 2, 2008. All cows were offered 45% forage and 55% grain diet three times a day. All data was analyzed using the PROC MIXED model of SAS (2004). Cow was the random effect, and milk yield, parity, and stage were the fixed effects. Cows were housed in a close-side barn with tie stalls and cooled with a combination of sprinklers and fans. Cows were milked three times a day. Milk samples were collected weekly from 3 consecutive milkings and analyzed for composition. At the end of the experiment, rumen fluid sample was collected from each cow at 5h post-feeding using stomach-tube. During the experiment, average temperature and THI were 27.9°C, 30.7°C and 27.6°C, and 79.5, 82.1 and 79.2 at 7:00h, 14:00h, and 22:00h, respectively. Milk yield reduced faster for high than medium milk producing cows (0.96 vs. 0.61 kg/

wk, P<0.01), primiparous than multiparous cows (0.95 vs. 0.62 kg/wk, P<0.01) and late than mid-lactation dairy cows (0.82 vs. 0.74 kg/wk, P=0.26). Milk protein contents were higher in high producing cows than mid producing cows (3.1% vs. 2.9%, P<0.01). Milk fat content did not differ among treatments. The ruminal fermentation parameters were the same among treatments except the ratio of acetate to propionate (3.26 vs. 2.54, P<0.01) was higher for mid than high milk producing dairy cows. Results from this study suggests that production of high producing and younger dairy cows is affected more than medium producing or older cows when exposed to 79-82 THI and fed similar diets.

Key Words: cows, hot weather, performance

Ruminant Nutrition: Forages

M335 Efficiency of different chemicals in deactivation of phenolic compounds in Sainfoin (*Onobrychis viciifolia Scop.*). H. Khalilvandi-Behroozyar, M. Dehghan-Banadaki*, and K. RezaYazdi, *Research Center of Excellence for Improving Sheep Carcass Quality and Quantity, Animal Science Department, University of Tehran, Karaj, Tehran, I.R. Iran*.

Sainfoin (*Onobrychis viciifolia*) is a member of the Fabaceae family (Leguminosae), tannin rich legume. Reports about condensed tannin content of sainfoin have very wide range from 25 to 100g/kg DM. No reports about effects of tannin destructive or binding matter on tannin deactivation of sainfoin were found. This study was conducted to determine (TP), total tannins (TT) and condensed tannins (CT) content of sainfoin. Samples of forage (from effects of different chemicals on total phenolics different regions of 30 bale) were chopped 3-5 cm length, and then treated with solutions of $KMnO_4$ (0.03 M), NaOH (0.05 M), sodium bicarbonate (0.1 M), wood ash (180 g/L) and water with forage to reagent volume ratio of 1:4 (W/V). 5% solution of PEG (6000 MW) was sprayed to forage with 1:1 ratio. Treatment with urea (20g/ 100 ml/1 kg of DM) was done using adhesive rubber to create anaerobic conditions for 1 week. All of above treatments were carried out in triplicates, in 25°C temperature, for 20 min, with hand shaking. Treated forages were then exposed to 40°C temperature in a forced air oven, for 48 hour. All forage samples were ground to pass 0.5 mm screen size (Wiley mill). Determinations of TP, TT and CT content of treated and control forages were done tenth time, using Folin Ciocalteu reagent, polyvinyl polypyrrolidone (PVPP) and Butanol-HCl reagent, respectively. For preparation of plant extracts 200 mg of dried (0.5 mm ground) plant material is taken in a glass beaker of approximately 25 ml capacity. Ten ml of aqueous acetone (70%) is added and the beaker is suspended in an ultrasonic water bath (Branson 3210) and subjected to ultrasonic treatment for 30 min at room temperature. Data were analyzed using by SAS 9.1, using GLM procedure with complete random design ($P \leq 0.05$). TP, TT and CTs content of sainfoin was 39.4±0.6, 38.5±1 and 21.3±0.4 g/kg of DM. Results (table 1) showed that PEG and water were more effective in CT deactivation. Although all of the chemicals reduced CT levels far from 90%, but TP and TT deactivation ranged from 54.12 to 75.40 and from 55.06 to 76.57 percent, respectively. In both cases, water was the best.

Tabble 1. Reduction of TP, TT and CT of treated sainfoin.

	Reduction of TP (%)	Reduction of TT (%)	Reduction of CT (%)	S.E.M
Water	75.40^{a}	76.57^{a}	92.06^{cd}	0.12
Urea	60.47^{d}	59.46^{d}	92.53^{c}	0.28
KMnO4	71.82^{b}	70.44^{b}	92.41^{c}	0.08
PEG	66.39^{c}	67.09^{c}	98.57^{a}	0.19
Wood ash	57.41^{e}	59.57^{d}	91.61^{d}	0.14
NaOH	54.12^{f}	55.11^{e}	93.79^{b}	0.19
Sodium bicarbonate	54.89^{f}	55.06^{e}	91.84^{d}	0.22

Key Words: sainfoin, condenced tannin, PEG

M336 The effect of high sugar grass on nitrogen and methane output in cattle: A modeling approach. J. L. Ellis*[1], A. Bannink[2], J. Dijkstra[3], A. J. Parsons[4], S. Rasmussen[4], G. R. Edwards[5], E. Kebreab[6], and J. France[1], [1]*Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*, [2]*Animal Sciences Group, Division Animal Production, Wageningen University and Research Centre, Lelystad, The Netherlands*, [3]*Animal Nutrition Group, Wageningen Institute of Animal Sciences, Wageningen University, Wageningen, Then Netherlands*, [4]*AgResearch, Palmerston North, New Zealand*, [5]*Lincoln University, Lincoln, New Zealand*, [6]*Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada*.

The potential of high sugar grass varieties to reduce nitrogen (N) excretion of pasture fed cattle has received considerable attention. It is the purpose of this work to (1) evaluate the prediction of N excretion within a dynamic mechanistic dairy cattle model, (2) evaluate the effect of high sugar grasses on N excretion across multiple studies, and (3) evaluate the effect of high sugar grasses on enteric methane production. The database consisted of 4 published studies for which high sugar grasses were being evaluated for their effect on N excretion. Root mean square prediction error (RMSPE, % observed mean) for urine N, fecal N and milk N (all g/d) were 23.7%, 22.3% and 11.4%, respectively, with the majority of error coming from regression slope deviation and random sources. Proc GLM in SAS was used to analyse the results with study as a fixed effect, and showed that total N excretion was negatively related to water soluble carbohydrate (WSC) content of the diet ($P = 0.006$) and the WSC:CP ratio ($P < 0.001$). Predicted methane production (% GE intake) was significantly affected by treatment, and was positively related to WSC content of the diet ($P < 0.001$), negatively related to N content of the diet ($P < 0.001$) and positively related to the WSC:CP ratio ($P = 0.001$). Results show that the model predicts N excretion adequately, that total N excretion, particularly urine N, is reduced with high sugar grasses, but that this mitigation strategy may also increase methane production (% GE intake).

Key Words: sugar grass, nitrogen, methane

M337 Lipolysis and biohydrogenation of forage species at vegetative and reproductive stages of growth. A. Cabiddu[1], M. R. F. Lee*[2], L. Salis[1], N. D. Scollan[1], and M. L. Sullivan[3], [1]*AGRIS, Sardinia, Italy*, [2]*Aberystwyth University, Wales, UK*, [3]*USDA-DFRC, Madison, WI*.

Fresh forage is known to increase polyunsaturated fatty acids (PUFA) in ruminant products. Besides forage′s proportionally high levels of PUFA, other factors such as plant secondary metabolites may play a role. In particular polyphenol oxidase (PPO) production of phenol bound protein (PBP) has been shown to reduce ruminal lipolysis. This study investigated the effect of forage species on ruminal lipolysis and C18:3 biohydrogenation (C18:3-Bio). Common vetch (CV); Crimson clover (CC), red clover (RC+) and PPO1 gene silenced red clover (RC-) were harvested, at reproductive (R) and vegetative (V) growth stages, freeze-

dried and ground. Samples were analysed for PBP (modified Lowry assay) and weighed (1 g DM) into incubation tubes to give triplicates of each forage at each growth stage for two time points (0 and 6 h). Buffer was dispensed into the tubes along with rumen liquor from 4 rumen fistulated dairy cows maintained on permanent pasture. At the allocated time points tubes were destructively harvested by freezing with liquid N2. Lipid was extracted using chloroform:methanol (2:1; v/v), fractionated by TLC and bimethylated (5% HCl, 0.5N NaOH in methanol) before analysis on GC. Data was analysed by ANOVA with species × growth stage as the treatment. Lipolysis and C18:3-Bio were calculated as the proportional loss of glycerol-based membrane lipid and total C18:3 between 0 and 6 h, respectively. PBP (mg/g DM): 0.54, 0.60, 2.62 and 1.98 (V) and 1.35, 1.15, 2.92 and 2.41 (R); Lipolysis: 0.78, 0.58, 0.82 and 0.85 (V) and 0.72, 0.61, 0.68, and 0.77 (R); C18:3-Bio: 0.72, 0.41, 0.63 and 0.77 (V) and 0.80, 0.70, 0.52 and 0.62 (R) for CV, CC, RC+ and RC-, respectively. There was a growth stage × species effect ($P<0.001$) for both lipolysis and C18:3-Bio. PBP was negatively correlated with lipolysis for all species except CC, which had the lowest lipolysis irrespective of growth stage and the lowest C18:3-Bio in V. CC and CV had lower levels of membrane lipid and C18:3 than RC which may have influenced the comparison. Low lipid metabolism of CC compared to CV warrants further investigation.

Key Words: lipolysis, forage species, growth stage

M338 Effects of maturity of alfalfa conserved as silage on intake, productivity, and rumen pools in lactating dairy cows. K. L. Kammes*, Y. Ying, and M. S. Allen, *Michigan State University*, *East Lansing*.

Effects of alfalfa maturity on dry matter intake (DMI), milk production, and ruminal pool sizes and the relationship of these effects with preliminary voluntary DMI (pVDMI) were evaluated using 16 ruminally cannulated Holstein cows in a crossover design experiment with a 14-d preliminary period and two 17-d treatment periods. During the preliminary period, pVDMI of individual cows ranged from 22.8 to 29.8 kg/d (mean = 25.8 kg/d) and 3.5% fat-corrected milk yield ranged from 34.1 to 68.2 kg/d (mean = 43.7 kg/d). The two treatments were diets containing alfalfa silage harvested from one field at either a) earlier maturity (EARLY) or b) later maturity (LATE) as the sole forage. Alfalfa silages contained 42.3 and 53.4% neutral detergent fiber (NDF) for EARLY and LATE, respectively; both diets contained ~20% forage NDF and 27% total NDF. The pVDMI determined during the last 4 d of the preliminary period was used as a covariate. Main effects of alfalfa maturity and their interaction with pVDMI were tested by ANOVA. Yield of milk and milk components were not affected by treatment or its interaction with pVDMI ($P > 0.15$). EARLY increased DMI 2.3 kg/d compared to LATE (29.8 vs. 27.5 kg/d) and ruminal turnover rates of DM, OM (organic matter), and NDF were greater for EARLY compared to LATE ($P < 0.001$) but no interaction of treatment and pVDMI was observed for these variables. Rumen contents wet weight and volume and rumen pool sizes of DM, OM, NDF, and indigestible NDF were all greater for LATE compared to EARLY ($P < 0.05$). Interactions were detected between alfalfa maturity and pVDMI for ruminal pool sizes; DM, OM, NDF, and indigestible NDF pools increased at a slower rate for EARLY compared to LATE as pVDMI increased. The greater turnover rate of rumen pools likely allowed greater DMI for EARLY compared to LATE, but the relative contribution of ruminal distension to satiety likely differed for the two treatments because rumen pool sizes were consistently greater for LATE compared to EARLY.

Key Words: alfalfa maturity, intake, milk production

M339 Alfalfa silage length of cut interacts with feed intake to affect concentration of milk components in Holstein cows. K. L. Kammes*, Y. Ying, and M. S. Allen, *Michigan State University*, *East Lansing*.

Effects of length of cut of alfalfa silage on dry matter intake (DMI), milk production, and ruminal pool sizes and the relationship of these effects with preliminary voluntary DMI (pVDMI) were evaluated using 14 ruminally cannulated Holstein cows in a crossover design with a 14-d preliminary period and two 19-d treatment periods. During the preliminary period, pVDMI of individual cows ranged from 16.8 to 30.8 kg/d (mean = 24.8 kg/d) and 3.5% fat-corrected milk yield ranged from 22.9 to 62.4 kg/d (mean = 34.4 kg/d). Experimental treatments were two diets containing alfalfa silage chopped to either a) 1.0 cm (SHORT) or b) 1.9 cm (LONG) theoretical length of cut as the sole forage. Alfalfa silages contained ~43% neutral detergent fiber (NDF); diets contained 47% forage, 18% forage NDF, and 25% total NDF. The pVDMI determined during the last 4 d of the preliminary period was used as a covariate. Main effects of particle size and their interaction with pVDMI were tested by ANOVA. DMI and milk yield were not affected by treatment or its interaction with pVDMI. However, response of milk fat, protein, and lactose concentrations (means = 4.00, 3.40, and 4.68%, respectively) to particle size depended on pVDMI, as indicated by a significant interaction between particle size and pVDMI. While LONG increased milk fat and lactose concentrations compared to SHORT for cows below 25 kg/d pVDMI and decreased them for cows with higher pVDMI, the reverse was observed for milk protein concentration. Ruminal digesta wet matter, volume, and pool sizes of nutrients were similar for SHORT and LONG. Ruminal turnover time of potentially digestible NDF was numerically lower for SHORT compared to LONG (8.1 vs. 9.5 h). Reducing the theoretical length of cut of alfalfa silage by half did not affect feed intake, milk production, or rumen pool sizes but treatment effect on milk components varied with preliminary feed intake.

Key Words: particle size, intake, milk production

M340 Protein fractionation of various whole crop silages, and effect of silage based TMR on fermentation characteristics and degradability in vitro, and ruminal degradability and whole tract digestibility of TMR by cattle. J. Shinekhuu*[1], G. L. Jin[1], S. H. Choi[1], B. J. Ji[1], X. Z. Li[2], and M. K. Song[1], [1]*Department of Animal Science, Chungbuk National University*, *Cheong-ju, Chungbuk, Korea*, [2]*Department of Animal Science, Yanbian University*, *Yanji, Jilin, China*.

Protein in silages of rice straw (RSS), and whole crop barley (BS), rye (RS) and Sudan grass (SGS) was partitioned by CNCPS method. Both silages and borate buffer extracted silages (ERSS, EBS, ERS, and ESGS) were mixed with concentrate in 40 to 60 ratio (DM) to prepare TMR. Rumen fluid was collected from four ruminally fistulated cow fed the each silage based TMR and strained through 12 layers of muslin and mixed with artificial saliva in same ratio under CO2 flushing to prepare culture solution. The four different silages and respecting buffer extracted silage based TMR (5g for each TMR) were added to 500 ml culture solution and incubated at 39 C up to 48h in culture jar with rotator (100rpm/min) placed in water bath. An in vivo study was also conducted in a 4 x 4 Latin square design with four ruminally fistulated cows for 4 silage TMRs to examine rumen fermentation characteristics, rumen degradability or whole tract digestibility. Highest total soluble protein fraction was obtained from the RS with lowest content from rice straw silage. Insoluble protein (B3) was highest in SGS and CC fraction was lowest in RSS. The pH of incubation solution was lowest in RS while was highest in RSS-TMR during 48h incubation. Opposite results to the

pH were found in ammonia-N and total VFA concentration. The DM and NDF degradability in culture solution was higher for TMRs of BS and RS than those for RSS and SGS TMRs (P<0.01). The CP degradability was lowest in SGS TMR (P<0.01). Degradability of DM, CP and NDF was higher for un-extracted silage TMRs than for extracted silage TMRs. The ruminal ammonia-N concentration was lowest in RSS TMR but the total VFA was not affected by silages and extraction. The whole tract digestibility of DM was lowest in RSS while that of NDF was highest in RS TMR. The whole tract digestibility of CP was not different among diets.

Key Words: protein fractionation, degradability, in vitro

M341 Fermentation profiles of brown midrib and non-brown midrib hybrid corn silage. K. E. Nestor Jr.*, P. Krueger, J. Anderson, J. Brouillette, and K. Emery, *Mycogen Seeds, Inc.*, *Indianapolis, IN*.

The objective of this study was to determine if brown midrib (bmr) corn silage hybrids have a similar fermentation profile over time of storage to non-bmr corn silage hybrids. The first four months of data are presented. A total of 24 non-bmr hybrids and 20 bmr hybrids were collected at harvest at 14 different locations. At each location, hybrids were selected with similar relative maturities. Samples were chopped and collected into vacuum sealed bags. Multiple samples of each hybrid were collected and stored in an environmentally controlled room. Samples were analyzed monthly for soluble protein, starch, sugar, 7 hr. in vitro starch degradability, pH, lactic acid, acetic acid, total volatile fatty acids (VFA), ammonia and 30 h in vitro neutral detergent fiber (NDF) digestibility. Samples were pooled by month for analysis. Data was anlayzed by ANOVA with hybrid and month as main effects. Thirty hour NDF digestibility was higher (P<0.01) in the bmr hybrid class within each month and was unchanged in the bmr hybrid class for each month of fermentation but tended to drop in the first four months of fermentation in the non-bmr hybrid class. Within month, there were no differences between hybrid classes in soluble protein, starch, sugar, 7 hr. in vitro starch degradability, lactic acid, acetic acid, and ammonia. Total VFA was higher in the bmr hybrid class (p<0.07) at month 4 but was not different in other months. The pH was lower (p<0.05) in the bmr hybrid class in month 3 but not in other months. Soluble protein increased (p<0.02) and pH decreased (p<0.01) by month of fermentation for each hybrid class. No difference by month of fermentation was observed in 7 hr in vitro starch degradability, starch, or sugar within each hybrid class. There was a trend (p<0.16) for an increase in acetic acid by month of fermentation. Lactic acid, ammonia, and total VFA increased between month one and two and stabilized afterwards. These data suggest that there is no difference in fermentation profiles of bmr and non-bmr hybrids in the first four months of fermentation.

Key Words: corn silage, brown midrib, fermentation profile

M342 Utilization of solid state fermentation of *Pleurotus sapidus* for sugar cane silages. A. Peláez-Acero[1], M. Meneses-Mayo[1], L. A. Miranda-Romero[2], S. S. González-Muñoz*[1], and O. Loera-Corral[3], [1]*Colegio de Postgraduados*, *Montecillo, Edo. de México, México*, [2]*Universidad Autónoma de Chapingo, Chapingo, Edo. de México, México*, [3]*UAM Iztapalapa*, *México D.F., México*.

The objective of this study was to evaluate production of cellulases, xylanases and laccases by *Pleurotus sapidus* using sugar cane (SC) as substrate after 15 days of solid state fermentation. Two trials were performed; in both the experimental design was completely randomized, data was analyzed using PROC GLM (SAS) and means were compared using the Tukey test (P≤0.05). In trial I, sugar cane was fermented 48 hours (SCF), then inoculated with 5% *P. sapidus* and fermented for 15 days (SCF-15). Results showed significant differences (P≤0.05) for: a) 1.96 IU/g DM cellulases, 2.08 IU/g DM xylanases, 5.25 IU/g DM laccases for SCF-15; b) CP was 7.43% for SCF-15 and 5.53% for SCF; c) NDF, ADF and *in vitro* DMD were 72.42, 41.48 and 64.80% for SCF-15, and 44.81, 29.08 and 63.71% for SCF; d) calculated metabolizable energy was 1.80 Mcal for SCF-15, and 2.28 Mcal for SCF. In trial II sugar cane was ensiled 24 days with 0, 10 and 20% SCF-15. There were significant differences (P≤0.05) between day 0 and 24 for: a) pH, 5.16 and 3.90; b) DM, 35.47 and 33.64%; c) soluble carbohydrates, 9.14 and 4.05%; d) NH_3-N, 3.80 and 9.26%; e) lactic acid, 10.32 and 19.44%; f) *in vitro* DMD, 64.28 and 70.13%. Besides, at day 24, significant differences (P≤0.05) were found between 0 and 20% SCF-15 for: a) NH_3-N, 9.89 and 5.65%; b) lactic acid, 12.40 and 18.52%; c) *in vitro* DMD, 66.65 and 71.53%. It may be concluded that fermented sugar cane may be used as substrate for producing fibrolytic enzymes, which then could be utilized to increase quality of sugar cane silages.

Key Words: solid state fermentation, fibrolytic enzymes, sugar cane

M343 As corn plants mature, NDF mass decreases. P. M. Walker[1], J. M. Carmack*[1], L. H. Brown[2], and F. N. Owens[2], [1]*Department of Agriculture, Illinois State University*, *Normal*, [2]*Pioneer Hi-Bred International, a DuPont Business*, *Johnston, IA*.

Determining corn silage value of the corn plant can be difficult. Nine Pioneer ® corn hybrids (107 to 116 day CRM) grown in 2008 near Normal, IL were harvested 15 cm above ground level weekly starting 102 days after seeding until plant DM content reached 50%. One thousandth of an acre was harvested on each date with ten plants from each hybrid being divided into two sections, the bottom 46 cm and the remaining top section. Top sections and total plants (recombined) were assayed commercially for nutrient composition (CP, starch, NDF, ADF, ash) and at the Pioneer Livestock Center for in situ NDF disappearance. Based on regression against harvest date, as harvest date advanced, NDF, ADF, sugars, and ash as a percentage of plant DM all decreased (P < 0.05) largely due to dilution by starch. As harvest date advanced, weight per plant of dry matter, protein, and starch per plant increased (P < 0.01) as expected. However, weight per plant of NDF, ADF, sugars, and ash all decreased (P < 0.01). Transformation to starch (increasing 3.6 g/d) can explain the decrease in sugar (0.8 g/d) mass of plants, but the decrease in weights of NDF and ADF (0.70 and 0.52 g/d per plant or 0.8 and 1.0% of total mass/d) indicates that some portion of these fiber fractions were mobilized. NDF digestibility typically is expressed as a fraction of total NDF. If the mass of NDF decreases as corn plants mature due to mobilization of digestible NDF, then digestibility expressed as a fraction of the remaining NDF is incomplete as an index of the relative energy availability for plants that are harvested at different stages of maturity. Whether the extent of NDF mobilization is altered by environmental conditions, hybrid, or the "stay-green" trait is not yet certain. For estimating energy availability of corn plants at harvest, both NDF content and NDF digestibility must be considered.

Key Words: NDF, corn silage, maturity

M344 Effects of moisture content and storage time on quality of baled TMR. J. Wang, J. Q. Wang*, W. J. Guo, Z. T. Song, J. Y. Zhang, and D. P. Bu, *The State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Influence of moisture content and time of storage of baled TMR was evaluated. The TMR were baled using stretch film in order to give support for the storage and delivery of TMR to small farms. TMR feed (F/C, 50:50; CP, 15.4%) containing 40%, 50%, and 60% moisture were wrapped and baled using YK–50 wrapping and baling machine. Three replicate bales were prepared for each sampling spot. After 0, 3, 7, 15, 30, and 60 d storage, the bales were opened and the sensory characteristics were evaluated. At the same time, core samples were taken using a modified boring device for nutrients and fermentation analysis. Data were analyzed statistically by using PROC MIXED of SAS. Results showed that there were no molds in baled TMR before 15 d storage, while some inequality of size molds appeared at the outer surface in part of the bales at 30 and 60 d. Along with the storage, DM content kept decreasing throughout the whole storage time (P>0.05). The CP, EE, ash, and lignin contents increased over storage time while NDF and ADF fluctuated. The pH of each treatment decreased significantly (P<0.01) along with the storage, and different moisture content TMR embodied pH was 4.67, 4.60 and 4.73 for 40%, 50%, and 60% moisture contents respectively at 60 d. NH_3–N/total–N of the baled TMR exhibited significantly increase (P<0.01) after storage, and the ratio were more in higher moisture content TMR (2.83, 3.24, and 4.05% for 40%, 50%, and 60% moisture content; respectively). The concentration of lactic acid, acetic acid and propionic acid were also increased along with the storage time (P<0.01), but butyric acid was not detected in the whole course. Lactic acid and volatile acid concentration were high in higher moisture content TMR. These results showed that there was no negative impact on nutrient content and quality after 15 d storage of TMR and baling technology could be used to achieve the effective storage and delivery of TMR.

Key Words: total mixed ration, baling technology, storage

M345 Chemical composition and nutritive value of total mixed ration (TMR) stored as wrapped round bales. J. Wang, J. Q. Wang*, W. J. Guo, Z. T. Song, J. Y. Zhang, and D. P. Bu, *The State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

his experiment was conducted to evaluate the storage effect of TMR baled by stretch film and its nutritive value on milk production of lactating diary cows in order to give support for the storage and delivery of TMR to small farms and make them also can use TMR diets. The TMR feed was produced based on forage to concentrate of 60:40 (DM basis) (DM, 50%; CP, 13.9%; NE_L, 1.38 Mcal/kg of DM) and then wrapped and baled using YK-50 wrapping and baling machine. Three bales were prepared for each sampling spot. After 0, 3, 7, 15, and 30 days storage, the bales were opened and core samples were taken using a modified boring device for nutrients analyses. Results showed that no mold was found in baled TMR before 15 days storage, while some inequality of size molds appeared at the outer surface on 30 d. Along with storage, CP, EE, ash, and lignin contents showed increasing over storage time compared with 0 d storage while NDF and ADF were manifested as a fluctuation. The pH of baled TMR was significantly decreased (P<0.01) from 5.17 at 0d to 4.44 at 30d. The proportion of NH_3-N/total-N of baled TMR significantly increased (P<0.01) after storage and reached 3.43% of total-N at 30 d of storage. The concentration of lactic acid and volatile acid also increased (P<0.05) along with the storage. Twenty-four late lactation cows average 182±25 DIM and average milk production of 15.9 kg/d were also selected to evaluate the effect of this baled TMR (stored 5-15d) on DMI, milk yield, and milk composition compared with traditional separate feeding of forage and concentrate. Experiment lasted 8 weeks. Cows fed baled TMR produced significantly more milk (14.4 vs. 12.4 kg/d) and more milk CP (0.55 vs. 0.48 kg/d), 3.5% FCM (14.7 vs. 12.9 kg/d) compared with separate feeding (P<0.05). It would be concluded that baled TMR may be a good selection for small-scale farmers to use TMR technique to improve their efficiency and income of dairy production.

Key Words: total mixed ration, baling technology, milk production

M346 Effect of supplementing sodium diacetate in baled-TMR on the performance of middle lactation dairy cows. W. J. Guo, J. Q. Wang*, J. Wang, Z. T. Song, J. Y. Zhang, and D. P. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science*, *Beijing, China*.

This experiment was conducted with thirty Holstein cows in mid-lactation (124±23 DIM, 16.4±6.1kg of milk/d) to examine the effects of supplementing sodium diacetate in baled total mixed ration (BTMR) on dry matter intake (DMI), milk yield, milk composition, body condition score (BCS), and some serum biochemistry parameters. Treatments were: 1) the forage and concentrate feeding separately (FS); 2) feeding in the form of BTMR; 3) BTMR supplemented with sodium diacetate (SDA). Animals were housed and individually fed 3 times daily to allow 5 to 10% orts (as-fed basis) in a tie-stall barn. Feeding intake and orts were recorded daily. Cows were milked twice daily at 0200 and 1400 h. Blood samples were collected monthly via venipuncture from coccygeal vein 3 h after morning feeding. The data were analyzed using the MIXED model of SAS 9.0 with a repeated measure. The results indicated that the DMI of the BTMR and SDA were significantly (P<0.01) higher than FS (18.9, 18.7 and 17.7 kg/d). The treatments of BTMR and SDA increased milk yield by 6.2% and 7.2% compared with FS. The milk protein, milk lactose, and solid non-fat (SNF) showed no significant differences among three treatments. However, the SDA treatment significantly (P<0.01) increased the milk fat compared with BTMR and FS (3.86, 3.27 and 3.4%). The BCS values of cows fed BTMR, SDA and FS diets were not significantly different. Serum urea nitrogen concentrations of the BTMR and SDA groups were significantly (P<0.01) lower than that of FS group (21.8, 20.9, and 26.4 mg/dL), and no significant differences existed among three treatments on serum protein, serum glucose and serum lipid concentrations. These results suggested that BTMR and SDA had positive effect on feed intake and milk production of lactating dairy cows compared with FS, while the addition of SDA increased milk fat significantly.

Key Words: dairy cow, sodium diacetate, total mixed ration

M347 An introductory animal cell culture course for animal science, biomanufacturing and biotechnology programs. P. E. Mozdziak*[1,2], J. N. Petitte[1,2], and S. Carson[1], [1]*Biotechnology Program, North Carolina State University, Raleigh*, [2]*Biomanufacturing Program, North Carolina State University, Raleigh*.

Animal cell culture is a core technique in many molecular biology, developmental biology, and biotechnology laboratories. It is also a core laboratory technique for biomanufacturing. The traditional methodology for acquiring cell culture training has been through trial and error, or instruction when hired for a specific cell culture position. However, cell culture is a critical course for any biotechnology-related training program because it is a technique that must be performed by investigators before they perform many molecular procedures. In addition, vertebrate cell culture is becoming increasingly important for biomanufacturing of therapeutic proteins. Therefore, a cell culture techniques course is an important offering for undergraduate students who aspire to graduate training, and those who will seek employment with biotechnology or biomanufacturing companies immediately after graduation. A core cell culture techniques course has been developed and delivered to students at North Carolina State University as a component of an undergraduate biotechnology minor curriculum, and it is now a key offering in the undergraduate biomanufacturing curriculum. The course has experienced considerable growth in both resources and enrollment. The course was first offered in 2001 with an initial enrollment of 8 students. Currently, 40 students complete the course per year. Key features of the course are acquiring practical critical reasoning skills, mastering record keeping skills, and developing effective communication skills. Subsequent courses in tissue engineering technologies, animal cell culture engineering, bioreactor culture, and stem cell technology serve as specialized follow-up topics to the introductory animal cell culture course.

Key Words: cell culture, undergraduate education, laboratory courses

M348 Justification of university equine extra-curricular activities. M. Nicodemus*, *Mississippi State University*, *Mississippi State*.

With current economic constraints University equine programs are forced to make cutbacks in their equine faculty and teaching horse herds. Equine extra-curricular activities such as equine clubs and teams are time consuming for the equine faculty and costly to the departments supporting such activities, and while these activities are popular recruiting tools for incoming freshmen, it does not reflect the participation of the students once they are enrolled in the University. Student participation is essential for justification for continuation of such activities. To determine student interest in the equine extra-curricular activities supported by the Animal & Dairy Sciences (ADS) department once students are enrolled in Mississippi State University, students (n=80) enrolled in equine courses were asked to fill out a researcher-developed, 9-item survey instrument with questions focusing on student academic and extra-curricular activities. 67% of those students that returned a survey were ADS majors with 50% of the students classified as underclassmen (freshmen or sophomores). 64% of ADS major and 13% of non-ADS majors had taken an equine course in a prior semester. While 26% of ADS majors and 10% of non-ADS majors were members of the University equine club, 60% of ADS majors and 70% of non-ADS majors were interested in becoming an equine club member. Similarly, although only 22% of ADS majors and 10% of non-ADS majors were competing members on an equine team (equestrian or rodeo team), 66% of ADS majors and 44% of non-ADS majors planned on competing on a team the following competition season. 68% of students currently participating or were planning to participate in an equine extra-curricular activity and that were not graduating at the end of the semester were planning to take another equine course in the following semesters, and of those students, 46% were students outside of the department. While memberships were small, intended participation in equine extra-curricular activities was strong and this continued growth in participation keeps students, particularly those outside of the ADS department, actively involved in the equine program.

Key Words: equine teaching programs, equine clubs

M349 A practical stem cell culture course for agricultural, life science, and engineering students. J. N. Petitte*[1,2], P. E. Mozdziak[1,2], and S. Carson[1], [1]*North Carolina State University, Biotechnology Program*, *Raleigh*, [2]*North Carolina State University, Biomanufacturing Program*, *Raleigh*.

During the last 20 years, the culture of stem cells has grown from a few laboratories utilizing embryonic stem cells for manipulation of the mouse genome to a field of science encompassing stem cells from embryos and adult tissues with a myriad of applications in biology, medicine, and engineering. Therefore, practical skills in the culture of stem cells of various types and sources is destined to become a fundamental aspect of animal cell culture in the future. Therefore, as a subsequent course to basic undergraduate animal cell culture, a practical course in the culture of stem cells was developed and offered to students at North Carolina State University as an elective component to an undergraduate/graduate Biotechnology minor. The course includes lectures to describe the historical development of stem cell biology and provides laboratory experience in the culture of embryonic stem cells and germ line stem cells. Lectures cover the establishment and characterization of embryonic stem cells, germ line stem cells, and adult stem cells. Subsequent lectures encompass the differentiation of stem cells and their therapeutic and industrial applications including ethical considerations of the technology. Laboratory exercises include culture systems for stem cells, growth factors in stem cell culture, initiation, maintenance, and characterization of stem cells. Targeted student outcomes include: 1) an understanding of the historical emergence of stem cell biology and current applications of the technology, 2) practical skills in the culture of embryonic stem cells and establishment of stem cell lines, 3) processes involved in the induction of stem cells toward differentiation into committed cell types, and 4) an appreciation of the ethical issues in stem cell biology.

Key Words: biotechnology, education, laboratory course

M350 Reliability of item scores on end-of-semester departmental course evaluation. M. A. Wattiaux* and P. M. Crump, *University of Wisconsin*, *Madison*.

Our objective was to determine whether students' scores for items on departmental course evaluation were reliable (i.e., repeatable). Eighty-two students including freshmen (5%), sophomores (20%), juniors (7%), seniors (34%), graduate students (28%) and guests (6%) from six classes (with enrollment ranging from 8 to 20) taught in 2008 by the same instructor, completed a 12-item departmental evaluation

(DPT) the last day of class using a 1 (=not at all) to 5 (=very much) likert-type scale. Ten of these items were dispersed in a 40 to 50 item instructor-generated tool (INSTR) administered with students' consent for a scholarship of teaching and learning project, one week before the last day of class using the following scale: 1-2=not at all, 3-4=a little, 5-6=somewhat, 7-8=a lot, and 9-10=a great deal. Items (I) were: I1: I value the material/topic covered in this course; I2: This course stimulated my interest in the subject; I3: This course encouraged me to think; I4: I learned a lot in this course; I5: Individual class meetings or lectures were well planned and effective; I6: This course was well organized and provided coherent understanding of the subject; I7: Useful supplementary materials were available outside of class; I9: The instructor was approachable and seemed to enjoy teaching; I10: The grading system was appropriate, clearly explained and fairly applied; I12: Overall I rank this class: (1=lowest 20% to 5=highest 20%). The I1 to I10 scores of the INSTR tool were re-categorized on a 1 to 5 scale before analysis with proc ANOVA of SAS. The overall score for INSTR and DPT tool was 4.2 and 4.1, respectively ($P=0.25$). Although scores for each item varied among courses ($P<.05$, data not shown), they were not influenced by tool (DPT vs. INSTR), except for I7 (see Table 1), which could be interpreted in different ways. Results suggest that students score unambiguous items reliably regardless of the evaluation tool's stated purpose, its item scale, the presence of distracting items, and the administration time in the last week of class.

Table 1.

Tool	I1	I2	I3	I4	I5	I6	I7	I9	I10	I12
DPT	4.3	4.1	4.1	4.0	3.6	3.8	4.2	4.8	3.9	3.9
INSTR	4.3	4.2	4.2	4.2	3.9	4.0	4.5	4.7	4.1	3.9
P value	.91	.55	.23	.32	.12	.19	.02	.18	.16	.82

Key Words: assessment, SoTL

M351 Effect of instructor on use of an informal consumer sensory panel to teach students concepts related to beef palatability. J. A. Daniel*[1], S. E. Kitts[1], and T. D. Pringle[2], [1]*Berry College, Mount Berry, GA*, [2]*University of Georgia, Athens*.

This experience was designed to test the effectiveness of use of an informal consumer sensory panel to teach concepts related to beef palatability with two separate instructors. This class experience was performed for four lab sections from one semester of Introduction to Agriculture (a general education science course for non-science majors) at Berry College for a total of 56 students. The students were enrolled in two separate sections of the class and had two different instructors. Students received no classroom instruction in beef palatability prior to this lab. At the beginning of the lab, students completed a quiz (pre-quiz) consisting of 12 questions. Ten of the questions were designed to test the students' knowledge of different attributes of beef quality, and two of the questions were designed to assess students' steak preferences. A rating sheet was then distributed to the students and they were presented with the bite-sized steak samples (approximately 2x2x2 cm cubes) for evaluation. Students were asked to take a bite of cracker and drink of apple juice between each sample. After completion of the sensory panel, evaluation sheets were collected, and results and beef palatability attributes were discussed with the class. Students then completed the previously mentioned quiz (post-quiz). Scores on the 10 questions designed to test students' knowledge of different attributes of beef quality were improved ($P < 0.0001$). Thirty-five out of 56 students changed at least one of the questions related to the students' steak preference, suggesting application of the students' newly acquired knowledge about beef palatability. Although there were significant differences in scores between lab sections, the differences did not appear to be due to instructor (the same instructor taught the lab sections with the highest and lowest post-quiz score). Thus, instructor does not appear to impact the effectiveness of the use of a consumer sensory panel to teach concepts related to beef palatability.

Key Words: beef, teaching

M352 Factors influencing student success in an introductory to animal science class. F. M. LeMieux*, T. H. Shields, and J. T. Compton, *McNeese State University, Lake Charles, LA*.

This study was conducted to determine factors that influence student performance in a traditional undergraduate Introduction to Animal Science class at McNeese State University. The study consisted of students enrolled (n = 133) over a 3 yr period (2006, 2007, and 2008) in a weekly 150 min lecture and 170 min laboratory covering basics of animal genetics, nutrition, reproduction, behavior, growth and development, and industry production systems. Gender, American College Testing (ACT) scores, animal experience, team involvement, major or concentration and participation in study sessions were evaluated to determine successful completion of the course. Female students (n = 65) performed better ($P < 0.05$) on tests and final course grades than male (n = 68) students. The average ACT score was 21 (range 14 to 28); students with increasing numerical ACT scores performed better on examinations and final grades. Prior animal experience was determined by a student survey, categories were 0 - no experience, 1 - companion animal, 2 - equine, and 3 - large animal (cattle, goat, sheep, or swine). Students with previous companion and large animal experience had the highest scores on examinations and final grades. Informal study sessions were offered before each examination. The instructor and a graduate assistant were available to answer questions and work problems for students. Study sessions lasted between 60 and 120 min. Students that participated in the session had higher ($P < 0.05$) test and final course grades. Students choosing the agricultural concentrations (Animal Science, Pre-Vet, Equine, and Agricultural Business) performed better ($P < 0.05$) on exams and subsequently final grades compared to Wildlife Management and Undecided students. Females, students with large and companion animal experience compared with those with previous equine experience or no animal experience, higher ACT scores, or participated in study sessions were more successful in an undergraduate introductory to animal science course.

Key Words: undergraduate, gender, ACT

M353 Introducing a "Nutritional Physiology Webinar" for animal scientists. K. J. Harvatine*, *Penn State University, University Park*.

With increasing specialization of researchers and decreasing size of Animal Science departments it has become difficult to sustain metabolism and nutritional physiology based seminars at many institutions. The "Nutritional Physiology Webinar" was created to provide a forum for departments without an active seminar and to complement existing seminar programs. Three beta-test webinars were hosted during Fall 2008 with a limited audience to test software and fine tune the approach. The webinar is hosted from a web-based platform. The speaker and audience members log into the webinar via a web browser and do not need to purchase or install additional software. The slide presentation

is displayed in the browser and the speaker has real-time control of the presentation and may use a suite of presentation aids including a white board, a pencil to draw on slides, and a pointer. Audio of the speaker and up to three participants is also broadcast through the web browser. Audience members participate by typing in a chat box or by having a microphone "passed" to them. In the current format speakers have presented a recently published paper or group of related papers that are of interest to animal nutritionists. Future webinars are expected to follow a similar format and possibly include invited speakers from outside the animal nutrition community. The webinar has the potential to promote dissemination of new concepts in nutrition and to stimulate collaboration between research programs. The expected impact will benefit training of students and further the progress of animal nutrition research.

Key Words: webinar, nutritional physiology, seminar

M354 Assessment of needs for teaching, research and extension for goat sector. S. Solaiman*, C. Hill, N. Gurung, O. Bolden-Tiller, and C. Okere, *Tuskegee University*, *Tuskegee, AL*.

A web based data search was conducted to assess current status for goat teaching, research and extension. Four different search engines, PubMed, PubMed Central, USDA website, and Agricola were used to retrieve number of records for goats. Key words used were goat, types of goats (dairy, meat, fiber), and production. Goat production was further defined as goat reproduction, genetics, parasites, immunity, and nutrition. Goat nutrition was searched for protein, energy, minerals, and vitamins. The website for more than 70 Land grant Universities' courses offered in Animal Sciences in 50 States and 7 US Commonwealth and Territories, were searched. Also number of records for goats, sheep and cattle for different management and production parameters were determined. The number of courses taught on Sheep and Goats, Small Ruminants, or Sheep Science/Production were 20, of which 16 (75%) were on sheep only. There was no course taught on goats only. The number of records for goat teaching produced only 3 hits, while for sheep and cattle were 4 and 12 folds higher, respectively. The number of records for goat research in all categories was much smaller than sheep and cattle except dairy goats and milk that were researched more than dairy sheep. According to the search, it is clear that within goat types, dairy goats have been investigated more than meat or fiber goats in all areas of goat production. Within production area, more data is available in the areas of reproduction and genetics followed by nutrition. In the area of nutrition, protein nutrition resulted in more records followed by energy nutrition. Energy nutrition of fiber goats has received more attention than other areas of their nutrition. Records on goat immune, vitamins and minerals are very limited. Search for extension and goats, resulted in higher numbers of records as compared to teaching. Similar records for sheep and cattle were 2 and 15 folds higher than goats, respectively. In conclusion, information regarding teaching, research and extension for goats are lacking and presents a challenge for educators and extension personnel in this sector of agriculture.

Key Words: goats, research, teaching

M355 Preferences and backgrounds of incoming students in animal sciences at Tuskegee University. O. U. Bolden-Tiller*, E. Bush, and S. Bruinton, *Tuskegee University*, *Tuskegee, AL*.

Statistics on African American students in the field of Animal Sciences are not readily available as the majority of said students attend 1890 Land Grant Institutions, which except for one do not have Departments of Animal Sciences. As universities, industry, and government work to diversify their workforce in the field of Animal Sciences, many are unclear as where to find well trained underrepresented students to meet the diversity demand. The Animal, Poultry, and Veterinary Sciences program within the Department of Agricultural and Environmental Sciences at Tuskegee University (TU) boasts one of the largest numbers of undergraduate African American students majoring in the field. The current report demonstrates that large numbers of African American students are interested in pursuing careers in the field of Animal Science. Here 100 minority students (77% Female, 33% Male) enrolled in the Orientation to Animal, Poultry, and Veterinary (APSC 100) course at TU were surveyed. Eighty percent of the students were 17-18 years of age with becoming a veterinarian as a 1st career choice. Sixty-five percent of the students reported their species of interested to be companion animals with horses coming in 2nd at a distant 13%. Forty-seven percent reported that their 1st choice for attending TU was with aspirations of attending the TU School of Veterinary Medicine with the appreciation of the university's history second at 6%. Of the students surveyed, 17% had attended Vet-Step, a two-week summer enrichment program at TU for high school students interested in veterinary medicine. Fifteen percent of the students had attended similar programs elsewhere. Only 19% were from rural areas. Forty-three percent had worked with a veterinarian; 62% had worked with companion animals. Only 23% had interacted with non-companion animals. In conclusion, incoming students majoring in Animal Sciences at TU have similar backgrounds and preferences of those at other institutions.

Key Words: undergraduates, minorities, diversity

SYMPOSIA AND ORAL SESSIONS

Alpharma Beef Cattle Nutrition Symposium

9 What routine analytical measurements best predict available energy content of feeds and co-products? F. N. Owens*, *Pioneer Hi-Bred International*, *Johnston, IA*.

Net energy for gain and lactation available from feeds traditionally has been predicted from an index of feed energy digestibility (e.g., TDN). At least 15 different equations are available to calculate TDN from nutrient content of a feed or a diet ranging in complexity from two assays (DM plus either ADF, NDF, or crude fiber) to 11 determinations (feed class, DM, ash, CP, ether extract, NDF, NDFn, ADF, ADFn, lignin, PAF). To test the validity of various prediction equations, energy availability (TDN or DE) must be measured independently from nutrient composition, not calculated from feed analysis as used in the Dairy NRC (2001). TDN and nutrient composition for individual feedstuffs (1,087 from Morrison′s Feeds and Feeding, 1961; 248 from Dairy NRC 1989; 71 from Beef NRC, 1996) were compiled; relationships between TDN estimates and nutrient concentration of feeds within and across data sets and feed classes were assessed by correlation and regression. Incomplete nutrient analysis limited the testing precision. However, based on stepwise regression, feed DM content was the primary factor responsible for differences among feeds in TDN content as a fraction of wet matter as might be expected. True digestibility of protein, fat, and NFE, estimated as the slope of digested amounts against feed concentrations across more than 500 feeds with digestibility values reported in Morrison′s tables, averaged 90 ± 1%, 93 ± 1%, and 107 ± 2%, respectively. Consequently, TDN on a DM basis was predicted most closely by deducting some multiple of fiber (crude fiber or ADF and, for wet forages, NDF) from a constant value both overall and within all feed classes (concentrates, dry forages, wet forages). This supports the concept of predicting TDN from fiber content. The second factor of importance was either ether extract (increasing TDN by 1.5 units for each 1% additional fat) or ash (decreasing TDN by 0.8 units for each 1% added ash), with ether extract content having a greater range and thereby being more important for predicting TDN for concentrates than forages.

Key Words: energy, digestibility, TDN

10 Interesting but minor ingredients available for use in feedlot formulations. R. A. Zinn*, J. Salinas, and P. Garces, *University of California*, *Davis*.

Recent changes in grain pricing structure in combination with generalized economic uncertainty have introduced portentous risks to grain contracting, prompting renewed interest in alternative energy sources for feedlot cattle. In this presentation we will discuss several of the "minor" high-energy feed ingredients including: bakery waste, confectionery waste (candy product), corn bran, cull beans, dehydrated sugar beets, malt sprouts, pelletized grain screenings, rice bran, and rice polishings. Their feeding value will be assessed in terms of nutrient composition, comparative net energy value, acceptability (palatability), handling and processing limitations, formulation constraints, and availability.

Key Words: grain, feedlot

11 Changes and evolution of corn based co-products for beef cattle. L. Berger* and V. Singh, *University of Illinois*, *Urbana*.

The number and nutrient composition of corn based co-products will expand as ethanol producers seek to optimize the efficiency of ethanol production and the value of the co-products. Several innovative technologies have been developed to fractionate corn and/or distiller dried grains with solubles (DDGS) for recovering additional co-products and improving nutritional composition of DDGS. Two (wet and dry) corn fractionation technologies have been developed to remove the germ, pericarp fiber and/or endosperm fiber before fermentation, resulting in a significant reduction in the amount of DDGS produced and a corresponding increase in its protein content. Other fractionation technologies include removal of oil (by centrifugation) after fermentation but prior to DDGS production or removal of oil (by solvent extraction) from DDGS. Technology to recover pericarp fiber (by sieving and aspiration) after DDGS production has also been developed. Germ, pericarp fiber, endosperm fiber, or oil can be used as feedstocks for producing other marketable co-products or can be used as ingredients in animal diets. One new corn co-product available to the beef industry will be bran cake. This product results from combining corn bran (pericarp fiber) and distillers solubles produced from a dry fractionation process. The bran cake contains less protein, slightly less fat, and similar fiber levels compared to traditional DDGS. When bran cake replaced corn up to 45% of a finishing diet, gains and feed efficiency were improved. In high-forage diets the corn bran had 85% the energy value of DDGS. How rapidly these technologies are adopted will be driven by the economics advantages achieved over the traditional dry and wet milling processes. Large quantities of DDGS and corn gluten feed will be available for the foreseeable future. Research at the University of Illinois has shown that combining these co-products with soybean hulls can be used to replace rolled-corn in finishing diets without a reduction in gain, feed efficiency, or carcass merit. Traditional methods of evaluating diets markedly underestimate the energy value of this mixture.

Key Words: corn co-products, beef cattle

12 Utilization and application of wet co-products. M. L. Nelson*, *Washington State University*, *Pullman*.

Wet co-products fed to beef cattle include processing co-products of the fruit, vegetable, juice, and beer industries. Considerations for their utilization in beef cattle diets include quantity available, feeding value, quality of animal products produced, economics (e.g., transportation of water), storage and preservation, consumer perception and nuisance concerns, contaminants and interactions with other diet ingredients. Potato (*Solanum tuberosum*) co-products from processing for frozen products may be quantitatively most important because the 10 million m tons of potatoes (fresh weight) processed in the United States and Canada in 2007 resulted in an estimated 3.5 million m tons (as is basis) of co-product. Chemical composition and feeding value of potato co-products depends on the type. The names of co-products vary among potato processors and some processors combine the types into one product commonly called slurry. The four main types are:

1) potato peels; 2) screen solids (small potatoes and pieces); 3) fried product (fries, hash browns, batter, crumbles; and 4) material from the water recovery systems (oxidation ditch, belt solids, filter cake). The co-products, except the fried products, ensile rapidly, reaching pH 5 in 7 d or less. Dry matter content varies from 10 to 30% and varies (DM basis) in CP (5 to 27%), starch (3 to 56%), NDF (4 to 41%), and ether extract (3 to 37%) content among types of potato co-product. Type of co-product and frying greatly affect the energy value (0.6 to 1.6 Mcal NEg/kg DM). Composition, quality and shelf-life of meat were not affected by potato co-product feeding in contrast to perceptions of some purveyors and chefs. Potato co-products are important energy sources in beef cattle diets, which, in turn, solve a potentially massive disposal problem for the food processing industry.

Key Words: beef cattle, potato co-products

13 Applying technology with newer feed ingredients – Do the old paradigms apply? M. L. Galyean* and N. DiLorenzo, *Texas Tech University, Lubbock.*

Use of co-products like corn and sorghum distillers grain (DG) and corn gluten feed (CGF) in beef cattle finishing diets has increased significantly in recent years, but research to evaluate the efficacy of traditional feeding practices and feed additives when co-products are fed has not kept pace. Grain processing methods that increase starch availability seem equally effective in traditional diets and diets with wet CGF; however, in wet DG diets, some studies have shown decreased efficacy of grain processing, whereas others have shown no evidence of an interaction. Limited data are available on the physical and nutritional value of the fiber in wet DG and CGF; however, CGF at levels ≥ 25% of the dietary DM seems to have some degree of "roughage value," whereas fiber in wet DG has less potential to replace traditional roughage sources. There is little evidence that efficacy of ionophores and antibiotics is changed with diets based on wet CGF or that they interact with addition of wet DG to finishing diets. In vitro data from our laboratory suggest no loss of monensin efficacy in substrates with 15% (DM basis) corn DG in terms of changes in VFA and gas production. Moreover, efficacy of ionophores was not affected in our data by diet substrates with increasing concentrations of S, and in vitro H_2S production in substrates containing wet DG seems predictable from substrate S concentrations. Nonetheless, limited in vivo data suggest lower acetate:propionate ratios with diets high in wet DG, which might affect ionophore efficacy. Likewise, in vivo results suggest that feeding wet DG might decrease ruminal pH; thus, to maximize DMI and minimize digestive upsets, optimal concentrations of roughage need to be evaluated in diets containing wet DG. The effects of yeast products and live microbial cultures in diets with co-product feeds have generally not been determined. Because of the high fiber concentration in CGF and DG, effects of exogenous enzyme preparations on ruminal fermentation and fiber digestion of diets containing these coproducts should be evaluated.

Key Words: coproduct feeds, high-concentrate diet, ionophores

Animal Health: Mastitis, Lameness, and Stress

14 Validation of a novel in-line milk analysis system designed to measure SCC and milk components. H. Karp* and C. S. Petersson-Wolfe, *Virginia Polytechnic and State Insitute, Blacksburg.*

The objective of the current study was to evaluate the accuracy of a novel in-line milk testing system for Holstein, Jersey and crossbred populations. The AfiLab system, developed and manufactured by the AfiMilk Corporation (Israel), measured milk components including fat percent, protein percent, lactose percent, milk urea nitrogen (MUN), presence of blood and SCC. Values were collected for each cow at each milking and data were stored using the AfiFarm software program, similar to conventional conductivity measures. The AfiLab system was designed and tested using a purebred Holstein population. However, validation was required for the Jersey and crossbred populations due to the distinct differences in milk components. Composite milk samples were collected daily from Holstein, Jersey and crossbred lactating cows at the Virginia Tech Dairy Center for an 8-wk period using DHI sampling bottles. All samples were preserved with bronopol and stored (4° C) until analysis. Milk analyses were conducted at the DHI Laboratory (Blacksburg, VA) and components measured included fat, protein and lactose percent, as well as, SCC and MUN. Results from the AfiLab system were compared to that from the DHI Laboratory (gold standard). Preliminary data analysis suggested a high level of correlation between the DHI and AfiLab results for both the Holstein and crossbred population. However, a lower correlation was found for the Jersey breed. These results were reported to the AfiMilk Corporation and an adjustment in the algorithms used to calculate the milk components was performed. Following the adjustment, accurate data was achieved for the Jersey breed. The dataset will be complete within 2 wk and a final analysis will be conducted to determine actual correlation values for the 3 breed populations examined. The use of daily milk component data may prove to be an effective way of identifying disease prior to clinical onset of signs.

Key Words: AfiLab, milk components, DHI laboratory

15 Reproduction and milk loss following clinical mastitis compared among J5 vaccinates and controls. D. J. Wilson*, *Utah State University, Logan.*

Milk loss and reproduction following clinical mastitis (CM) were compared among J5 vaccinates and controls on 3 commercial dairy farms. Contagious mastitis was well controlled and milk production was approximately 11,350 kg/cow/305 d. Cows were randomly assigned as vaccinates or controls. The vaccine was administered subcutaneously in the supramammary region at dryoff, and again 21-28 d before calving due date. At onset of CM, milk samples were aseptically collected for bacterial culture. Among 306 controls and 251 vaccinates, there were 221 new cases of CM affecting 120 cows. 90% (159/176) of milk isolates were environmental pathogens. Factors significantly associated (general linear model) with change in daily milk production following CM were J5 vaccination, DIM at onset of CM, and herd effect as well as each 2-way interaction between the 3 factors. The adjusted daily milk for 21 d following CM (all agents) was 7.6 kg higher among J5 vaccinates than controls; this protective effect of vaccination waned with increasing DIM at onset of CM. A mixed linear model with AR(1) correlation structure estimated the daily milk production of any cow (whether or not she had CM) on a given DIM. Cows with CM caused by Strep spp., S. aureus, E. coli, and Klebsiella all lost significant daily milk production for the entire lactation relative to non-mastitic cows. Another mixed linear model evaluated only coliform CM cases within

the first 50 DIM. For 21 d following coliform CM less milk was lost by J5 vaccinates than controls, 6 to 15 kg/day. Pregnancy was less likely (chi-square) among cows that had CM caused by E. coli (42% pregnant) or Strep spp. (38% pregnant), while 78% of cows with no mastitis conceived. Days open averaged 131 d for cows with no CM, 162 d for cows that had at least one case of CM. Days until conception, days open, times bred, days until last breeding, and percent pregnant by 200 DIM were not changed with J5 vaccination. An important benefit of use of J5 bacterin appears to be reduction of the loss of daily milk production following clinical mastitis, whether all cases or only those caused by coliform bacteria.

Key Words: mastitis, bovine, J5 vaccination

16 Relationships between rumen lipopolysaccharide and mediators of inflammatory response with milk fat production and efficiency in dairy cows. Q. Zebeli, S. M. Dunn, and B. N. Ametaj*, *University of Alberta, Edmonton, Alberta, Canada*.

Milk fat depression is commonly observed in lactating dairy cows fed diets rich in polyunsaturated fatty acids and easily digestible carbohydrates. The objective of this study was to evaluate relationships between rumen lipopolysaccharide (LPS) and mediators of acute phase response with milk fat yield and milk energy efficiency (MEE) in Holstein dairy cows challenged with graded amounts of barley grain in the diet. Eight primiparous, lactating Holstein cows (60 DIM) were assigned to one of the four diets containing barley grain at 0, 15, 30, and 45% (DM basis) in a replicated 4 × 4 Latin square design with 21-d periods (first 11d of adaptation diet). Rumen and blood samples were collected on d 1, 3, 5, 7, and 10 and milk samples on d 5 and 7 of the measurements period and rumen pH and LPS as well as plasma serum amyloid A (SAA), LPS-binding protein (LBP), C-reactive protein (CRP), haptoglobin, and milk fat content were measured. Results showed a linear increase in the DMI and milk yield with increasing the amount of grain in the diet ($P<0.01$). Data also indicated that rumen fluid pH ($P<0.05$; quadratically), milk fat content ($P<0.01$), milk fat yield ($P=0.04$), 3.5% fat-corrected milk ($P=0.04$), and MEE ($P<0.01$) decreased linearly as the dietary grain to forage ratio increased. Additionally, higher grain diets were associated with greater concentration of rumen fluid LPS and of plasma SAA, LBP, and CRP ($P<0.01$). Interestingly, data revealed strong negative correlations between rumen LPS and plasma CRP with milk-fat content and yield as well as with MEE ($R^2=0.45$ to 0.69, $P<0.0001$). Furthermore, a high inter-individual variation with regards to rumen LPS, plasma CRP, and milk fat production was obtained. Further research is warranted to understand the mechanism(s) by which rumen LPS and inflammatory responses to LPS lower milk fat synthesis and MEE and to develop novel strategies for its prevention.

Key Words: milk fat depression, rumen lipopolysaccharide, acute phase response

17 Joint association of some *Staphylococcus aureus* genes with *in-vitro* biofilm formation and sub-clinical intramammary infection. B. V. Le Thanh[1,3], C. L. Jacob[2,3], S. Messier[1,3], F. Malouin[2,3], K. Pépin Gaudreau[2], and D. Scholl*[1,3], [1]*University of Montreal, Saint-Hyacinthe, QC, Canada*, [2]*Univesity of Sherbrooke, Sherbrooke, QC, Canada*, [3]*Canadian Bovine Mastitis Research Network, Saint-Hyacinthe, QC, Canada*.

Chronic infection is one of the problematic results of intramammary infection (IMI) of dairy cows by *Staphylococcus aureus*. If bacterial characteristics could be identified that render an *S. aureus* strain more likely to persist as chronic IMI, it could be possible to diagnose these infections for purposes of selective case management. Using a cohort of 91 Canadian dairy farms, a longitudinal study was conducted of the associations of several *S. aureus* genes and biofilm formation with pre-dry off subclinical IMI versus moderate to sever clinical IMI. Biofilm was determined by an *in-vitro* optical density assay and the presence of *S. aureus* genes were determined by multiple multiplex polymerase chain reactions. Isolates that were recovered from sub-clinical pre-dry off IMI displayed a more widely positive distribution of *in-vitro* biofilm formation than did isolates that were recovered from moderate to severe clinical IMI (MW ANOVA $p<0.01$). The absence of *S. aureus* enterotoxin genes *seg*, *sec*, and *tst*, were each associated with sub-clinical IMI (p-values < 0.03, mixed-random effects logistic regression with herd and parity effects), but the *sen* gene was not, despite having a binary similarity coefficient of 0.80 with *seg*. Absence of the genes *seg*, *sec*, and *tst* were associated with greater biofilm formation as well (MW ANOVA p values < 0.02). The *agr* genotype 1, versus 2 or 3, was also associated with sub-clinical pre-dry off IMI. Moreover, *seg* occurring in the absence of *sen* was associated with the lower biofilm formation (KW ANOVA $p<0.01$) and lower odds of non-clinical pre-dry off IMI (Pearson Chi-square $p<0.01$) compared to all other combinations of occurrence of *seg* and *sen*. These observations suggest direct or indirect effects of some *S. aureus* enterotoxin genes on the likelihood of sub-clinical, presumably chrnonic IMI and that biofilm formation may play a role in the effect.

Key Words: intramammary infection, *Staphylococcus aureus*, molecular epidemiology

18 Effect of flunixin meglumine treatment following parturition on cow health and milk production. T. F. Duffield*[1], H. Putnam-Dingwell[1], D. Weary[2], A. Skidmore[5], L. Neuder[4], W. Raphael[4], S. Millman[3], N. Newby[1], and K. E. Leslie[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*University of British Columbia, Vancouver, ON, Canada*, [3]*Iowa State University, Ames*, [4]*Michigan State University, East Lansing*, [5]*Intervet-Schering Plough, Desoto, KS*.

A double-blind randomized clinical trial was conducted on two Holstein dairy farms: a research facility in Ontario, Canada and a large commercial dairy farm in Michigan. At both sites, cows received flunixin meglumine (Banamine) at a dose of 1.1 to 2.2 mg/kg intravenously based on a fixed volume of 25 ml and 22 ml for cows and heifers, respectively, approximately 2 hours following calving; and a second injection at the same dose and by the same route, approximately 24 hours later. Weekly milk production and clinical health outcomes were recorded. Dichotomous data was analyzed using logistic regression, while milk production was analyzed using mixed linear models. A total of 148 and 1174 cows were enrolled on the study at the Ontario and Michigan sites, respectively. No significant effect of treatment was identified for milk fever, abomasal displacement, clinical ketosis, or mastitis. However, significant effects of treatment were identified for both risk of retained placenta and metritis. Cows treated with flunixin meglumine shortly following calving were 2.5 (OR=2.5, $P<0.001$) times more likely to have a retained placenta and 1.5 (OR=2.5, $P=0.001$) times more likely to be diagnosed with metritis. Milk yield was not significantly different between the two treatment groups. Treatment with a non steroidal anti-inflammatory drug (NSAID) on the day of calving increased the risk of retained placenta and metritis. Based on these results, NSAID therapy on the day of calving is not recommended.

Key Words: flunixin meglumine, parturition, retained placenta

19 Use of dermal fibroblasts to identify cows with high and low innate immune response potential. S. Kandasamy* and D. E. Kerr, *University of Vermont*, *Burlington*.

Resistance to mastitis is dependent on pathogen detection and subsequent activation of the innate immune system. An impaired response may be associated with decreased resistance to infection. We have explored between-cow variation in the ability of their dermal fibroblasts to respond to inflammatory stimuli (IL-1B or *E. coli* LPS) by producing IL-8 and IL-6 as markers of the innate immune response. Fibroblast cultures were established from skin biopsies obtained from 37 mid-lactation cows. Confluent cultures were each challenged with LPS (100 ng/ml) and separately with IL-1B (100 ng/ml). After 24 h the media concentrations of IL-8 and IL-6 were determined and used to rank the animals from high to low (unstimulated cells produced very little IL-8 or IL-6). The five animals with highest and lowest average rankings were designated as high and low responders, respectively. Average IL-8 measured in response to LPS was much greater ($P<0.01$) in fibroblast cultures from high (2.62 ± 0.30 ng/ml) than low (0.52 ± 0.09 ng/ml) responders. Likewise, the LPS-induced concentration of IL-6 (ng/ml) was greater ($P<0.01$) in high (2.05 ± 0.43) than in low (0.15 ± 0.04) responders. The IL-IB-induced IL-8 concentrations in the high responder fibroblasts (16.72 ± 2.85 ng/ml) were approximately 10-fold greater ($P<0.01$) than with the low responder cells, while the IL-1B-induced IL-6 concentrations in the high responder fibroblasts (28.24 ± 4.02 ng/ml) were approximately 15-fold greater than the low ($P<0.01$). The in vivo response was evaluated in 4 high and 4 low responder cows that were challenged in late lactation with *E. coli* (strain P4; 200 cfu) in one quarter. All cows developed clinical mastitis in the challenged quarter, which in one high responder cow ceased lactating. Milk SCC in the other cows began to decline earlier in the low responder group and was lower ($P\leq0.05$) than the high responder group 12 and 15 days post-infusion (last sample day). These results document substantial between-cow variation in fibroblast production of cytokine markers of the innate immune response, and differences between high and low responders appear to have effects on the resolution of *E. coli* mastitis.

20 Effect of farm, housing and management practices on the occurrence of clinical mastitis and pathogen isolation. Y. B. Hunt[2] and J. K . Margerison*[1], [1]*Massey University*, *Palmerston North, New Zealand*, [2]*Plymouth University*, *Newton Abbot, UK*.

The aim of the study was to analyse the incidence of mastitis on the sample farms and compare these with farm management practices. A total of 9 commercial dairy farms were selected at random from the South West of England, they had a full farm assurance audit and matched according to; herd size, housing type, feeding levels and milk yield. Mean herd size was 231, with the greatest proportion of cows being housed in free stalls (cubicles) (0.78) followed by beep bedded (0.22) systems and the mean milk yield was 7,800 l/cow (305 d). Milk samples were collected aseptically from 664 cows, exhibiting clinical mastitis during the first 110 days of lactation. Standard microbiological procedures for culturing mastitis casing pathogens were applied, pathogen presence was assessed using suitably trained and experienced technical staff, while antibiotic susceptibility was assessed by applying antibiotic multidiscs to estimate the effect of the pathogens cultured. Environmental bacteria *E-coli* (25 samples) and *Staph aureus* (17 cows) and *Strep uberis* (16 cows) were the main organisms isolated. Synulox was significantly more effective against *E-coli* and *Staph aureus*. There was no significant difference between farms of the types of bacteria found. In terms of management practices, two farms had significantly lower levels of mastitis, which coincided with free stall housing with sand or sawdust with cow mats, and hot and cold water parlor washing. In conclusion, mastitis levels were found to be higher on farms with poor hygiene and housing management practices.

Key Words: mastitis, dairy, management

21 The effect of lameness in Holstein Friesian dairy cattle on live weight, milk yield, milk let down and milking duration. J. A. Hollis[2] and J. K. Margerison*[1], [1]*Massey University*, *Palmerston North, New Zealand*, [2]*Plymouth University*, *Newton Abbot, UK*.

The aim of this study was to assess the effect of lameness on yield, milking duration, body condition score and live weight. A total of 40 multiparous Holstein Friesian dairy cattle were selected at random and were split into two groups of either; 20 lame (L) or 20 non lame (NL) according to the locomotion score (0 to 5 point scale) at 110 d postpartum, such that the cows in each if the two group were paired according to calving date, milk yield, body condition and live weight. Data was normally distributed and means were compared using a General linear model ANOVA to establish the existence of significance differences ($P<0.05$). Following selection, the lame cows had a significantly greater ($P<0.001$) locomotion score compared with non-lame cows (NL: 1.01, L: 3.57 (±0.445)). Lame cows had a significantly ($P<0.05$) lower body condition score (1 to 5) (NL: 3.24, L: 2.87 (±0.064)), a significantly ($P<0.05$) lower mean milk yield (NL: 42.3, L: 38.7 (±0.60)) and significantly ($P<0.05$) lower milking duration (m) (NL: 7.03, L: 6.06, (±0.224)) compared with non-lame cows. While, no significant difference was found between live weight per se (NL: 654, L: 646 (±5.5)) the change in live weight was significantly different ($P<0.05$) as lame cows lost weight compared with non lame cows which gained weight. In conclusion, lameness reduced milk yield, body condition score, milking duration and increased liveweight loss compared with non lame cows.

Key Words: lameness, live weight, milk yield

22 A comparison of measures of stress following administration of either lipopolysaccharide (LPS) or corticotropin-releasing hormone (CRH) to Brahman bulls and heifers. L. E. Hulbert*[1], J. A. Carroll[1], M. A. Ballou[4], J. W. Dailey[1], L. C. Caldwell[2,3], A. N. Loyd[2,3], N. C. Burdick[2,1], R. C. Vann[5], T. H. Welsh, Jr.[2], and R. D. Randel[3], [1]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*, [2]*Texas AgriLife Research, Texas A&M System*, *College Station*, [3]*Texas AgriLife Research, Texas A&M System*, *Overton*, [4]*Department of Animal and Food Sciences, Texas Tech University*, *Lubbock*, [5]*MAFES, Mississippi State University*, *Raymond*.

A better understanding of cattle responses to various stressors is needed for production and health improvement, yet it is often difficult to decipher if stressor-specific physiological effects are neurendocrinological, immunological or both. The objective of this study was to compare and contrast the temporal aspects of rectal temperature (RT), heart rate (HR), white blood cell (WBC) counts and WBC differentials following either a LPS or CRH challenge. Brahman heifer (H) and bull (B) calves were fitted with indwelling jugular catheters, HR monitors and RT devices. The following day, calves were challenged with an i.v. bolus of LPS (0.25 μg/kg BW; H:n=6, B:n=5) or CRH (0.5 μg/kg BW; H:n=6, B:n=6). Blood samples were collected at 1-h intervals from 2 h prior to challenge through 8 h, and at 12 and 24 h. Blood was analyzed using a Cell Dyn for WBC (10^6 cells/mL) and differentials. HR (beats

per min, bpm) and RT (°C) data were continuously collected from 10 h before to 24 h following challenge and were averaged into 10-min intervals prior to analysis. Data were analyzed using ANOVA specific for repeated measures. Baseline measures were defined as data collected prior to the challenge and were averaged and used as a covariate. The first increase in RT from baseline ($P \leq 0.01$) was at 1 h and 7 h for LPS and CRH, respectively. A peak in RT was observed at 4.5 and 9.3 h following LPS and CRH, respectively, returning to baseline for both treatments by 21 h ($P \leq 0.10$). Increases ($P \leq 0.01$) in HR above baseline were observed at 1.5 h after LPS and 2 h after CRH. Overall, HR was 26±0.1% greater ($P \leq 0.05$) in LPS- than CRH-treated calves from 2.7 to 7.2 h, with both returning to baseline by 23 h ($P \geq 0.10$). After LPS, WBC and neutrophil:lymphocyte (N:L) ratio decreased from 1 to 5 h with a recovery above baseline ($P \leq 0.01$) observed at 8 h. In contrast, WBC and N:L ratio increased 3 to 4 h post-CRH ($P \leq 0.01$). Based upon the parameters evaluated in the current study, a CRH-simulated stress and an acute immunological stress induced by LPS elicit uniquely different physiological and immunological responses.

Key Words: bovine, endotoxin

23 Peripartum measures of stress, inflammation and energy status as predictors for postpartum health disorders in transition dairy cows. J. M. Huzzey*[1], T. R. Overton[1], D. V. Nydam[1], and R. J. Grant[2], [1]*Cornell University, Ithaca, NY*, [2]*W. H. Miner Agricultural Research Institute, Chazy, NY*.

The objective of this study was to measure physiological markers related to stress, inflammation, and energy status during the period around calving to determine if these markers could identify cows at greater risk for health disorders postpartum. Blood was collected weekly from 414 Holstein dairy cows during wk -3, -2, -1 and +1 relative to calving and analyzed for cortisol, haptoglobin (Hp) and non-esterified fatty acids (NEFA). Dairy Comp 305 records were used to collect health events up to 100 days in milk. Data for healthy cows (no health events, n = 195) and those with ketosis (KET; n = 68), displaced abomasum (DA; n = 26) and/or retained placenta (RP; n = 45) are presented; cows experiencing disorders other than KET, DA, or RP were not included in this analysis. NEFA concentrations were higher in the KET, RP, and DA groups relative to the healthy group during each week relative to calving ($P < 0.001$). Cortisol was higher during wk +1 for cows with RP compared to healthy cows (0.9 ± 0.2 vs. 0.5 ± 0.04 μg/dl respectively, $P = 0.009$); however, no other differences in cortisol were detected. During wk +1 plasma Hp levels were higher ($P \leq 0.01$) in cows with RP (1.6 ± 0.2 mg/ml), KET (1.1 ± 0.1 mg/ml) and DA (1.2 ± 0.2 mg/ml) compared to healthy cows (0.7 ± 0.05 mg/ml). During wk -1 Hp was higher for cows that developed DA postpartum compared to healthy cows (0.5 ± 0.2 vs. 0.2 ± 0.02 mg/ml; $P = 0.02$). For every 0.5 mg/ml increase in Hp during wk -1, the odds of developing a DA postpartum were 2 times greater (OR = 1.99, 95% CI = 1.3, 3.0, $P < 0.001$) and the odds of having a DA were 3.1 times greater if the cow had a Hp concentration ≥ 0.8 mg/ml during this period (sensitivity = 19.2%, specificity = 92.8%, $P = 0.04$). Prepartum NEFA and Hp may be useful diagnostic tools to assess risk for health disorders after calving thus providing opportunities for early intervention or management changes.

Key Words: transition cow, health, metabolites

24 Use of rumen temperature for health monitoring in cattle. L. E. Sims*[1], T. K. Dye-Rose[1], C. L. Goad[2], B. P. Holland[1], L. O. Burciaga-Robles[1], D. L. Step[3], C. R. Krehbiel[1], and C. J. Richards[1], [1]*Department of Animal Science, Oklahoma State University*, [2]*Department of Statistics, Oklahoma State University*, [3]*Veterinary Clinical Sciences, Oklahoma State University*.

Heifer calves (241±17kg) were purchased in western Kentucky, comingled, dosed with a remote, continuous monitoring rumen temperature bolus (SmartStock, LLC), and delivered to the Oklahoma State University Willard Sparks Beef Research Center to evaluate the effectiveness of rumen temperature boluses as a health management tool during a 42d receiving period. After arrival, calves were stratified according to High, Medium, or Low arrival blood haptoglobin level. Calves were evaluated each day by two trained individuals to assess calves for signs of respiratory or other diseases. Each calf was given a visual severity score of: 0) normal, 1) mild, 2) moderate, 3) severe, or 4) morbid based on clinical signs. Any animal scored 1 or higher was transferred to processing facility (pulled) for further examination. At examination, if rectal temperature was greater than 40°C, the calf was treated according to a predetermined antimicrobial regimen. Two hundred sixty five calves were used for 21d observation and 168 calves were used for 42d observation. Calves with high haptoglobin levels had a 21d average rumen temperature that was higher than medium (P=0.05) and tended to be higher than low haptoglobin levels (P=0.08). No differences were detected in 42d average rumen temperature across haptoglobin levels (P=0.22). As the number of times calves were treated increased, average 21d rumen temperature increased ($P < 0.01$) and 7 and 21d ADG decreased ($P < 0.01$). Calves were also classified by one of three ADG categories; 1) Low (≤0.68 kg), 2) Medium (>0.68 kg and <1.59 kg), and 3) High (>1.59 kg). Calves with low 0-21 and 0-42d ADG had the greatest 21 and 42d average temperature and average maximum temperature ($P < 0.01$), whereas calves with high 0-21 and 0-42d ADG had the lowest 21 and 42d average temperature and average maximum temperature ($P < 0.01$). These results indicate potential benefits of using rumen temperature boluses to assist in health management of receiving cattle.

Key Words: temperature, receiving cattle, health

25 Relationship between milk fat depression and laminitis in early lactating Holstein cows. M. Vazirigohar*, A. Nejati Javaremi, and A. Nikkhah, *University of Tehran, Karaj, Tehran, Iran*.

The objective of this study was to assess association between milk fat depression (MFD) and clinical laminitis in early lactating Holstein cows. In this study, production data were obtained from the Dairy Herd Improvement Center, and laminitis data were collected from 3 large Holstein dairy herds. There was 3380 milk fat-test day in 2 months of early lactating, 1387 cases of MFD (milk fat: protein ratio less than 1), and 344 cases of clinical laminitis up to 4 months of early lactation. Logistic data regression was used to evaluate the association between the occurrence of MFD and subsequent clinical laminitis. This study found that cows that had MFD during 2 months of early lactation were (odds ratio=0.767; 95% confidence interval=0.594 to 0.991) lower risk of clinical laminitis within the next 2 months than were cows without MFD. Risk of laminitis was greater for cows in second, third and fourth lactation (odds ratio = 1.038, 2.784 and 4.764, resp.; 95% confidence interval = 0.668 to 1.1.613, 1.91 to 4.057, and 3.374 to 6.677) than first lactation cows.

Key Words: milk fat depression, laminitis, early lactating Holstein cows

Bioethics: A Scientist's Guide to Approaching Bioethics

26 Bioethical considerations of food animal products and production. W. R. Stricklin*, *University of Maryland, College Park*.

Humans obtain a number of products from animals. These include food, clothing, medical materials, companionship and research knowledge to name a few. A valued ethic contends that it is inappropriate for one to treat another as a means to an end. In short, it is wrong to treat another as simply a product. Historically, non-human beings have not been included as "others" and thus their treatment as products has been generally accepted. However, a growing view holds that animals are "subjects of a life" and deserving of consideration beyond their economic worth. Accordingly, the public asks increasingly for assurance of appropriate animal well-being. At the same time, polls indicate that the public majority does not wish to give up using animal products. The research community has dealt with these somewhat conflicting viewpoints by adopting animal care and use committees (ACUC). Research animals continue to provide a product (i.e., data points) for researchers, but the ACUC, not the researcher, is responsible for the animal's life, i.e., its care, treatment and well-being. This uncoupling of the research animal's life from the animal as a product via the ACUC has generally been successful and may serve somewhat as a model. But ultimately, animal agriculture faces the challenge of developing its own methodology for uncoupling the animal "as a subject of a life" from the animal product, and doing so without destroying the integrity and economic viability of animal agriculture. Third-party accreditation programs can help, but input from educators and possibly additional methods from industry leaders are also needed. Addressing the ethical implications of treating animals as subjects of a life, and not simply as products, meets with the longterm goal of animal scientists. Accordingly, developing an animal agriculture that is bioethically grounded should be consistent with developing a system that is sustainable.

Key Words: bioethics, animal products, animal welfare

27 Thinking critically about bioethical issues. K. K. Schillo*, *University of Kentucky*, *Lexington*.

Animal scientists embrace a humanist ideology; i.e., a perspective that emphasizes the characteristics, experiences and interests of *Homo sapiens*. According to this view, humans are so different from all other organisms that they deserve supreme status over the rest of nature. The ability to reason in an abstract manner is the basis for this distinction. Humanists believe that this degree of intellectual ability allows humans to ascertain a true understanding of nature and that such knowledge can and should be used to advance the species. This idea underlies an ethical framework that assumes that rational analysis leads to discovery of what is right and wrong thereby perpetuating moral progress and improving the human condition. No matter how popular and appealing this approach might be it should not be immune to critical analysis. Before we begin to think critically about bioethical issues we should think critically about ethics itself. I should like to establish a framework for doing so, by discussing two major concerns. First, we should recognize that humanism is an anthropocentric perspective and may not be compatible with the overall structure and function of nature. More specifically, we should consider whether the notion of ethics is compatible with the biological principles that govern all life, including humans. Second, it is questionable that human intelligence provides the only or best means to understand or cope with nature. Basic emotions may be just as useful as or even more useful than reason in helping humans live skillfully, if not ethically.

Key Words: bioethics, humanism, rationalism

28 A pedagogical tool for scientists faced with ethical issues. C. C. Croney*, *The Ohio State University*, *Columbus*.

In the United States, escalating concerns about current farm animal science and production methods have resulted not just in increased food animal protection policies, but also, animal welfare legislation. Animal scientists and industry leaders are apprehensive that such policies may primarily be driven by emotion and lack of scientific understanding, and thus, may have unforeseen consequences. The potential impacts of animal care and use decisions on producers, animals, concerned citizens, and implications for the environment and food prices must also be considered. Balancing the interests and values of all stakeholders has presented a considerable challenge. An ethics assessment process developed for addressing biomedical ethics issues presents a more inclusive model to combine socio-ethical concerns with relevant factual information, thereby facilitating decision-making that is both ethically responsible and pragmatic. A case study will illustrate application of this model, which includes identification of the ethical problems, the embedded values, the relevant facts and moral tests that can be applied.

Key Words: ethics, science, values

Breeding and Genetics: Dairy Cattle Breeding I

29 Using veterinary and milk recording data for a genetic analysis of health traits. J. Moro-Méndez*[1], E. Bouchard[2], and R. I. Cue[1], [1]*McGill University*, *Ste-Anne-de-Bellevue, QC, Canada*, [2]*Université de Montréal, Faculté de Médecine Vétérinaire*, *Saint-Hyacinthe, QC, Canada*.

The objective was to estimate clinical incidence of diseases (CI) and the genetic variability of health traits in commercial dairy herds. Health events from a veterinary health database were obtained from Dossier Sante Animal (DS@HR); 296,170 cow-calving dates from 123,867 cows. Animal identification and pedigree information were obtained via Valacta and CDN and merged with the health event data. Merges were performed for Holstein (HO) and Ayrshire (AY). This process produced 155,740 and 8,130 herd-cow-date of calving records from 70,168 HO and 3,365 AY cows, in common between DS@HR and Valacta/CDN files, with 197,755 and 10,797 HO and AY health event records, respectively. Then, binary traits were created for each health event-parity combination: coded 1 when the cow had the disease during the lactation, otherwise the trait was coded as 0. Binary traits were created for milk fever (MF), retained placenta (RP), cystic ovaries (CO), displaced abomasum (DA), mastitis 1st case and 2nd cases (M1, M2, respectively), reproductive (RP), digestive (DG), locomotive (LO), and metabolic (ME) problems. Lactational incidence rates (LIR) were calculated from the CI and the number of lactations at risk for each herd.

For HO, LIR for first to third parities ranged from 0.10% (MF) to 13% (M1). Using a sire model (year of calving and age at calving as fixed effects, herd and sire as random effects) heritabilities were calculated. Each analysis was performed specifying a binomial distribution for the dependant variable, and a logit link function (using the procedure Glimmix of SAS). The heritabilities showed low to moderate values (HO, first parity): 0.15 (DG), 0.27 (RP), 0.15 (CO), 0.09 mastitis (1st and 2nd cases combined), 0.05 (LO), and 0.05 (ME). Combining health and milk recording data is not trivial and overall correct permanent identification and recording of date of calving are critical.

Key Words: health traits, incidence, heritability

30 Use of linear and threshold models for analysis of producer-recorded health data in Holstein cattle. T. F.-O. Neuenschwander[1], F. Miglior*[2,3], J. Jamrozik[1], and L. R. Schaeffer[1], [1]*CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*, [2]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [3]*Canadian Dairy Network, Guelph, ON, Canada*.

Eight health traits (mastitis, lameness, cystic ovarian disease, left displaced abomasum, ketosis, metritis, milk fever and retained placenta) are recorded by dairy producers in Canada since April 2007. The objectives of this study were 1) to estimate variance components for 8 diseases recorded in Canadian Holsteins using univariate or multivariate analyses, 2) to compare threshold and linear models and 3) to estimate the effect of days at risk on the estimates of variance components. Binary traits (0=sick, 1=healthy) were analyzed either individually or grouped according to biological similarities. Minimum number of disease recordings per herd was applied to ensure a sufficient quality of disease recording in the herds included in the analysis. Eight different models were implemented for each trait; 4 of them were sire linear models and the other 4 sire threshold models. The differences among the 4 linear or threshold models were the inclusion of days at risk and/or permanent environmental effect in addition to herd, parity and sire effects. Data included 46,104 cases of any of the above diseases. Incidences ranged from 2.6% for ketosis and 9.7% for mastitis. Metritis and milk fever had an incidence below 4.0%. Heritability for all traits with all models was below 0.04 with a linear model. The highest heritability was for left displaced abomasum (0.034). Heritabilities for lameness and metritis were below 0.01. Heritabilities on the liability scale calculated with a threshold models were between 0.003 (metritis) and 0.216 (left displaced abomasum). Converted to the observable scale, these values were close to those estimated with a linear model. There was a moderate positive genetic correlation between left displaced abomasum and ketosis as well as between metritis and retained placenta. The effect of days at risk was not significant and showed a negative sign for some traits. This may be due to the short period at risk of these traits and the highest risk of culling of sick animals.

Key Words: variance components, health traits, threshold models

31 Comparison of service-sire fertility evaluations formerly or currently available to the US dairy industry. H. D. Norman*, J. L. Hutchison, and J. R. Wright, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

A new service-sire fertility evaluation, Sire Conception Rate (SCR), was initiated in August 2008 to replace the previous evaluation, Estimated Relative Conception Rate (ERCR), used by the dairy industry for 20 yr. This study derived and compared evaluations from these 2 procedures using both an August 2008 and January 2009 data cutoff (using data from the same herds) with the Western Bull Fertility Analysis (WBFA). SCR and ERCR inputs were from 3 dairy records processing centers; WBFA data was from 1. The SCR model includes 10 effects to help predict bulls' conception rate (CR). Minimum inseminations/bull in the last 4 yr to publish SCR was 300 for Holsteins (HO), 100 or 200 for other breeds. ERCR uses only first services, and WBFA and SCR use inseminations through fifth and seventh service, respectively. Comparing the January 2009 evaluations, the most bulls were summarized with SCR; number of HO bulls with SCR, ERCR, and WBFA were 2358, 956, and 1594; number of Jersey (JE) bulls were 210, 82, and 98. Mean of bull evaluations from all 3 methods were near zero. Standard deviations (SD) for HO and JE for SCR were 2.42 and 2.51, 1.76 and 1.88 for ERCR, and 2.02 and 2.72 for WBFA. Holsteins bulls that were <3, 3 to 4, 4 to 5, 5 to 6, and >6 yr had mean SCR of -0.76, -0.12, 2.30, 1.48, and 1.31%, respectively. Comparable means for ERCR were 0.89, 0.10, 0.82, 0.06 and 0.02, and for WBFA were -0.14, -0.01, -0.13, 0.38, and 0.53. Standard deviations for SCR for these same were 2.20, 2.47, 2.29, 2.22, and 2.05. Standard deviations for ERCR were 1.68, 1.79, 1.74, 1.74, and 1.98, and for WBFA were 1.85, 1.96, 2.19, 2.10, and 1.93. Correlations between SCR and ERCR for HO and JE were 0.73 and 0.76. Correlations between SCR and WBFA were 0.65 and 0.68, and between ERCR and WBFA were 0.63 and 0.73. Correlations between August 2008 and January 2009 SCR were 0.95 and 0.94. Correlations between August 2008 and January 2009 ERCR were 0.91 and 0.90, and between the same for WBFA were 0.97 and 0.96.

Key Words: bull fertility, conception rate, evaluation

32 Analysis of accounting for production in the genetic evaluation of direct herd life in Canadian Holsteins. A. Sewalem*[1,2], G. Kistemaker[2], and F. Miglior[1,2], [1]*Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada*, [2]*Canadian Dairy Network, Guelph, ON, Canada*.

In Canada, the genetic evaluation for direct herd life (DHL) is based on cows' survival from 1st calving to 120 DIM, from 120 DIM to 240 DIM, from 240 DIM to 2nd calving, survival from 2nd to 3rd calving, and survival from 3rd to 4th calving, The multiple-trait animal model includes the fixed effect of herd year, fixed effect of registry status x herd size change x season of calving (RHS), linear and quadratic regression of age at first calving, protein yield by RHS, protein and fat yields linear, quadratic, and cubic regressions and the random effect of animal and residual (Model 1). Two additional models were developed: a) same as Model 1 without production traits (Model 2) and b) same as Model 1 except that linear and quadratic regression of protein and fat yields were fitted within quota year (Model 3). The three models were compared in terms of: a) correlation analyses of DHL bull proofs with production traits; b) predictability of DHL bull proofs; and c) Genetic trends. The same genetic parameters were used for all the three models. The results showed that the correlations between direct herd life and production traits were negative in Model 1 and positive in Model 2. However, Model 3 has resulted in zero correlations with the main production traits. There were no major noticeable differences among three models in terms of predictability and genetic trends. Therefore, modifying the current genetic evaluation model system, by fitting production traits as a regression within quota year will result a desirable correlation with production traits and will better account for potential changes over time of culling for production.

Key Words: herd life, multiple-trait animal model, accounting for production

33 Estimates of residual feed intake in Holstein dairy cattle using an automated, continuous feed intake monitoring system. E. E. Connor*[1], J. L. Hutchison[2], H. D. Norman[2], and R. L. Baldwin, VI[1], [1]*USDA-ARS, Bovine Functional Genomics Laboratory*, *Beltsville, MD*, [2]*USDA-ARS, Animal Improvement Programs Laboratory*, *Beltsville, MD*.

Improving feed efficiency of cattle is a primary goal in livestock production to reduce feed costs and production impacts on the environment. In dairy cattle, studies to estimate efficiency of feed conversion to milk production based on residual feed intake (RFI) are limited primarily due to a lack of individual feed intake measurements available for lactating cows. The goal of this study was to apply state-of-the-art radio-frequency identification equipment to measure feed intake in Holstein cows during the first 90 days of lactation (DIM) and characterize the RFI trait in dairy cattle. A total of 107 animals (55 first-lactation heifers [L1]; 32 second-lactation cows [L2]; twenty ≥3 lactation cows [L3+]) were evaluated between Oct 2007 and Nov 2008. Animals were housed in a free-stall barn and individual daily feed consumption was monitored continuously using the GrowSafe 4000 System (GrowSafe Systems, Airdrie, Canada; 33 nodes), at a maximal density of < 2 cows per node. Cows were fed a total mixed ration 3× daily, milked 2× per day, and weighed every 10 to 14 d. Milk yield was measured at each milking. Feed %DM was measured daily and nutrient composition was analyzed from a weekly composite. Milk composition was analyzed weekly, alternating AM and PM milking periods. Estimates of RFI were determined as the difference between actual intake and predicted feed and energy intake based on the equation $b0 + b1 * BW^{0.75} + b2 * gain + b3 * energy\text{-}corrected\ milk$. A subset of 11 L1 heifers was evaluated for a 305-d lactation to determine the relationship between RFI during the first 90 DIM and the full lactation. Using this system, RFI ranged from -2.2 to 3.6 kg/d for L1, -3.0 to 2.6 kg/d for L2 and -2.9 to 3.2 kg/d for L3+, meaning a difference of 6.6 kg/d in DMI between the most and least efficient animals across all lactational groups. Regression analysis indicated RFI of L1 during the first 90 DIM was predictive of RFI during the full lactation ($r^2 = 0.48$; $P = 0.02$). Based on our small sample size, heritability of the RFI trait was estimated to be very low ($h^2 = 0.05$).

Key Words: dairy cattle, feed efficiency, residual feed intake

34 Trends for monthly changes in days open in Holsteins. M. Pszczola*[1,2], I. Aguilar[1,3], and I. Misztal[1], [1]*University of Georgia*, *Athens*, [2]*Animal Breeding and Genetics Group, Wageningen University*, *Wageningen, the Netherlands*, [3]*Instituto Nacional de Investigación Agropecuaria*, *Las Brujas, Uruguay*.

A reaction norm approach was used to estimate trends for days open (DO) with a model that indirectly accounted for heat stress. Data included 3.4 million first-parity records of DO of US Holsteins. A fixed effect model included herd-year, month of calving within region (MOC), age class, and regression on 305-d milk yield. An index calculated from the standardized solutions to MOC derived from the fixed effect model was treated as a proxy for an index on heat stress (SI). The lowest index for any region was set to zero. The highest index was one for the Southeast, 0.56 for the Northeast, 0.54 for the Midwest, 0.33 for the Northwest, and 0.42 for the Southwest. In all regions except the Northwest, the highest DO and the corresponding highest indices were in March-April. Compared to the fixed model, the reaction norm model also included the effect of an animal and a random regression on the SI; the two animal solutions are subsequently referred to as an intercept and a slope. Genetic trends were calculated for all animals and separately for sires. For all the animals, the trend for the intercept was -0.1 d/year, while the trend for the slope was 1 d/year. For sires, the same trends were -0.3 and 1.5, respectively. Official proofs were used to characterize the 100 top and the 100 bottom bulls with at least 50 daughters for the intercept and the slope. Compared to the top bulls, the bottom bulls for the intercept gave 56 kg more milk, and their type performance index (TPI) was higher by 212 points. For the slope, the same numbers were -435 kg and -242 pt., respectively. Trends for seasonal changes of days open are unfavorable.

Key Words: dairy cattle, fertility, heat stress

35 Effects of milk fat composition, DGAT1 and SCD1 on fertility traits in Dutch Holstein cattle. R. M. Demeter*[1,2], G. C. B. Schopen[1], A. G. J. M. Oude Lansink[2], M. P. M. Meuwissen[2], and J. A. M. van Arendonk[1], [1]*Animal Breeding and Genetics Centre, Wageningen University, Wageningen, the Netherlands*, [2]*Business Economics Group, Wageningen University*, *Wageningen, the Netherlands*.

Recently, selective breeding was proposed as a means of changing the fat composition of milk to improve its nutritional quality. Before implementing such breeding strategies, effects on other economically important traits should be investigated. The objective of this study was to examine the effect of milkfat composition, DGAT1 gene, and SCD1 gene on fertility traits in commercial Holstein Friesian dairy cattle in the Netherlands. Morning milk samples from 1,745 first-lactation Holstein Friesian cows were collected. From the records on reproductive performance, eight fertility traits were derived. Linear mixed models were fitted as randomized block designs, with herds as random blocks and individual cows as units of analysis. The model included days in milk, age at first calving, season of calving, and sire type. Relationships between individuals were accounted for. We found that greater concentrations of trans fatty acids (TFAs) and conjugated linoleic acid (CLA) within total milkfat had a negative effect on fertility. Increased proportions of TFAs are associated with longer intervals between calving and first insemination, larger numbers of inseminations, lower calving rates, lower nonreturn rates for insemination after first service, and lower calving rates after first service. Greater proportions of CLA were associated with longer periods to first insemination and lower nonreturn rates for insemination 90d after first service. DGAT1 affected nonreturn rates for insemination 28d and 56d after first service. Results for DGAT1 displayed a nonlinear pattern, with heterozygous genotypes associated with lower estimates than homozygous genotypes. Results suggest that breeding to decrease TFA concentrations could improve fertility, whereas breeding to increase CLA content might impair some of the reproductive traits. Regarding DGAT1, results suggest that selecting for animals with the AA genotype would be the most desirable with regard to the nutritional quality of milk and the reproductive performance of cows. Results of this study can be used to assess the economic effects of breeding to change milk fat composition on reproduction.

Key Words: dairy cattle, milk fat composition, fertility

36 Deriving final score from linear traits for the Italian Holstein cattle. S. Biffani, F. Canavesi*, and R. Finocchiaro, *ANAFI*, *Cremona, Italy*.

Over the past ten years the definition of Final Score has been changed quite a few times due to the harmonisation of type traits evaluation. Moreover, the increasing importance of cow functionality, with particular emphasis on feet & legs, has not been completely taken into account.

All these changes can affect the robustness of genetic evaluation since the definition of the trait is not the same across time. To address this issue, and to guarantee a better comparison of bull and cow EBVs across time and between national and foreign bulls, a formula to derive final score from linear conformation traits EBVs has been developed using the selection index theory. At first a new phenotypic definition of Final Score was defined combining 15 different linear traits according to the last recommendations of the international harmonisation group. Subsequently genetic correlations were estimated between the new definition of Final Score and each of the 15 linear traits scored in Italy. Selection index theory was then applied to maximize genetic gain for Final Score making use of the correlated traits. A total of 15 linear traits were used to estimate Final Score resulting in 31% contribution linked to frame and dairy strength traits, 21% to feet & legs and 48% to udder traits. The new Final Score will be introduced officially in Italy during 2009.

Key Words: EBV, final score, linear conformation traits

37 Modelling technical parameters of individual extended lactation curves in Italian Holsteins. R. Steri[1], E. L Nicolazzi[2], G. Gaspa[1], F. Canavesi[2], C. Dimauro[1], and N. P. P. Macciotta*[1], [1]*Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italia*, [2]*Associazione Nazionale Allevatori Frisona Italiana, Cremona, Italia*.

In several countries, the average length of lactation is increasing due both to reproductive failure but also to management strategies. The investigation of basic traits of individual extended lactations may be of interest for selection programmes. In this study, 68,899 individual lactations of 45,132 Italian Holstein cows were fitted with two mathematical functions that have been previously tested on extended lactations: the Ali and Schaeffer multiple regression function (AS) and the non linear modification of the Dijkstra model (DJ). Lactations were of three parities (first, second and thirty) and were classified into four lactation length classes (1<350 d; 2= from 351 to 450d; 3= from 451 to 650d; 4>651 to 1000d). Both models were fitted to individual lactation curves for milk yield (MY), fat (FP) and protein (PP) percentage and somatic cell score (SCS). Peak yield (Ym), time of peak yield (Tm), time et inflection point (Tf) and final test day production (for AS) or asymptotic production (for DJ) were calculated. AS and DJ function show a good fit when modeling lactations curves of milk yield and protein content in 651-1000d class: the percentage of curves having an R-square higher than 0.7 was about 75% for MY, 60% for PP, 15% for FP and 15% for SCS. Estimates of technical parameters show a remarkable variability. As an example, for milk yield the median of asymptotic level of production estimated with DJ was kg -7.3, kg 11.5 and kg 8.51 for first, second and third parity respectively, whereas the production at last test estimated by AS function was kg 5.5 kg, kg 8.4 and kg 5.5 for the same parities. Time of inflection (Tf) also show a great variability between models: for first parity cows; for example, it was estimated as 137.7 d by DJ and 596 by AS. Finally, time at peak occurrence (Tm) was at days 82.5, 53.6 and 52.9 for DJ and 49.5, 33.7 and 41 days for AS. Both models were able to highlight some basic traits of the curve shape for individual extended lactations, although a great variability has been also detected.

Key Words: extended lactations, individual curves, mathematical modelling

Breeding and Genetics: Molecular Genetics I

38 Hybridization quality diagnostics using control probes on long-oligonucleotide microarrays: An application to the Pigoligoarray. J. P. Steibel*[1], M. Wysocki[2], V. D. Rilington[1], A. M. Ramos[1,3], J. K. Lunney[2], and C. W. Ernst[1], [1]*Michigan State University, East Lansing*, [2]*ANRI, BARC, ARS, USDA, Beltsville, MD*, [3]*Wageningen University, Wageningen, the Netherlands*.

Long oligonucleotide microarrays are composed of 40- to 70-mer oligonucleotides spotted on glass slides. This type of expression profiling platform has been recently made available to several livestock species. Such microarrays commonly include negative control oligonucleotides (scrambled sequences) and perfect match/mismatch oligonucleotide sets (PM/MM). Graphical diagnostics (e.g. MA plots) are commonly used in exploratory microarray analysis, but they do not explicitly consider control oligonucleotides. The objective of this work was to develop graphical diagnostics that use control oligos to evaluate hybridization specificity. We re-analyzed data from 8 previously conducted experiments using the Pigoligoarray. A total of 160 microarray slides were processed under a range of stringency and hybridization conditions that resulted in various degrees of non-specific hybridization. The arrays were classified as "good" or "poor" hybridization quality depending on the extent of cross-hybridization. Negative control oligos had median signal intensities similar to or lower than non-control oligos for the "good" arrays whereas for the "poor" arrays negatives exhibited an almost symmetric distribution of intensities around the median for non-control oligos. The analysis of PM/MM sets was even more informative, clearly indicating whole experiments or arrays with extensive non-specific binding. In experiments with specific hybridization, individual probe analyses of PM/MM sets revealed the expected decrease in signal intensity with increased MM number. Additionally, the dispersion around the median intensity decreased as the number of mismatches decreased. Such patterns were not present on arrays with nonspecific hybridization. While these diagnostics were developed using the Pigoligoarray, the proposed applications could be straightforwardly implemented for other long-oligonucleotide microarrays that include the same types of control probes, such as for the bovine and turkey. In summary, we successfully used PM/MM and negative oligos to elaborate graphical diagnostics of hybridization quality.

Key Words: microarrays, cross-hybridization, graphical diagnostics

39 Low density SNP chip for non-genotyped animals. H. Wang*[1] and R. Rekaya[1,2], [1]*Department of Animal and Dairy Science*, [2]*University of Georgia, Athens*.

Availability of reliable and inexpensive genotyping platforms for single nucleotide polymorphism markers (SNP) has made the possibility for genomic breeding value estimation in several livestock species a reality. Unfortunately, at above two hundred dollars per animal this technology is still too expensive for massive use at the commercial level. Currently, this technology is mainly used for genotyping top animals and then used in two step procedures for estimating genomic breeding values. For its use at the population level, the SNPs genotypes of non-typed animals have to be inferred somehow from the already genotyped animals and their relationships. In fact, several attempts have been proposed ranging from the calculation of gene content to the construction of a covariance matrix similar to the classical additive relationship matrix.

However, in all cases the only information used is the one available from the allele frequencies and the relationship between animals. This information could be limited especially in pedigrees that span several generations as it is the case in food producing animals. In this study, we propose using low-density chips with few hundred SNPs for large scale genotyping. This low cost chip will provide an additional source of information, linkage disequilibrium, in inferring genotypes of non-typed animals. For that purpose a simulation was conducted where 1 and 5% of the population was genotyped for 50 K SNPs and 10 and 25% of the remaining animals were genotyped for 500, 1,000 and 2,000 SNPs selected jointly using an ant colony algorithm. The results showed an increase in the probability of predicting the true SNP genotypes by 5 to 12% and an increase in the accuracy of breeding values estimation by 3 to 6% depending on the number of SNPs in the low cost chips and number of animals genotyped.

Key Words: low-cost chip, SNP, GBV

40 An approach to predict and manage Mendelian sampling variation based on dense SNP data. G. Abdel-Azim*, *Genex Cooperative Inc., Shawano, WI.*

An approach to predict the variance of Mendelian sampling (MS) in future progeny, based on high density SNP marker genotypes of pre-selected parents, is introduced. Simple formulas have been derived to calculate the variance of MS for each SNP marker according to their natural segregation from parents to offspring; pre-estimated SNP effects, and population allele frequencies were utilized. The total variance of MS was obtained as the sum of single MS variances predicted from each SNP. Formulas were validated for theoretical accuracy by simulation. In addition, variability across families was studied and found to be generally sufficient for selection. Comparing variances of MS in future progeny has many applications in genetics. One obvious application is selective genotyping to reduce cost. Another application is management of genetic variability in future progeny of pre-selected parents. A stochastic simulation of 200 sires and 200 dams with 10,000 SNP markers was run a 100 times. The simulation showed a correlation of up to 0.68 between marker-predicted MS variance and realized within-family absolute deviations. The correlation increased from 0.21 to 0.68 with increasing full-sib family size from 1 to 40. A 19% average reduction in deviations from parent average was possible by selecting the bottom 10% of candidate parents for marker-predicted MS variance. Extending formulas to non additive genetic variation and application to multiple traits add extra benefit to the current approach.

Key Words: genetic variation, high density SNP, Mendelian sampling

41 Selection of SNPs for an optimal low-density assay for genomic prediction of transmitting abilities. A. Vazquez*, G. de los Campos, K. A. Weigel, G. J. M. Rosa, and D. Gianola, *University of Wisconsin, Madison*.

A 50K single nucleotide polymorphism (SNP) bovine chip seems to predict transmitting abilities (PTAs) of young dairy sires effectively. However, the cost of the assay may limit its use in commercial herds. A low-cost chip with a subset of informative SNPs may be useful for evaluating young males and females. This study: (a) evaluated different strategies for selecting subsets of SNPs; and (b) quantified the predictive ability of chips of different sizes. Data were from the USDA and consisted of SNP genotypes (32,518 SNPs, after editing) and progeny-test PTAs for 4,783 sires. A training set (sires born before 1998) was used to fit the models, and predictive ability was evaluated using bulls born between 1999 and 2003. SNP effects were estimated using the Bayesian LASSO. First, "full models" (32,518 SNPs) were fitted to PTAs of net merit (NM), productive life (PL), fat (F), and protein (P). Three selection strategies were evaluated: (1) top SNPs (Top) selected based on the absolute value of their estimated effects on the full model for the corresponding trait; (2) top SNPs chosen based on the absolute value of their estimated effects on the full model for NM (TopNM); and (3) SNPs evenly spaced (ES) along the chromosomes. TopNM and ES yield the same chip for all traits, while other Top chips are trait-specific. For each selection strategy, different chip sizes were evaluated (300, 500, 750, 1000, 1250, 1500 and 2000 SNPs), and predictive ability was assessed via the correlation between genomic PTAs and progeny test PTAs in the testing set. Full models had the best predictive ability. Among models based on subsets of SNPs, predictive ability increased with assay size for all traits; however, benefits of going from 1,000 to 2,000 SNPs were relatively small. Pre-selecting SNPs either with Top or TopNM increased predictive ability relative to ES, however the difference diminished as the size of the chip increased. The TopNM chip with 1500 SNPs achieved correlations between progeny test and genomic PTAs of 0.56, 0.61, 0.60, 0.63, which represent about 90% of those of the full model for NM, PL, F and P, respectively.

Key Words: feature selection, genomic PTAs, low density chip

42 Transcriptional profiling during fetal skeletal muscle development of Piau and commercial pigs. B. P. Sollero*[1,2], V. D. Rilington[1], R. J. Tempelman[1], S. E. F. Guimarães[2], J. D. Guimarães[2], M. S. Lopes[2], N. E. Raney[1], J. P. Steibel[1], and C. W. Ernst[1], [1]*Michigan State University, East Lansing*, [2]*Federal University of Viçosa, Viçosa, MG, Brazil*.

Mammalian myogenesis and prenatal skeletal muscle fiber formation are under genetic control. However, little is known about the genes involved in this process or how differences in genotype affect gene expression. The aim of this study was to identify differentially expressed genes in *longissimus dorsi* (LD) of pigs at 40 and 70 d of gestation (stages encompassing the transition from primary to secondary fiber formation) in U.S. commercial crossbred pigs (Yorkshire × Landrace) and Brazilian native Piau pigs. Total RNA was isolated from fetuses obtained from gilts at each gestational age (n=3 commercial gilts; n=4 Piau gilts) and RNA from 3 fetuses per litter was pooled. Transcriptional profiling was performed using the Pigoligoarray (www.pigoligoarray.org) comprised of 20,400 70-mer oligos. Thirteen slides were screened using the Amino Allyl MessageAmp II aRNA Kit (Ambion), and Cy3 and Cy5 dyes. Fluorescence intensity data was LOESS normalized and analyzed with a mixed model using SAS. A total of 937 unique genes with Human Gene Nomenclature (HGNC) annotation were differentially expressed (false discovery rate, FDR < 0.05) between 40 and 70 d gestation in either commercial or Piau pigs. Interestingly, only 226 (24%) of these genes were common to the two breed types, whereas 422 (45%) were preferential to the Piau breed and 270 (29%) were preferential to the commercial pigs. The remaining 19 genes (2%) had multiple oligos on the array for which different oligos were differentially expressed in each breed. Among the 226 genes, most exhibited similar fold-changes between the two ages in each breed. However, a few genes exhibited much greater differences in one breed including DYSFIP1 and NRAP with higher abundance in 40 d Piau fetuses (5.2- vs. 2.6-fold and 4.7- vs. 2.0-fold, respectively), and CA3, FABP4 and GRN with higher abundance in 40 d commercial fetuses (12.2- vs. 5.5-fold, 9.0- vs. 4.0-fold and 3.8- vs.

1.8-fold, respectively). This study reveals transcriptional profiles in LD at 40 and 70 d gestation for commercial and Piau pigs, which helps elucidate phenotypic differences between these breed types.

Key Words: myogenesis, microarray, skeletal muscle

43 Extent of linkage disequilibrium in purebred and crossbred beef cattle. D. Lu*[1], M. Sargolzaei[1], M. Kelly[1], G. Vander Voort[1], Z. Wang[2], J. Mah[2], G. Plastow[2], S. Moore[2], and S. Miller[1], [1]*University of Guelph, Guelph, Ontario, Canada*, [2]*University of Alberta, Edmonton, Alberta, Canada*.

Knowledge of linkage disequilibrium (LD) is important in genomic selection, QTL mapping and single nucleotide polymorphism (SNP) chip design. Knowledge of LD in crossbred beef cattle is limited. The objective of this study was to understand the extent of LD and persistence of LD phase in beef cattle. 56,947 SNP were genotyped (38,745 used) across 29 chromosomes of 60 Angus (AN), 43 Piedmontese (PI) bulls, and 400 crossbred beef cattle. Average distance between adjacent SNP was 60kb. The squared correlation of the alleles at 2 loci (r^2) and r were used to measure LD and phase persistence, respectively. Pattern of LD across the genome was investigated using the sliding window approach. Average LD within a given sized window was calculated as it slid along the chromosome. Amount of LD decreased rapidly from 0.31 to 0.22 to 0.15 when the distance range between markers changed from 0-30kb to 30-60kb and then to 60-100kb, respectively. The effect of distance between markers, breeds, and chromosomes on LD decay was tested using least squares. Breeds and chromosomes had significant effects ($P<0.001$) on LD decay. There were significant interactions between distance and chromosomes ($P<0.001$) as well as between breeds and chromosomes ($P<0.05$). There existed 1Mb-regions of consistently high LD ($r^2>0.3$) on chromosomes 1, 4, 5, 7, 9, 14, 16, 19 in purebred and crossbred animals. Correlations of LD phase were high between crossbred animals and either AN or PI (0.82), and between AN and PI (0.78) in 60kb-regions. These dropped when the regions expanded. The marker density in this study should be sufficient for accurate genomic selection within breed when LD of 0.2 between marker and QTL is required. High LD chromosomal segments should be investigated further. Marker effect estimates across breed may not be similar due to observed change in LD phase.

Key Words: linkage disequilibrium, linkage phase, single nucleotide polymorphism

44 Construction of LD maps for SNPs linked to susceptibility loci. L. Gomez-Raya*, *University of Nevada*, *Reno*.

The extension of linkage disequilibrium (LD) in human and animal genomes allows linkage disequilibrium mapping without requiring a family structure. The objective of this study was the construction of a maximum likelihood model for LD mapping in which only estimates of a disequilibrium parameter and penetrances (Ψ_{TT} ; Ψ_{Tt} ; and Ψ_{tt} ; where Ψ_i =probability of developing the disease given the i-th genotype) corresponding to the three genotypes at a susceptibility locus (T/t) are estimated. A second objective was to carry out a MonteCarlo computer simulation to test if the novel maximum likelihood method can provide unbiased estimates of the linkage disequilibrium parameter and penetrances. It is shown that all disequilibria between a pair of alleles at two loci can be put in terms of allele frequencies and a single disequilibrium parameter, which allows the construction of maximum likelihood equations. Montecarlo computer results are presented for a variety of scenarios regarding number of individuals, linkage disequilibrium parameter and penetrances for the three genotypes. For example, a population was simulated with 200 individuals, an incidence of disease of 30% and frequencies of 0.5 for both the susceptibility allele and the SNP alleles. The simulated disequilibrium parameter was 0.125 (50% of the maximum possible disequilibrium). Penetrances were Ψ_{TT} =0.60; Ψ_{Tt}=0.20 ; and Ψ_{tt} =0.20. The average of the disequilibrium parameter over 1500 replicates was 0.132 (SD=0.048). The averages of estimates of penetrances over replicates were Ψ_{TT} =0.62 (SD=0.17); Ψ_{Tt}=0.20 (SD=0.13); and Ψ_{tt} =0.19 (SD=0.12). Empirical statistical power was 0.77 at a significance level of 0.05. The results suggest some confounding in the estimation of the disequilibrium parameter and penetrances which may lead to bias in the estimation of the linkage disequilibrium parameter. The proposed maximum likelihood method is suitable for fine LD mapping since it allows estimation of a single disequilibrium parameter for each of a number of SNPs in a chromosomal fragment where a susceptibility locus has been mapped.

Key Words: linkage disequilibrium, SNP, genetic mapping

45 Characterization of a whole-genome map of single nucleotide polymorphisms applied to two selection lines in British dairy cattle. G. Banos*[1] and M. P. Coffey[2], [1]*Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece*, [2]*Sustainable Livestock Systems, Scottish Agricultural College, Edinburgh, Scotland, UK*.

The objective was to study genotyping results from the bovine 50K SNP chip and assess the extent of Linkage Disequilibrium (LD) in two divergent selection lines. DNA extracted from 299 Holstein cows was used to determine genotypes in 54,001 SNP loci with the Illumina BovineSNP50 array. These animals were from two selection experiment lines (166 genetically selected vs. 133 control) raised on the Scottish Agricultural College research farm. Data edits removed loci with a major allele frequency greater than 0.95, call rate less than 65% and missing valid chromosomal assignment or position. The Hardy-Weinberg equilibrium (HWE) state was assessed in each locus with a chi-square test. Pairwise haplotypes were determined using parsimony. LD values were calculated both within and across selection lines for all possible syntenic SNP pairs within 1 Mb as the squared correlation between alleles at two loci. After edits, 41,859 loci (78% of the original total) were kept for analysis. There were, on average, 17.5 SNP per Mb with the highest concentrations on chromosomes 1, 2 and 4. The majority (96%) of the loci were in HWE ($P>0.05$). Observed heterozygosity levels were very close to theoretical expectation. The average LD calculated across all chromosomes was 0.0691, 0.0705 and 0.0746 for all, control and selected line cows, respectively. LD was not uniformly distributed across regions. Looking at adjacent SNP, overall average distance was 0.063 Mb and average LD 0.125 in the three datasets. Of all SNP pairs studied, 6.7-12.8% were in LD greater than 0.30, which is considered the minimum useful for mapping purposes and genomic selection. A few SNP loci pairs (844, 984 and 1070 in the three datasets) were found in nearly perfect (>0.99) LD, suggesting that genotyping only one of them would be sufficient. The overall product-moment correlation of LD values calculated within the control and selected lines was 0.79 ($P<0.001$), ranging from 0.71 to 0.84 for different chromosomes. Results suggest that genetic selection has influenced the LD level in the studied population. Results can be used to support gene detection and genomic prediction studies.

46 Evaluation of supplemental dried bovine colostrum in milk replacer fed dairy calves. V. Bielmann*, T. J. DeVries, S. J. LeBlanc, K. Lissemore, and K. E. Leslie, *University of Guelph*, *Guelph, Ontario, Canada*.

Supplementing neonatal calves with immunoglobulins (Ig) in the diet may enhance local immunity in the gut. The goal of this study was to evaluate feeding supplemental IgG on health and growth in pre-weaned dairy calves. Calves (61 bulls and 59 heifers) housed in individual pens in a calf barn were randomly assigned to receive 0 (control), 5g, or 10g of IgG per feeding from dried bovine colostrum, added twice daily for 14 d into a 22% protein 17% fat milk replacer, adjusted to provide similar total protein and fat intakes among groups. Serum samples were collected at d 1 of age to determine passive transfer and again at 11-14 d of age. Mean IgG levels at d 1 were 23± 8.4g/L and were similar among groups (P = 0.36); serum IgG at 2 weeks of age was 17 ± 6.0g/L and were similar among groups (P=0.33). Calves were weighed weekly and intakes were measured daily until weaning at 45 d of age. Average daily gain (ADG) over the 6 week period was 0.63, 0.67 and 0.65 kg/d in the control, 5g, and 10 g groups, respectively (P = 0.45). Fecal scores (0 - 3) were recorded weekly for 6 weeks with fecal samples collected at 7-13 d, 14-20 d and 21-28 d of age. The prevalence of scours (fecal score &ge#2) at 7-13 d was 36%, 34%, and 32% (P=0.95) in the control, 5g, and 10 g groups, respectively, and at 14-20 d was 39%, 30% and 35% (P = 0.75). BioX™ test strips were used to measure fecal shedding of *Cryptosporidium parvum*, rotavirus, coronavirus and *E. coli* K99. The prevalence of shedding of *C. parvum* at 7-13 d was 28%, 33% and 25% (P = 0.76) in the control, 5g, and 10 g groups, respectively, and at 14-20 d was 35%, 23% and 22%, respectively (P = 0.35). At 21-28 d the prevalence of fecal shedding of rotavirus was 14%, 18%, 14% (P = 0.84) in the control, 5g, and 10 g groups, respectively. Under the conditions of this pilot study, no associations were detected between treatment groups in ADG, fecal scores and the prevalence of pathogens being shed in pre-weaned calves. Consistent numerical differences may indicate the need for further research to determine if the addition of Ig plays a role in providing a local immunological effect under conditions of greater exposure.

Key Words: dried bovine colostrum, IgG, calves

47 Feeding anionic salts in the prefresh period, the addition of sodium bicarbonate to colostrum replacer and their effects on IgG absorption in the neonate. K. M. Morrill*, S. P. Marston, N. L. Whitehouse, and P. S. Erickson, *University of New Hampshire*, *Durham*.

The objective of this experiment was to determine if feeding anionic salts to Holstein cows pre-partum affected their calf 's ability to obtain passive transfer, and if adding sodium bicarbonate to colostrum replacer would increase the efficiency of IgG absorption in these calves. Forty Holstein cows and their calves were assigned to a 2 × 2 factorial arrangement of treatments in a randomized complete block design based on expected date of calving. Three weeks prior to projected due date, cows were placed on one of two diets: a ration without anionic salts (+77 meq/kg), or a ration with anionic salts (-100 meq/kg). Urine pH and DMI were lower for cows receiving anionic salts, as compared to cows not receiving anionic salts. At calving, calves received a commercially available colostrum replacer with or without supplemental sodium bicarbonate (19.75 g/dose). One dose of colostrum replacer was fed within 45 minutes of birth and one half dose was fed at 6 h of age for a total of 198 g IgG. Calves received milk replacer at 12, 24, 36 and 48 h. Blood samples were taken from calves prior to feeding at 0, 6, 12, 24 and 48 h and analyzed for serum IgG concentration. Calves born from dams receiving anionic salts had similar serum IgG concentrations (14.4 vs. 15.1 g/L) and 24 h apparent efficiency of absorption (28.2 vs. 29.2%) to calves born from dams that did not receive anionic salts. Calves receiving supplemental sodium bicarbonate added to colostrum replacer had higher serum IgG concentrations at 12 (14.4 vs. 12.0 g/L), 24 (16.3 vs. 13.2 g/L) and 48 h (14.6 vs. 11.2 g/L) and higher 24 h apparent efficiency of absorption (31.2 vs. 26.1%) as compared to calves that did not receive supplemental sodium bicarbonate in colostrum replacer. Of the forty calves on the study, 90% obtained successful passive transfer (serum IgG concentration > 10 mg/ml).

Key Words: anionic salts, sodium bicarbonate, colostrum replacer

48 Intramammary infections in pasture-based dairy cows supplemented with barium selenate before calving. A. Ceballos*[1], J. Kruze[2], I. R. Dohoo[1], J. Sanchez[3], H. W. Barkema[4], J. J. Wichtel[1], and F. Wittwer[5], [1]*Centre for Veterinary Epidemiologic Research, University of Prince Edward Island*, *Charlottetown, Prince Edward Island, Canada*, [2]*Institute of Microbiology, Universidad Austral de Chile*, *Valdivia, Chile*, [3]*Canadian Food and Inspection Agency*, *Charlottetown, Prince Edward Island, Canada*, [4]*Department of Production Animal Health, University of Calgary*, *Calgary, Alberta, Canada*, [5]*Institute of Veterinary Clinical Sciences, Universidad Austral de Chile*, *Valdivia, Chile*.

Sub-optimal selenium (Se) intake has been associated to several diseases (eg. mastitis). The objective was to evaluate the effect of single Se supplementation before calving on the incidence risk of intramammary infection (IMI) and incidence rate of new IMI, and on milk somatic cell count (SCC) in pasture-based dairy cows. Forty-nine Holstein-Friesian cows were fed a suboptimal Se diet (<0.05 ppm DM). Cows were divided in two groups; supplemented cows (n=24) received a single injection of barium selenate (1 mL/50 kg BW; Deposel®, Novartis. NZ) approx. 60 days prior to calving, control group (n=25) remained unsupplemented. Duplicate foremilk samples were collected within 6 days after calving, and every 2 weeks until drying-off for bacteriological culture. Composite milk samples were collected monthly to evaluate SCC. Se status was established through the blood glutathione peroxidase (GPx) activity from samples collected at the beginning of the trial, and 30, 90, 180 and 270 DIM. Data were analyzed using linear, logistic, and Poisson mixed models. The mean of blood GPx activity was higher for supplemented cows than for unsupplemented ones (P<0.05). In total 4136 milk samples were submitted for culturing, 17 (0.4%) were culture-positive at calving, and 1028 (24.9%) were positive during lactation. Cor. bovis, CNS, and Staph. aureus were mostly isolated pathogens. A trend towards a higher risk of IMI during lactation was observed in supplemented cows (OR: 2.52; 95% IC: 0.78, 8.11) (P=0.12). The OR for specific-pathogen IMI was not affected by Se supplementation (P>0.05). The overall IR of new IMI per quarter-time (14-day interval) at risk was not affected by Se supplementation (IR: 1.40; 95% CI: 0.90, 2.17) (P=0.14). The geometric mean of SCC increased from 29,260 cells/mL (30 DIM) to 148,240 cells/mL at drying-off (P<0.05), not affected by Se supplementation itself (P>0.05). These results indicated that Se supplementation before calving in pasture-based dairy cows resulted in higher blood activity of GPx. Nevertheless, the difference in Se status was not associated with significant changes either IMI or SCC pattern.

Key Words: supplementation, selenium, intramammary infection

49 Prevalence, risk factors, and impact of postpartum uterine diseases in dairy cows. J. Dubuc*, T. F. Duffield, K. E. Leslie, J. S. Walton, and S. J. LeBlanc, [1]*Population Medicine, University of Guelph, Guelph, Ontario, Canada*, [2]*Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada*.

The objectives of this study were to determine the prevalence, to identify risk factors for, and to quantify the impact on pregnancy risk of postpartum metritis and endometritis in dairy cows. Data were available for 1273 Holstein cows from 3 herds. Calving history, periparturient disease incidence, and body condition score at calving were recorded. During the week prior to expected calving, serum NEFA were measured. At 4, 11, and 18 (± 3.5) DIM, serum BHB, NEFA and haptoglobin were measured. Metritis (MET) was defined as both rectal temperature ≥ 39.5 C and a foul-smelling discharge occurring ≤ 11 DIM; clinical endometritis (CE) as mucopurulent or purulent discharge in the vagina (Metricheck device); and subclinical endometritis (SCE) as ≥ 9% neutrophils (cytobrush technique). All cows were examined for CE and SCE at 35 DIM. The probability of MET, CE, and SCE were analyzed using multivariable logistic regression models; their incidences were 9%, 17%, and 18%, respectively. Cows experiencing retained placenta had greater risk of developing uterine diseases (OR: MET=11.0; CE=2.2; SCE=2.6; P < 0.01). Cows having serum haptoglobin level ≥ 1.0 g/L during the first week postpartum were 2.8 times more likely to develop MET (P < 0.03). Cows experiencing MET were 2.8 and 2.4 times more likely to develop CE and SCE (P < 0.01). Cows experiencing CE were 3.0 times more likely to be diagnosed with SCE (P < 0.01), but among animals with CE, only 42% were diagnosed with SCE at the same time. Cows experiencing at least one of MET, CE, or SCE were 2.1 times less likely to become pregnant at first breeding (P = 0.02). Compared to unaffected cows, pregnancy at first AI was lower in cows with CE (21 vs. 28%, P = 0.04) or with SCE (15 vs. 26%, P < 0.01). Although MET, CE, and SCE are strongly associated with each other they appear to be somewhat distinct manifestations of the interactions between uterine pathogens and the immune response of the cow.

Key Words: dairy cow, uterine disease, metritis

50 Effects of level of concentrate supplementation on milk production and ruminal pH in lactating cows on pasture. G. R. Clevenger*, L. R. Tager, and K. M. Krause, *West Virginia University*, *Morgantown*.

Six ruminally cannulated lactating Holstein dairy cows were used in Latin rectangle design to evaluate the effects of varying levels of concentrate supplementation on milk production and ruminal fermentation. Cows were allowed access to 14 kg DM/cow/d of pasture containing: 31.2% ADF, 44.5% NDF, 15.7% CP and 2.9% fat. Cows were fed a concentrate supplement consisting of (DM basis): 75.18% ground corn grain, 18.02% soybean meal, 3.0% sugarcane molasses, 2.0% hydrolyzed feather meal, 0.6% limestone, 0.5% salt, 0.4% vitamin premix, and 0.3% calcium diphosphate. The treatments were: C4 (4 kg concentrate/d), C8 (8 kg concentrate/d) and C12 (12 kg concentrate/d), on a DM basis. Cows were fed twice daily after milking. Concentrate DM intake was greater in C8 (6.4 kg; *P = 0.04*) and C12 (8.4 kg; *P < 0.003*) compared to C4 (3.5 kg), with no difference between C8 and C12. Milk yield was lower in C4 (19.9 kg/day) compared with C12 (22.7 kg/day; *P < 0.02*). Daily fat and lactose production were less in C4 (0.66 kg and 0 .85 kg, respectively) compared to C8 (0.8 kg; *P < 0.03* and 0 .98 kg; *P = 0.03*, respectively) and C12 (0.82 kg; *P = 0.02* and 1.03 kg; *P = 0.01*, respectively), but % milk fat was similar for C4, C8 and C12 (3.4%, 3.7%, and 3.7%, respectively) as was % milk protein (2.8%, 2.8%, and 2.8% for C4, C8, and C12, respectively). Continuous ruminal pH data was collected during the last 4 days of sampling. Daily mean ruminal pH was similar for C4, C8, and C12 (6.37, 6.27, and 6.27, respectively) as was daily minimum pH (5.86, 5.75, and 5.74 for C4, C8, and C12, respectively). Time spent below pH 5.8 increased linearly (*P = 0.007*; 27.1, 71.2, and 162.4 min/d for C4, C8, and C12, respectively) and daily number of bouts of pH below 5.8 tended (*P = 0.09*) to increase linearly with increasing level of supplementation (1.0, 4.4, and 7.5 bouts/d for C4, C8, and C12, respectively). Although increasing levels of supplementation will increase milk production of cows on pasture it might also affect ruminal fermentation.

Key Words: pasture, supplementation, ruminal pH

51 Use of in vitro and in vivo tests to characterize gastrointestinal nematode anthelmintic resistance on sheep and goat farms in the mid-Atlantic U.S. E. K. Crook*[1], D. J. O'Brien[1], N. C. Whitley[2], R. M. Kaplan[3], and J. M. Burke[4], [1]*Delaware State University*, *Dover*, [2]*North Carolina A&T State University*, *Greensboro*, [3]*University of Georgia*, *Athens*, [4]*USDA, ARS*, *Booneville, AR*.

DrenchRite® Larval Development Assays (LDA) and fecal egg count reduction tests (FECRT) were used to evaluate anthelmintic resistance of gastrointestinal nematodes in 4 sheep (Farms A, B, D, and E) and 5 goat (C, F, G, H, and I) farms in the mid–Atlantic U.S. Fecal samples were collected rectally from individual animals and pooled for LDA to determine potential gastrointestinal nematode resistance to benzimidazole (BZ), moxidectin (MOX), ivermectin (IVM), and levamisole (LEV). To validate results, at the time of fecal collection for LDA, FECRT were conducted on each farm using anthelmintics determined based upon prior anthelmintic use by individual farms. Anthelmintics tested included BZ (n = 5 farms), MOX (n = 6 farms), IVM (n = 3 farms), and LEV (n = 5 farms) with a minimum of 10 animals per anthelmintic and 10 untreated control animals included in each test. An anthelmintic was considered effective for FECRT when gastrointestinal nematode fecal egg counts were reduced by ≥ 95% 7 to 14 d after treatment. Based on LDA results, all farms (5/5) tested were resistant to BZ. A low level of resistance to MOX was noted for 2/5 goat (Farms G and F) and 1/4 sheep farms (Farm B) and resistance to MOX was found on 1/5 goat (Farm I) and 2/4 sheep farms (Farms A and E). All goat farms (5/5) and 3/4 sheep farms tested were resistant to IVM (Farms A, B, and E). The LDA further indicated that while all goat farms tested were susceptible to LEV, 1/4 sheep farms (Farm G) had suspected resistance to LEV. The FECRT validated results of LDA with the exception of one farm (H) in which BZ susceptibility by LDA was not confirmed with results from the FECRT. Overall, similar to what has been seen in other areas of the U.S., anthelmintic resistance is a problem in sheep and goat farms in the Mid–Atlantic region of the U.S. with FECRT and LDA both supporting this conclusion.

Key Words: FECRT, LDA, small ruminant

52 Effects of cinnamaldehyde, eugenol, and capsicum on rumen fermentation in continuous culture. L. R. Tager* and K. M. Krause, *West Virginia University*, *Morgantown*.

A 12-unit continuous culture system was used in a complete randomized design to study the effects of cinnamaldehyde (CIN), eugenol

(EUG), and capsicum (CAP) fed with a 45:55 forage:concentrate ratio (DM basis) ration on rumen fermentation. Treatments, including a control (CON), were replicated 3 times over 10 days with 7 days equilibration and 3 days sampling. Essential oils were supplemented at a dosage of 500 mg/L rumen fluid per d. Inoculum was obtained from 2 ruminally cannulated, lactating Holstein dairy cows receiving a 45:55 forage:concentrate ratio (DM basis). Dry matter digestibility did not differ among treatments (P = 0.97). Organic matter digestibility tended to be lowest in CIN (36.4%; P = 0.06). Digestibility of NDF was highest (37.8%; P = 0.04), and ADF digestibility tended to be highest (46.1%; P = 0.08), in CAP. Crude protein digestibility was lower in CIN and EUG (44.7% and 49.4%) than in CAP and CON (64.4% and 60.8%; P = 0.01). Bacterial nitrogen flow was lower in CIN and EUG (1.1 and 1.2 g/d) than CAP and CON (1.6 and 1.6 g/d; P < 0.01). Efficiency of microbial protein synthesis in CIN tended to be lower (34.6 g bacterial N/kg digested OM; P = 0.06) than CON and CAP (40.2 and 39.8 g bacterial N/kg digested OM). Effluent ammonia N tended to be higher in CIN than CON (3.7 vs. 2.5 mg/dL; P = 0.06). Total VFA production was unaffected by EO (P = 0.16). Supplementation with EUG caused lower production of propionate (103.9 mM/d; P < 0.01), higher production of butyrate (59.3 mM/d; P < 0.01), and the highest acetate:propionate (1.6; P = 0.02) compared to other treatments. Isovalerate production tended to be highest in CAP (1.5 mM/d; P = 0.10). Fermenters with CIN or EUG had higher mean pH than CAP and CON (5.9 vs. 5.7; P < 0.01), spent fewer hr/d (2.0 and 0.9 vs. 9.6 and 10.5; P < 0.01), and had smaller area under the curve (0.1 and 0.1 vs. 0.9 and 1.0; P < 0.01) at pH < 5.6. Supplementation with CIN or EUG at high dosages may be unfavorable to rumen efficiency.

Key Words: dairy nutrition, essential oil, continuous culture

Graduate Student Paper Competition-CSAS Oral Competition: CSAS Graduate Student Competition 1

53 Plant-based diets enriched with linseed oil or marine algae and organic selenium modify sperm fertility parameters in broiler breeders over the reproductive cycle. C. Coss*[1,2], C. Brèque[1,2], R. Gervais[2], C. Lessard[1,2], D. Venne[3], M. R. Lefrançois[2], P. Y. Chouinard[2], G. Vandenberg[2], and J. L. Bailey[1,2], [1]*Centre de recherche en biologie de la reproduction, Québec, QC, Canada*, [2]*Département des sciences animales,Université Laval, Québec, QC, Canada*, [3]*Couvoir Scott Ltée, Scott Jonction, QC, Canada*.

There are indications that plant-based diets and organic (org) Se alter fertility in broiler breeders. We hypothesised that supplementing plant-based diets with n-3 fatty acids (FA), org Se, and vitamin (vit) E improves male reproductive parameters. Individually caged, 23 week old Ross broiler breeders were fed 8 diets (n=15/diet). The control diet contained meat meal + 50 IU/kg vit E, while the others were plant-based: 2.3% of soya oil (rich in C18 n-6 FA) + 50 IU/kg vit E, 2.3% of soya oil + 100 IU/kg vit E, 2.3% of soya oil + 100 IU/kg vit E + 0.3 ppm org Se, 2.3% of linseed oil (rich in C18 n-3 FA) + 100 IU/kg vit E, 2.3% of linseed oil + 100 IU/kg vit E + 0.3 ppm org Se , 2.2% soya oil + 1% of marine algae (42% oil, rich in C22 n-3 FA) + 100 IU/kg vit E, and 2.2% soya oil + 1% of marine algae + 100 IU/kg vit E + 0.3 ppm org Se. Diets were isoproteic and isoenergetic. After 7, 13, and 25 weeks of feeding (corresponding to 33, 38, and 50 weeks of age), semen was evaluated. Data were analysed as a completely randomized design using the SAS MIXED procedure. The Sperm Chromatin Structure Assay showed that the DNA Fragmentation Index (DFI), which reflects the % of sperm with weakened chromatin, increased from 33 to 50 weeks of age for the group fed soya oil + 50 IU/kg vit E (P<0.05), while no effect was observed for the other dietary treatments. DFI standard deviation increased with age (P<0.05). Sperm viability (LIVE/DEAD® assay by flow cytometry) decreased with age (P<0.05). Computer Assisted Sperm Analysis revealed that various parameters increased with age (motility, progressive motility, elongation; P<0.05), whereas others decreased (straightness, linearity; P<0.05). These results show that aging had an effect on fertility parameters, whereas dietary treatments had little or no effect.

Key Words: broiler breeder, sperm, omega-3

54 The effect of two calving seasons on cow and calf performance in western Canada. L. C. Girardin*[1], H. A. Lardner[2], A. D. Iwaasa[3], S. L. Scott[4], and S. H. Hendrick[1], [1]*University of Saskatchewan, Saskatoon, SK, Canada*, [2]*Western Beef Development Centre, Lanigan, SK, Canada*, [3]*Agriculture and Agri-Food Canada - Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada*, [4]*Agriculture and Agri-Food Canada - Brandon Research Centre, Brandon, MB, Canada*.

A 2-yr study was conducted to evaluate the effects of calving season on cow and calf performance. Two calving seasons, Early (March) vs. Late (June), were compared at 3 locations, Lanigan, Saskatchewan (LA), Swift Current (SC), Saskatchewan, and Brandon (BR) Manitoba. One-hundred crossbred cows at LA, 50 crossbred cows at SC and 120 crossbred cows at BR were randomly allocated to 1 of 2 replicated (n=2) calving seasons. Experimental design was a randomized complete block, analyzed using PROC MIXED repeated measures. Cow body weights and condition scores (5-pt scale [1=thin, 5=fat]) were taken at calving, breeding and weaning. Calf body weights were taken at birth, 60 d of age and weaning (205 d). Pregnancy and weaning rates were based on the number of cows exposed at breeding. At BR, cow body weights were not different (P>0.05) between calving seasons, however rump fat of Early-calving cows was greater (P<0.05) than Late-calving cows. Cow body condition at weaning at SC was lower (P<0.05) for Early-calving cows than Late-calving cows. Cow body condition at calving at LA was greater (P<0.05) for Late-calving cows as compared to Early-calving cows. At all locations, birth weights were numerically lower for Early-born calves compared to Late-born calves. Weaning weights were lower (P<0.05) for Late-born calves compared to Early-born calves at all locations (BR, 253 vs. 287 kg(SE=8.58); SC, 239 vs. 270 kg(SE=13.42); LA, 228 vs. 260 kg(SE=7.24)). Calf growth from birth to weaning at BR (SE=0.07), SC (SE=0.06) and LA (SE=0.03) for Early-born and Late-born calves was 1.18, 1.13, 1.09 kg d^{-1} and 0.99, 0.95, 0.91 kg d^{-1}, respectively. Neither weaning rate nor pregnancy rate was affected by calving season or location. Results indicate that calving season impacts cow performance differently depending on location and may impact calf weaning weights.

Key Words: calving season, beef cattle, reproductive traits

55 Evaluation of swine group-housing systems for breed-to-wean herds using a sow investment model. M. A. Fynn*, N. J. Lewis, M. L. Connor, and G. V. Johnson, *University of Manitoba*, *Winnipeg, MB, Canada*.

With the current trend in the North American swine industry to move away from the use of gestation crates, group-housing systems for gestating sows need careful investigation. The objective of this study was to compare two group-housing systems – one a partial-slatted concrete-floor system (conventional) and the other a straw-based solid-floor system (alternative) – for sows in breed-to-wean operations taking into consideration both animal well-being and economic profitability. Experimental data was collected between March 2006 and March 2009 from two genetically-identical breed-to-wean herds in southern Manitoba. A sample representing average breeding gilts was selected from each barn – 63 in the conventional and 62 in the alternative – with data being collected throughout their productive lives at breeding, 30-days post-breeding, farrowing, weaning, and prior to culling. A dynamic programming model was built using sow condition and production data to determine optimal replacement criteria for breeding sows in each respective housing system. The model used a profit function that optimizes the present value of net revenues. Inherent to this model was the identification of a sow production function. The profit function was estimated using regression analysis, and culling data was analyzed by chi-square analysis. All data analysis was performed in SAS. Production in the alternative system had a higher trend, suggesting increased revenues, as compared to the conventional system. Further, sows in the conventional system were found to be subjected to higher risk of involuntary culling in the first 3 parities than sows in the alternative system (P<0.05) implying improved longevity in the straw-based system. This finding is important since longevity has been shown to be a good indicator of animal well-being. This study suggests that the alternative system favours both higher welfare for the animals and higher production for the farmers. However, a similar model detailing costs for the entire breed-to-wean operation needs to be developed to fully assess the economics.

Key Words: economic, sow replacement, housing

56 Effect of ruminal protozoa on urea-nitrogen recycling in growing lambs fed varying dietary protein concentrations. D. Kiran* and T. Mutsvangwa, *University of Saskatchewan*, *Saskatoon, SK, Canada*.

The objectives were to examine the effects of ruminal protozoa and level of dietary crude protein (CP) on urea-N recycling to the gastrointestinal tract (GIT), microbial protein synthesis and N balance in growing lambs. Four Suffolk ram lambs (43.9 ± 1.4 kg BW) were used in a 4 × 4 Latin square design with 28-d periods and a 2 × 2 factorial arrangement of treatments. Treatments were: 1) partial defaunation vs. faunation; and 2) 10% (LOW) vs. 15% (HIGH) dietary CP (DM basis). Partial defaunation refers to substantial decreases (up to 85%) in ruminal protozoal counts. Linoleic acid-rich sunflower oil was fed (6% of DM) as an anti-protozoal agent. Nitrogen balance was measured from d 22 to d 26, with concurrent measurements of urea-N kinetics using continuous intra-jugular infusions of [$^{15}N^{15}N$]-urea. There were only minor interactions between ruminal protozoal status and level of dietary CP. Feeding sunflower oil decreased (P < 0.01) total protozoal counts by 85%, and this was accompanied by a decrease (P < 0.01) in ruminal NH_3-N concentrations. Intake of N was lower (P = 0.04), and N retention (as a % of N intake) was higher (P = 0.05) in partially-defaunated compared to faunated lambs. Endogenous production of urea-N (UER; 26.1 vs. 34.6 g/d) and urea-N loss in urine (UUE; 10.1 vs. 15.7 g/d) were lower (P < 0.01), and urea-N entering the GIT (GER; 16.0 vs. 18.9 g/d) tended to be lower (P = 0.06) in partially-defaunated compared to faunated lambs. However, as a proportion of UER, GER was higher (P < 0.01) and its anabolic use tended to be higher (P = 0.09) in partially-defaunated compared to faunated lambs. Partial defaunation increased (P < 0.01) microbial N supply. Endogenous production of urea-N (38.2 vs. 22.5 g/d), GER (20.8 vs. 14.2 g/d), and UUE (17.4 vs. 8.3 g/d) were higher (P < 0.01) in lambs fed the HIGH diet compared to those fed the LOW diet. However, as a proportion of UER, GER and its anabolic use were higher (P < 0.01) in lambs fed the LOW diet compared to those fed the HIGH diet. In summary, partial defaunation increased urea-N transfer to the GIT, while also increasing microbial N supply.

Key Words: dietary protein, ruminal protozoa, urea-N recycling

57 Comparison of NRC–2001 chemical approach with biological approach (in situ animal study) in the determination of digestible nutrients and energy values of dry distillers grains with solubles in ruminants. W. G. Nuez Ortin* and P. Yu, *University of Saskatchewan*, *Saskatoon, SK, Canada.*

Dry distillers grains with solubles (DDGS) are not natural but man–made feed products from bio–energy production. It is a question whether chemical approach (NRC–2001 formula), which was developed based on natural feeds, can accurately estimate energy values of different types of DDGS based on chemical composition. The objective of this study was to compare the NRC–2001 chemical approach with biological approach (in situ animal study) in the determination of digestible (DE3X) and metabolizable energy (ME3X) at a production level, net energy for lactation (NEL3X), net energy for maintenance (NEm), and net energy for gain (NEg) of DDGS. Corn DDGS, wheat DDGS and blend DDGS (70% wheat: 30% corn) from different batches were obtained during 2007 in Canada. In situ study was used to determine digestible nutrients (tdNFC, tdFA, tdCP, tdNDF) and total digestible nutrients (TDN1X), from which energy values were estimated. Statistical analyses were performed using the Mixed and Correlation procedures of SAS (version 9.1.3). Experimental design was a Completely Randomized Design. The results showed significant differences (P<0.001) in the estimation of energy values as well as nonsignificant correlation (P>0.05) between the NRC–2001 chemical and biological approach. The highest Pearson correlation coefficient found was 0.39 for NEL3X (P=0.229). Compared with the biological approach, NRC–2001 estimated lower values for TDN1x [TDN1x (NRC)–TDN1x (In situ)= –18.28% DM], DE3X (–0.672 Mcal/kg DM), ME3X (–0.679 Mcal/kg DM), NEL3X(–0.351 Mcal/kg DM), NEm (–0.475 Mcal/kg DM) and NEg (–0.392 Mcal/kg DM). Energy values of DDGS estimated by the biological approach are not predictable from the chemical approach. Thus, refinement of the NRC-2001 formula is needed in order to more accurately predict energy values in ruminants.

Key Words: energy values, dried distillers grains with solubles, NRC–2001 chemical approach

58 Effect of butyrate absorption on the severity of subacute ruminal acidosis. G. B Penner*[1], J. R. Aschenbach[2], G. Gäbel[2], and M. Oba[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Universität Leipzig*, *Leipzig, Germany*.

This study aimed to determine the effect of subacute ruminal acidosis (SARA) on the absorption of butyrate across the ruminal epithelia.

Twenty-four German Merino sheep (72.3 ± 10.1 kg of BW) individually housed and fed a hay diet were assigned to a glucose (GLU; n = 17) or control (CON, n = 7) treatment. The GLU was designed to induce SARA by administering an orally dosed glucose solution (2.2 *M*) to supply 5 g glucose/kg BW; whereas, CON sheep received and equal volume of water. Ruminal pH was measured continuously for 3-h following the oral dose. Sheep were euthanized and ruminal epithelia from the ventral sac were collected. Epithelia were mounted in Ussing chambers with separate mucosal and serosal solutions (pH 6.1 and 7.4, respectively). In vitro treatment included Ussing chamber solutions that contained bicarbonate or excluded bicarbonate. 1-^{14}C-butyrate was used to determine the apical uptake as a measure for butyrate import into the cell and the mucosal-to-serosal flux as an estimate of butyrate absorption. In vivo data were analyzed as a randomized complete block design and Ussing chamber data as a split-plot design. Means ± SEM are presented. Mean ruminal pH was lower (5.77 ± 0.06 vs. 6.67 ± 0.09; $P < 0.001$) and the severity of SARA, indicated by the area that pH < 5.8, was higher for GLU than CON sheep (27 ± 5.0 vs. 0 ± 7.8 pH × min/180 min; $P = 0.009$). Total butyrate uptake and flux were not affected by in vivo treatment averaging 10.23 nmol/mg protein/min and 2.83 µmol/cm^2/h, respectively. Bicarbonate-dependent butyrate uptake was lower ($P < 0.001$) than bicarbonate-independent uptake (3.06 ± 0.55 vs. 7.23 ± 0.55 nmol/mg protein/min) and bicarbonate-dependent butyrate flux was lower than bicarbonate-independent flux (1.25 ± 0.11 vs. 1.58 ± 0.11 µmol/cm^2/h; $P = 0.0497$). Total butyrate uptake and butyrate flux tended ($P \leq 0.088$) to be negatively related to the severity of ruminal acidosis ($r^2 = 0.133$ and 0.127, respectively) indicating that efficient absorption of butyrate may ameliorate the severity of SARA.

Key Words: butyrate, ruminal acdiosis, rumen pH

59 Comparison of wheat or corn dried distillers grains with solubles (DDGS) on performance and carcass characteristics of feedlot steers. L. J. Walter*[1], J. L. Aalhus[2], W. M. Robertson[2], T. A. McAllister[3], D. J. Gibb[3], M. E. R. Dugan[2], N. Aldai[2], and J. J. McKinnon[1], [1]*University of Saskatchewan, Saskatoon, SK, Canada*, [2]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*.

A study was conducted to evaluate performance and carcass quality of cattle fed wheat or corn DDGS. Crossbred steers (N=275) weighing 376 ±24kgs were randomly assigned to one of 25 pens and fed one of 5 treatment rations. The control ration contained 86.6% rolled barley grain, 5.7% supplement and 7.7% barley silage (DM basis) and was formulated to 12% crude protein and 1.95 and 1.30 Mcal/kg NE_m and NE_g, respectively. The 4 treatments included replacement of barley grain at 20 or 40% of the diet (DM basis) with wheat or corn DDGS. Data was analyzed as a CRD using the mixed model with pen as the experimental unit. Relative to control fed cattle (10.4 kg/d), cattle fed 40% wheat DDGS (10.9 kg/d) had the highest (P<0.0001) DMI while those fed 40% corn DDGS (8.8 kg/d) had the lowest (P<0.0001). No effect (P>0.05) of 20% addition of wheat or corn DDGS on DMI was noted. ADG was not influenced (P>0.1) by DDGS feeding. The cattle fed 40% corn DDGS had a lower (P<0.0001) feed to gain relative to all other treatments (5.2 vs. 6.3). In contrast to the steers fed the control and 20% wheat DDGS treatments, steers fed 40% wheat DDGS had fewer (P<0.05) days on feed. Carcass traits including weight, *l. dorsi* area, grade fat and marbling score were not affected (P>0.05) by treatment, although steers fed the control ration had a lower (P<0.05) dressing % than steers fed 40% wheat DDGS and 20 and 40% corn DDGS. Yield of boneless boxed beef sub-primals as determined by carcass cutout was not (P>0.05) affected by treatment. The results of this study indicate that replacement of barley grain with corn or wheat DDGS at 40% of the diet DM can lead to superior performance (improved feed efficiency or reduced days on feed, respectively) with no detrimental effect on carcass retail yield or quality grade.

Key Words: DDGS, cattle performance, carcass characteristics

60 Effect of graded levels of wheat-based dried distillers grains with solubles on rumen fermentation in finishing cattle. R. M. Beliveau*[1,2] and J. J. McKinnon[2], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [2]*University of Saskatchewan, Saskatoon, SK, Canada*.

A 4×4 Latin square experiment using ruminally cannulated heifers (388±25kg) was conducted to evaluate the effects of graded levels of wheat-based dried distiller's grains with solubles (DDGS) on the rumen fermentation characteristics and eating behaviour of finishing cattle fed barley-based diets. Animals were randomly assigned to one of four treatments of 0, 7, 14 or 21% DDGS replacing barley in a finishing ration. Rumen fermentation measurements included in-dwelling 23h pH measurements, total volatile fatty acid (VFA) levels, molar proportions of individual VFA's, osmolality and ammonia nitrogen levels. Mean rumen pH, at the sub-acute and acute acidosis benchmark values of pH 5.8 or less (P=0.02) and 5.5 or less (P=0.004), decreased in a cubic fashion as DDGS inclusion level increased resulting in a theoretical maximum pH at DDGS inclusion levels of 2.5 and 2.6% and theoretical minimum pH at DDGS inclusion level of 14.7% (DM basis). A cubic effect of DDGS inclusion level (P=0.03) was also noted for total time below pH 5.2 where a theoretical minima was found at 2.9% DDGS and a maxima at 15.0% DDGS (DM basis). Ammonia nitrogen (P=0.003) levels and the molar proportions of acetate (P=0.02) and butyrate (P=0.04), as well as the acetate: propionate ratio (P=0.01) increased linearly with DDGS inclusion level. In contrast, propionate decreased (P=0.006) linearly as the level of DDGS increased. Time spent eating increased (P=0.03) linearly with DDGS inclusion level; however, no differences ($P \geq 0.05$) were seen for ruminating, chewing (eating + ruminating), drinking, lying or standing. It was concluded that despite the high fibre, low starch nature of wheat-based DDGS, substitution for barley did not improve the acidic rumen fermentation conditions associated with feeding high grain rations. As such, metabolic disturbances such as sub-acute ruminal acidosis (SARA) are still a concern when feeding wheat-based DDGS as a substitute for barley in finishing rations for feedlot cattle.

Key Words: distiller's grains, pH, acidosis

61 Impact of feed waste on the nutrition and economics of wintering beef cows. B. J. Yaremcio*[1], E. K. Okine[2], M. Oba[2], and D. McCartney[3], [1]*Alberta Agriculture and Rural Development, Canada*, [2]*University of Alberta, Canada*, [3]*Agriculture and Agri-Food Canada, Canada*.

Many cowherds in western Canada are fed forage on snow during winter using extensive feeding systems to reduce feeding costs. Newer technologies claim to be more economical and efficient than other feeding systems. The main objective was to compare two feeding systems, the old bale unroller (BU), and newer bale shredder (BSHR), to determine the amount of feed waste (FW) that occurs when meadow brome alfalfa hay (MBAH) was fed on snow at 1.8% of body weight on a dry matter basis (DMB). The feeding rate was 90% of recommended rates (NRC Beef 2000). The control for this experiment was feeding MBAH into

portable feed bunks (PFB) delivered by BSHR. Four replicates of each treatment were completed, with four samples per replicate were collected. Treatments were blocked by week and analyzed by proc mixed and pdiff (SAS, 2002). The second objective was to calculate the impact of FW on nutrients consumed compared to amounts supplied. The third objective was to calculate the economic impact caused by FW and the amount of additional feed required to replace lost nutrients. FW was 12.1% and 19.2% DMB respectively for BU and BSHR ($P<0.0001$) when fed on snow. Forage placed into PFB had 0% waste. More fine material (78.5%) was lost ($P<0.0001$) with the BSHR feeding system than the BU (46%). CP losses were 23.3% and 21.5% compared to physical losses of 12.3% and 19.2% respectively for the BU and BSHR. Losses of Ca, P, Mg, K and Na were also greater than the physical feed loss. Ration CP content was reduced from the delivered feed at 11% DMB to 8.4% and 8.6% when waste was considered with the BU and BSHR respectively. Over a 175 d feeding period, replacing nutrients lost in the FW with additional forage and additional equipment operating time increased winter feed costs by C$28.52 and C$56.52 per head for the BU and BSHR respectively.

Key Words: snow, feed waste, cows

62 A temporal characterization of the rumen epithelium response to dramatic shifts in dietary fermentable carbohydrates. M. A. Steele*, O. AlZahal, S. E. Hook, S. Greenwood, and B. W. McBride, *University of Guelph*, *Guelph, ON, Canada*.

The rumen epithelium performs a vital role in whole-animal energy metabolism through the absorption and the metabolism of volatile fatty acids (VFA). In spite of this, very little is known about how the rumen epithelium responds to dramatic shifts in dietary carbohydrates and the resulting microbial products. The first objective of this study was to temporally characterize how shifts in dietary carbohydrates influence rumen pH and epithelial ketogenesis. The second objective was to temporally quantify mRNA expression levels of ketogenic enzymes in rumen papillae. To meet these objectives, four mature, rumen fistulated dairy cattle were utilized to facilitate continuous rumen pH recording on a weekly basis. The cattle were maintained on a control (CON) diet prior to transitioning to an acidosis (AD) diet, which was fed for three weeks (weeks 1-3). The cattle were then switched back to the original CON diet for three additional weeks (weeks 4-6). A mixed model with repeated measures was used to contrast ruminal pH, blood metabolites and mRNA expression data between and within treatments. Mean ruminal pH was depressed ($P<0.01$) and SARA was diagnosed during the first week of the AD diet however pH was not significantly different from the CON during the second and third week on the AD diet, indicative of improved VFA clearance from the rumen. Plasma BHBA levels were elevated ($P<0.01$) when cattle were fed the AD compared to the CON diets, suggesting increased ketogenesis in the rumen epithelium. The expression of HMG-CoA Synthase mRNA increased during the first week of the AD diet ($P<0.05$) however was down-regulated 2.0-fold ± 0.08 ($P<0.01$) by the third week. Acyl-CoA Synthase mRNA expression was also decreased 1.8-fold ± 0.11 ($P<0.01$) by the third week of the AD diet. To our knowledge, this is the first in-vivo study to demonstrate that rumen epithelial metabolism adapts to shifts in the form of dietary carbohydrates.

Key Words: rumen epithelium, acidosis, ketogenesis

63 Fertility of Alpine goats following oestrus synchronisation with CIDR and artificial insemination with cryopreserved semen. M.-E. Marier*[1,2], F. Castonguay[3], M. Theriault[3], D. Cinq-Mars[2], C. Lessard[1,2], and J. L. Bailey[1,2], [1]*Centre de recherche en biologie de la reproduction*, [2]*Département des sciences animales, Université Laval*, *Québec City*, [3]*Dairy & Swine Research and Development Center, AAFC*, *Lennoxville*.

The demand for goat milk by Canada's manufacturing industry far outweighs that produced by its dairy herd. In contrast, France has been proactive in improving the genetic make-up and productivity of their herd using artificial insemination (AI). Our goal is to encourage AI in Canada by developing a protocol based on that used in France but modified for Canada's industry, where sponges are no longer available. A total of 48 female Alpine goats under an artificial photoperiod regime were assigned to 3 treatments (n=16 goats/treatment; 8 adult and 8 yearling) during the non-breeding season (spring): NAT+AI – females were inseminated with frozen semen 12 h after natural oestrus; CIDR+AI - oestrus was synchronized with CIDRs (progesterone-releasing device) and females were inseminated with frozen semen 43 h after CIDR removal; CIDR+buck - oestrus was synchronised with CIDRs and females were placed with bucks 24 h after CIDR removal. For CIDR groups, females were treated with CIDRs on Day 0, injected with eCG+cloprostenol on Day 9, and CIDRs were removed on Day 11. Semen straws from the same lots were used for both AI groups, and sperm parameters (computer-assisted sperm motility, viability, DNA stability, and % acrosome reactions) were analysed to assess the relationship with fertility. Data were analysed by PROC LOGISTIC with SAS. Overall birth rate was 25% for NAT+AI, which was inferior to the 63%, and 100% for CIDR+AI and CIDR+buck, respectively ($P<0.05$). Female age did not affect fertility. Post-thaw semen analyses were not predictive of fertility. This study demonstrates that AI with frozen semen yields satisfactory fertility in adults and yearlings in the non-breeding season with oestrus being synchronised by a CIDR-based protocol. While natural mating yields the best fertility, the 63% obtained with AI allows a much faster genetic improvement.

Key Words: goat, CIDR, AI

Graduate Student Paper Competition: National ADSA Dairy Foods

64 Growth of *Lactobacillus casei* at 8°C in Cheddar cheese extract requires supplementation. W. S. Tan*[1], M. F. Budinich[1], R. Ward[2], J. R. Broadbent[2], and J. L. Steele[1], [1]*University of Wisconsin*, *Madison*, [2]*Utah State University*, *Logan*.

Flavor development in ripening Cheddar cheese is a complex microbial and biochemical system that is difficult to study in its natural form. Therefore, we developed a model system, Cheddar cheese extract (CCE), derived from the aqueous phase of ripening Cheddar cheese to study the complex interactions between the cheese microbiota, the conditions present in the cheese (e.g. composition of the microbiota, substrates present, NaCl concentration, temperature, pH, and organic acids) and flavor development. Previous studies in our laboratory have demonstrated that CCE supports the growth of strains of *Lactobacillus casei* at 37°C from

10^4 to 10^8 CFUs/ml. However, when we attempted to repeat this CCE growth experiment at 8°C, the final cell density was 10^6 CFUs/ml. When growth experiments were done at 8 and 37°C in MRS, no significant differences were observed in the final cell densities obtained. These results suggested that CCE was lacking an essential nutrient for growth of *Lb. casei* strains in CCE at 8°C to the levels observed at 37°C. To identify the lacking nutrient, CCE was supplemented with various media components present in MRS or a chemically defined media formulated for *Lb. casei*. These results indicated that addition of tween 80 to CCE allowed for growth of *Lb. casei* strains at 8°C to levels similar to that observed at 37°C. To determine if a similar growth enhancement would result from the addition of milk fat, 1% (v/v) milk fat was added to CCE and growth studies were conducted at 8°C. Milk fat was capable of enhancing the growth of *Lb. casei* strains at 8°C in CCE, but not to the same level observed with tween 80. Future studies will include the membrane fatty acid analysis of *Lb. casei* strains growing in CCE with and without milk fat supplementation at different incubation temperatures. These results suggest that milk fat plays an essential role in the growth of *Lb. casei* in ripening Cheddar cheese. Therefore, CCE with 1% milk fat will be use as a cheddar cheese model system to further understand the interactions within the cheese aqueous phase and flavor development in Cheddar cheese.

Key Words: Cheddar cheese, *Lactobacillus casei*, milk fat

65 Structure-function relationship of exopolysaccharides from lactic acid bacteria in fermented milk. M.-C. Gentès*[1,2], D. St-Gelais[2], and S. L. Turgeon[1], [1]*STELA Dairy Research Centre and Institute of Nutraceuticals and Functional Foods, Laval University, Quebec city, Quebec, Canada, G1K 7P4*, [2]*Food Research and Development Centre, Agriculture and Agri-Food Canada, St-Hyacinthe, Quebec, Canada, J2S 8E3*.

Exopolysaccharides (EPS) produced by lactic acid bacteria (LAB) can be used as stabilizers in fermented milk. Literature indicates that their properties to bind water and modulate viscosity are not correlated to EPS concentration but to their structure and interactions with milk compounds. In order to produce fermented milk with desirable rheological properties, it is essential to know their structure-function relationship. The aim of this work was to evaluate the gelation profile and the rheological properties of reconstituted skim milk (RSM) made with LAB producing different EPS. Three *Streptococcus thermophilus*: ST1 (EPS-), ST2 (neutral ropy EPS+), ST3 (charged ropy EPS+) and four *Lactobacillus delbrueckii* ssp. *bulgaricus*: LB1 (EPS-), LB2 (neutral nonropy EPS+), LB3 (charged nonropy EPS+), LB4 (neutral ropy EPS+) were compared. Each strain was grown at 42°C in RSM at 12% (DM) until pH reached 4.6. Glucono-delta-lactone (GDL) was used as control. Analysis of variance, according to completely randomized design, was applied to determine the effect of EPS on rheological properties. Significant differences were tested at $P \leq 0.05$. Whey retention (centrifugation: 210 x *g*), firmness (TA-XT2 texture analyser) and apparent viscosity at $10s^{-1}$ (rheometer) were significantly higher in RSM with ropy strains. Gel formation (elastic modulus: G′>1Pa) was observed from pH 5.6 to 5.2 for all strains while ST3 formed gel at pH 5.0. Casein aggregation seemed to be affected by the EPS produced by ST3. EPS- strains, GDL and ST3 had similar G′ (242Pa) at 10Hz while for others, the G′ was significantly lower (135Pa). For LB3, the G′ was intermediate (178Pa). This work showed that casein aggregation during gel formation and rheological properties of fermented milk are modified by the type of EPS produced by LAB.

Key Words: exopolysaccharide, structure-function relationship, rheological properties

66 Modifying whey proteins to improve heat stability and clarity. K. N. Ryan*, B. Vardhanabhuti, and E. A. Foegeding, *North Carolina State University, Raleigh*.

Heat-induced aggregation, resulting in excessive turbidity, phase separation, or precipitation, limits the application of whey proteins in beverages. Whey proteins with increased heat stability, especially in the presence of salts, are desirable for existing meal replacement beverages and new beverage applications. Therefore, the objective of this research was to determine the factors that influence heat stability of unmodified and modified (mild heat treatment) whey proteins in the presence of salt in order to achieve maximum protein stability. Solutions containing 7% w/v whey protein isolate (WPI) or β-lactoglobulin (BLG), pH 7, were heated at 90°C for 10 min to produce "modified" proteins. Subsequently, unheated (native) and modified WPI or BLG were diluted to 3% w/v protein and underwent a second heating at 90°C for 5 min in the presence of 0-30 mM NaCl after pH was adjusted to 6.8. Sample turbidity was determined by optical density at 400 nm. Solution viscosity (shear rate sweep) and protein solubility (BCA assay) were determined. Surface hydrophobicity of proteins was measured using the fluorescent probe 1-anilinonaphthalene-8-sulfonic acid (ANS). Modified proteins produced solutions with significantly lower turbidity ($p \leq 0.05$) than their native counterparts, where a greater than 40% decrease in turbidity was observed at high NaCl concentrations. Modified samples with reduced turbidity also showed reduced viscosity as indicated by lower consistency coefficients when modeled using a power law model, with modified BLG showing a greater viscosity reduction than WPI. Solubility was close to two times greater for the modified proteins at 30 mM NaCl compared to native proteins. Surface hydrophobicity could not explain the stability of the modified proteins, suggesting another mechanism is responsible for greater heat and salt stability of the modified whey proteins. This research is important as it shows how modification of whey proteins results in higher solubility of proteins and reduced viscosity and turbidity of solutions containing salts, which is often desired in nutritional beverages.

Key Words: whey protien, stability, modified

67 Evaluation of heated milkfat flavor profile and its effect on buttery flavor in cheese. E. L. Harvey* and S. A. Rankin, *University of Wisconsin, Madison*.

Milky and buttery flavor notes are highly desirable in many cheeses. Developing a simple means to potentiate these flavor notes would improve consumer acceptance of bland products such as low fat cheese. One mechanism for increasing buttery notes involves the thermal treatment of milkfat such as in ghee production. The objective of this work was to study the impact of heat treatment on the volatile and flavor profile of milkfat for flavor improvement of mild cheese. Milkfat was separated from pasteurized (87.2°C, 19s) 37% fat cream in a pilot-scale variable speed churn. Fresh butter samples were placed in glass vials with Teflon-lined closure and rapidly heated to 90, 120, 150 and 180°C by immersion in a mineral oil bath for 15 and 30 minutes. The volatile fractions of the heated samples were analyzed using SPME-GC/MS, and the results were compared with those of fresh butter. The heated samples contained numerous volatiles associated with the Maillard reaction and lipid oxidation products, including lactones, which are known to contribute to sweet milkfat flavors in dairy products. Trained descriptive panel assessments demonstrated relationships between heating and several sensory descriptors such as cooked and caramelized. To examine the application of heated milkfat flavor in mild cheese, salted curd of a fresh, acid-set cheese was combined, hooped, and pressed

(40psi, 1.5hrs) with fresh and heated (139°C ± 7°C, 5min) milkfat. A consumer panel (n=100) involving the three treatments was conducted to assess perception and intensity of the buttery notes in the samples. Statistical analysis (ANOVA) of the results showed that significantly (α=0.05) stronger buttery flavors were detected in the samples containing both heated and fresh added milkfat. Also, an increased overall flavor was recognized in the sample containing heated milkfat. This data indicates that incorporation of heated milkfat markedly enhances buttery notes in mild cheese. Producing cheese with heated butter flavor characteristics could have application in improving flavor performance in low fat cheeses.

Key Words: flavor, cheese, buttery

68 Are the physico-chemical properties of the casein micelle modified by ultrafiltration? M. A. Ferrer*[1,2], M. Alexander[2], and M. Corredig[2], [1]*University of Zulia, Maracaibo, Zulia, Venezuela*, [2]*University of Guelph, Guelph, Ontario, Canada*.

The aim of this work was to determine if concentration of milk using ultrafiltration (UF) (with no diafiltration) affects the structure of casein micelles once they are brought back to their original environment (pH and ionic strength) in milk. Despite the amount of information available on ultrafiltration of milk, no information is available on how (or if) ultrafiltration irreversibly modifies the properties of the micelles. Casein micelles were concentrated by ultrafiltration of skim milk to 2-fold (light UF) and 5-fold (high UF) casein volume fraction, and their light scattering properties were immediately observed by diffusing wave spectroscopy and dynamic light scattering. Casein micelles were then re-dispersed in their own permeates and dialyzed against raw skim milk. Scattering properties were then observed on all samples after 24h of equilibration. This allowed us to examine the stability of casein micelles (which underwent different UF treatments) under the same volume fraction and ionic conditions. The light scattering properties (size, ζ-potential and turbidity parameter) of casein micelles modified by "light" ultrafiltration (2-fold concentration) were not different from those of the skim milk control. However, the inverse of the transport mean free path, defined as the turbidity parameter, $1/l^*$, was significantly lower for the casein micelles modified by "high" ultrafiltration (5-fold concentration) compared to "light" UF and the skim milk control. Analysis of serums obtained by centrifugation of the samples revealed no differences in the soluble caseins profile, proving that ultrafiltration did not induce solubilization of caseins from the micelle structure. These results suggest that the process of ultrafiltration does have some lasting effects on the structure of the casein micelles. These changes are most probably due to variations in the mineral equilibrium of the casein/environment system during the UF process and not to the protein structure itself.

Key Words: casein micelle, light scattering, ultrafiltration

69 Isolation of a whey fraction rich in α-lactalbumin from skim milk through microfiltration. B. Holland*[1], J. Kacmar[2], and M. Corredig[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*NCSRT, Raleigh, NC*.

Currently microfiltration is used extensively in the dairy industry for removal of bacteria and spores from raw milk, and to concentrate proteins for preparation of milk protein and whey protein concentrates and isolates. The objective of this work was to be able to isolate a high purity α-lactalbumin rich stream from pasteurized skim milk through only filtration techniques. The microfiltration system used for isolation was a pilot plant scale novel Purposep™ filtration system (NCSRT. inc, North Carolina). Various filters and operating conditions were tested, and the amount of whey protein transmitted in the permeate was quantified using high performance size exclusion chromatography and calibration curves using previously purified –whey proteins. The CONSEP™ RC 100 membrane filter cartridge used was regenerated cellulose (RC) and had a 100kDa MWCO (molecular weight cut-off). Final conditions were 26°C with a TMP (trans-membrane pressure) of 186 kPa (27psi). These were found to be optimal for the isolation of α-lactalbumin to levels of up to 90% of total protein. This would be sufficient for use in human baby milk powders as they require only 80% purity. DSC tests confirmed that the protein is still in a state close to native and is not further damaged (after pasteurization) by the filtration process. This process results in a very high value product with minimal inputs as the skim milk can go on to be used in many processes, most notably for cheese making.

Key Words: ultrafiltration, α-lactalbumin, whey protein

70 Production efficiency of a serum protein (SP) reduced micellar casein concentrate (MCC) produced with polymeric spiral-wound microfiltration (MF) membranes. S. L. Beckman*[1], J. Zulewska[2], M. Newbold[1], and D. M. Barbano[1], [1]*Cornell University, Ithaca, NY*, [2]*University of Warmia and Mazury, Olsztyn, Poland*.

The purpose of this research was to determine the process necessary to create a 95% SP reduced MCC using polymeric spiral-wound MF diafiltration. Separation of micellar casein and serum proteins by MF is an emerging process that could be used to produce a range of protein ingredients for use in both dairy and non-dairy foods and beverages. Pasteurized (79°C, 18s) skim milk (3 lots) was microfiltered at 50°C [about 3× concentration] using a 0.3µm polyvinylidene fluoride spiral-wound membrane bleed-and-feed 3-stage process, using 2 diafiltration stages, where the retentate was diluted 1:2 with reverse osmosis water. The measured CN content of the MF permeate was 0.02%, so there was not a large loss of CN in the permeate. MF retentate TP content decreased progressively with stage, 7.58, 6.27 and 5.55%. These decreases were larger than expected, given the concentration factors were not different, 2.79, 2.82 and 2.90 for the 3 stages, respectively showing an apparent loss of protein in the system. This disappearance may be due to adsorption of protein to polymeric components of the MF system or the imbalance between actual concentration factor and the diafiltration factor used for water addition. Flux increased progressively with stage, 15.7, 24.3, and 35.1 kg/m^2 per hour, indicating that membrane fouling decreased with stage. The SP removal was determined by Kjeldahl [SP times the mass of permeate divided by the mass of SP in the skim milk]. Theoretical SP removal for this process is 68, 22 and 7% for the 1st, 2nd and 3rd stages, respectively with a total removal of 97%. Based on the Kjeldahl, 38.6, 20.8 and 11.0% of skim milk SP was removed in the 1st, 2nd and 3rd stages, respectively for an overall SP reduction of 70.4% compared with 90 to 95% reported for ceramic MF. Therefore, the membrane was partially blocking the passage of SP. The percentage of starting SP for each stage that passed through the membrane was 39, 34 and 27%, respectively. To achieve a 95% serum protein reduction in MCC it is estimated that an additional 5 diafiltration stages would be necessary.

Key Words: microfiltration, micellar casein concentrate

71 Retention of vitamin D fortified emulsions in bench-top cheese. M. Tippetts*[1,2], S. Martini[1,2], C. Brothersen[2,1], and D. McMahon[1,2], [1]*Utah State University*, *Logan*, [2]*Western Dairy Centrer*, *Logan, UT*.

The objective of this research was to evaluate the retention of vitamin D in bench-top cheese by using different delivery matrices. Vitamin D was incorporated in the cheese using a 5% oil-in-water emulsion. Emulsions were formulated with different emulsifiers (non-fat dairy powder, whey protein concentrate, calcium and sodium caseinates) in triplicate to determine the efficiency in vitamin D delivery. The oil phase was composed of 50:50 wt% of vitamin D and soybean oil; the water phase consisted of 2 wt% protein in a 0.01M Na2HPO4-7H2O buffer (pH 7). The amount of each emulsifier added varied according to protein content. The oil and water phases were homogenized using a high shear force for 1 min at 18,000 rpm and then passed through a microfluidizer (2,500psi). Vitamin D dissolved in medium chain triacylglycerides (Continental Custom Ingredients; 40,000 IU/mL) was used as a control. Bench-top cheese was made in triplicate with pasteurized (72 °C 15 s) whole (non-homogenized) milk. For each sample, 200 µl of vitamin D emulsion or 125 µl pre-emulsified vitamin D (control) was added to 200 ml of milk (250 IU per gram of curd). Each fortified milk solution was prepared in 250 ml polycarbonate Nalgene centrifuge bottles. Glucono-delta-lactone (2% w/v) and double strength rennet diluted to 1.8 rennet units per ml with cold water (0.2% v/v) were added to each. Mixtures were incubated 30 min at 35°C for coagulum formation, then coagulum was cut and centrifuged at 1000 x g at 25 °C for 30 min. The curd and whey were measured and 100 g of whey and 5 g of curd were retained and frozen for vitamin D analysis (O'Neil Laboratories). Results from this research show that the retention of vitamin D in the curd was 98.4 ± 0.2% for the samples formulated with non-fat dairy powder, 97.1 ± 0.5% for samples with calcium caseinate, 98.1 ± 0.1% for samples with sodium caseinate and 97.1 ± 0.2% for samples with whey protein. These values were significantly higher than the ones obtained for the control delivery matrix (93.3 ± 0.7%). These results suggest that using an oil-in-water emulsion is a better delivery matrix than using the vitamin D dissolved in medium chain triacylglycerides.

Key Words: vitamin D, cheese, retention

72 Low fat Mozzarella cheese with improved baking and melting properties. R. Wadhwani* and D. J. McMahon, *Utah State University*, *Logan*.

Low fat cheeses dehydrate too quickly when baked using a forced air convection that prevents proper melting on a pizza. Low fat Mozzarella cheeses were made using direct acidification with citric acid to pH 5.9, containing 1.5, 3.0, 4.5, or 6.0% fat. The cheese curd was salted and placed in a bowl chopper and 4.5, 3.0, 1.5, or 0.0% respectively, of melted butter was added along with glucono-δlactone. The curd mixture was comminuted, hooped, and pressed into a block using 100 kPa pressure. Cheese was analyzed for melting, texture, free oil, and performance when baked on a pizza at 250°C for 6 min in an Impinger oven after 15, 30, 60, and 120 days of storage at 5°C. All cheeses contained 5.5-6.0% fat and 52-53% moisture. Compared to the control cheese in which all 6% fat was from the curd, the treated cheese had higher stretchability tested using a fork test after baking the pizza. Melting also increased which was particularly evident after baking on a pizza. The control cheese remained in the form of shreds and did not melt, while the cheeses made with added butter melted and flowed together. The cheeses with added butter had higher free oil and less hardness, gumminess, and chewiness than the control. Low fat Mozzarella cheese with free oil availability during baking is very important for retaining moisture. This study helped in availing free oil in cheese using melted butter.

Key Words: Mozzarella, melting, baking

73 Effects of starch addition on a low-fat cheese model system. K. M. Larsen*[1,2], D. J. McMahon[1,2], and W. R. McManus[1,2], [1]*Western Dairy Center*, *Logan, UT*, [2]*Utah State University*, *Logan*.

Addition of starch to low-fat cheese has the potential to create discontinuities in the protein matrix and alleviate formation of a rubbery texture. The purpose of this research was to 1) determine if various starches are retained with casein when a rennet curd is formed, and to quantify the percentage of starch lost into the whey during syneresis, and 2) determine starch impact on microstructure of rennet-induced milk gels using laser scanning confocal microscopy (LSCM). Model low-fat cheeses were made by renneting and acidifying skim milk containing one of five starches at 0.5% (wt./vol). Starches used included modified waxy cornstarch (WC), waxy rice starch (RS), instant tapioca starch (IT), dextrin (D), and modified food starch (MF). Milks were heated prior to renneting to gelatinize starch. After curd formation, curd was cut and centrifuged at 25°C at 500 x g then 1,000 x g for 15 min each. Starch content in whey was determined by alcohol precipitation. Curd samples for LSCM imaging were fixed in osmium tetroxide. Acriflavin HCl at 2% in water was used to stain carbohydrate, and 0.01% Rhodamine B in water was used for protein. Curd yields were 18.9, 21.7, 14.0, 25.1, 21.2, and 13.4% for WC, RS, D, MF, IT and control cheeses, respectively. Apparent starch losses in whey were 0, 0.7, 15.4, 18.6, and 0%, from centrifuged curd containing WC, RS, D, MF, and IT, respectively. The proportion of carbohydrate observed in the curd structure with LCSM was related to the level of starch retention. There were differences in the distribution of starch between the protein matrix and the serum pockets depending on the starch used. The MF apparently interacts most strongly with the matrix, D interacts less, and WC, RS and IT are intermediate.

Key Words: starch, cheese, low-fat

Graduate Student Paper Competition: National ADSA Production Division Oral MS Competition

74 Effects of conjugated linoleic acid isomers on mammary gland development in BALB/cJ mice. J. M. Gloviczki*[1], J. Kraft[2], A. L. Lock[2], J. F. Trott[1], and R. C. Hovey[1], [1]*University of California*, *Davis*, [2]*University of Vermont*, *Burlington*.

Conjugated linoleic acids (CLA) are isomers of octadecadienoic acid that are present in ruminant-derived products. *Cis*-9, *trans*-11 (9,11) CLA is the most abundant, while the less abundant *trans*-10, *cis*-12 (10,12) isomer is a major constituent of mixed isomer supplements. Both isomers suppress mammary gland (MG) tumorigenesis *in vitro* and *in vivo*, whereas 10,12 CLA has been implicated as affecting the incidence of obesity and insulin resistance. Intriguingly, recent data indicate that a diet supplemented with 10,12 CLA stimulates MG tumorigenesis in transgenic mice overexpressing the ErbB2 oncogene. These conflicting data emphasize the need to further investigate MG development

in response to the intake of specific CLA isomers. The objective of these studies was to determine the effects of these CLA isomers on MG development in female BALB/cJ mice and the responsiveness of their MG to ovarian hormone stimulation. In the first study, mice were weaned onto a control diet (ctrl) (AIN-93G) or the same diet with 1% of the fat from soybean oil replaced with either 9,11 CLA or 10,12 CLA. The MG were collected at 35d and 55d of age for tissue analysis. At 35d mice fed 10,12 CLA had increased ductal elongation in the MG ($P<0.05$) in comparison to mice fed ctrl. The females fed 10,12 CLA had an increase in supramammary lymph node size at 55d ($P<0.01$). At both ages the MG from females fed 10,12 CLA weighed less than those fed ctrl ($P<0.01$). MG weight from females fed 9,11 CLA was reduced at 55d ($P<0.05$). In the second study, pubertal mice were fed either the control diet or one of the treatment diets for 28d. Mice were then ovariectomized, and 7d later commenced receiving 17β-estradiol (1ug) and/or progesterone (1mg), or vehicle for 4d. The MG from females fed 9,11 CLA or 10,12 CLA weighed less than those from females fed ctrl ($P<0.05$ and $P<0.001$). Mice fed 10,12 CLA also had larger ($P<0.001$) supramammary lymph nodes ($P<0.001$). There was no interactive response between hormone treatment and diet on MG weight($P>0.05$). Taken together, these data support previous suggestions that 10,12 CLA stimulates ductal elongation in the developing mouse MG, potentially via its effects on the adipose stroma.

75 The effects of TGF-β1 on mammary stroma during the dry period of dairy cows. L. De Vries*, J. Liesman, K. Weiss, H. Dover, T. Casey, M. VandeHaar, and K. Plaut, *Michigan State University*, *East Lansing*.

During the dry period in dairy cows, the mammary gland undergoes remodeling in preparation for the next lactation. This remodeling occurs in part through the coordination and activation of various cell types, and the production of structural proteins, growth factors and proteases. Transforming growth factor-β1 (TGF-β1) can activate human mammary fibroblasts, and TGF-β mRNAs are present in the bovine mammary gland. Therefore, we hypothesized that TGF-β1 plays a role in bovine mammary remodeling during involution and mammogenesis. Our objective was to determine if TGF-β1 affects the expression of stromelysin-1 and fibronectin, and the activation of stromal cells during the dry period. Tissue was biopsied from 7 multigravid Holstein cows at 4 time points: late lactation, 7 d after dry-off, 21 d before expected calving and 7 d before expected calving. Explants of biopsied tissue were incubated for 2 h in Waymouth's media containing insulin, hydrocortisone, and 0 or 5 ng/ml TGF-β1. Immunohistochemistries of 5-μm sections of formalin-fixed, paraffin-embedded explant tissue were analyzed with Image Pro Plus software, and a mixed model analysis was performed with Statistical Analysis Software. TGF-β1 increased the total number of stromal cells expressing smooth muscle α-actin (SMA, a marker of stromal cell activation) from 640 to 760 cells per mm^2 *($P=0.03$)* across all 4 mammary biopsies. TGF-β1 also tended to increase the percent of stromal cells expressing SMA from 22% to 26% *($P=0.06$)*. TGF-β1 had no effect on the percent of the intralobular stroma area expressing fibronectin or stromelysin-1. The effect of TGF-β1 was similar for all biopsies for all variables measured (no significant treatment × biopsy interaction). These findings support our hypothesis that TGF-β1 plays a role in mammary remodeling of dry cows through the activation of stromal cells. *This project was supported by National Research Initiative Competitive Grant no. 2006-35206-16719 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: transforming growth factor β1, remodeling, dry period

76 Comparison of real-time PCR and culture for detection and speciation of *Mycoplasma* species in bulk tank milk samples. A. Justice-Allen*[1], G. Goodell[2], J. Trujillo[1], and D. Wilson[1], [1]*Utah State University*, *Logan*, [2]*Dairy Authority*, *Greeley, CO*.

Intra-mammary infections caused by mycoplasma species have been recognized for more than fifty years. In addition to causing mastitis, these organisms also cause pneumonia, joint infections, and otitis. The impact of a herd level outbreak of disease can be a marked decrease in milk production, and result in the culling of a significant percentage of animals. The standard detection method for mycoplasma mastitis at the herd level has been repeated bulk-tank sampling and culture using specialized media. The goal of our research was to develop a real-time PCR method which could detect and differentiate mycoplasma species in bulk tank milk at rates comparable to standard culture techniques. 180 previously cultured bulk tank samples were extracted with a Qiagen DNEasy DNA isolation kit. The PCR reaction was carried out using a PerfeCTa Sybr master mix and two primers keyed to the 16S-23S ribosome RNA spacer region of *M. bovis*. This protocol had been previously tested with several mycoplasma type species from American Type Culture Collection (ATCC). The results from the bulk tank samples were compared to these standards. For 70% of the samples, the culture and PCR methods of detection agreed. PCR detected mycoplasma organisms in 24 (13%) samples that were culture negative. In 20 samples, the mycoplasma species identified was not *M. bovis*. Twelve samples had *M. bovis* and a second species. Four dairies had two different species of mycoplasma in bulk tank milk. Three dairies had only non-*M. bovis* mycoplasma. PCR did not detect *M. bovis* in 10 (5.5%) culture positive samples. Samples that were not in agreement or that identified a species of mycoplasma other than *M. bovis* were confirmed by sequencing the amplicon. The failure of the PCR to detect organisms in 10 samples is under investigation. This could be attributed to the loss of DNA during storage and shipment or the presence of inhibiting substances in the milk. Since the impact of mycoplasma mastitis varies with the species involved, a diagnostic method which can rapidly and accurately identify the species will greatly assist in the management of the disease.

Key Words: mycoplasma, mastitis, real-time PCR

77 Intermediates of linoleic acid biohydrogenation in ruminal batch cultures dosed with uniformly ^{13}C labeled linoleic acid. C. M. Klein* and T. C. Jenkins, *Clemson University*, *Clemson, SC*.

Most depictions of linoleic acid biohydrogenation do not explain all of the fatty acid isomers found in the rumen. Linoleic acid is generally accepted to be converted to *cis*-9 *trans*-11 conjugated linoleic acid (CLA), *trans*-C18:1 and then stearic acid. In this study ^{13}13C labeled linoleic acid was used as a metabolic tracer to determine other intermediates of linoleic acid biohydrogenation. Ruminal microorganisms were maintained in 10 ml batch cultures for 3, 6, 12 and 24 h. A 0 h sample was taken by acidifying media prior to addition of mixed ruminal microorganisms. Duplicate cultures were methylated and then separated on a 100-m CP-Sil 88 column and abundances of the quasimolecular (M) and M+18 ions were determined by mass spectroscopy in electron impact ionization mode. Enrichment was calculated as [M+18/M]*100 in labeled minus unlabeled cultures and tested for their difference from zero by t-test ($P<0.05$). Enrichments for linoleic acid were not different for 0 through 12 h (12.5, 13.6, 14.0, 14.2%), with an increase ($P<0.05$) to 17.9% at 24 h. By 24 h incubation significant tracer was found in 5 isomers of C18:2, 4 isomers of C18:1 and stearic acid ($P<0.01$). No enrichment of stearic acid was seen from 0 to 6 h, which then increased ($P<0.05$) to 0.43 and 3.05% at 12 and 24 h respectively, *trans*-9 C18:1

was not enriched before 6h and increased (P<0.05) to 6.4 and 9.4% from 12 to 24 h. There was no linolenic acid enrichment at any time point. The appearance of tracer in 4 isomers of C18:2 indicate that linoleic acid is acted on by isomerase enzymes and converted into a multitude of CLA isomers. *Cis*-9 *trans*-11 CLA enrichment increased from 0 at 0 and 3h to 5.4, 8.4 and 7.9% at 6, 12 and 24 h. *Trans*-10 *cis*-12 CLA enrichment averaged 0.0, 3.6, 5.3, 7.5 and 7.4% at 0, 3, 6, 12 and 24 h, respectively. Two currently unidentified C18:2 isomers in the CLA range were also found to be labeled (P<0.01). These results indicate that linoleic acid is converted into several CLA and *trans* monoene isomers prior to complete saturation to stearic acid.

Key Words: linoleic acid, biohydrogenation, conjugated linoleic acid

78 Effect of an exogenous fibrolytic enzyme or ammonia on fiber concentration, feed intake, digestibility, and ruminal pH of steers fed bermudagrass hay harvested at two maturity stages. J. J. Romero*, A. T. Adesogan, M. A. Zarate, O. C. M. Queiroz, J. Han, K. G. Arriola, C. M. Huisden, C. R. Staples, and M. Garcia, *University of Florida*, *Gainesville*.

The objectives were to compare the effect of treatment without (control) or with either a fibrolytic enzyme (ENZ) (Biocellulase A) or anhydrous ammonia (NH3; 4% DM) on the quality of bermudagrass (Cynodon dactylon) hay harvested as 5- and 10-wk regrowths and the performance of steers. Six ruminally cannulated Brangus steers (average BW 216.4 ± 5.9kg) were used in an experiment with a 6 × 6 Latin Square design with a 3 (treatments) × 2 (maturities) factorial arrangement. Each period consisted of 14 days of adaptation, followed by 7 days of digestibility (total collection) measurements and 1 day of ruminal pH measurement. Steers were housed in individual pens and fed 110% of their previous days hay consumption twice daily (1000 and 1600 h) with 2.66 kg DM/hd/d of a supplement consisting of sugar cane molasses, distillers grain and a mineral and vitamin supplement. Urea (0.03 kg/hd/d) was provided to steers fed Control and enzyme-treated hays to ensure diets were isonitrogenous. No treatment × maturity interactions existed (P>0.05) for performance measures except CP and NDF%. Ammoniation reduced NDF% (P=0.01) and increased CP% (P<0.001) to a lesser extent (P<0.01) at 5 wk (74.7 vs. 78.6 and 78.1; 17.8 vs 12.9 and 12.1) than at 10 wk (68.0 vs vs 74.4 and 71.1;16.3 vs 9.1 and 9.2). The ADF % of hays were lower at 10 vs 5 wk (39.0 vs 40.6). Hay (4.8 kg/d) and total (7.51 kg/d) DMI and ruminal pH (6.50) were unaffected (P>0.05) by treatment or maturity. Dry matter digestibility decreased with maturity (64.3 vs. 63.1; P<0.05) and was increased by NH3 (65.9 vs. 62.4%; P<0.001) but not ENZ (62.9%; P>0.09).

Key Words: enzyme, ammonia, beef cattle

79 Supplemental starch in postpartum dairy cow diets: 2. Effects on reproduction. B. L. Dyck*[1], M. G. Colazo[2], D. J. Ambrose[1,2], M. K. Dyck[1], and L. Doepel[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Alberta Agriculture and Rural Development*, *Edmonton, AB, Canada*.

Negative energy balance in early lactation cows has been associated with reduced reproductive performance. This study was conducted to determine if increasing the level of dietary starch would improve energy balance and positively impact reproduction. One of 3 diets was fed in a randomized block design to Holstein cows from calving until 70 DIM. All diets contained 45% barley-based concentrate and 10% alfalfa hay. In addition, the low (LSD, n=14) medium (MSD, n=13) and high starch diets (HSD, n=13) contained 45% barley silage, 45% alfalfa silage, and 41% barley silage + 4% corn starch, respectively. Resulting starch levels were 23.5%, 25.3% and 26.9% for LSD, MSD, and HSD, respectively. Transrectal ultrasonography was performed biweekly from 7 d after calving until 1st ovulation or 62 DIM, and a complete estrous cycle was monitored for ovarian dynamics in 8 LSD, 7 MSD and 9 HSD cows. Blood samples were collected every 2nd d during the cycle for determination of progesterone and estradiol concentrations; LH pulsatility was determined (5 cows/trt) approximately 15 d post calving. Cows fed HSD had a shorter interval from calving to 1st ovulation than cows fed MSD (30.6 vs. 43.2 d; *P*<0.01) and those fed LSD (38.1 d; *P*=0.07). The incidence of double 1st ovulation was higher (*P*=0.03) in cows fed HSD (39%) and MSD (27%) compared to those fed LSD (0%). There were no treatment effects on LH pulse frequency or amplitude, ovarian dynamics, or progesterone and estradiol concentrations during the observed estrous cycle. Energy balance did not differ between the 3 treatments and averaged -2.6±1.4 Mcal/d. Number of cows confirmed pregnant 30 d after 1st AI did not differ between treatments and averaged 36%. Increasing dietary starch decreased the interval from calving to 1st ovulation without improving energy balance but had no impact on pregnancy to 1st AI.

Key Words: starch, energy balance, ovulation

80 Accuracy of an on-farm blood test for pregnancy in dairy and beef cattle. J. C. Green*[1], D. H. Volkmann[1], S. E. Poock[1], M. F. McGrath[2], M. Ehrhardt[2], A. E. Moseley[2], and M. C. Lucy[1], [1]*University of Missouri*, *Columbia*, [2]*Monsanto Co.*, *St. Louis, MO*.

The ruminant placenta produces pregnancy-associated glycoproteins (PAG) that can be detected in the blood. The objective was to determine the accuracy of an on-farm PAG test for the purpose of pregnancy detection. Blood was sampled from dairy cattle (539 Holstein cows, 173 Holstein heifers, 73 Guernsey cows, 22 Guernsey heifers, and 12 Jersey heifers) and crossbred beef cattle (145 cows and 46 heifers) that were greater than or equal to 25 d after insemination (range = 25 to 45 d for dairy and 29 to 56 d for beef). Cattle were ultrasounded for detection of pregnancy within 2 d of blood collection. Blood was collected in EDTA-coated tubes and assayed either as whole blood or plasma. Whole blood or plasma was incubated in a polystyrene tube coated with a monoclonal PAG antibody for 15 min. The tubes were then washed with a phosphate-buffered saline-tween (PBST) solution and subjected to sequential incubations with a biotinylated polyclonal PAG antibody (15 min, followed by PBST wash), a horseradish peroxidase-streptavidin solution (15 min, followed by PBST wash) and a peroxidase substrate. Tubes were visually assessed for color (i.e., PAG/pregnancy status) after 15 min (clear solution = PAG negative, not pregnant; blue solution = PAG positive, pregnant). Total assay time was approximately 90 min. The ultrasound exam was used as the gold standard for pregnancy diagnosis. The sensitivity (99.8 ± 0.2%), specificity (91.7 ± 1.4%), and negative predictive value (99.7 ± 0.3%) for the PAG test used in dairy cattle were similar for different breeds and for cows and heifers (P>0.10). The positive predictive value for the test was greater in dairy heifers when compared with dairy cows (96.5 ± 1.4% versus 90.5 ± 1.7%, respectively; P<0.05). In beef cattle, the sensitivity (100%), specificity (92.3 ± 3.0%), positive predictive value (95.0 ± 2.0%), and negative predictive value (100%) for the PAG test were similar for cows and heifers (P>0.10). The accuracy of the test was similar for dairy and beef cattle (P>0.10). The conclusion was that the on-farm pregnancy test

based on PAG is highly sensitive and specific for pregnancy detection in dairy and beef cattle.

Key Words: pregnancy test, PAG, cattle

81 Financial analysis of direct comparison of natural service sires and timed artificial insemination in a dairy herd. F. Lima*, A. deVries, and C. Risco, *University of Florida*, *Gainesville*.

Objective was to compare the cost and profitability of natural service (NS) vs. timed artificial insemination (TAI) as the sole reproductive program on a commercial dairy farm in random allocated field study. Both programs were directly compared in 2007 and managed by the researchers. The NS group had a bull/cow ratio of 1/28 including open and pregnant cows. Bulls rested for 2 wk after 2 wks of exposure with cows. Both groups were presynchronized with 2 injections of PGF 14 days a part and the TAI group received Ovsynch and Ovsynch+CIDR for resynchronization of non-pregnant cows with 35 d intervals between AI up to 5 services. Pregnancy rate (PR) for NS (70 to 230 d) was 25.1% and for TAI (80 to 230 d) was 24.2%. Direct net cost of the NS program during the trial was $92.87/cow/yr. Direct net cost of the TAI program during the trial was $52.76/cow/yr. Costs per eligible day were estimated at $1.32 for the NS program and $0.76 for the TAI program. A herd budget was developed to account for the effects of differences in voluntary waiting periods and pregnancy rates on cost and profitability. The advantage of the TAI program after inclusion of these costs was $31.44/cow/yr (default). The advantage of the TAI program was $16.72 if genetic progress was not considered. A decrease in milk price from $20 to $14/cwt reduced the advantage of the TAI program to $26.44/cow/yr. Considering opportunity cost, if each bull was replaced by an additional cow, the advantage of the TAI program was $98.95/slot/yr. When milk price was reduced from $20 to $14/cwt, the advantage of the TAI program was $58.30/slot/yr. Changing PR for each program for 16.5% resulted in an advantage of $50.52/cow/yr for the TAI program. Considering opportunity cost, the advantage rose to $138.68/slot/yr, mainly because more bulls were needed. In conclusion, PR of the NS and TAI programs were similar and if well managed could both be much better than typical on US dairy farms. The TAI program was cheaper and its advantage increased substantially when opportunity costs of additional cows were considered.

Key Words: economics, bulls, estrus synchronization

82 Fecal and urinary estrogens in dairy heifers during the estrous cycle. H. A. Tucker*[1], K. F. Knowlton[1], and N. G. Love[2], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*University of Michigan*, *Ann Arbor*.

The US EPA has identified estrogens from animal feeding operations as a major environmental concern, but little data is available quantifying estrogen excretion by dairy cattle. The objectives of this study were to quantify estrogenic activity in feces and urine during the estrous cycle in dairy heifers, and evaluate relationships with plasma 17-β estradiol (E2). Seven Holstein heifers were fed a common diet for the 28 d study. Plasma was obtained via jugular venipuncture and grab samples of feces and urine were collected daily. Plasma E2 was quantified with RIA and used to confirm day of estrous. Feces and urine samples from days -12, -6, -2, -1, 0, 1, 2, 6, 12 of the estrous cycle were analyzed with Yeast Estrogen Screen (YES) bioassay. The YES assay utilizes a recombinant yeast strain (*Saccharomyces cerevisiae*) containing the human estrogen receptor gene and a chromogenic reporter system to indicate total estrogenic activity. Proc Mixed (SAS) was used to evaluate the effect of day on concentration of estrogens. The effect of day was significant, and patterns of estrogenic activity in feces and urine mirrored plasma E2 concentrations during the estrous cycle. Feces and urine estrogenic activity peaked a day after plasma E2 peaked. Identifying sources of variation in estrogen excretion by livestock will aid in the development of practices to reduce environmental estrogen accumulation.

Table 1. Average concentrations of plasma 17-β estradiol and fecal and urinary estrogenic activity by day of estrous

	Day of Estrous								
	-12	-6	-2	-1	0	1	2	6	12
Plasma[1], pg/mL	1.66	0.88	0.92	1.57	22.86	2.48	1.54	1.12	0.89
Feces[2], µg/mL	11.74	18.94	53.61	73.31	87.00	106.79	82.21	20.10	15.85
Urine[3], µg/mL	10.87	20.42	36.00	79.09	90.18	112.58	89.65	14.27	9.47

[1] SEM=2.39 [2]SEM=12.15 [3]SEM= 13.67

Key Words: estrogen, estrous, feces

83 Low progesterone concentration during the development of the first follicular wave impairs fertility of lactating dairy cows. A. C. Denicol*[1], G. Lopes Jr.[1], L. G. D. Mendonça[1], F. A. Rivera[1], F. Guagnini[1], R. V. Perez[1], J. R. Lima[1], R. G. S. Bruno[1], J. E. P. Santos[2], and R. C. Chebel[1], [1]*University of California*, *Tulare*, [2]*University of Florida*, *Gainesville*.

Objectives were to determine the influence of progesterone (P4) concentration on fertility of lactating dairy cows induced to ovulate follicles of the first follicular wave. Lactating dairy cows (n = 988) received 2 injections of PGF2α 14 d apart (Presynch). Cows were then randomly assigned to first follicular wave (FW), first follicular wave with CIDR (FWC), or second follicular wave (SW) treatments. FW and FWC cows started the timed AI (TAI) protocol 3 d after the last PGF2α of the Presynch protocol, whereas SW cows received GnRH 3 d after the last PGF2α of the Presynch and started the TAI protocol 7 d later. The TAI protocol consisted of GnRH on d 0, PGF2α on d 7, and GnRH + TAI on d 10. FWC cows received 2 CIDR inserts from d 2 to 7. A subgroup of cows (n = 719) had their ovaries scanned by ultrasound on d 0, 7, and 17. Pregnancy was diagnosed at 38 d after AI. Although similar (P = 0.49) proportion of cows ovulated in response to the first GnRH of the TAI protocol (66.9%), FW cows had larger (P < 0.06) follicles on d 7 than FWC and SW cows (FW = 17.8 ± 0.4, FWC = 16.8 ± 0.4, SW = 16.0 ± 0.4 mm). Pregnancy per AI (P/AI) at 38 d tended (P = 0.06) to be and was smaller (P = 0.02) for FW (28.7%) cows than FWC (35.9%) and SW (37.2%) cows, respectively. Among cows scanned by ultrasound, the interaction between treatment and ovulation in response to the first GnRH injection tended (P = 0.10) to affect P/AI, because among FW (21.1 vs. 34.9%) and SW (26.0 vs. 40.2%) cows those that did not ovulate had smaller P/AI, but among FWC cows ovulation to the first GnRH did not affect P/AI (35.4 vs. 34.5%). FW cows had more (P = 0.04) corpora lutea 7 d after AI than FWC and SW cows (FW = 1.26 ± 0.04, FWC = 1.13 ± 0.04, SW = 1.12 ± 0.04) and were more likely (P<0.01) to experience double ovulation (FW = 32.2, FWC = 18.7, SW = 20.6%). Exposure to low concentrations of P4 during follicle development resulted in larger follicles before ovulation, increased multiple ovulations, and reduced fertility in lactating dairy cows induced to ovulate follicles of the first follicular wave.

Key Words: progesterone, first follicular wave, lactating cow

Graduate Student Paper Competition: National ADSA Production Division PhD Oral Competition

84 Expression of inducible nitric oxide synthase is up-regulated by production of 1,25-dihydroxyvitamin D_3 in bovine monocytes in response to toll-like receptor signaling. C. D. Nelson*[1,2], D. C. Beitz[1], T. A. Reinhardt[2], and J. D. Lippolis[2], [1]*Iowa State University, Ames*, [2]*National Animal Disease Center, United States Department of Agriculture, Ames, IA*.

In the endocrine pathway of vitamin D signaling 1,25-dihydroxyvitamin D_3 ($1,25(OH)_2D_3$) is produced from 25-hydroxyvitamin D_3 ($25(OH)D_3$) by the enzyme CYP27B1 in the kidney. Production of $1,25(OH)_2D_3$ in the kidney functions to regulate gene expression systemically. However, recent studies have shown that human monocytes express CYP27B1 and produce $1,25(OH)_2D_3$ in response to toll-like receptor recognition of bacterial cell wall components. Activation of $25(OH)D_3$ by CYP27B1 in human monocytes improves antimicrobial activity via an autocrine pathway. The purpose of this study was to determine if $1,25(OH)_2D_3$ is produced by CYP27B1 in bovine monocytes upon TLR signaling and if $1,25(OH)_2D_3$ production in bovine monocytes increases expression of antimicrobial genes. Monocytes were isolated from peripheral blood of six lactating Holstein cows and cultured in media containing 10% FBS. Monocyte cultures were treated with 0 - 75 ng/mL $25(OH)D_3$ or 0 – 4 ng/mL $1,25(OH)_2D_3$ and stimulated for 24 hours with lipopolysaccharide (LPS) a tripalmitoylated lipopeptide (Pam3CSK4) or peptidoglycan (PGN). Relative expression of CYP27B1, cathelicidin 4 (CATH4), CATH5, CATH6 and inducible nitric oxide synthase (iNOS) mRNA in monocytes was measured using quantitative real-time PCR. CYP27B1 expression in monocyte cultures was induced by stimulation with LPS, Pam3CSK4 or PGN ($p < 0.05$). Treatment of stimulated monocyte cultures with $25(OH)D_3$ or $1,25(OH)_2D_3$ increased iNOS expression ($p < 0.05$). Treatment of unstimulated monocyte cultures with $1,25(OH)_2D_3$, but not $25(OH)D_3$, increased iNOS expression. Expression of CATH4, CATH5 and CATH6 genes in stimulated monocytes was not affected by $25(OH)D_3$ or $1,25(OH)_2D_3$ treatment. In conclusion, bovine monocytes convert $25(OH)D_3$ to $1,25(OH)_2D_3$ in response to TLR signaling and $1,25(OH)_2D_3$ production up-regulates iNOS expression. This study is the first to show that an autocrine pathway of vitamin D signaling has an impact on the innate immune response in cattle.

Key Words: iNOS, vitamin D, toll-like receptor

85 Regulation of bovine pyruvate carboxylase mRNA and promoter expression by heat stress. H. M. White*, S. L. Koser, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Pyruvate carboxylase (PC) catalyzes a rate limiting step in gluconeogenesis and TCA cycle flux. Bovine PC is the product of a gene containing three promoter regions (P3, P2, and P1, 5′ to 3′) and is responsive to physiological and nutritional stressors. The objectives of this study were to investigate the effects of heat exposure (42°C) on PC expression in bovine hepatocyte monolayer cultures and in rat hepatoma (H4IIE) cells. Hepatocytes were isolated from three Holstein calves less than 7 d of age and used to prepare monolayer cultures. Rat hepatoma cells were obtained from American Type Culture Collection and utilized by eight passage. Cells from both lines were maintained in 10% FBS for 24 h following plating, and treatments were applied in triplicate in three independent groups of cells or three primary hepatocyte preparations. Expression of PC mRNA relative to 18S mRNA (arbitrary units) increased ($P \leq 0.1$) with 24h exposure to heat (1.31 vs. 2.79, control vs. heat). Conversely, endogenous PC mRNA expression decreased ($P \leq 0.1$) in H4IIE cells (0.47 vs. 0.30, control vs. heat). There was an interaction of cell type and PC mRNA expression with heat exposure ($P \leq 0.05$). There were no changes in phosphoenolpyruvate carboxykinase (PEPCK) mRNA expression in either cell types. To further investigate the regulation of PC, H4IIE cells were transiently transfected with bovine promoter-luciferase constructs containing either P1, P2, or P3 and exposed to heat for 23 h. Activity of P1 was suppressed (arbitrary units of luciferase activity; $P \leq 0.05$) with heat exposure (5.85 vs. 1.25, control vs. heat) but P3 activity was enhanced ($P \leq 0.1$; 0.34 vs. 2.57, control vs. heat). These data indicate that there is a cell type interaction of PC expression with heat exposure. Furthermore, induction of gene expression by heat stress appears specific to bovine PC compared with PEPCK. The promoter response data indicate unique characteristics of bovine PC promoters that may be part of the physiological response to heat stress.

Key Words: pyruvate carboxylase, heat, bovine hepatocytes

86 Activation of AMP-activated protein kinase (AMPK) inhibits *de novo* fatty acid synthesis in bovine mammary epithelial cells. J. W. McFadden* and B. A. Corl, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Activation of AMP-activated protein kinase (AMPK), a heterotrimeric energy-sensing protein, decreases lipid synthesis in liver tissue of various species; however, little is known about the role of AMPK in the regulation of lipid synthesis in bovine mammary epithelial cells. Our objectives were to identify the presence of AMPK in bovine mammary tissue and a bovine mammary epithelial cell line (MAC-T) and determine the effect of AMPK activation on *de novo* fatty acid synthesis in MAC-T. Expression of AMPK subunits (α1, α2, β1, β2, γ1, γ2, and γ3) was determined using real-time PCR. The α, β, and γ subunits of AMPK were found in mammary tissue and MAC-T; however, the α2 isoform was not expressed in MAC-T nor was the γ3 isoform found in mammary tissue or MAC-T. Treatment of MAC-T with the AMPK activator AICAR for 4 h (acute) or 24 h (chronic) resulted in 85 and 92% decreases ($P<0.05$) in radiolabeled-acetate incorporation into fatty acids, respectively. Treatment of MAC-T with AICAR for 1 h increased the ratio of inactive acetyl-CoA carboxylase (ACC) to total ACC by 959% ($P<0.0001$). Chronic treatment of MAC-T with AICAR decreased the mRNA expression of glycerol phosphate acyltransferase, lipoprotein lipase, and peroxisome proliferator-activated receptor-γ by 44-80% ($P<0.05$). Chronic AICAR increased the mRNA expression of fatty acid binding protein-3, fatty acid synthase, and sterol regulatory element binding protein-1 by 39-65% ($P<0.01$). Expression of ACC mRNA was unaffected by AICAR. AMP-activated protein kinase is sensitive to decreases in energy supply. Incubating MAC-T without glucose for 4 h resulted in a 251% increase in the ratio of inactive ACC to total ACC ($P<0.0001$). Ionomycin is a potential activator of Ca^{2+}/calmodulin-dependent kinase kinase, an AMPK kinase. Treatment of MAC-T with ionomycin for 1 h resulted in a 308% increase in the ratio of inactive ACC to total ACC ($P<0.0001$). Results confirm that AMPK activation dramatically decreases *de novo* fatty acid synthesis in MAC-T. Therefore, in the lactating mammary gland, AMPK may sense energy availability and regulate milk fat synthesis to control energy utilization.

Key Words: ACC, AMPK, fatty acid

87 Evaluation of effects of fibrolytic enzyme application on the digestibility of corn silage, alfalfa hay, and two concentrates and complete diets under simulated ruminal and preruminal conditions. K. G. Arriola* and A. T. Adesogan, *University of Florida*, *Gainesville*.

Previous work showed that when added to the TMR prior to feeding, a fibrolytic enzyme containing 880 U/ml of endoglucanase activity, 3633 U/ml of xylanase activity, and 0.1 umol/mg/minute of esterase activity improved DM (DMD) and NDF digestibility (NDFD) and the level and efficiency of milk production by dairy cows. This study determined if the enzyme exerts its hydrolytic effect on different dietary substrates preruminally or ruminally. Substrates evaluated included corn silage (CS), alfalfa hay (AH), low (LC) and high (HC) -energy concentrates (22 and 37% corn meal) and low- (33%) and high-(48%) concentrate TMRs (TMRL and TMRH). The enzyme was diluted in 1 ml of citrate phosphate buffer (pH 6.0) and applied to six replicates of 0.5 g of each substrate within 250 ml culture bottles in each of 2 runs. Twenty-four h later, 40 ml of either distilled water (W) or buffered-rumen fluid (RF) was added to the substrates. Samples were incubated at 39°C for 24 h after which, residues were analyzed for DM and NDF, and digestibility of DM and NDF were calculated. Substrates incubated in RF had greater ($P < 0.01$) DMD than those incubated in W except for AH, which had greater DMD in water and TMRH which, had similar DMD in both media. On average, DMD in RF was 5.5% greater than DMD in W. Due to a substrate × medium interaction; AH had the greatest ($P < 0.01$) DMD in W and CS had the lowest ($P < 0.01$) DMD, whereas, LC had the greatest DMD in RF and TMRH had the lowest DMD. All substrates except AH had greater ($P < 0.001$) NDFD when incubated in RF than in W. On average, NDFD in rumen fluid was 74% greater than NDFD in W. Due to a substrate x medium interaction, AH had the greatest NDFD in W and CS had the lowest, whereas TMRL had the greatest NDFD in RF and AH had the lowest. The fibrolytic enzyme hydrolyzed the substrates in the presence and absence of rumen fluid suggesting that it can improve digestion both preruminally and ruminally.

Key Words: fibrolytic enzymes, digestibility, diet

88 Comparison of a controlled-energy high-fiber diet fed throughout the dry period to a two-stage far-off and close-up dietary strategy. B. F. Richards*[1], N. A. Janovick[1], K. M. Moyes[1], D. E. Beever[2], and J. K. Drackley[1], [1]*University of Illinois*, *Urbana*, [2]*Richard Keenan & Co.*, *County Carlow, Ireland*.

Our objective was to determine if a controlled-energy, high-fiber diet fed during the dry period improves metabolic status and production of dairy cows compared with a higher-energy diet or a two-stage system (controlled energy far-off and higher energy close-up to calving). Twenty-five Holstein cows (10 primiparous) were assigned to 1 of 3 treatments at 60 d before expected calving. Treatment LE was a controlled-energy diet (1.32 Mcal NE_L/kg DM; 12.3% CP) to meet but not exceed NRC recommendations at ad libitum intake from dry-off until calving. The diet included wheat straw (42% of the DM) processed directly into the TMR using Keenan Klassik mixer wagon technology. Treatment HE was a moderate-energy diet (1.61 Mcal NE_L/kg DM; 12.7% CP) fed ad libitum from dry-off until calving. For the LEHE treatment, the LE diet was fed ad libitum from dry-off until 21 d prepartum, followed by the HE diet until parturition. After parturition all cows were fed the same lactation diet (1.66 Mcal NE_L/kg DM; 18% CP) mixed in a Calan Data Ranger through 63 d postpartum. The DMI and BW were greater for HE cows prepartum ($P<0.01$, $P<0.01$), but not postpartum ($P=0.47$, $P=0.59$). Cows fed HE had greater gain of body condition score (BCS) before calving ($P<0.01$) but lost more BCS postpartum ($P=0.06$). Milk production did not differ across treatments ($P=0.80$). Milk fat (kg/d) was higher for HE ($P<0.01$); milk protein (kg/d) did not differ ($P=0.38$). The LE cows had lower serum NEFA ($P<0.01$), serum β-hydroxybutyrate ($P<0.01$) and liver total lipid ($P<0.01$) postpartum than HE cows and lower liver total lipid ($P<0.05$) than LEHE cows. Serum glucose ($P<0.01$) and insulin ($P=0.02$) were lower for LE than HE and LEHE prepartum; insulin was lower for LE than LEHE postpartum ($P<0.01$). Controlling energy intake to near requirements during the dry period by use of a high-straw diet improved metabolic status with no adverse effects on production. A two-stage feeding strategy provided little benefit over the single-group controlled-energy diet.

Key Words: dry period, transition cow, energy balance

89 Effects of addition of live bacterial inoculants and glycerol to the diet of lactating dairy cows on apparent efficiency and milk yield during heat stress. J. Boyd*[1], J. W. West[1], J. Bernard[1], J. Loften[2], and D. R. Ware[2], [1]*University of Georgia*, *Tifton*, [2]*Nutrition Physiology Corporation*, *St. Cloud, MN*.

A study was conducted to evaluate the effects of a live bacterial inoculant and dietary glycerol on milk yield, efficiency of yield, and nutrient digestibility during hot weather. Sixty Holstein cows averaging 120 DIM and 36.2 kg/d of milk were used. The study was conducted from June through Sept. 2008. Cows were fed a common diet during the 2 wk standardization period and then divided into 4 groups of 15 by parity, milk yield, ECM, and DIM and randomly assigned to 1 of 4 treatments for 10 wks. Experimental design was a randomized complete block with a 2x2 factorial treatment arrangement. Treatments included control **(**C), Bovamine® (B), Bovamine® w/ 400g h/d glycerol (BG), and control w/ 400g h/d glycerol **(**G**)**. Bovamine® contained $4x10^9$ CFU/h/d of a combination of *Lactobacillus acidophilus NP51* and *Propionibacterium freudenreichii NP24*. Diets were based on corn and ryegrass silages and balanced to be iso-caloric and iso-nitrogenous. DMI ($P<0.52$) was 23.0, 22.2, 23.3, and 22.8 kg/d (treatments C, B, BG, and G respectively). Milk yield ($P<0.52$) was 32.5, 32.8, 34.5, and 32.4 kg/d (treatments C, B, BG, and G respectively). A trend for improved milk yield with BG versus G of 2.1 kg/d was noted. No effect was noted for milk fat percentage or ECM among diets. A decrease in milk protein percentage was noted ($P<0.06$) for cows offered G (2.72 ± 0.02) compared with C (2.8 ± 0.02). No effect on respiratory rate, skin temperature, body temperature or concentration of serum glucose or urea N was noted. An increase in efficiency ($P<0.02$) defined as milk yield/DMI was noted with G (1.51 ± 0.02) and BG (1.54 ± 0.02) compared with C (1.42 ± 0.02). Also, improved efficiency ($P<0.06$) for B (1.5 ± 0.02) versus C (1.42 ± 0.02) was noted. The addition of Bovamine® alone and with glycerol had a positive effect on apparent efficiency compared with C. Results suggest that the addition of Bovamine®, glycerol or a combination of both may improve yield efficiency for cows subject to heat stress.

Key Words: bacterial inoculant, glycerol, heat stress

90 Subacute ruminal acidosis decreases acetate absorption across the isolated ruminal epithelia. G. B. Penner*[1], J. R. Aschenbach[2], G. Gäbel[2], and M. Oba[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Universität Leipzig*, *Leipzig, Germany*.

This study aimed to determine the effect of subacute ruminal acidosis (SARA) on the absorption of acetate across ruminal epithelia. Twenty-four German Merino sheep (72.3 ± 10.1 kg of BW), fed a hay diet,

were assigned to the glucose (GLU; n = 17) or control (CON, n = 7) treatments. The GLU sheep were orally dosed with a 2.2 *M* glucose solution to supply 5 g glucose/kg BW; whereas, CON sheep received an equal volume of water. Ruminal pH was measured for 48 h prior to and extending for 3 h after the oral dose. Following the 3 h challenge period, sheep were euthanized and ruminal epithelia from the ventral sac were collected. Epithelia were mounted in Ussing chambers with isolated mucosal and serosal solutions buffered at pH 6.1 and 7.4, respectively. In vitro treatment was Ussing chamber buffer solutions that 1) contained bicarbonate, 2) excluded bicarbonate, or 3) excluded bicarbonate and included nitrate. ^{3}H-acetate was used to determine the mucosal-to-serosal flux of acetate in order to estimate absorption. This allowed for the calculation of total, bicarbonate-dependent, bicarbonate-independent, and bicarbonate-independent and nitrate-sensitive absorption of acetate. Data were analyzed as a split-plot design with the main-plot factors of in vivo treatment and the sub-plot factors of in vitro treatment. The severity of SARA, as indicated by area that ruminal pH < 5.8, was greater (P = 0.009) for GLU than CON sheep (27 vs. 0 pH × min/180 min) during the 3 h challenge. Inducing SARA decreased acetate absorption (P = 0.037), where total absorption was reduced by 37% for epithelia from GLU compared to CON sheep (0.64 vs. 0.43 μmol/cm^2/h). Correlation analysis revealed that as the severity of SARA increased, the bicarbonate-dependent absorption of acetate decreased (r^2 = 0.263; P = 0.035). This study indicates that SARA decreases acetate absorption across the ruminal epithelia primarily due to a reduction in bicarbonate-dependent absorption.

Key Words: acetate, ruminal acidosis, ruminal epithelia

91 Effect of feed bin stocking density on the feeding and standing behavior of postpartum dairy cows. P. D. Krawczel*[1,2], D. M. Weary[3], R. J. Grant[1], and M. A. G. von Keyserlingk[3], [1]*William H. Miner Agricultural Research Institute*, *Chazy, NY*, [2]*The University of Vermont*, *Burlington*, [3]*University of British Columbia*, *Vancouver, BC, Canada*.

There are limited data on the effect of overcrowding feed bins, within a range that is representative of on-farm conditions, on the behavior of dairy cows during the postpartum period. The objective of this study was to determine the effects of feed bin stocking densities of 100% (1:1, bin:cow), 133% (1: 1.33), 150% (1:1.5), and 200% (1:2) on the behavior of cows during 21 d following parturition. Two groups of multiparous, Holstein cows (n = 24) were housed sequentially in a pen containing 36 freestalls (freestall stocking density was 67%) and 18 feed bins. To keep stocking density constant, the pen was managed as a dynamic group. Dry matter intake, water intake, feeding rate, and total feeding time were recorded on a daily basis and used to assess feeding behavior. Standing behavior was quantified by daily standing time and daily standing bouts, which were averaged for each of the 3 wk. Data were analyzed as a randomized design using the mixed procedure of SAS. The model included day as the repeated measure for feeding behavior and week as the repeated measure for standing behavior. Dry matter and water intake increased (P < 0.001) from 1 d to 21 d (13.9 ± 0.4 kg/d to 22.1 ± 0.4 kg/d and from 64.8 ± 2.5 kg/d to 102.4 ± 2.5 kg/d, respectively), but were not affected by treatment (P < 0.20) or treatment by day interaction (P < 0.10). Feeding rate tended (P = 0.06) to increase with treatment (from 1.6 ± 0.1 g/s at 100% to 2.0 ± 0.1 g/s at 200%). Time spent feeding was affected (P < 0.001) by day and there was a trend (P = 0.08) for a treatment by day interaction. Standing time (14.0 ± 0.6 h/d) was not affected by treatment (P = 0.40) or week (P = 0.87). Although standing bouts decreased (P = 0.02) during the trial (from 9.4 ± 0.4 during wk 1 to 8.7 ± 0.4 during wk 3), no treatment by week interaction (P = 0.99) occurred. In absence of freestall overcrowding, feed bin stocking density did not affect dry matter intake, water intake, or standing behavior. Trends for increased feeding rate and altered feeding time suggest that overstocking feed bins may alter feeding behavior.

Key Words: dairy cow, behavior, competition

92 Evaluation of NEFA and β-hydroxybutyrate (BHB) as predictors of clinical disease, milk production and reproductive performance in dairy cattle. P. A. Ospina*, D. V. Nydam, T. Stokol, and T. R. Overton, *Cornell University*, *Ithaca, NY*.

Data from 100 freestall, TMR-fed herds in the Northeastern U.S. were used in a prospective cohort study to establish cow-level critical thresholds for non-esterified fatty acids (NEFA) mEq/L and β-hydroxybutyrate (BHB) mg/dL as predictors of disease outcomes, milk production and reproductive performance.Blood samples were collected from two different sets of 15 pre- and 15 post-partum transition animals in each herd and a total of 2758 cows were analyzed.The outcomes of interest were: diseases (DA, clinical ketosis, and metritis or retained placenta); milk production (estimated by ME 305 kg at 120 DIM), and reproductive performance (time to conception within 70 d post-voluntary waiting period).NEFA was measured in the pre-partum group while both NEFA and BHB were measured post-partum. ROC- curve analysis and multivariable models were used to evaluate NEFA and BHB as predictors of disease. Mixed effect models were used to predict milk production with herd as a random effect. Reproductive performance was evaluated using time to event analysis. There was a significant change in risk of disease ($p<0.05$), the risk doubled when pre-partum NEFA levels were ≥0.29 quadrupled when post-partum NEFA ≥0.57, and increased by 4% when BHB levels were ≥10.ME 305 was decreased by 616 kg in all animals when pre-partum NEFA was ≥0.33 ($p<0.05$) and by 662 kg when post-partum NEFA was ≥0.72 ($p<0.05$)and 328 kg when BHB was ≥ 10 in cows ($p=0.09$).ME 305 was increased by 482 kg when post-partum NEFA was ≥0.57 ($p<0.05$)and by 381 when BHB was ≥9 in heifers ($p=0.05$).The probability of pregnancy within 70 d post-VWP was reduced by 20% when pre-partum NEFA was ≥ 0.27 ($p=0.01$)and 16% when post-partum NEFA was ≥0.72 ($p=0.05$).Similar results were seen when BHB was ≥10 ($p=0.1$).This study indicates that increased levels of NEFA and BHB increased the risk of developing disease, and had detrimental effects on reproductive performance and milk production. However, further investigation about homeorhesis in heifers is warranted.

Key Words: transition cow, nonesterified fatty acids, ketosis

93 Heterogeneous relationship between milk production and reproduction in dairy cows: Preliminary evidence. N. M. Bello*, R. J. Erskine, and R. J. Tempelman, *Michigan State University*, *East Lansing*.

Although it is generally perceived that an antagonistic relationship exists between dairy cow milk yield and fertility, some recent studies have suggested otherwise. We hypothesize that the relationship between milk production and reproductive performance in dairy cows is thereby heterogeneous and depends upon various herd-related and management factors. In this study, we provide preliminary ad-hoc evidence for heterogeneity in the correlation between 305-d milk yield (305Milk) and projected calving interval (ProjCI) in dairy cows. Dairy Herd Improvement data for 776,957 lactation records from 1,033 Michigan

herds recorded from 1998 to 2007 were used to jointly estimate residual (cow-level) (co)variances for 305Milk and ProjCI for each herd-year using a bivariate restricted maximum likelihood approach. (Co)variance estimates were then used to compute the cow-level correlation for each herd-year. The distribution of the estimated 305Milk-ProjCI correlation was symmetrical, centered at 0.26 and ranged from highly positive to negative values (i.e., unfavorable to favorable relationships between milk production and reproductive performance, respectively). A total of 16 selected herd performance indicators and management factors were evaluated as potential sources of correlation heterogeneity using stepwise model selection based on Bayesian Information Criteria. The final model indicated that the cow-level correlation between 305Milk and ProjCI was greater in herds with 2X versus 3+X milking frequency (P<0.01) and was lower in herds that used bST compared to those that did not (P<0.01). Also, the 305Milk-ProjCI correlation increased in herds undergoing expansion (P<0.01) but was not associated with herd size (P = 0.08). The correlation between 305Milk and ProjCI increased linearly over the 10-year period considered (P<0.01). In summary, this study provides preliminary evidence for heterogeneity in the relationship between milk production and reproductive performance of dairy cows, as a function of herd-related and management factors.

Key Words: dairy production, heterogeneous correlation, management

94 Effects of maternal lineage on production and fertility traits of Holstein cattle. C. N. Vierhout*, S. P. Washburn, R. L. McCraw, and E. J. Eisen, *North Carolina State University*, *Raleigh*.

The objective of this study was to determine effect maternal lineage has on production and fertility in Holstein cattle. Data included Holstein historical lactation records dating from 1980 to August 2005 from 13 states obtained from Animal Improvement Laboratory of USDA. Cows were included from historical records dating back to birth year of 1980 or 1981 as the foundation cows. Historical records included cows calving and completing lactations through August, 2005. Cows were then put in maternal family groups using dam identification within herd. A family value was calculated by averaging the first and second lactations across parity by degree of relationship to the individual (free of progeny information) for generations one though four. Each family was entered into top, middle, and bottom groups based on average deviations for milk production, pregnancy rate, or by combining pregnancy rate and milk into a selection index. Analyses were performed on fifth generation cows to determine if milk production and pregnancy rates were significantly associated with historical performance of the respective cow families. After adjustments for sire predicted transmitting ability (PTA), maternal-grandsire PTA, and family group for milk in the model the effect of maternal cow family was significant for pregnancy rate (P < 0.05; -1.05 percentage units) and milk production (P < 0.05; +913 kg) in an inverse relationship. When using deviations of pregnancy rate, the effect of maternal cow family was significant for both pregnancy rate (P < 0.05; +7.73 percentage units) and milk production (P < 0.05; -128 kg). A selection index with equal weights for milk and pregnancy rate resulted in an effect of maternal cow family for milk (P < 0.05; +133 kg) but not for pregnancy rate (P > 0.05; -0.22 percentage units). Although pregnancy rate and milk production have an antagonistic relationship, simultaneous consideration of both traits could allow for moderate genetic gain in production without adversely affecting reproduction. Consideration of maternal family history for pregnancy rate may be useful when selecting future bull dams.

Key Words: milk yield, pregnancy rate, selection index

95 Use of acaricides and gastrointestinal anthelminthes in developing countries: A case study among livestock farmers in Ghana. W. Addah*[1], J. Baah[2], and E. K. Okine[1], [1]*University of Alberta*, *Edmonton, Alberta, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre*, *Lethbridge, Alberta, Canada*.

Logistical constraints facing regulatory agencies in developing countries limit their capacity to enforce laws on importation, packaging and appropriate use of agro-parasiticides. A survey of 100 ruminant livestock farmers was conducted to assess their knowledge and administration of acaricides and gastrointestinal anthelminthes to ruminant livestock in the Sissila East district of the Upper West region of Ghana. Respondents were interviewed with a semi-structured questionnaire and data analyzed using Statistical Package for Social Sciences (SPSS 11). Inspection of labels of acaricides and anthelminthes showed that 4% and 30% respectively were not certified by the Foods and Drugs Boards of Ghana. Only 10% of farmers (P<0.05) used anthelminthes at the recommended rate. Majority of respondents (72%; P<0.05) reported underdosing of anthelminthes while overdosing of acaricides was 18% (P>0.05). Administration of both parasiticides was not done by the livestock owners themselves (30%), hired herdsmen (50%); none of whom were literate in the English language nor had any formal training in the use of agro-parasiticides, veterinary personnel (9%) and community-based livestock health workers (11%). Most farmers (35%; P<0.05) did not practice parasiticide withdrawal prior to slaughter or sale of livestock. Thirty eight percent (P<0.05) of anthelminthes had no expiry dates on their labels. The commonest place for storage of both parasiticides was under the bed in the bedrooms of farmers (43%; P<0.05). Animals that did not respond to treatment were slaughtered and consumed in the household (65%; P<0.05). The study found that inappropriate handling and use of livestock parasiticides were prevalent and raised serious public health and food safety concerns in the region.

Key Words: anthelminthes, acaricides, livestock

Nonruminant Nutrition: Feed Ingredients

96 A comparative evaluation of a new dried cheese and milk product (Gold Star Milk) versus other milk protein sources for weanling pigs. G. L. Cromwell*, M. C. Ulery, Y. L. Ma, I. F. Hung, and M. D. Lindemann, *University of Kentucky*, *Lexington*.

Gold Star Milk (International Ingredient Corp., St. Louis, MO) is a product resulting from the blending of dried cheese powder and specialty dairy powders such as dried milk and whey protein concentrate. It has a pleasant cheese aroma and an attractive dairy flavor. The product typically contains 24% CP, 15% fat, and 38% lactose. A 21-d experiment involving 90 pigs weaned at 21 d and averaging 7.6 kg BW was conducted to compare Gold Star Milk with 3 other sources of milk protein in Phase I (7 d) and Phase II (14 d) diets. There were 4 replications of 4 or 5 pigs/pen. Treatments were (1) basal diet with no milk protein, and 4 diets with 1.82% milk protein provided by (2) dried skim milk, (3) whey protein concentrate, (4) Gold Star Milk, or (5) casein. The 4 milk protein sources analyzed 35.9, 35.2, 23.1, and 88.7% CP, respectively. In addition, the Gold Star Milk product analyzed 96.1% DM, 17.1% fat, 35.6% lactose, 0.42% Ca, 0.57% P, and 1.92% lysine.

The milk products were substituted for starch (3.5% starch was in the basal diet), and lactose was equalized across diets at 20 and 15% during the 2 phases. Levels of fat, Ca, and P also were equalized across diets. Lysine levels in the basal and in diets 2-5 were 1.14 and 1.40% during Phase I, and 1.00 and 1.24% during Phase II, respectively. The basal diet was purposely made slightly deficient in lysine to better assess the contribution of the milk protein sources. Pigs fed 3 of the dried milk sources tended to gain more rapidly than controls during Phase I of the study (255, 243, 273, 282, 278 g/d for diets 1 to 5, respectively), but the differences were not significant (P = 0.40). Overall ADG, ADFI, and feed:gain for the 21-d study were, respectively: 424, 459, 450, 446, 466 g/d; 639, 628, 632, 601, 656 g/d; and 1.51, 1.37, 1.40, 1.35, 1.41. Pigs fed the 4 milk protein sources gained faster (P < 0.10) and more efficiently (P < 0.01) than controls, but feed intake was not affected (P = 0.72). These results indicate that Gold Star Milk is as effective in improving performance in weanling pigs as other milk protein sources when fed in Phase I and II nursery diets.

Key Words: pigs, milk protein

97 Canola meals from yellow-seeded *Brassica napus* and *B. juncea* have a higher digestible and net energy content in pigs than the meal from black-seeded *B. napus*. C. A. Montoya, K. Neufeld, P. Kish, and P. Leterme*, *Prairie Swine Centre Inc., Saskatoon, SK, Canada*.

The digestible (DE) and net (NE) energy content of canola meal (CM) in monogastric animals is limited by its high dietary fiber content. A breeding program based on yellow cultivars of *Brassica napus* and *Brassica junceae* has been initiated to develop canola seeds with lower fiber content, especially that of lignin. Also, the defatted meal is normally toasted to destroy antinutritional factors and evaporate solvent residues but excessive toasting can negatively affect digestibility. Therefore, an experiment (factorial 3x2) was conducted in growing pigs to determine the DE content and estimate the NE content of 3 different CM: yellow *B. napus* (YBN); black *B. napus* (BBN) and yellow *B. junceae* (YBJ) that were toasted (95 °C) or not (60 °C). A basal diet and 6 CM-based diets (2/3 basal diet, 1/3 CM) were prepared. A total of 42 growing pigs (28 kg; 6/treatment) were kept in metabolic cages for 18 d and their feces totally collected for the last 10 d. The digestibilities (DM, N and energy), DE and NE content were tested for CM type and flake type. The NE content was estimated by means of a prediction equation based on the DE content and chemical composition of the CM. Dry matter and energy digestibilities were greater (P < 0.05) for the YBN and BJ types compared to the BBN type. This could be ascribed to a lower NDF content (162 vs 217 g/kg, respectively) for the yellow-seeded canolas. A higher DE and NE content was observed for YBN and YBJ as compared to BBN (P < 0.01). There was no impact (P > 0.05) of toasting, or any interaction between toasting and canola type on nutrient digestibility or DE or NE content. In conclusion, toasting had no negative effect on digestibility in growing pigs whereas canola meals from yellow-seeded *B. napus* and *B. junceae* presented higher DE and NE content than the CM of black *B. napus* seeds.

Key Words: pigs, canola meal, digestible energy

98 Chemical composition and nutritive value of yellow-seeded canola for broiler chickens. W. Jia*[1], B. A. Slominski[1], G. Rakow[2], and D. Hickling[3], [1]*University of Manitoba, Winnipeg, MB, Canada*, [2]*Agriculture and Agri-Food Canada, Saskatoon, SK, Canada*, [3]*Canola Council of Canada, Winnipeg, MB, Canada*.

An evaluation of the chemical composition and nutritive value of meals derived from black- and yellow-seeded *Brassica napus* canola and canola-quality yellow-seeded *B. juncea* was undertaken. Two different seed processing technologies: the conventional prepress solvent extraction process (regular meal) and a new cold process of meal desolventization (white flake) were employed. In comparison with its black-seeded counterpart, and irrespective of the process used, yellow-seeded *B. napus* contained more protein (49.8 vs. 43.8% DM), less dietary fiber (21.3 vs. 27.4% DM) and less glucosinolates (20.0 vs. 30.7 μmol/g). Lower fiber content in yellow-seeded *B. napus* meal was reflected in lower content of nonstarch polysaccharides (15.9 vs. 17.6%) and lignin with associated polyphenols (3.6 vs. 7.1%). *B. juncea* meal showed intermediate levels of crude protein (47.4%), total dietary fiber (24.6%), and the lowest glucosinolate (18.8 μmol/g) content. Regardless of the genotype, the white flake samples contained higher myrosinase activities than the regular meals (0.60 vs. 0.08 U/g). The effects of seed coat color and processing technology on the nutritive value of the meals were investigated in a 2 week broiler chicken trial with 3×2 factorial arrangement of treatments. Birds were fed corn/soybean meal-based diets containing 30% of canola meals. On average, chickens fed diets containing white flakes consumed significantly (P<0.01) less feed (531 vs. 572 g/bird/14 days) and gained less weight (375 vs. 425 g/bird/14 days) than those fed regular meals. Consequently, an inferior FCR was observed (1.42 vs. 1.35). Such a response may have resulted from the myrosinase activity present in the white flake samples. Although different in the nutritive content, similar growth performance data was observed for the meals derived from yellow- and black-seeded canola.

Key Words: yellow-seeded canola, chemical composition, nutritive value

99 Effect of grinding on the digestible and net energy content of field peas (*Pisum sativum*) in growing pigs. C. A. Montoya, K. Neufeld, P. Kish, and P. Leterme*, *Prairie Swine Centre Inc., Saskatoon, SK, Canada*.

An experiment was conducted to determine the effect of the particle size of field peas on their digestible (DE) and net energy (NE) content in growing pigs. A factorial design (11 pea cultivars × 3 screen openings of the mill) was used, with 204 growing pigs (28 ± 2 kg). The 11 pea cultivars were ground at 3 different screen-opening sizes: fine, medium and coarse. The calculated mean particle size was 156, 650 and 1035 μm for the peas ground with fine (0.74 mm), medium (3.28 mm) and coarse (5.4 mm) screen opening size, respectively. A basal diet and 33 pea-based diets (70% basal diet and 30% peas) were supplemented with Celite®, a source of acid-insoluble ash, used as an indigestible marker. After an adaptation period of 10 d, faecal samples were collected by the grab sampling method for 3 d. The total tract digestibility values (DM, N and energy) and the DE and NE content were tested for pea sample and particle size. The NE content was estimated by means of a prediction equation based on the pea DE content and its chemical composition. Differences in digestibility values, DE or NE content were observed among the field peas (P < 0.05). The Pekoe pea cultivar presented the lowest values and Mozart the highest (e.g. 3.20 and 3.84 Mcal DE/kg). The digestibility values and energy content increased linearly as the mean particle size decreased from 1035 to 156 μm (P < 0.001). The average DE content was 3.84, 3.52 and 3.34 Mcal/kg and the NE content 2.69, 2.47 and 2.34 Mcal/kg for fine, medium and coarse grinding peas, respectively (P < 0.001). No difference was observed for the ′pea cultivar x screen opening size′ interaction (P > 0.05). In conclusion, the DE and NE content of peas in growing pigs increased linearly as the

particle size of pea decreased. Differences in DE and NE content were observed between pea cultivars.

Key Words: pig, field peas, digestible energy

100 Various levels of guar meal supplementation on growth performance and meat quality in growing-finishing pigs. P. S. Heo, S. W. Lee*, D. H. Kim, G. Y. Lee, K. H. Kim, and Y. Y. Kim, *Seoul National University, Seoul, Korea*.

The objective of this experiment was to evaluate different levels of guar meal supplementation on growth performance and meat quality in growing-finishing pigs. Treatments were : 1) CON - basal diet(NRC, 1998), 2) GM3 - basal diet + guar meal 3%, 3) GM6 - basal diet + guar meal 6%, 4) GM9 - basal diet + guar meal 9% and 5) GM12 - basal diet + guar meal 12%. A total of 120 crossbred ([LxY]xD) pigs with initial body weight 29.72 ± 0.1kg, were allotted in 5 treatments based on body weight and sex by a RCB design with 6 replicates and 4 pigs per pen. During the whole experimental period, GM12 treatment was significantly lower in body weight (P<0.01, 103.93, 100.97, 100.36, 97.67 and 90.14 kg for CON, GM3, GM6, GM9 and GM12, respectively) and ADG (P<0.05, 757, 727, 722, 693, and 616g for CON, GM3, GM6, GM9 and GM12, respectively) than other treatments. There was no significant difference in ADFI among treatments. Inclusion of guar meal over 6% resulted in a lower G:F ratio than other treatments(P<0.01), (0.320, 0.316, 0.300, 0.309 and 0.287 for CON, GM3, GM6, GM9 and GM12, respectively). Carcass weight of GM12 treatment was significantly lower than that of other treatments (P<0.05), (91.30, 89.62, 89.98, 89.24 and 86.48kg for CON, GM3, GM6, GM9 and GM12, respectively). However, dressing percentage (P<0.01), (76.34, 76.35, 76.26, 76.40 and 77.21% for CON, GM3, GM6, GM9 and GM12, respectively) and initial pH of the loin (P<0.01), (5.66, 5.64, 5.52, 5.62 and 5.99 for CON, GM3, GM6, GM9 and GM12, respectively) in GM12 treatment was significantly higher than those of other treatments. No significant differences were observed in meat color, cooking loss and backfat thickness after slaughtering. In conclusion, these results suggested that the inclusion of guar meal up to 6% has no negative effects on growth performance and 12% supplementation of guar meal in pig's diet may reduce growth performance but pork quality was not affected by guar meal treatments.

Key Words: guar meal, pig, growth performance

101 Prediction of barley grain feed value for swine using near infrared reflectance spectroscopy (NIRS). M. L. Swift*[1], L. Oatway[1], R. T. Zijlstra[2], W. C. Sauer[2], and J. H. Helm[1], [1]*Alberta Agriculture and Rural Development, Lacombe, AB, Canada*, [2]*University of Alberta, Edmonton, AB, Canada*.

A rapid and accurate prediction of feeding value would enable grain and livestock industries to fairly evaluate the economic value of barley. Barley breeders use near infrared reflectance spectroscopy (NIRS) to evaluate feed value of new cultivars. Original calibrations to predict the apparent total tract digestibility (ATTD) of energy and DE content were based on mobile nylon bag (MNB) studies using 270 and 30 samples of hull-less and hulled barley, respectively. Recently, 175 hulled and 26 hull-less barley samples were collected. In-vitro digestibility of DM (IVDMD) and energy (IVED) was determined using a 3-step assay. In-vivo ATTD of energy was determined for a subset of 55 (39 hulled, 16 hull-less) samples. Calibration models were compared using cross validation statistics, namely 1-VR (1 minus ratio of unexplained to explained variance) and standard error of cross validation (SECV). The 1-VR for IVDMD and IVED were 0.92, 0.88, respectively; the SECV was 1.02 and 1.21 for IVDMD and IVED, respectively. The SECV in predicting the DE content of barley calculated using the IVED data was 62 with a 1-VR of 0.86. The model for ATTD of energy and DE content had a 1-VR of 0.83, 0.81, and SECV of 1.12 and 72, respectively. To merge the original MNB and new IV data into a new calibration model, a variable was added to indicate the specific methods used to predict ATTD of energy. The IVED values were adjusted using the formula Y=1.23x-25.33 to predict ATTD of energy. The best model for ATTD of energy had a 1-VR of 0.83 and a SECV of 1.87. The best model for DE content had a 1-VR of 0.66 and a SECV of 99.3. This data set is the first large scale validation to show that NIRS can predict ATTD of energy and DE content of barley with prediction errors less than 100 kcal/kg. The combined model using MNB and IV data sets can be used to screen new barley cultivars for energy digestibility.

Key Words: barley, energy, NIRS

102 Prediction of metabolizable energy value of meat and bone meal for swine using near infrared reflectance analysis. O. A. Olukosi* and O. Adeola, *Purdue University, West Lafayette, IN*.

The study was conducted to investigate the possibility of developing a prediction equation for apparent metabolizable energy (AME), and apparent nitrogen-corrected metabolizable energy (AMEn) for 33 meat and bone meal samples (MBM) for growing pigs using Near Infrared Reflectance Analysis (NIRA). Thirty-three MBM samples, used in previous AME assays with pigs were used for NIRA. The samples were scanned using a FOSS 6500 scanning monochromator. Duplicate scanning per sample was conducted in reflectance between 400 and 2500 nm at 2 nm increments. The data were transformed to log of inverse reflectance and average spectra of duplicate scans were used to develop calibrations. Spectra were mathematically corrected for light scattering by using standard normal variate and detrend corrections. Calibration performance was calculated as the multiple coefficient of determination (R^2) and standard error of cross validation (SECV). Multivariate calibration was performed with partial least squares regression. The coefficient of determination was greatest for GE (0.89) and lowest for AME (0.10). In addition, R^2 was greater for AMEn compared to AME (0.45 vs. 0.39, respectively). Other parameters for NIRA including standard error of calibration (SEC) and SECV were greater for AME and AMEn compared to the values for GE of the samples. The averages of AME and AMEn for the MBM samples were 2,962 and 2,885 kcal/kg, respectively. The standard error of calibration was 301 for AME and 296 for AMEn. Similarly SECV was 368 for AME and 367 for AME. Both values were greater than the values for GE. Sample number of only 33 is too small to generate a robust NIRA prediction equation for AME and AMEn, however the high values obtained for the parameters of NIRA with regards to GE, CP, fat, Ca, and P indicate the promise of NIRA as an alternative to wet chemistry. In conclusion, these data show that NIRA may be useful in predicting AME and AMEn values for MBM, but this will require the use of much greater sample numbers.

Key Words: near infrared reflectance spectroscopy, meat and bone meal, metabolizable energy

103 Nutritive value of distillers dried grains with solubles (DDGS) for poultry. A. Rogiewicz*, B. A. Slominski, M. Mogielnicka, C. M. Nyachoti, and K. M. Wittenberg, *University of Manitoba*, *Winnipeg, Canada*.

An evaluation of the nutritive profiles of several samples of wheat, wheat/corn, and corn DDGS was undertaken. On average, and in comparison to corn, wheat DDGS were found to be higher in protein (40.7 vs. 30.5% DM), and non-phytate P (0.9 vs. 0.6% DM), similar in lysine (1.0% DM), but lower in fat (4.5 vs. 10.7% DM), carbohydrates (7.1 vs. 10.5% DM) and total fiber (33.3 vs. 35.5% DM) contents. The wheat/corn (70:30 wt/wt) DDGS sample revealed intermediate values for protein (36.7% DM), non-phytate P (0.7% DM), fat (6.4% DM), carbohydrate (8.2% DM), but was higher in lysine (1.05% DM) and total fiber (37.6% DM). In comparison to wheat, high fat and carbohydrate contents of corn DDGS was reflected in higher (P<0.01) AME_n (2,428 vs. 2,097 kcal/kg DM) and TME_n (3,488 vs. 3,160 kcal/kg DM) values. The wheat/corn DDGS sample showed intermediate values for AME_n (2,136 kcal/kg DM) and TME_n (3,238 kcal/kg DM). Substantial differences between the AME_n and TME_n values observed for wheat and corn DDGS (i.e., around 1,000 kcal/kg) would indicate that the energy utilization by broiler chickens of 3-wk of age would be much lower than that of adult birds. Little or no detectable levels of mycotoxins were observed in the DDGS samples. Three experiments were conducted to evaluate the effect of dietary inclusion rate of wheat, corn or wheat/corn DDGS (0, 10, 15 or 15% with carbohydrase addition) on growth performance of chickens (1-21d). Each treatment had 10 replicate pens, 5 broilers per pen. No significant differences (P>0.05) in growth performance were observed between treatments. When compared with the 10% DDGS diet, however, a small but consistent increase in FCR (from 1.38 to 1.41), irrespective of the type of DDGS used, was observed for the 15% DDGS diets. This potentially negative effect was reversed when the 15% DDGS diets were supplemented with enzymes. The improvement in FCR with enzyme addition averaged 2.1% and 2.8% for wheat and corn DDGS, respectively, with the FCR values being similar to those of 10% DDGS diets.

Key Words: DDGS, nutritive value, broiler chicken

104 Effects of distillers dried grains with solubles on the digestibility of energy, DM, AA, and fiber, and intestinal transit time in a corn-soybean meal diet fed to growing pigs. P. E. Urriola* and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was condcuted to measure the effect of distillers dried gains with solubles (DDGS) on the digestibility of energy, DM, AA, NDF, and total dietary fiber (TDF), and the transit time of digesta in a corn-soybean meal diet (control) fed to growing pigs. Sixteen pigs (initial BW: 38.0 ± 1.6 kg) were prepared with a T-cannula in the distal ileum and another T-cannula in the cecum. Pigs were allotted to 2 treatments with 8 pigs per treatment. In period 1, all pigs were fed the control diet, but in periods 2, 3, and 4 pigs were fed the control diet or the control with 30% DDGS. Rate of passage of digesta at the end of the ileum, to the cecum, and over the total tract was measured at the end of period 4. Apparent ileal digestibility (AID) of energy, DM, AA, NDF, and TDF, and the apparent total tract digestibility (ATTD) of energy, DM, NDF, and TDF were measured. Concentration of VFA and pH were analyzed in ileal, cecal, and fecal samples. The AID of Lys (74.1%) was lower ($P < 0.05$) in the DDGS diet than in the control diet (78.6%). The AID of GE, NDF, and TDF were not affected by the inclusion of 30% DDGS in the diet, but the AID of DM in the diet containing 30% DDGS (71.2%) was lower ($P < 0.05$) than the AID of DM in the control diet (74.0%). The ATTD of GE (81.0%), NDF (57.2%), TDF (55.5%), and DM (82.6%) were also lower ($P < 0.05$) in the diet containing DDGS than in the control diet (86.0, 69.3, 66.0, 88.1%, respectively). The concentration of VFA in ileal, cecal, and fecal samples was not different between diets. The pH of ileal and cecal digesta of pigs fed the diet with 30% DDGS (5.48 and 5.48) were greater ($P < 0.01$) than for pigs fed the control diet (5.34 and 5.35, respectively). There was no effect of inclusion of 30% DDGS on the pH of feces. The transit time of digesta from the mouth to the ileum, the cecum, or over the total tract was not affected by DDGS. In conclusion, addition of DDGS to a corn-soybean meal diet fed to growing pigs resulted in a reduction in digestibility of Lys, energy, NDF, and TDF.

Key Words: distillers dried grains with solubles, digestibility, pigs

105 Copra meal and palm kernel meal on growth performance, blood urea nitrogen concentration and meat quality in growing-finishing pigs. Y. H. Choi, G. Y. Lee*, K. H. Kim, S. W. Lee, P. S. Heo, D. H. Kim, H. K. Oh, and Y. Y. Kim, *Seoul National University*, *Seoul, Korea*.

The objective of this experiment was to evaluate the effect of copra meal and palm kernel meal on growth performance, blood urea nitrogen concentration and meat quality in growing-finishing pigs. Treatments were: 1) CON - basal diet(NRC, 1998), 2) C5 - basal diet + copra meal 5%, 3) C10 - basal diet + copra meal 10%, 4) P5 - basal diet + palm kernel meal 5%, 5) P10 - basal diet + palm kernel meal 10%. A total of 120 crossbred ([Landrace × Yorkshire] × Duroc) pigs with an initial body weight of 26.97 ± 0.3kg, were allotted in 5 treatments based on body weight and sex by a RCB design with 6 replicates and 4 pigs per pen. At the end of the experimental, C5, C10 and P5 treatments were numerically similar with CON in body weight (99.75, 98.52, 98.58, 98.53 and 94.60 kg for CON, C5, C10, P5 and P10, respectively) and ADG (792, 769, 770, 770, 727 g for CON, C5, C10, P5 and P10, respectively). The P10 treatment showed lower G:F (P<0.02, 0.3574, 0.3463, 0.3485, 0.3553 and .3371 for CON, C5, C10, P5 and P10, respectively). There were no significant differences in ADFI or blood urea nitrogen (BUN) concentration among all treatments. No significant differences were observed in TBARS value, drip loss, cooking loss, pH of the loin and meat color between CON and other treatments containing copra meal or palm kernel meal. In conclusion, these results suggested that copra meal and palm kernel meal could be supplemented up to 10 or 5%, respectively with no detrimental effects on growth performance, BUN concentration or pork quality. Moreover when copra or palm kernel meal was utilized in growing-finishing pig's diets, approximately 3 to 5% feed cost could be reduced based upon the results of this experiment.

Key Words: copra meal, palm kernel meal, pig

106 Emissions of ammonia and methane from concentrated dairy production facilities in Southern Idaho. A. B. Leytem*, D. L. Bjorneberg, and R. S. Dungan, *USDA-ARS, Kimberly, ID*.

The number of dairy cows in Idaho has increased by approximately 80% in the last decade with concentrated dairy production facilities being the norm. The majority of these production facilities are located in southern Idaho, which has generated regional air quality concerns. To determine the potential air quality impacts of these facilities, we determined emissions of ammonia (NH_3) and methane (CH_4) during four seasons on a 700 cow open-lot dairy (small) using open-path Fourier transform infrared spectrometry (OP/FT-IR) and over a one-year period at a 10,000 cow open-lot dairy (large) using a photoacoustic field gas monitor. Measurements were made at a background location and over the open lots at the small dairy or at the center of the lots at the large dairy. Average NH_3 concentrations over the lots at the small dairy were between 0.13 to 0.41 ppmv, while concentrations at the large dairy were between 0.39 and 0.74 ppmv. Average CH_4 concentrations over the lots at the small dairy were between 2.2 to 3.0, while concentrations at the large dairy were between 2.1 and 6.6 ppmv. Ammonia emission rates, calculated by the WindTrax model, ranged between 0.04 to 0.25 kg NH_3/cow/day for the small dairy and 0.12 to 0.19 kg NH_3/cow/day at the large dairy. Methane emission ranged between 0.20 to 0.55 kg CH_4/cow/day for the small dairy and 0.33 to 1.23 kg CH_4/cow/day for the large dairy. At these average emission rates, farms with greater than approximately 1,650 cows would be required by the State of Idaho to adopt best management practices to reduce ammonia emissions through a permit by rule.

Key Words: emissions, ammonia, methane

107 Ammonia emissions from beef feedlot cattle fed corn-based backgrounding and finishing diets varying in protein concentration and source. K. M. Koenig*, S. M. McGinn, and K. A. Beauchemin, *Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*.

Ammonia (NH_3) emissions are becoming an important environmental and human health issue facing the livestock industry. The objectives of this study were to determine the effects of protein feeding strategies (varying in concentration and ruminal degradability) on NH_3 emissions and growth performance of feedlot cattle fed corn-based backgrounding and finishing diets. Steers (305 kg ± 0.4 kg initial BW) were ranked according to BW, allocated to 24 pens of 13 steers each, and 6 pens were randomly assigned to 4 dietary treatments. The basal diets were corn-based and consisted of 54% silage and 46% concentrate for the backgrounding phase and 9% silage and 91% concentrate for the finishing phase. The 4 dietary treatments included a control (11% CP) and the control diet supplemented (13% CP) with urea and canola meal, canola meal, or corn distillers grains. Feed was offered once per day for ad libitum intake (5% feed refusal). Every 3 wk, 1 pen of steers fed the control diet and 1 pen fed one of the protein supplemented diets were moved to 2 isolated pens for the measurement of NH_3 emissions using the passive diffusion technique. Ammonia traps were replaced daily over 4 consecutive days at heights of 0.5, 1, 2 and 3 m on the north, south, east and west sides of the isolated pens. Growth performance (DMI, ADG, G:F) was improved ($P < 0.05$) in steers fed the urea and canola, and canola supplemented diets during the backgrounding phase, but there was no effect ($P > 0.05$) of protein supplementation on performance of cattle during the finishing phase. Ammonia emissions for the control and protein supplemented diets averaged 3.0 and 4.2 g N/(steer d) for the backgrounding phase and 7.7 and 11.3 g N/(steer d), respectively, for the finishing phase. Feeding the diets with 11% CP compared to 13% CP, lowered NH_3 emissions by 30% with no effect on growth performance during the finishing phase, but performance was reduced during the backgrounding phase.

Key Words: ammonia emissions, protein, beef cattle

108 Methane emissions from finishing beef cattle offered maize silages harvested at four different stages of maturity. E. Mc Geough*[1,2], P. O'Kiely[1], T. M. Boland[2], K. J. Hart[2], P. A. Foley[2], and D. A. Kenny[2], [1]*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*, [2]*School of Agri., Food Sci. & Vet. Med., University College Dublin, Belfield, Dublin, Ireland*.

Sixty cross-bred beef steers, mean initial BW 531 (s.d. 23.8) kg were blocked by weight and randomly allocated to one of five dietary treatments over a 110-day finishing period. The four maize silage harvest dates (treatments I - IV) were, (I) 13 Sept., (II) 28 Sept., (III) 09 Oct., (IV) 23 Oct, with maize silage offered *ad libitum* and supplemented with 3 kg concentrates daily per head. A fifth treatment, *ad libitum* concentrates (ALC) supplemented with 5 kg grass silage daily per head was used as a positive dietary control. Daily methane (CH_4) emissions were measured using the SF_6 tracer technique over 5-day sampling periods. Data were analysed by two way ANOVA accounting for block and treatment using the PROC GLM procedure of SAS. The mean dry matter (DM) (uncorrected for volatiles) of maize silages I to IV was 274, 310, 333 and 328 g/kg respectively, with corresponding *in vitro* DM digestibilities of 710, 723, 734 and 715 g/kg, neutral detergent fibres of 485, 447, 437 and 434 g/kg DM and starches of 315, 362, 381 and 386 g/kg DM. Advancing maize maturity at harvest had no effect on absolute daily CH_4 emissions but all maize treatments were higher (297, 295, 284, 279, g/day; $P < 0.05$) than ALC (226 g/day). Methane emissions, when expressed relative to carcass gain (CG), tended to decrease linearly (354, 354, 311, 314 g/kg CG; $P = 0.06$) across maize treatments and were lowest (236 g/kg CG; $P < 0.05$) for ALC. When expressed on a DM intake basis, CH_4 emissions were higher ($P < 0.05$) for maize silage I than II and IV while ALC again exhibited the lowest CH_4 emissions overall. Maize maturity at harvest did not affect carcass gain, however, an increase in DM intake ($P < 0.01$) was observed with cattle offered harvest II maize silage. The ALC diet consistently reduced CH_4 emissions and supported superior rates of carcass gain when compared with the maize silage treatments.

Key Words: maize, harvest date, methane

109 Effect of ammonia volatilization on manure nitrogen isotope composition. C. H. Lee*[1], A. N. Hristov[1], and S. Silva[2], [1]*Pennsylvania State University, University Park*, [2]*U.S. Geological Survey, Menlo Park, CA*.

The objective of this experiment was to investigate the effect of ammonia losses from dairy manure on manure N isotopic composition *in vitro*. Feces and urine collected from a dairy cow fed a 16% CP diet were mixed (1:1, w/v) and incubated at 21°C for 20 d in 2-L capacity fermentation jars (n = 3). Samples from manure and emitted ammonia were collected daily for chemical and isotopic analyses. Initial concentration of ammonium in manure was negligible, but rapidly increased through d 5 due to hydrolysis of urinary urea. Concentration of urea in manure

decreased from 3.7±0.14 (d 0) to 0.7±0.02 mg/ml in 24 h. Ammonia emission rate peaked on d 5 (144±6.4 mg N/d) and declined thereafter. Cumulative ammonia losses increased exponentially ($r^2 = 90$; $P < 0.001$) during the incubation and were negatively correlated (r = -0.88; $P < 0.001$) with the amount of N in manure, which declined exponentially by 0.7 mg/g manure DM per d ($r^2 = 86$; $P < 0.001$) reaching a plateau by d 5. Similar to our previous observations, ^{15}N abundance of manure N rapidly increased from $\delta^{15}N$ of 0.1±0.36 (d 0) to 6.7±0.80 (d 2) and reached a plateau by d 5 (10.1±0.42‰). This rapid increase in $\delta^{15}N$ was due to the loss of depleted in ^{15}N ammonia. Delta ^{15}N of volatilized ammonia increased quadratically ($r^2 = 88$; $P < 0.001$) from -22.5±0.68 (d 1) to -16.5±0.09 (d 5) and -1.3±2.55‰ (d 20). At the maximum $\delta^{15}N$ of manure (d 5 and beyond), the decreasing concentration of ammonium in manure counterbalanced its increasing $\delta^{15}N$ as a result of volatilization. Cumulative ammonia loss (mg N) was best described ($r^2 = 92$; $P < 0.001$) by a 3-parameter model including an intercept (1778, SE=395), $\delta^{15}N$ of emitted ammonia (61.4‰, SE=4.1) and manure N (67.5‰, SE=19.0), and manure N concentration (-14.7 mg/g DM, SE=6.5). This experiment demonstrated that ammonia volatilization from manure is very rapid in the first 2-3 d (originating primarily from urinary urea) and that $\delta^{15}N$ of aged manure and emitted ammonia can be successfully used to predict ammonia emissions from cattle manure.

Key Words: manure, ammonia, ^{15}N isotope

110 On-farm evaluation and demonstration of ammonia reduction best management practices (BMPs) for feedlots and dairies. N. M. Marcillac-Embertson*, J. Pritchett, J. L. Collett, and J. G. Davis, *Colorado State University*, *Fort Collins*.

Globally, agriculture is the largest source of atmospheric ammonia (NH3), with livestock accounting for up to 60% of the total emissions. The purpose of this four part study was to minimize the negative impacts of NH3 through the adoption of field-tested, effective, and economical BMPs for Colorado dairies and feedlots. First, a comprehensive literature review was conducted to identify proven BMPs that had potential for NH3 reduction on dairies and feedlots. Second, a detailed survey was sent to dairy and feedlot producers in Colorado, Iowa, Kansas, and Nebraska to learn about producers current BMP practices and constraints to adoption of additional BMPs. Third, selected BMPs were tested on 6 dairy and 6 feedlot operations from June to October, 2007, 2008, to evaluate NH3 reduction potential, ease of use, and economic viability. Some of the 12 BMPs tested were: bedding, alum, scraping feedlot pens, freestall manure removal type, natural vs conventionally fed cattle, water application to drylots, composting vs stockpiling of manure, harrowing woodchips into drylots, and natural lagoon covers. Ammonia concentration was measured from surfaces using a real-time NH3 analyzer (Nitrolux-S, Pranalytica) at eight coincident measurements per sample location (multiple locations per sample area). Results for each BMP sampling model were analyzed using a mixed model that accounted for day and weather effects. Significance was evaluated at P=0.05 using lsmeans. Compost bedding in freestalls had 43% lower NH3 than sand over 30 days (P=0.06); alum application to feedlot pen surfaces was not economical, and had limited effectiveness (56% for 2 days, than back to baseline); scraping feedlot surfaces decreased NH3 by 10% (P=0.51); wood chips decreased ammonia in drylots by 40% (P=0.19). Part four was the development of BMP educational resources (i.e., website, handbook, online factsheets, a BMP photo gallery, and an NH3 reduction and implementation cost-estimator). The overall goal of the project was to provide producers with the necessary information to make good management choices, while preserving agricultural in Colorado.

Key Words: livestock, ammonia, BMP

111 Nitrogen volatilization losses from bed pack in dairy cow barns. A. S. Atzori*, R. Boe, P. Carta, A. H. D. Francesconi, and A. Cannas, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Sardinia, Italy*.

The objective of this work was to measure N volatilization (NVOL) from bedded-pack lactating dairy cow barns. Feed intake, milk production, bedding material used and air temperature were monitored in 3 dairy farms near the town of Arborea (Sardinia, Italy; 39°46'26" N, 08°34'53" E, 7 m a.s.l.) during one month per season from summer 2007 to spring 2008. In each season the bed pack of each farm was sampled and analyzed about once per week during the 1-month interval between excretion and removal of bed packs from barn floors. The N to P ratio marker method was used to estimate NVOL, considering P as an internal non-volatile marker in milk and manure. Nitrogen and P excretions were estimated by nutrient balance as intake minus N and P excreted in milk. The results showed limited variation among seasonal means of NVOL, with significantly higher values in summer than in fall (Table 1). NVOL losses were associated to bed-pack temperature (r = 0.32; $P<0.03$), DM (r = 0.40; $P<0.004$) and N content (r = -0.30; $P<0.04$) but not to mean air temperature (r = 0.18; $P>0.20$). As average, the measured annual mean NVOL in bed pack was equal to 39.1% of excreted N (Table 1). However, since concrete floor, instead of bed pack, covered the feeding and walking areas of the barns, a NVOL of 42.5% of N excreted (as measured in cubicle barns by Atzori et al., 2008) was considered for those areas. Therefore, the annual coefficient of NVOL in bedded-pack barns was equal to 40.8% of N excreted. This value is much higher than that considered by the regulations of many European countries.

Table 1. Air temperature, bed-pack characteristics and NVOL in bedded-pack barns.

Samplings		Air temperature	Bed-pack temperature	Bed-pack density	Bed-pack DM	Bed-pack N	NVOL
Season	n	C°	C°	kg/m^3	%	% DM	% of N excreted
Summer	12	24.4	26.4^{A}	268.0^{B}	35.8^{A}	2.06^{b}	44.1^{a}
Fall	9	17.2	26.2^{AB}	462.7^{A}	27.1^{B}	2.15^{ab}	35.9^{b}
Winter	12	9.3	23.1^{B}	502.6^{A}	24.8^{B}	2.22^{ab}	37.9^{ab}
Spring	16	17.3	24.7^{AB}	511.9^{A}	25.2^{B}	2.37^{a}	38.6^{ab}
Annual mean	4	17.1	25.1	436	28.2	2.20	39.1
SEM		2.7	0.7	49	2.2	0.06	1.5

^{A,B} = $P<0.01$; ^{a,b} = $P<0.05$

Key Words: bed pack, N volatilization, dairy cow

112 DairyGHG: A tool for evaluating the greenhouse gas emissions and carbon footprint of dairy production systems. C. A. Rotz* and F. Montes, *USDA/ARS*, *University Park, PA*.

Greenhouse gas (GHG) emissions and their potential impact on the environment have become important national and international concerns. Dairy production, along with all other animal agriculture, is a recognized source of GHG emissions, but little information exists on the net emissions from our farms. Component models for predicting all important sources of methane, nitrous oxide, and carbon dioxide emissions from

primary and secondary sources in dairy production were integrated in a software tool called the Dairy Greenhouse Gas Model or DairyGHG. This tool calculates the carbon footprint of a production system as the net exchange of all GHGs in carbon dioxide equivalent (CO2e) units per unit of milk produced. Primary emission sources include enteric fermentation, manure handling facilities, cropland used in feed production, and the combustion of fuel in the machinery used to produce feed and handle manure. Secondary emissions are those occurring during the production of resources used on the farm, which can include fuel, electricity, machinery, fertilizer, pesticides, plastic, and purchased replacement animals. A long-term C balance is assumed, which does not account for potential depletion or sequestration of soil carbon. Depending upon farm size, milk production level, and the feeding and manure handling strategies used, the carbon footprint of production systems was found to range from 0.4 to 0.8 kg CO2e per kg of milk produced. This footprint was most sensitive to the amount of methane produced through enteric fermentation, moderately sensitive to the GHG emissions during long-term manure storage, and mildly sensitive to the amount of fuel, electricity and inorganic fertilizer used on the farm. DairyGHG provides a relatively simple tool for evaluating management effects on net GHG emissions and the overall carbon footprint of dairy production systems. This tool is available at http://www.ars.usda.gov/Main/docs.htm?docid=17355 for download and installation on computers using Windows® operating systems.

Key Words: greenhouse gas, carbon footprint, dairy farm

113 Greenhouse gas emission rates from Holstein and Black Angus-Cross feedlot steers and calves. K. R. Stackhouse*, Y. Pan, Y. J. Zhao, M. J. Tobias, and F. M. Mitloehner, *University of California*, *Davis*.

According to United Nations estimates, livestock contributes 18% of the global anthropogenic greenhouse gasses (GHG); however, actual emission data that help verify emission models remain sparse. The present study quantified GHG emissions from a total of 56 steers and calves. Animal types were assigned to three replicate groups (n = 3) of three animals per group and included: 1) 544 kg Holstein steers (1200H), 2) 544 kg Black Angus-Cross steers (1200BA), 3) 340 kg Holstein steers (750H), 4) 340 kg Black Angus-Cross steers (750BA), 5) 159 kg Holstein steers (350BA), and 6) 54 kg Holstein calves (120H). Cattle were housed in an environmental chamber for 24 h, after which waste remained for an additional 24 h. Steers were fed a 90% concentrate diet and calves were milk bottle and grain fed. Greenhouse gasses carbon dioxide (CO_2), methane (CH_4) and nitrous oxide (N_2O) were measured in 20 min intervals, using a photoacoustic gas analyzer. Emission rates ($g^{-1}cow^{-1}h$) were analyzed over time using PROC MIXED in SAS. Compared to the background, GHG emissions increased when steers entered the chamber; e.g., 1200BA emissions of (CO_2) increased by 366.67 ($g^{-1}cow^{-1}h$), (CH_4) by 3.78 ($g^{-1}cow^{-1}h$)and (N_2O) by 0.05 ($g^{-1}cow^{-1}h$) ($P < 0.001$). Associations of GHG to body weight and cattle breed were identified ($P < 0.05$). In summary, GHG are mainly produced by enteric fermentation and respiration, rather than by the animals' fresh waste, and differ greatly across life stages of cattle. The present data will be useful to verify models and to enhance emission inventories for enteric fermentation, respiration, and fresh waste for numerous cattle life stages across the U.S. beef industries.

Key Words: beef cattle, greenhouse gas, environmental chamber

114 Effects of urine application on chemistry of feedlot pen surfaces. N. A. Cole*[1], A. M. Mason[1], R. W. Todd[1], and D. B. Parker[2], [1]*USDA-ARS-CPRL*, *Bushland, TX*, [2]*West Texas A&M University*, *Canyon*.

Beef cattle feedlots can emit significant quantities of ammonia that may adversely affect air quality and decrease the fertilizer value of manure. The major source of ammonia loss may be urinary urea. We conducted three studies to evaluate the effects of urine on the chemistry of feedlot pen surfaces. In Exp.1, samples were collected from the loose surface manure and the underlying layers (dry hard pack, wet hard pack, soil) of nine pens at each of three commercial feedyards. Samples were collected from an area that had recent (< 10 minutes) urine deposition, and a pen area devoid of urine. The samples were analyzed for DM, ash, pH, electrical conductivity (EC), nitrate-N, ammonium-N, and total N, C, and P. The loose surface manure from urine spots had lower ($P < 0.05$) DM content (59.7 vs. 88.2%), and greater ($P < 0.05$) pH (8.08 vs. 7.80), EC (1.45 vs. 1.22 S/m), ammonium-N (6,755 vs. 2,381 ppm), total N (3.00 vs. 2.73%), and ammonium-N:total N (21.8 vs. 8.5%) than urine-free areas. In Exp. 2 (Summer) and 3 (Spring), 4 L of deionized water or artificial urine (21.4 g of urea/L) were applied to 1 m square plots (6/treatment) on a feedlot surface. The loose manure on the pen surface was sampled for 7 d and chemically analyzed. Compared to untreated plots, ammonium-N concentrations of plots treated with artificial urine increased ($P < 0.001$) from 391 to 6,343 ppm and pH of plots increased from 8.1 to 8.5 in less than 5 min following application and remained elevated ($P < 0.05$) for 79 to 96 h. Water applications caused a short term (2 to 4 h) increase in ammonium-N concentrations. These results support the hypothesis that ammonia losses from feedlot pens occur rapidly from urine spots. Therefore, we conclude that 1) methods which do not take this spatial variability into account will greatly underestimate ammonia emissions, and 2) pen surface amendments used to control ammonia losses must be on the pen surface continuously for optimal efficacy.

Key Words: cattle, urine, ammonia

115 Modifying available grazing time to increase dairy cow urine capture. C. E. F. Clark*[1], K. L. M. McLeod[1], C. B. Glassey[1], P. Gregorini[1], K. Betteridge[2], and J. G. Jago[1], [1]*DairyNZ, Hamilton, Waikato, New Zealand*, [2]*AgResearch*, *Palmerston North, Manawatu, New Zealand*.

A major source of nitrogen in New Zealand's ground and river water is dairy cow urinary nitrogen excreted as a result of excess dietary protein in grazed pasture. Nitrogen loss to the environment may be reduced by modifying available grazing time to capture urinary nitrogen. Forty-eight Holstein Friesian cows milked twice a day in early lactation (Days in milk = 35±9 days) were allocated to three treatments replicated twice. Cows were offered perennial ryegrass pasture for four hours after each milking (2x4), eight hours between milkings (1x8) or for the 24 hour period excluding milking times (control). The 2x4 and 1x8 treatments were on a bark pad when not grazing or being milked to capture urination. During the experimental period, each treatment group was allocated the same daily herbage allowance of 33 kg DM per cow (pre-grazing cover 3,200 kg DM/ha, P=0.38). No supplements were fed. The frequency and location of cow urination events were determined for 6 cows within each treatment using urination sensors (AgResearch, Palmerston North, New Zealand) on day 1, 2, 7 and 8 after a 10 day adaptation period. There was no difference (P=0.10) between treatments in the number of urinations per cow per day nor the milk urea concentration (P=0.44). However, the 2x4 and 1x8 treatments captured approximately 25% more urinations (P<0.05) on the bark pad than the control. These findings highlight an opportunity to reduce nitrogen loss to the environment.

Table 1. Cow urination frequency and location for the 2x4, 1x8 and control treatments

	2x4[#]	1x8	Control	sed
Urinations/cow/day	13.82	12.73	14.28	6.02
Captured (pad + parlour)	0.35[a]	0.38[a]	0.10[b]	0.07
Uncaptured (pasture + race)	0.65[a]	0.62[a]	0.90[b]	0.07
Pasture	0.45[a]	0.51[a]	0.82[b]	0.06
Bark pad	0.13	0.23		0.08
Race	0.20[a]	0.11[ab]	0.07[b]	0.04
Milking parlour	0.22[a]	0.15[b]	0.10[b]	0.02
Milk urea (ng/mL)	7.76	8.20	7.29	0.61

[#]Different superscripts indicate significantly different means (P<0.05)

Key Words: pasture, urine capture, dairy

Ruminant Nutrition: Dairy 1

116 Production of angiopoietin-like protein 4 in ruminal tissue is decreased with increasing dietary fermentability. L. K. Mamedova*[1], G. B. Penner[2], K. A. Beauchemin[3], M. Oba[2], and B. J. Bradford[1], [1]*Kansas State University, Manhattan*, [2]*University of Alberta, Edmonton*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, Canada*.

Angiopoietin-like protein 4 (ANGPTL4, also known as FIAF) is a secreted protein that functions as a lipoprotein lipase inhibitor and a modulator of angiogenesis. Although it is produced by multiple tissues, gut secretion of ANGPTL4 has been implicated in host/microbe interactions, making the ruminal epithelium a site of interest. Ruminal tissues from 2 studies were used to assess effects of dietary fermentability on ANGPTL4 expression. In the first study, 12 mature, non-lactating, non-gestating Holstein cows were randomly assigned to low-concentrate (8% of dietary DM) or high-concentrate (64% of dietary DM) diets for a minimum of 28 d. Ruminal pH was monitored continuously for 3 d and ruminal fluid samples were collected for VFA analysis, then animals were euthanized and ruminal tissue was collected. In the second study, 8 beef heifers (700 kg final BW) were fed a finishing diet (90% concentrate, DM basis) for 140 d and then either left on the finishing diet or assigned to a backgrounding diet (60% concentrate, DM basis) for another 75 d. Ruminal pH was monitored continuously for 6 d prior to euthanization and ruminal tissue collection. Abundance of ANGPTL4 mRNA was measured by quantitative real-time PCR and protein by Western blotting. Diet effects were analyzed by ANOVA and correlations with rumen parameters were assessed by regression analysis. In the first study, the low-concentrate diet tended to increase ANGPTL4 mRNA by 120% ($P = 0.08$), although no effect on protein abundance was detected. Transcript abundance tended to correlate with mean ruminal pH ($P = 0.07$) and was inversely correlated with total VFA concentration ($P = 0.03$). In the second study, the backgrounding diet increased ANGPTL4 protein abundance ($P < 0.001$), and a positive relationship with ruminal pH was also observed ($P < 0.01$). These findings suggest that increased ruminal fermentation results in decreased expression of ANGPTL4 in ruminal tissue.

Key Words: rumen, epithelium, fermentability

117 Mammary transcriptomics response to milk fat-depressing or milk fat-enhancing diets in lactating dairy cows. G. Invernizzi*[1,2], B. J. Thering[1], D. E. Graugnard[1], P. Piantoni[1], M. A. McGuire[3], G. Savoini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana*, [2]*University of Milan, Milan, Italy*, [3]*University of Idaho, Moscow*.

Gene networks regulating lipid metabolism were studied in mammary tissue biopsied at 0, 7, and 21 d of feeding mid-lactation cows (n = 5-6/diet) a milk fat-depressing (MFD, fish/soybean oil (1:2) at 3.5% of DM) or a milk fat-enhancing (MFE, EnergyBooster100, 3.5% of DM) diet for 28 d. Quantitative PCR was used for transcript profiling of 28 genes. Milk yield was not affected ($P > 0.05$) by diets (29 kg/d), but milk fat % (FP) decreased ($P < 0.05$) gradually (3.7% to ≈2.5%) with MFD and reached a nadir essentially by d 13 of feeding. MFE did not increase FP above controls and averaged 3.7%. MFE increased (interaction effect) genes associated with fatty acid (FA) import into cells (LPL, CD36), FA activation (ACSL1), intracellular transport (FABP3), and triacylglycerol synthesis (GPAM, LPIN1) mRNA at 7 and 21 d; whereas, MFD increased CD36, FABP3, GPAM, and ACSL1 mRNA only by 21 d. In addition, MFE increased mRNA expression of genes associated with fatty acid synthesis (ACSS2, ACACA, FASN) and synthesis of 20:5n3 (FADS1) during the treatment period. SCD abundance increased linearly through 21 d with MFE, whereas feeding MDF resulted in marked increase by 7 d followed by a return to basal expression by 21 d. ACACA was not affected by MFD and FASN increased by 21 d. Genes associated with lipid droplet formation and fat secretion (XDH, ADFP) in mammary tissue increased over time only with MFE. Among transcription regulators, MFE increased SREBF1 and INSIG1 throughout the study. MFD, however, resulted in higher expression of INSIG1 by d 7 and lower SREBF1 by d 21 vs. 0. Stearic, oleic, and palmitic acid molar yield was markedly lower by 7 through 21 d with MFD vs. MFE. Overall gene expression profiles with MFE agreed with production of milk fat and major fatty acids. Data also suggested a role for endogenous synthesis of oleic acid via SCD as well as INSIG1 in milk fat synthesis regulation.

Key Words: genomics, lipid nutrition, fatty acids

118 Mammary glucose metabolism in response to energy and/or protein supply in lactating dairy cows. S. Lemosquet*[1,2], F. Bardey[1,2], H. Rulquin[1,2], H. Lapierre[3], and J. Guinard-Flament[2,1], [1]*INRA, Rennes, France*, [2]*Agrocampus ouest, Rennes, France*, [3]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*.

Milk yield usually increases in response to increased supply of energy (E) and protein (P), alone or in combination, in cows fed under require-

ments. Does this increment occur through a similar mechanism: a higher mammary glucose (GLC) uptake leading to an increased lactose yield? Four multiparous dairy cows received 4 diets providing 70% (LP: 1324 g PDI/d) or 125% (HP: 2247 g PDI/d) of protein requirements and 70% (LE: 22.8 Mcal NE_L /d) or 100% (HE: 30.9 Mcal NE_L /d) of energy requirements, in a Latin Square design with 14-d periods. Requirements (INRA, 1989) were determined based on milk yield predicted at mid experiment using a milk persistency of 98%. Cows were fitted with an ultrasonic flow probe to measure blood flow on half udder and with two catheters to determine arterio venous differences in concentrations on d 12 of each period (with samples collected every 2 h between the 12h milking interval). Milk yield increased from 25.3 to 29.7 kg/d with P supply (P<0.01) and from 25.9 to 29.1 kg/d with E supply (P<0.01), with no interaction between E and P. Lactose yield on half udder (d 12) increased (P<0.01) by 17% and 15% with P and E, respectively. Mammary GLC uptake increased by 7% with P (from 222 to 238 mmol/h; P = 0.05) and by 19% (from 210 to 250 mmol/h; P<0.01) with E, with no interaction. The increment observed with E was mainly due to an increased mammary plasma flow. The ratio of lactose yield to GLC uptake averaged 62%, 63%, 56% and 64% in LELP, LEHP, HELP, HEHP, respectively, and tended to be lower in HELP (P×E interaction, P = 0.09). These results suggest different mammary regulations of glucose metabolism with P and E. Increased P supply could improve lactose yield with a concomitant higher GLC uptake and a more efficient lactose synthesis whereas E supply could improve it through a higher GLC uptake, even associated with a less efficient conversion of GLC towards lactose when P supply remained low.

Key Words: dairy cow, glucose, mammary gland

119 Regulation of adipose tissue metabolism in dairy cattle as affected by genetic merit and dietary efficiency. S. Rocco, A. M. Youngquist, G. Duncan, C. Schachtschneider, J. Miller, J. L. Vierck, A. Hutjens, J. P. McNamara*, and A. Lowe, *Washington State University*, *Pullman*.

To continue to define mechanisms of control of energy metabolism in the most efficient dairy cattle, 48 cows were allotted to High Genetic (sire PTAM = 870 kg), or Low Genetic (PTAM = 378); and half of each group was fed either to energy requirements (HE) or to 90% of requirements (LE), other components fed to requirements, from 21 d prepartum to 56 DIM. Samples of adipose tissue were taken at -21, -7, 7, and 28 days around parturition and lipolysis, lipogenesis and expression of key genes that control these pathways were measured. Feed intake in the dry period (-21 to -1 d prepartum) was 13.6 and 12.7 kg DMI/d for HE and LE (SE = 1.5); during lactation (1 to 56 DIM) it was 21.2 and 17.4 kg/d (SE = 1.4). Milk yield was 36.1 and 33. 3 kg/d for HG and LG for 27-56 DIM (P<0.05) across diets and parities. Milk yield was 28.6, 26.0 for HG in parity 1 and 2; and 38.1 and 38.0 (SE 1.2) kg/d for LG in parity 1 and 2. The genetic dietary interaction for the LGHE, HGHE, LGLE and HGLE groups was 33.7, 32.8, 31.7, 31.5 kg/d. Thus HG was slightly more protective of milk production when challenged with LE. Loss of BW, BCS and body fat were greater (P<0.05) on LE diet and in parity 2. Rates of lipolysis in adipose tissue increased in early lactation and were greater on the LE diet. Lipogenesis was similar in the dry period on LE and HE, but on the LE was less than (P < 0.05) 50% of that on the HE diet. In HG animals, lipogenesis was faster in the dry period and first week of lactation, but was lower at 28 DIM. Expression of genes that control lipolysis was similar to higher in lactation, those that control lipogenesis decreased in early lactation and were highly related (P <0.05) to rates of lipogenesis. Animal of greater genetic merit (sire PTAM) peaked with greater milk production on the same amount of energy, and protected milk production and body energy stores better than those from sires with lesser PTAM.

Key Words: lactation, adipose tissue, genetic merit

120 Changes in deposition of visceral adipose tissues and expression of lipogenesis-related genes induced by diets with different energy levels in non-lactating cows. P. Ji*, J. J. Loor, A. Nikkhah, M. Bionaz, N. A. Janovick, and J. K. Drackley, *Department of Animal Science, University of Illinois*, *Urbana*.

Over-accumulation of adipose lipid prepartum increases susceptibility to metabolic disorders postpartum. Effects of moderate excess (M) or low dietary energy (L) on visceral adipose tissue deposition and expression of lipogenic genes were assessed in 18 non-pregnant dry cows. Cows were blocked by BCS and randomly assigned to either an M (NEL = 1.61 Mcal/kg) or L (NEL = 1.37 Mcal/kg) diet. The M diet contained 74.5% (DM basis) forage without straw, while the L diet contained 84.6% forage including 41.9% wheat straw. Cows were euthanized after 8 wk of feeding. Visceral adipose tissues were weighed and sub-samples from subcutaneous (Su), mesenteric (Me), and omental (Om) adipose were snap-frozen in liquid-N. Cows fed M had greater (P < 0.05) DMI than L (15.7 vs. 10.9 ± 0.6 kg), as well as greater Om (28.07 vs. 17.49 ± 1.31 kg) and Me weights (21.99 vs. 12.1 ± 2.35, kg). BCS did not differ between groups (3.62 vs. 3.55 ± 0.11 for M and L). Thirty genes with roles in insulin resistance, inflammation, and/or lipogenesis were chosen for quantitative PCR. Among 6 lipogenic genes studied initially, abundance of thyroid hormone responsive SPOT 14 (THRSP) and stearoyl-CoA desaturase (SCD) was greater for M than L. Abundance of SCD (Su, Me, and Om = 3.86, 2.92, and 3.32 ± 0.25), acyl-CoA synthetase long-chain family member 1 (ACSL1) (Su, Me and Om = 3.71, 4.15 and 3.82 ± 0.15) and adipose differentiation related protein (ADFP) (Su, Me and Om = 4.21, 4.04 and 3.77 ± 0.09) varied among tissue sites. No treatment or tissue source effects were detected for mRNA abundance of acetyl-coenzyme A carboxylase alpha (ACACA) or peroxisome proliferator-activated receptor gamma (PPARG). A moderate excess of dietary energy increased visceral lipid deposition which was undetectable by BCS. Transcriptomics revealed that lipogenic genes across adipose sites differ in sensitivity to altered dietary energy intake.

Key Words: visceral adipose tissue, dry period, gene expression

121 Contribution of changes in gene transcription in dairy cattle adipose tissue to control of metabolic pathways dictating increased overall efficiency. J. M. Sumner, C. Shachtschneider, A. Hutchins, A. M. Youngquist, G. Duncan, S. Rocco, J. Miller, J. L. Vierck, J. P. McNamara*, and A. Lowe, *Washington State University*, *Pullman*.

Metabolic adaptations in adipose tissue contribute to establishment and maintenance of lactation. Previous work determined that several enzymes and pathways are controlled by gene transcription for enzyme synthesis, and hormonal and neurocrine regulation of enzyme activity. Our objective was to evaluate the mechanisms of gene transcriptome changes underlying the adipose response to lactation. We tested the hypothesis that genes encoding for proteins that regulate metabolism would change expression in adipose tissue of dairy cattle in early lactation. Animals (n = 24) from two different experiments were used and ranged from 8.8 to 52.2 kg/d milk production, and from 8 to 32

kg/d DMI. They lost a range of +9.1 to -113.6 kg BW, from 0 to -1.0 BCS units. Subcutaneous adipose tissue biopsies were obtained at -30 adn 30 DIM, tissue extracted RNA, and hybridized to the Affymetrix Genechip® Bovine Genome Array. Genes that control anabolic pathways decreased from 30 d prepartum to 30 DIM ($P < 0.05$), including (mean (% change), (SEM)): SREBP, -25.1, (6.2); GLUT1, - 57.3 (14.1); THRSP14, -30.8 (7.4); LPL, -48.4 (7.7) and AcCoA Carboxylase, -60.6 (13.0), ribosomal S2 expression did not change. These genes were all highly correlated ($r > .80$, $P < 0.05$) with in vitro rates of lipogenesis from acetate, and regression of transcript change on milk production was 0.18 for AcCoA carb and 0.26 for ATP-CL ($P < 0.05$). Expression of genes directing lipolytic pathways were much more varied, including Ca channel subunit 338% (203); B2AR 52.0 (8.8); PKC receptor 10.1 (2.6) and HSL mRNA 23.0 (17.9). The regression of transcript change on milk was 0.30 and 0.25 for B2AR and HSL mRNA. We have confirmed and extended earlier observations that reductions in lipogenesis are primarily due to a systematic reduction in enzyme synthesis, while increases in lipolysis are a combination of increases in transcription and metabolic flux. Both are directly related to milk productive ability and efficiency and can help to identify the mechanisms that direct the most efficient milk production.

Key Words: gene transcription, efficiency, lactation

122 Nitrogen recycling in lactating dairy cows consuming diets predicted by CPM Dairy to be deficient in either ruminal N or metabolizable protein. E. B. Recktenwald*, D. A. Ross, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

Twelve ruminally fistulated, lactating dairy cows (155 DIM ± 13d, 609 kg BW ± 32 kg) were assigned to three diets in a randomized complete block to observe the effects of nitrogen (N) source and quantity consumed on urea N recycling. Diets consisted of approximately 45% corn silage, 2% wheat straw, and 53% concentrates and were as follows: 16% CP and balanced for ruminal N and MP (Diet P), 14% CP and deficient in MP (Diet N), 14% CP and deficient in ruminal N (Diet T). Cows were infused in the jugular vein with 15N15N urea (0.0208 g urea/h) in saline for 72 hr, after which samples of feces, urine, plasma, milk, rumen fluid and total rumen contents were collected. Protozoa, liquid associated bacteria, and solid associated bacteria were isolated based on several published methods. Microbial and fecal samples were analyzed for 15N enrichment by IRMS. Urinary urea was isolated by fractionation on a AG 50W-X8 Dowex column and analyzed by IRMS. Urea kinetics were determined by fecal 15N and urinary 14N15N and 15N15N-urea enrichments using the model of Lobley et al. (2000). Due to total collection problems, urinary urea excretion was estimated according to Nennich et al. 2006 and CPM Dairy v3.0. Nitrogen intake was lower ($P<0.05$) for cows fed Diet T (443 g N/d) compared with cows fed Diets P (620 g N/d) and N (546 g N/d). Urea entry rate followed N intake with 208, 293, and 222 g urea-N/d, but were not different ($P > 0.05$) among diets. Urea entry to the GIT and urea-N return to the ornithine cycle averaged 98 and 69 g urea-N/d, respectively, with no differences ($P > 0.05$) among treatment. The portion of urea production excreted in the urine or contributing to anabolic use averaged 0.65 and 0.27, with no differences ($P > 0.05$) among treatment. The atom percent excess (APE) of liquid associated bacteria (9.4, 6.1, and 6.2 APE, Diets T, P, and N, respectively) and protozoa (7.8, 5.3, and 5.1 APE) were higher for cows on the T diet, but were significant only for the protozoa. Solid bacterial APE averaged 5.1 APE, and were not different ($P > 0.05$) among diets.

Key Words: urea recycling, metabolizable protein, ruminal nitrogen

123 Effect of metabolizable methionine (MET) and lysine (LYS) concentrations on milk production and N utilization in lactating dairy cows. Z. H. Chen*[1], G. A. Broderick[2], N. D. Luchini[3], B. K. Sloan[3], and E. Devillard[4], [1]*University of Wisconsin*, *Madison*, [2]*U. S. Dairy Forage Research Center*, *Madison, WI*, [3]*Adisseo USA Inc.*, *Alpharetta, GA*, [4]*Adisseo, France S.A.S.*, *Commentry, France*.

The amino acids methionine and lysine are considered the two most limiting AA in high producing dairy cows. Balancing rations for MET and LYS according to NRC 2001 may allow lower levels of MP and CP to be fed, without compromising yield of milk components, reducing urinary N excretion and improving feed efficiency. Different commercial sources of methionine are proposed as effective sources of MET. The isopropyl ester of HMB (HMBi) appears to be partly absorbed across the rumen wall with the balance being ruminally metabolized. Seventy cows were blocked by parity and DIM into 14 blocks and randomly assigned within blocks to diets based on alfalfa and corn silage with (DM basis) 28% NDF: 1 diet with 16.9% CP, 6.17 LYS and 1.85 MET as % of MP (positive control; PC), 1 diet with 15.7% CP, 6.60 LYS and 1.84 MET as a % of MP (negative control; NC); the 3 supplements added to NC were 0.16% MetaSmart (0.57 HMBi), 0.06% Smartamine M (SM) + 0.1% HMB (Rhodimet AT 88), or 0.06% Smartamine M; all were estimated to improve the LYS to MET ratio from 3.6 to 3.0. After a 2-wk covariate on the same diet, cows were fed test diets continuously for 12 wk. Data will be analyzed as a randomized complete block using Mixed Model of SAS with covariate production and repeated measures in the model. Diet did not affect DMI, milk yield, or Milk N/N intake. However, adding HMBi to the NC increased yield of energy corrected milk (ECM), milk protein and SNF contents. Moreover, there were trends for effects on milk fat content, fat and protein yield. Feeding the PC elevated MUN without improving production. Results with the different Met sources were similar, suggesting that using HMBi with an assumed rumen absorption of 50% is equivalent to using Smartamine M with an assumed MET contribution of 0.6g/g.

Table 1.

Item	NC	HMBi	HMB+SM	SM	PC	SEM	P > F
DMI, kg/d	24.9	25.7	25.1	24.6	24.7	0.4	0.44
Milk, kg/d	41.8	42.1	41.7	41.7	41.2	0.9	0.98
ECM, kg/d	37.9^{b}	41.0^{a}	39.0^{ab}	40.2^{ab}	39.4^{ab}	0.95	0.02
ECM/DMI	1.54^{b}	1.59^{ab}	1.57^{ab}	1.63^{a}	1.61^{ab}	0.04	0.04
Fat, %	3.52	3.93	3.66	3.77	3.85	0.11	0.08
Fat, kg/d	1.42	1.60	1.54	1.62	1.61	0.06	0.07
Protein, %	3.03^{c}	3.19^{a}	3.17^{a}	3.15^{ab}	3.05^{bc}	0.04	0.01
Protein, kg/d	1.24	1.30	1.33	1.33	1.25	0.03	0.09
SNF, %	8.73^{b}	8.94^{a}	8.92^{a}	8.84^{ab}	8.73^{b}	0.05	0.01
Milk N/N Intake, %	32.7	32.7	33.2	34.1	30.9	0.92	0.14
MUN, mg/dl	10.0^{c}	10.2^{c}	10.8^{bc}	11.2^{b}	13.2^{a}	0.33	<0.01

Key Words: methionine, HMB, HMBi

124 Effects of jugular infused branched-chain amino acid supplementation on milk protein synthesis in high producing dairy cows. J. A. D. R. N. Appuhamy*[1], J. R. Knapp[2], C. A. Umberger[1], and M. D. Hanigan[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Fox Hollow Consulting, LLC*, *Colombus, OH*.

In addition to lysine (Lys) and methionine (Met), current ration balancing programs suggest that branched chain amino acid (BCAA) supply

may also be limiting in dairy cows. The objective of this study was to investigate whether BCAA become limiting for milk protein synthesis when Met and Lys supply were not limiting. Nine multiparous Holstein cows with average milk production of 53.5 ± 7.11 kg/day were randomly assigned to 7 d continuous jugular infusion treatments of saline (CTL), Met and Lys (ML; 12 g and 18 g /d respectively), and ML plus leucine, isoleucine, and valine (ML+BCAA; 35 g, 15 g, and 15 g/d respectively) in 3 x 3 Latin square design with three infusion periods separated by 7 d non-infusion periods. The basal diet consisted of 40% corn silage, 14% alfalfa hay, and a concentrate mix. During the last 3 d of each infusion period, milk and feed samples were collected for composition analysis. Daily feed intake and milk production of individual cows were recorded. Infusion treatments had non-significant effects on dry matter intake, milk yield, fat percentage and fat yield. Protein yield (kg/d) and protein percentage (%) were not significantly different between ML (1.56 ± 0.10 and 2.88 ± 0.03 respectively) and ML+BCAA (1.52 ± 0.11 and 2.81 ± 0.03 respectively), but they were significantly greater than that of CTL (1.41 ± 0.11 and 2.71 ± 0.03 respectively). Protein efficiency, expressed as milk protein yield divided by total crude protein intake (feed plus infusate), was not significantly different between ML (0.41 ± 0.02) and ML+BCAA (0.38 ± 0.03) but that of CTL (0.37± 0.02) was significantly less than that of ML. While high producing cows responded positively to Met and Lys supplementation, there were no apparent benefits of BCAA supplementation.

Key Words: milk protein synthesis, branched chain amino acids, methionine

125 Effect of carbohydrate source on rumen fuid pH and in vitro gas production (GP) in heifers fed pasture silage. A. Britos*[1], A. Mendoza[2], M. Claramunt[1], M. Karlen[1], G. Kelly[1], L. Magallanes[1], S. Ramírez[1], A. Zunini[1], J. L. Repetto[2], and C. Cajarville[1], [1]*Department of Animal Nutrition, Faculty of Veterinary, UdelaR, Montevideo, Uruguay*, [2]*Department of Bovines, Faculty of Veterinary, UdelaR, Montevideo, Uruguay*.

Hereford heifers (n=24; mean BW=224kg; SEM=4) were randomly assigned to four treatments: no supplement (N), soybean hulls (S), corn grain (C) and barley grain (B), to test if carbohydrate source affects the pH and GP of rumen fluid. Heifers were housed in metabolic cages and supplements were offered at 1% of BW in one meal at 0700h. Pasture silage was offered ad libitum from 0700 to 2000h. In supplemented heifers forage was immediately offered after the supplements were consumed. After 21d of adaptation, rumen fluid samples were collected from each heifer through tubes inserted in rumen every hour for 24 hours (hour 0=0700h), and pH was measured with a digital pH-meter. Inoculum for GP was collected and mixed within groups. Pasture silage, S, C, B, wheat straw, oats and lotus were weighed (0.5g DM) in triplicate for each inoculum into 125mL flasks and 38.5mL of media was added before injection of 10mL of inoculum. GP was measured at 2, 4, 6, 8, 10, 12, 18, 24, 48, 72 and 96h. Data were fitted to V=Vf/{1+exp[2+4*Rf*(T-L)]}+Vs/{1+exp[2+4*Rs*(T-L)]}: V=total GP volume (mL/g DM), Vf=fast pool volume (mL/g DM), Vs=slow pool volume (mL/g DM), Rf and Rs=rates (h^{-1}) of fast and slow pools respectively, T=time, L=lag (h). pH and GP data were analyzed by a mixed or general linear model, respectively. Mean (SEM=0.05) and minimum (SEM=0.11) pH values were 6.82 and 6.55, 6.45 and 6.14, 6.48 and 6.16, 6.48 and 6.10 for treatment N, S, C and B, respectively, and were lower for supplemented heifers (P<0.01) but did not differ between carbohydrate sources. pH decreased after the start of the meal until a nadir of 6.27 (SEM=0.05). GP parameters were affected by inoculum, substrate and interaction. Vf decreased according to inoculum as B>S>C>N. *Funded by PEDECIBA; PDT 78/12; ANII.*

Table 1. Effect of inoculum source on in vitro gas production parameters

Inoculum	V	Vf	Rf	Vs	Rs	L
N	210.3^{b}	82.5^{d}	0.138^{a}	127.9^{a}	0.022^{a}	6.2^{a}
S	213.3^{ab}	112.6^{b}	0.114^{b}	100.7^{c}	0.022^{a}	4.3^{bc}
B	216.5^{ab}	118.1^{a}	0.112^{b}	98.4^{c}	0.019^{b}	3.6^{c}
C	220.5^{a}	104.9^{c}	0.130^{a}	115.6^{b}	0.022^{a}	4.7^{b}
SEM	2.793	1.902	0.004	2.451	0.0004	0.348
P(inoculum)	0.080	<.001	<.001	<.001	<.001	<.001
P(substrate)	<.001	<.001	<.001	<.001	<.001	<.001
P(inoculum*substrate)	<.001	<.001	<.001	<.001	<.001	0.048

^{abcd}Superscripts within column differ (P<0.05)

Key Words: carbohydrate source, in vitro gas production, rumen pH

126 TMR particles breakdown through ingestive mastication of dairy cows. I. Schadt*[1], J. D. Ferguson[2], G. Azzaro[1], C. Guardiano[1], R. Petriglieri[1], and G. Licitra[1,3], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*University of Pennsylvania, School of Veterinary Medicine, Kennett Square*, [3]*D.A.C.P.A. University of Catania, Italy*.

The study of feed particle breakdown through mastication might help to understand the formation and characteristics of the ruminal mat, and in consequence might help to explain how feed particle size can affect animal health and productivity. In the present study we examined particle breakdown of TMR samples differing in composition and distribution on the Penn State Particle Separator (PSPS). In particular, TMR and fecal samples from 10 farms were collected. The TMR samples were shaken through the PSPS with an additional sieve of 0.25 cm openings added between the middle and the lower screen to obtain the following treatments 1-6: unprocessed TMR, and TMR components retained on screens of 1.91, 0.79, 0.25, and 0.13 cm, and bottom pan, respectively. Three nonlactating, rumen fistulated cows had rumens evacuated and were offered 1 kg of each treatment in a randomized sequence. Swallowed boli were manually retrieved from the reticulo-rumen at the esophagal orifice. All samples were horizontally, wet sieved through a 0.16 cm screen and proportional dry residues (RES1.6) were determined. Residues of unprocessed TMRs, their respective boli and fecal samples were further analyzed through image analysis for particle distribution and mean size. Mean sizes of the unprocessed TMRs ranged from 1.49 to 2.06 cm (mean = 1.71 ± 0.17 cm). Contents of dry matter (DM), NDF, and crude protein ranged from 49 to 64% (mean = 55 ± 5.5%), from 26 to 35% DM (mean = 31 ± 2.8% DM), and from 15 to 25% DM (mean = 19 ± 3.4% DM), respectively. TMR mean size was positively related to fecal mean size (r = 0.63, P < 0.05, n =10). There was a positive linear response of boli RES1.6 to their respective treatments RES1.6, Y = 0.79X + 0.03 (r = 0.98, P < 0.01, n = 58). Boli RES1.6 differed between cows (P < 0.01).

Key Words: TMR particles, bolus particles, dairy cattle

127 Relationship between metabolizable protein balance, purine derivative excretion, 3-methyl histidine excretion, to feed efficiency in individually-fed heifers. W. A. Griffin*, G. I. Crawford, K. M. Rolfe, T. J. Klopfenstein, G. E. Erickson, P. S. Miller, and R. M. Diedrichsen, *University of Nebraska, Lincoln*.

Data from an experiment utilizing 78 individually fed heifers (407 ± 32 kg) were used to determine relationships of G: F and residual feed intake (RFI) to metabolizable protein balance (MPB), purine derivative excretion to creatinine excretion (PD:C) and 3-methyl histidine excretion to creatinine excretion(3MH:C). Heifers were fed steam-flaked corn based diets containing either 0 (NEG) or 1.5% (POS) urea for 95 d, resulting in CP levels of 9.6 and 13.7% for NEG and POS, respectively. Animal BW and urine samples were collected at 3 different times (28, 56, and 84 d) and urine was analyzed for PD: C and 3MH: C. To determine MPB, ADG, DMI, and final BW adjusted to equal (28%) empty body fat were used as inputs for the 1996 NRC model. Data were analyzed from 3 periods: early (d 1 to 55; urine 28 d), late (d 56 to 95; urine 84 d), and overall (d 1 to 95; urine d 28, 56, and 84). Relationships between MPB and RFI were inconsistent and poor. A positive relationship between PD: C and G: F was observed within both NEG ($r2 = 0.54$; $P < 0.01$) and POS ($r2 = 0.38$; $P = 0.02$) treatments during the early period. No relationship between 3MH: C and G: F was observed ($P > 0.10$). A negative relationship between MPB and G: F was observed for both POS ($r2 = -0.79$; $P < 0.01$) and NEG ($r2 = -0.65$; $P < 0.01$) in all periods. The more negative MPB was primarily due to greater ADG for cattle with greater G: F. The positive relationship between early period PD: C and G: F suggests that increased microbial protein leads to greater G: F. The lack of a relationship between 3MH: C and G: F suggests that protein turnover does not impact G: F and perhaps differences in G: F related to protein metabolism are due to differences in microbial efficiency.

Key Words: cattle, feed efficiency, metabolizable protein

128 Residual feed intake in Nellore heifers selected for growth. R. H. Branco[1], S. F. M. Bonilha[1], D. P. D. Lanna*[2], L. A. Figueiredo[1], L. Calegare[3], and A. G. Razook[1], [1]*Instituto de Zootecnia, Agência Paulista de Tecnologia dos Agronegócios, Sertãozinho, São Paulo, Brazil*, [2]*Departamento de Zootecnia, Esalq/USP, Piracicaba, São Paulo, Brazil*, [3]*Nutron Alimentos LTDA, Toledo, Paraná, Brazil*.

Recent studies of beef cattle feed efficiency suggest an opportunity to select animals to reduce required inputs. Proposed feed efficiency parameters suggested a statistical model to adjust feed intake for differences in average BW and gain (residual feed intake - RFI) or gain adjusted for feed intake (residual gain). RFI is an alternative measurement of feed efficiency, which is theoretically independent of production level and body size. RFI is established by the difference between observed and estimated feed intake based on BW and ADG. The objective of this work was to evaluate the effect of 30 yr selection for post-weaning growth in Nellore on ADG, feed intake, feed conversion efficiency, and RFI. The experiment was conducted at CAPTA Pecuária de Corte - Instituto de Zootecnia, Sertãozinho - São Paulo/Brazil. Feedlot test used 128 heifers from 24 and 25th calf crops, selected for BW and ADG at 550 d of age, from the Selection Program for Zebu Breeds of Sertãozinho. Final BW and ADG were different between lines of selection (control Nellore - NeC; and selected Nellore - NeS), being NeS heifers greater in BW (280 vs 214 kg, $P<.001$)) and ADG (1.033 vs 0.777 kg/d, $P<.001$) than NeC. DMI expressed in kg (6.90 vs 5.08 kg/d, $P<.01$) and in BW percentage (2.82 vs 2.68%BW, $P<.001$) were significantly different. Feed efficiency parameters did not differ ($p>.05$): feed:gain ratio (7.12 vs 6.93); gain:feed ratio efficiency (154 vs 157) and RFI (0.045 vs -0.009 kg/d) for lines NeS and NeC, respectively. RFI was favorably correlated to BW, although not different between NeS and NeC lines. Selection for growth did not have influence on efficiency parameters of Nellore heifers.

Key Words: efficiency, feed conversion, selection

129 Relationships between residual feed intake and apparent nutrient digestibility, in vitro methane producing activity and VFA concentrations in growing Brangus heifers. W. K. Krueger[1,2], G. E. Carstens[1,2], R. R. Gomez*[2], B. M. Bourg[2], P. A. Lancaster[2], L. J. Slay[2], J. C. Miller[2], R. C. Anderson[3], S. M. Horrocks[3], N. A. Krueger[3], and T. D. A. Forbes[4], [1]*Intercollegiate Faculty of Nutrition - Texas A&M University, College Station*, [2]*Department of Animal Science - Texas A&M University, College Station*, [3]*USDA, ARS, Food and Feed Safety Research Unit, College Station, TX*, [4]*Texas AgriLife Research - Texas A&M University, Uvalde*.

The objective of this study was to determine if animal variation in residual feed intake (RFI) was associated with variation in apparent nutrient digestibilities, in vitro methane producing activity (MPA), and VFA concentration. A four-year study was conducted with Brangus heifers (N = 114-116/yr) with initial BW of 273 ± 28 kg. Heifers were fed a high-roughage diet (ME = 2.1 Mcal/kg DM), and individual DMI and BW measured for 70 d. RFI was calculated as the residual from the linear regression of DMI on mid-test $BW^{0.75}$ and ADG. Within year, heifers were ranked by RFI and those with the lowest (n = 18–20) and the highest (n = 18–20) RFI selected to measure nutrient digestibilities, MPA, and VFA. Daily fecal and ort samples were collected for 7 or 10 consecutive d and AIA used to estimate nutrient digestibilities. Rumen samples were collected for MPA and VFA analysis in yr 2, 3, 4. RFI was not correlated with initial BW or ADG, but was correlated ($P < 0.001$) with DMI (0.70) and feed:gain ratio (0.68). Heifers with low RFI (n = 78) consumed 23% less DMI and had 20% lower feed:gain ratios than heifers with high RFI (n = 77). RFI was negatively correlated ($P < 0.001$) with DM, NDF, ADF, CP, P, Ca, Zn, and Cu digestibilities. Heifers with low RFI had higher DM (762.2 vs. 734.7 ± 33 g/kg DM) and NDF, ADF, CP and P digestibilities that were 4.0 to 5.5 percentage units higher ($P < 0.05$) compared to heifers with high RFI. Heifers with low RFI had lower ($P = 0.04$) propionate concentrations and higher ($P = 0.03$) acetate:propionate ratio than high RFI heifers. Differences in acetate and butyrate concentrations, and MPA were not detected between heifers with divergent RFI. Estimates of fecal nitrogen and P excretion rates, and methane emissions (Blaxter and Clapperton, 1965) were 36, 32 and 16% lower ($P < 0.001$), respectively, in heifers with low vs. high RFI. Results from this study suggest that inter-animal variation in apparent digestibility and ruminal VFA concentrations contributes to observed phenotypic differences in RFI of growing Brangus heifers.

Key Words: residual feed intake, nutrient digestibility, methane

130 Relationship between residual feed intake, temperament, blood constituents and serum cortisol in growing Brangus heifers. R. R. Gomez*, G. E. Carstens, T. H. Welsh, P. A. Lancaster, W. K. Krueger, and L. J. Slay, *Texas A&M University, College Station*.

The objective of this study was to examine the relationships between residual feed intake (RFI) and temperament traits in growing heifers.

A 4 yr study (N = 114-119 hd/yr) was conducted with Brangus heifers (Camp Cooley Ranch). Heifers were weaned for 25.5 ± 8.6 d prior to transport to the TAMU research facility where they were adapted to the diet for 28 d before the start of the studies. Average initial BW was 273 ±28 kg. Heifers were fed a high roughage diet (ME = 2.0 Mcal/kg DM) using Calan gate feeders and individual DMI and BW were measured for 70 d. Exit velocity (EV) was measured as the rate of distance traveled (m/s) while exiting a confined area at weaning and d 0. Blood samples were collected on d 0 of the studies. RFI was calculated as the residual from the linear regression of DMI on mid-test BW0.75 and ADG. Within year, heifers were ranked by RFI; the 20 lowest and 20 highest heifers assayed for serum cortisol, glucose and complete cell counts. RFI was positively correlated with DMI (0.66) and feed:gain ratio (0.52), but not with ADG. Heifers with low RFI (n = 80) consumed 18.6% less DMI and had 16% lower feed:gain ratio than heifers with high RFI (n = 80). Across all heifers, weak correlations ($P < 0.05$) between EV at weaning and d 0 and initial BW (-0.17, -0.12) and DMI (-0.10, -0.15) were found. However, EV was not correlated with ADG or RFI. For heifers in the divergent RFI groups, initial glucose was correlated ($P < 0.05$) with ADG (-0.29), and DMI (-0.24) but was not correlated with feed:gain or RFI. Initial cortisol was correlated ($P < 0.05$) with weaning EV and d 0 EV (0.31, 0.24) and correlated ($P < 0.06$) with initial BW and DMI (-0.15, -0.15) but not final BW, feed:gain or RFI. Low RFI heifers had lower ($P < 0.05$) WBC (9.4 vs. 10.6 ± .27 x 10^3/μL), higher RBC (10.2 vs. 9.8 ± 0.1 x 10^6/μL), and Hb (13.1 vs. 12.6 ± 0.1 g/dL) than high RFI heifers. These results suggest that heifers with excitable temperaments tended to have smaller initial BW, consumed less feed and had higher serum cortisol than calm heifers. However, EV and serum cortisol were not associated with RFI in growing heifers.

Key Words: RFI, cortisol, temperament

131 Frequency of supplementation of a soyhull/corn gluten feed mix does not affect performance of growing cattle fed hay. M. E. Drewnoski* and M. H. Poore, *North Carolina State University*, *Raliegh*.

A mixture of soyhulls and corn gluten feed (SH/CGF) has become a common feed supplement in the Southeastern US. The labor cost of hand feeding supplements is often very high therefore feeding a supplement less frequently would potentially increase profit depending on the resulting performance. The objective of this study was to determine the effect of reducing supplementation frequency on steer performance when supplementing hay with SH/CGF. The supplement contained 47% soyhull pellets, 47% corn gluten feed pellets and 2% limestone. The 86-d feeding trial was replicated over 4 years. Each yr, 40 steers (~ 270 kg) were stratified by weight assigned to 8 groups which were randomly assigned to treatment. During yr 1 and 2, treatments consisted of ad-libitum medium quality fescue hay that was supplemented daily (7X) with 2.73 kg/hd, supplemented on Monday, Wednesday and Friday (3X) with 6.36 kg/hd, or not supplemented (Hay). During yr 3 and 4, a fourth treatment was added in which steers were supplemented on Monday and Thursday with 9.55 kg/hd of SH/CGF (2X). Average daily gain was greater in supplemented steers compared to non-supplemented steers, but did not differ due to supplementation frequency. Hay intake was reduced by supplementation, was greater for 7X compared to 3X and did not differ between 3X and 2X. Gain to feed was improved by feeding supplement, and was also improved with less frequent supplementation. These results suggest that when given the same amount of supplement weekly, supplementation of growing steers with SH/CGF as little as two times a week will not reduce rate of gain, while improving feed efficiency.

Table 1.

		Treatment			
Item	Hay	7X	3X	2X	SEM
Model 1					
n	8	10	10	-	
ADG, kg/d	0.24^{b}	0.75^{a}	0.73^{a}	-	0.01
Hay intake, kg•hd^{-1}•d	5.95^{a}	5.33^{b}	4.68^{c}	-	0.10
Gain to feed	0.042^{c}	0.099^{b}	0.107^{a}	-	0.002
Model 2					
n	4	4	4	4	
ADG, kg/d	0.31^{b}	0.85^{a}	0.84^{a}	0.85^{a}	0.02
Hay intake, kg•hd^{-1}•d	5.25^{a}	4.53^{b}	4.03^{c}	3.81^{c}	0.14
Gain to feed	0.058^{c}	0.120^{b}	0.129^{ab}	0.135^{a}	0.003

Treatment effect ($P < 0.01$). n=group of 5 steers. Model 1 includes hay, 7x and 3x across all yrs. Model 2 includes all treatments in yr 3 and 4. Means within a row not sharing a superscript differ ($P < 0.05$).

Key Words: supplementation frequency, growing cattle

132 Effect of energy source on leucine utilization and nitrogen retention in growing steers. K. S. Spivey*, E. C. Titgemeyer, and M. L. Jones, *Kansas State University*, *Manhattan*.

Previous research demonstrated that energy supplementation increases the efficiency of leucine utilization in growing cattle. We studied the effects of energy source on leucine utilization and nitrogen retention in growing steers. Six ruminally cannulated Holstein steers (134 kg) housed in metabolism crates were used in a 6x6 Latin square. All steers were limit-fed a soybean hull based diet (2.3 kg/d DM) and received basal ruminal infusions of 150 g/d acetate, 150 g/d propionate, and 50 g/d butyrate, and abomasal infusions of a mixture (215 g/d) that contained all essential AA except leucine. Treatments were arranged in a 2x3 factorial with 2 levels of leucine (0 and 4 g/d) and 3 energy treatments: 1) control, 2) ruminal infusion of an additional 150 g/d acetate, 150 g/d propionate, and 50 g/d butyrate, and 3) abomasal infusion of 420 g/d glucose. Leucine supplementation increased N retention when no additional energy was supplied (34.8 g/d and 39.2 g/d for 0 and 4 g/d leucine), indicating that leucine was the most limiting nutrient. Both energy sources as well as leucine supplementation decreased urinary N excretion ($P<0.05$). Glucose supplementation numerically ($P=0.29$) increased N retention when either 0 or 4 g/d of leucine was provided (35.9 g/d and 40.7 g/d, respectively). VFA infusion tended ($P=0.07$) to increase N retention when no leucine was supplemented (37.9 g/d), but not when 4 g/d of leucine was provided (38.6 g/d). Leucine supplementation tended to reduce plasma urea concentrations (2.2 vs. 2.5 mM; $P=0.11$). Plasma urea concentrations were less ($P<0.01$) for the cattle receiving glucose (1.9 mM) than for control steers (2.7 mM), whereas plasma urea concentrations were not affected by the VFA treatment (2.5 mM). Data support previous observations that increased energy supply may slightly improve the efficiency of leucine utilization, but the response was not large. *This project was supported by National Research Initiative Competitive Grant no. 2007-35206-17848 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: leucine, N retention

133 Steer performance and digestibility when fed stocker diets with soyhull, corn gluten feed and distillers grain. G. M. Hill*[1], V. A. Corriher[2], D. J. Renney[1], and A. J. Nichols[1], [1]*The University of Georgia, Tifton*, [2]*Texas AgriLife Ext. Ctr., Overton, TX*.

Steers were fed corn silage (CS; 40% DM, 7.6% CP) or Tifton 85 hay (T85; 91.7% DM, 11.8%CP) with supplements (SUP) of pelleted soyhulls (SH), corn gluten feed (CGF) or distillers dried grains with solubles (DG) with respective DM and CP (%) of : 89.7, 13.7; 88.5, 20.8; 87.8, 32.6. Exp.1. After weaning, 48 steers (311.5 ± 34.5 kg; 27 Brangus; 21 Angus sired) were randomly assigned to treatments (TR). Steers were fed SUP of corn/SH [CSH; 47% SH, 38% soybean meal (SBM), 15% corn], corn gluten feed (CGFL) or corn/DG (CDG; 36.4% corn, 63.6% DG), top-dressed on CS fed free-choice in sheltered feed bunks for 60 d. The SUP DMI, total DMI, 60-d ADG (kg) and gain/feed, respectively, by SUP TR, were: CSH 2.24, 8.06, 1.64, 0.203; CGFL 2.00 , 8.31, 1.40, 0.169; and CDG 1.99, 7.30, 1.46, 0.200; ADG (*P*=0.331), SE 0.10. Exp. 2. In an 18-d digestion trial, 28 steers (265.9, SE 5.8 kg; 10 mo old; 19 Angus sired, 9 Brangus) were randomly assigned to SUP TR: corn/SBM (CSB; 77.8% corn, 22.2% SBM); SH/SBM (SHS; 80% SH, 20% SBM); CGF/corn (CGC; 75% CGF, 25% corn), DG/corn (DGC; 59% DG, 50% corn). Steers were individually-fed SUP with T85 hay; chromic oxide was fed (10 g/steer, d 8 to d 18), and fecal samples (11/steer, d 14 to d 18) were analyzed to determine apparent digestion. The SUP DMI, total DMI (kg) and dietary CP (%), respectively, for CSB, SHS, CGC, and DGC, were: 1.83, 5.4, 14.0; 2.05, 5.8, 14.8; 1.60, 5.3, 13.8; 1.64, 5.3, 13.3; total DMI ($P < 0.10$; SE 0.14). Digestibility (%) for CSB, SHS, CGC, and DGC, respectively, were: OM 65.8, 70.6, 68.6, 69.3, ($P < 0.05$; SE 1.09); CP 65.2, 70.0, 70.1, 69.2, ($P < 0.01$; SE 0.90); ADF 42.4, 60.6, 50.7, 50.8, ($P < 0.01$; SE 1.90); NDF 50.8, 63.5, 56.1, 57.9, ($P < 0.01$; SE 1.85). Steers had similar ADG for TR in Exp. 1; and CSB had lower OM, CP, ADF and NDF digestibility than other SUP TR in Exp. 2.

Key Words: steer, digestion, distillers grain

134 Effects of supplemental energy and protein on forage digestion. E. A. Bailey*, E. C. Titgemeyer, K. C. Olson, K. S. Spivey, D. W. Brake, D. E. Anderson, and M. L. Jones, *Kansas State University*, *Manhattan*.

We quantified effects of supplemental energy from differing sources on nutrient digestibility at 2 levels of DIP supply. The study was a 6x6 Latin square with treatments as a 3x2 factorial. Energy treatments included control, 600 g glucose (GLC) dosed ruminally once daily, and 480 g VFA (192 g C2, 144 g C3, 144 g C4) infused ruminally over 8 h daily. Casein (120 or 240 g) was dosed once daily as the DIP supplement. Six ruminally and duodenally cannulated steers had ad libitum access to prairie hay (5.8% CP). Each period had 9 d for adaption, 4 d for total fecal collection, and 1 d for rumen and duodenal collections. ADIA was used to determine ruminal digestion. VFA infusion decreased (P<0.01) forage intake by 27%; decreases in forage intake due to glucose (7%) and increases due to increasing casein (4.5%) were not significant. GLC decreased total tract NDF digestibility (P<0.01) and tended to decrease ruminal NDF digestibility; these depressions in response to GLC tended to be greater at the low level of casein. Duodenal N flow tended (P=0.15) to be increased by increasing casein, but was not affected by supplemental energy (P=0.55). Increasing DIP decreased ruminal pH (P<0.02). GLC decreased pH 2 h after dosing, and VFA infusion decreased pH during the infusions, but not at other times. Increasing casein increased and GLC decreased ruminal NH_3 (P<0.01). Ruminal acetate and propionate concentrations decreased and butyrate increased when GLC was supplemented. VFA infusion increased ruminal propionate and butyrate concentrations during the infusion period (P<0.01). Increasing casein increased (P<0.01) concentrations of acetate, propionate, isobutyrate, and isovalerate. Overall, provision of supplemental energy decreased forage intake and/or digestion, but had no impact on duodenal N flow. GLC supplementation may have exacerbated a ruminal NH_3 deficiency. *This project was supported by National Research Initiative Competitive Grant no. 2007-35206-17848 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: forage, energy, protein

135 Feeding dried distillers grains in lieu of standard range cubes to pregnant beef cows consuming low quality roughages improved economic returns with limited impacts on serum urea nitrogen or trace mineral status of the cows or their offspring. K. L. Swyers*[1], M. J. Jarosz[1], L. W. Douglass[2], and S. L. Archibeque[1], [1]*Colorado State University, Department of Animal Sciences*, *Fort Collins*, [2]*University of Maryland, Department of Animal and Avian Sciences*, *College Park*.

The effects of dried distillers grains with solubles (**DDGS**) on performance, serum urea nitrogen (**SUN**), and trace mineral status of pregnant beef cows and their offspring was evaluated. Two-hundred sixteen cross-bred, multiparious beef cows in the last third of pregnancy were blocked by age (young cows, < 3 vs mature cows, > 3 yrs of age) and randomly assigned to one of six pasture replicates, with 3 pastures per treatment. The dietary factor was either range cube (**CON**; 33.7% CP (DM basis)) or DDGS (**DDG**; 37.1% CP (DM basis)) supplementation, fed thrice weekly at 3.5 and 3.4 kg DM × cow^{-1} × $feeding^{-1}$, respectively. Cows had access to pasture, hay, and ad libitum mineral (target intake of 110 g × cow^{-1} × d^{-1} (DM)). Treatments were fed from d 200 of gestation through calving. Samples were collected on individuals on d -8, 28, 54, and 77 of the study. Disappearance of mineral was 127 and 162 g × cow^{-1} × d^{-1} for CON and DDG cows, respectively. Young cows had reduced BW (545 vs. 627 kg), and higher BCS (4.93 vs. 4.85) and SUN (9.24 vs. 7.63 mM; young vs. mature cows, respectively; $P < 0.05$) than mature cows. Cows fed DDGS had higher BW on d 77 and BCS on d 28 and 54 (treatment × day, $P < 0.01$), and higher ($P = 0.01$) ADG than CON cows. There was no effect of treatment ($P = 0.30$) on cow SUN. Cows fed DDGS had increased (treatment × day, $P \leq 0.05$) hepatic Cu, Co, and Mn concentrations, decreased (treatment × day, $P = 0.02$) Fe, and Zn status tended to be higher ($P = 0.08$) by d 77 than CON cows. There was no effect of treatment on calf weaning wt, SUN, or trace mineral status ($P \geq 0.39$), but DDGS tended to increase calf birth wt ($P = 0.10$). Feeding DDGS yielded a savings of $13.86 per cow over the trial period. These data indicate that supplementing DDGS to pregnant range cows on winter range renders the cow-calf producer with both a cost benefit and improved cow performance at no detriment to SUN or hepatic trace mineral status.

Key Words: dried distiller's grains, beef cows, pasture

136 A meta-analysis evaluation of supplementing dried distillers grains plus solubles to cattle consuming forage based diets. W. A. Griffin*[1], V. R. Bremer[1], T. J. Klopfenstein[1], L. A. Stalker[2], L. W. Lomas[3], J. L. Moyer[3], and G. E. Erickson[1], [1]*University of Nebraska*, *Lincoln*, [2]*West Central Research and Extension Center*, *North Platte, NE*, [3]*Southeast Agricultural Research Center*, *Parsons, KS*.

Data from nineteen (12 grazing and 7 confinement) studies utilizing 790 growing steers and heifers supplemented dried distillers grains (DDGS)

were analyzed using mixed models to determine the response to supplementing different levels of DDGS on gain and forage intake. Thirty-eight treatment means (442 hd) were from grazing cattle managed on pasture and supplemented DDGS (range: 0.00 to 1.03% of BW/d). Twenty-eight treatment means (348 hd) were from pen fed cattle consuming forage based diets and supplemented DDGS (range: 0.00 to 1.27% of BW/d). In both the grazing studies and pen studies, statistics of interest were relationships between DDGS intake and ADG or ending BW. Additionally, in pen studies, forage intake was measured and relationships between DDGS intake and forage intake were used to determine forage replacement. In pasture grazing studies, ending BW increased linearly ($P < 0.01$) and tended to increase quadratically ($P = 0.07$) with increasing DDGS supplementation. Daily gain increased linearly ($ADG = 0.37x + 0.70$; $P < 0.01$) with increased DDGS supplementation. Results from pen fed studies indicate that ending BW ($P < 0.01$) and ADG ($ADG = -0.09x2 + 0.15x + 0.55$; $P < 0.01$) increase quadratically with increasing DDGS supplementation. Intakes measured in the pen studies suggest that increasing DDGS supplementation increases total DMI ($P < 0.01$) quadratically, even though forage intake decreases ($P < 0.01$) quadratically with increased DDGS supplementation. Results from all studies indicate that increasing DDGS supplementation increases ADG and ending BW, additionally, results from pen studies suggest that DDGS intake replaces forage intake in growing cattle consuming forage based diets.

Key Words: dried distillers grains plus solubles, forage intake, supplementation

137 Effects of dam's dietary prepartum energy source on post-natal skeletal muscle development and growth in offspring of beef cattle. A. E. Radunz*, H. N. Zerby, F. L. Fluharty, and S. C. Loerch, *The Ohio State University*, *Wooster*.

Mature Angus-cross (n = 180) beef cows were used to determine prepartum dietary energy source impacts on post-natal skeletal muscle development and growth in offspring of beef cattle. Cows were blocked by location (n = 3) and stratified by body weight, body condition score and age (5 pens/treatment). Cows were adapted to diets starting at approximately 200 d of gestation and fed until 1 wk prior to expected calving date. Cows were fed 1 of 3 energy sources: hay (HAY); corn (LFC); or dried distiller grains (DDGS) at isocaloric intakes. Following parturition, cows were fed a common diet and managed as one group per location. Body weight and *Longissimus dorsi* area (LMA) between 12th and 13th rib measured via ultrasonography was collected postpartum at birth (24-72 hr) and weaning (184 ± 7 d). *Longissimus dorsi* muscle biopsy samples posterior to the 13th rib were taken for histology measurements on a subset of male calves (6 calves/trt; n = 18) within 7 d of parturition. Muscle samples were measured for muscle fiber width and bundle length. Calves resulting from LFC and DDGS prepartum diets had greater ($P = 0.003$) birth weight than those from HAY diets (44.6, 43.5, and 39.0 ± 1.3 kg, respectively). The adjusted weaning weights of calves from cows fed LFC, DDGS, and HAY diets were 284.9, 277.8, and 272.4 ± 5.1 kg, respectively; with LFC greater than HAY ($P = 0.01$), and DDGS intermediate and similar to both LFC and HAY. From birth to weaning, ADG tended to be greater ($P = 0.07$) for calves from cows fed LFC than either HAY or DDGS. Ultrasound LMA measurements were not different ($P > 0.20$) among treatments at birth or weaning. Muscle fiber width was greatest ($P = 0.05$) in calves from dams fed LFC and HAY vs DDGS while muscle bundle length was greatest ($P = 0.03$) in calves from dams fed LFC vs HAY and DDGS. Type of energy source in late gestation, even when fed at isocaloric amounts, can impact calf birth weight and skeletal muscle characteristics as well as post-natal growth and weaning weight.

Key Words: prepartum nutrition, muscle development, beef cattle

138 Effect of ZADO®, as enzymes from anaerobic bacterium, on extent of ruminal fermentation, nutrient digestibilities and average daily gain in steers. H. Gado*[1] and B. E. A. Borhami[2], [1]*Ain-Shams University, Dept. of Animal Production, Faculty of Agriculture*, *Cairo, Egypt*, [2]*Alexandria University, Dept. of Animal Production, Faculty of Agriculture*, *Alexandria, Egypt*.

Forty crossbred steers (Baladi x Friesian) were randomly assigned to two groups of twenty animals each. The average initial weight was 153.5 kg. The experiment lasted for 219 days. Two steers fitted with ruminal cannulas were used to take ruminal samples. The objectives were to evaluate the effects of exogenous enzyme supplementation (ZADO®) on nutrient digestibilities, ruminal ammonia and volatile fatty acids(VFA) and average daily gain (ADG). The enzyme mixture, which contained mainly xylanase , cellulase , protease and alpha amylase, was added to the concentrate to supply 40 g/ animal/day. The concentrate mixture contained 11% cracked corn, 8.5% agwa (minced date), 26.5% biscuits (bakery waste), 10% sugar cane molasses, 19% sesame cake, 2% soya bean meal ,6% beans, 14.2% rihan straw, 1% salt, 1% limestone and, 0.3 mixture of mineral and vitamins and 0.5% mineral mixture. Total digestibility of nutrients was significantly increased ($p<0.01$) by ZADO treatment vs control (dry matter, 61.7 vs. 69.1%; %; crude protein, 60.3 vs. 68.9%, neutral detergent fiber, 41.7 vs. 50.8%; acid detergent fiber, 32.2 vs. 40.8%)., ADG was 1.25 vs. 1.45 kg/d in control vs ZADO ($p<0.05$). VFA, (mM/100ml) was higher ($p<.05$) in the ZADO group in comparison with the control group (120 vs 110, respectively). Ammonia-nitrogen in the rumen (mg/N) was higher ($p<0.05$) in the ZADO group 65 vs 54 in the control group. Supplementing of steer diets with an enzyme mixture has the potential to enhance ADG and nutrient digestibility of fattening steers.

Key Words: ZADO, enzyme supplement, rumen fermentations

Teaching/Undergraduate and Graduate Education: Symposium: Enhancing the Writing Experience

139 Making the writing experience right. D. K. Aaron*, *University of Kentucky*, *Lexington*.

Over a decade ago Writing Across the Curriculum programs were initiated in universities across the U.S. Shortly thereafter Writing in the Discipline programs followed. The premise of the former was *writing to learn* course material; for the latter it was *learning to write* using discipline-specific conventions. Both have been successful. However, as they were first initiated into animal science courses, students and teachers had to change their attitudes about student writing. Students were generally apprehensive and often responded with a "this is *NOT* English" attitude. They were being asked to do something they did not like in courses where they did not expect it. And, past experiences had often reinforced the idea that they did not do it well. Teachers were perhaps more enthusiastic, but most did not know where or how to begin

or how to find time to add another component to classroom instruction. Today writing in many animal science courses is routine, but getting it right is still a challenge. To make it right for students, writing has to be incorporated through use of innovative, real-world activities. Good writing assignments cause students to think about what they have been taught and to solve problems. To make it right for teachers, incorporation of writing has to be done in such a way that it does not "steal" time from course content. Also, grading has to be kept to a manageable level. The pioneering *writing to learn* and *learning to write* programs provided valuable techniques for making the writing right. Journal entries, case studies, scenarios, policy analyses, article reviews, briefing notes, grant proposals, editorials, and press releases are some of the activities promoted as alternatives to the traditional term paper. These types of activities are still used successfully. However, as the world students live in changes, teachers have to look to new ways of engaging them. Integrating writing into animal science courses is an ongoing process that can improve student thinking and learning, enhance communication skills, and better prepare students for the workplace. When this happens, the writing has been made right.

Key Words: writing, students, teachers

140 Creating effective writing assignments in the animal sciences. M. W. Orth* and T. T. Barry, *Michigan State University, East Lansing*.

Future employers of our animal science students highly value good written communication skills. However, trying to develop those skills in our academic programs can be challenging, given the amount of material, skills, and opportunities that we as faculty members want students to explore during their undergraduate career. Furthermore, many of us do not feel qualified to teach our students how to write. The purpose of this presentation is to provide some ideas for how faculty in the Animal Sciences can incorporate writing in the classroom that both improves students' writing skills and their mastery of concepts pertinent to their fields of study. First, design assignments that meet course goals. Identify the most important concepts or information that students need to learn and then develop writing assignments specific to that area. Have students write to a targeted audience to facilitate personal comprehension of the subject. Second, put the assignment in writing and discuss it in class. Clarify the purpose and expectations to reduce anxiety and improve engagement. Third, provide opportunities for students to approach writing as a process. As faculty, we rarely produce a writing piece in one draft; neither should students. We need to provide students with opportunities for constructive peer and faculty feedback that promotes learning and leads to thoughtful revision, which is important for a thorough reflection on both the subject and how it is communicated. Assignments do not have to be long. Many objectives can be met in a writing piece the length of an abstract. Several student outcomes can be anticipated. For example, putting ideas into their own words helps students better comprehend course material. Students can get a clearer understanding of scientific genres, leading to deeper development of critical thinking skills. If we devote time to teaching scientific writing, students will recognize the value of writing in the sciences. Good writing takes practice. Increasing the number of courses in the Animal Sciences that incorporate even one or two assignments that include feedback ultimately should improve students' written expression.

Key Words: effective writing assignments, feedback, course goals

141 Incorporating journals and journal writing into the teaching and learning process. A. Zimmerman*, *The Ohio State University, Wooster*.

Journal writing is a type of reflective writing with the purpose of finding out what the writer thinks, feels, and knows. As such, it is informal, writer based, exploratory, and resembles speech. A journal provides a written record of an individual's observations, experiences, and thoughts. Journal writing is "thinking on paper" and a journal is written from a combined subjective/objective perspective. Therefore, journals differ from diaries (subjective recordings of a personal nature) and logs and notebooks (objective records of information and data). Journal writing is quite different from the formal writing typically required in educational settings, which is undertaken for the purpose of communicating to a designated audience. Clearly, individuals need to master formal writing as applicable to their particular disciplines. However, journal writing is a powerful thinking and learning mechanism in its own right and can be incorporated into the teaching and learning process as an important component of student-centered learning activities. This workshop will provide an overview and materials related to the use of journals and journal writing in the teaching and learning process. The session will be informal and interactive. Participants will be actively involved in writing and sharing their ideas.

Key Words: journals, journal writing, writing assignments

142 Incorporating writing assignments in large animal science courses. J. A. Sterle*, *Texas A&M University, College Station*.

Numerous studies show the importance and value of writing across the curriculum, however, incorporating writing into science-based animal science courses can be difficult. Enrollment in many Animal Science courses has increased in recent years. The demographics of students enrolled in animal science courses has changed, with fewer students having an agricultural background, causing teachers to provide more basic knowledge. When all of these elements combine into a single course, incorporating writing, and subsequent grading into a course can be intimidating at best. The purpose is to encourage students to write to learn, not necessarily learn to write and incorporating simple grading strategies can improve both the students' writing skills and the knowledge gained from the course. Integrating writing assignments, which need not be lengthy, into the course content can serve multiple goals. Incorporating critical thinking and problem-solving skills into the writing adds another component. Students can write responses to a situation or issue individually first, then work in groups on an overall response. This also requires cooperation and teamwork skills to formulate the final writing. Not all writing has to be graded. Previous studies have shown that it is the act of writing itself, more than evaluation and feedback, which improves writing. While students appreciate feedback, and most educators feel the need to give feedback, it does not have to come from the instructor. Evaluation from peers, with activities such as think-pair-share, or comments from teaching assistants can be valuable to both the writer and the evaluator. Regardless of class size, writing can enhance the student learning experience without creating an insurmountable amount of work for the instructor.

Key Words: writing, teaching, assignments

143 Journal writing. C. L. Hicks*, *University of Kentucky, Lexington*.

Students doing summer internships within the Food Science Group at University of Kentucky are required to keep a journal. After the internship is acquired the student signs a contract where they agree to make daily entries into a journal about what they did and learned each day. The contract also requires that the student check in with their advisor on a monthly basis and give a presentation about what they learned during the internship the following semester. Once the contract is completed, the student is automatically registered for the internship course the semester following the internship. As the internship proceeds the student meets with his/her advisor who checks their journal and makes suggestions as to how the journal can be improved. Under this system most students keep fairly detailed journals. Many students not only keep information about their internships but also include information about other personal events. Students are encouraged to keep the raw notes in their journal, so many journals are filled with sticky notes attached to the pages where the journal entries were made. Many students prefer to keep their journals in an electronic format. The journal serves as a primary source of information that the presentation is developed from the following semester. Advisors do not correct journal entries, but do encourage that journals are legible and contain insights about the internship. Most students have shorter daily entries in their journals at the beginning of the internship and more extensive entries near the end of the internship. Most students state that by keeping a journal for an extensive period their writing fluidity is enhanced and as a result they write term papers in a more succinct flowing manner.

Key Words: teaching, internships, journal

144 Students' perception of writing assignments in contrasting learning environments. M. Wattiaux*, *University of Wisconsin, Madison*.

Our objective was to determine students' perception of writing (W), reading (R), discussion (D), and practical hands-on activities (A) in six classes taught in 2008. Classes included sophomores enrolled in 272 Precapstone Seminar; freshmen and seniors in 302 Dairy Cattle Husbandry Practicum; students of mixed standing enrolled in 375 Mexico Seminar; seniors in 414 Ruminant Nutrition; juniors, seniors and master students enrolled in 468 Managing the Environmental Impacts of Livestock Operations; and doctoral candidates enrolled in 875 College Classroom: Teaching in Sciences and Engineering. The W assignments included the submission of a draft and a final resume (272), a weekly question and answer notebook (302), weekly journal entries (375), a take-home case study (468), and weekly thought papers (875). Students scored how the W, R, D, and A of the class helped their learning on the following scale: 1-2=not at all, 3-4=a little, 5-6=somewhat, 7-8=a lot, and 9-10=a great deal. Data were analyzed with proc mixed of SAS (see results in Table). Except for 875, W scores were the lowest scores in all classes in which they were evaluated. The score (means ± SD) for the item "I learned in this class" (L score) was: 7.8 ± 1.2, 9.1 ± 1.1, 8.5 ± 1.7, 6.4 ± 2.6, 8.7 ± 1.1 and 8.4 ± 1.3 for 272, 302, 375, 414, 468 and 875, respectively. The L score minus the W score differed among classes (*P=0.03*) and was the lowest for 272 (L-W = 0.4) and 875 (L-W=1.2), intermediate for 302 (L-W=1.6) and 468 (L-W=2.3), and highest for 375 (L-W=3.3) suggesting that the sophomores writing their resume and the doctoral candidates writing their thought papers perceived a relatively higher contribution of the W assignment to their overall learning than the W assigned in 302, 375 and 468. The design of successful W assignments must consider student standing, learning objectives, and the other pedagogical elements of the course environment.

Table 1.

Class	N	W score	R score	D score	A score	P value
272	14	7.4	na	na	9.3	<.01
302	8	7.5	na	na	10.0	.01
375	13	5.2[a]	8.7[b]	8.5[a]	na	<.01
414	19	na	6.2[b]	6.6[a]	7.3[a]	.09
468	11	6.5[b]	8.1[a]	8.8[a]	7.2[b]	<.01
875	16	6.8	7.2	7.7	6.6	.47

na = not applicable; a, b: means in a row with different superscripts differ, *P<.05*.

Key Words: assessment, SoTL

ASAS Cell Biology Symposium

145 Redox regulation of cysteine-dependent enzymes. R. P. Guttmann*, *University of Kentucky, Lexington*.

It is well-established that maintenance of the intracellular redox state is critical for cell survival and that prolonged or abnormal perturbations towards oxidation result in cell dysfunction. This is exemplified by the widespread observation of oxidative stress in many pathological conditions as well as the positive effects of anti-oxidants in treating certain conditions or extending life-span itself. In addition to the effects of oxidation on the lipid bi-layer and modification of DNA in the nucleus, proteins are also modulated by redox state. One of the primary targets of oxidation within a protein is the amino acid cysteine, whose thiol-side chain is highly sensitive to all types of oxidizing agents. While this sensitivity is used within the cell as potent defense mechanisms to prevent oxidation such as glutathione, the use of cysteine in the active site of enzymes leaves them open to oxidant-mediated damage. Whether the damage is due to a pathological condition or to post-mortem mediated loss of redox homeostasis, cysteine-dependent enzymes are targets of all forms of reactive oxygen, nitrogen and sulfur species. A greater understanding the redox-mediated control of cysteine-dependent enzymes opens the door to the selective use of anti-oxidants to prevent or reverse the cellular damage their inhibition causes.

Key Words: anti-oxidant, glutathione, cell death

146 Redox regulation of cell function in skeletal muscle: Effects of contractile activity and implications for aging muscle. G. L. Close*, E. D. O'Neill, and M. J. Jackson, *University of Liverpool, UK*.

Skeletal muscle comprises approximately 40% of the human body and could be described as the largest organ system in the human body (1). Skeletal muscle is terminally differentiated post-mitotic tissue that is subjected to considerable day to day stresses. Fortunately, skeletal

muscle has the remarkable ability to adapt and remodel providing protection against future stresses (2). Skeletal muscle fibres continually generate reactive oxygen species (ROS) (3) and this production is increased during physical activity (4). For many years, this potentially deleterious effect of increased ROS generation has been termed oxidative stress and attempts to prevent ROS generation have been, and continue to be, advocated (5). However, there is emerging evidence that ROS also play physiological roles mediating cell signalling and adaptation (6; 7). Redox regulation of skeletal muscle function may therefore be essential in cellular adaptation. Inconsistencies in the literature may be due to the difficulties in assessing ROS production. Our group has utilised novel techniques to study ROS in skeletal muscle such as fluorescent microscopy (8), microdialysis (9) and transgenic mouse models (10). We have been able to identify the site of ROS production and identify a number of redox regulated transcription factors that play a fundamental role in skeletal muscle adaptation to stresses (6). Data will be presented on these adaptations in skeletal muscle and provide evidence that dysregulation of redox regulated processes may impair cellular adaptations (11) and promote muscle atrophy. 1. Close GL et al., Sports Med 35:413-427, 2005 2. McArdle A et al Ageing Res Rev 1:79-93, 2002 3. Jackson MJ, IUBMB Life 60:497-501, 2008 4. Reid MB, Free Radic Biol Med 44:169-179, 2008 5. Close GL et al., Comp Biochem Physiol A Mol Integr Physiol 142:257-266, 2005 6. Vasilaki A, et al., Mech Ageing Dev 127:830-839, 2006 7. Gomez-Cabrera MC et al., J Physiol 567:113-120, 2005 8. Pye D et al., J Physiol, 2007 9. Close GL et al., Free Radic Biol Med 39:1460-1467, 2005 10. Broome CS et al., Faseb J 20:1549-1551, 2006 11. Khassaf M et al., J Physiol 549:645-652, 2003

Key Words: skeletal muscle

147 Mammalian epididymal glutathione peroxidases control the maintenance of sperm DNA integrity. E. Chabory, P. Vernet, R. Cadet, F. Saez, and J. R. Drevet*, *GReD, Clermont Université*, *Aubiere, France*.

In mammals, post-testicular epididymal sperm maturation is considered an essential step for the transformation of immature testicular gametes to mature spermatozoa capable of fertilization. Reactive oxygen species (ROS) have clearly been shown to be key actors in this maturation process. However, spermatozoa are extremely sensitive to oxidative attacks that were correlated with lipid peroxidation, DNA damage and impaired sperm motility. To precisely control the level of hydrogen peroxide in the vicinity of the male gamete the mammalian epididymis uses a panel of non enzymatic and enzymatic scavengers among which the glutathione peroxidase (GPx) family is highly represented. Within the various GPx proteins expressed in the mammalian epididymis, GPx5, occupies a unique position since it is the sole secreted GPx that will be directly in contact with the male gamete during its journey in the epididymal luminal environment. To find out how important this protein is for the epididymis physiology and the male gamete, GPx5-null mice were generated. Histological analyses of the GPx5-/- epididymides followed by cytological sperm examination did not show any obvious signs of morphological alterations. Overall, fertility parameters of GPx5-/- sexually mature male mice were not affected. However, a clear increase in developmental defects were noticed when WT females were crossed with aging GPx5 deficient males (over one year old). Cytometry analyses have shown a significant decrease in sperm DNA compaction in cauda epididymides from GPx5 null mice. In addition, sperm DNA oxidation was noticed in GPx5-/- mice using β-oxodG as a marker. Nuclear peroxidative attacks were also observed in cauda epididymidis epithelium. Quantitative PCR analyses have confirmed that the cauda epididymidis of the GPx5-/- mice is engaged in an antioxidant response. Overall, the data collected show that the lack of GPx5 protein leads to oxidative stress within the epididymis resulting in sperm nucleic alterations. *This work was supported by the CNRS, the French Ministry of Education, the Ernst Schering Research Foundation (Berlin, Germany) and CONRAD (Contraceptive Research & Development, New York, USA).*

148 A theoretical approach to sperm preservation based upon mitochondrial energetics. D. P. Froman*, *Oregon State University*, *Corvallis*.

To date, sperm preservation has depended upon a trial-and-error experimental approach. Even though this approach enabled bovine sperm to become a commodity, semen preservation remains problematic for many species. The present work outlines an alternative approach. In previous work, mitochondrial calcium cycling and phospholipase A_2 were proven critical to fowl sperm motility. Thus, it was inferred that fowl sperm use an endogenous substrate to ascend the hen's vagina. It is noteworthy that fowl sperm reside with the oviduct's sperm storage tubules (SST) over an interval of days to weeks after insemination. In this regard, additional previous work outlined a model wherein in vivo sperm storage was explained in terms of exogenous long chain fatty acids (released from SST epithelial cells) and sperm cell oxidative phosphorylation. Moreover, this model afforded an explanation for sperm egress from the SST based on mitochondrial senescence. Collectively, these facts and inferences presented the possibility that sperm could be inactivated by disrupting mitochondrial calcium cycling and thereby preserved. However, this possibility also posed a problem: maintenance of the mitochondrion's inner membrane potential within inactivated sperm. The present work details a series of experiments in which fowl sperm were inactivated by treatment with the calcium chelator BAPTA and then reactivated by treatment with calcium ions. Cessation of mitochondrial calcium cycling was proven by flow cytometry and fluorescence microscopy. When treated sperm were cooled to 10 C, inactivated sperm could be reactivated over a 5-h interval. When stored sperm were held for 3 h prior to reactivation and insemination, fertility was 88% of the control. Storage did not affect hatchability. In summary, short-term storage was realized by manipulating mitochondrial function. It is proposed that: (1) Complex V consumes ATP within inactivated sperm and by doing so maintains the mitochondrion's inner membrane potential, (2) ATP is regenerated from phosphocreatine by creatine kinase, and (3) necrosis follows depletion of intracellular phosphocreatine.

Key Words: calcium, mitochondria, sperm

149 Consumer fluid milk choices: Balancing nutrition, safety, cost, and emotions. K. Bolen* and L. Timms, *Iowa State University, Ames*.

In the past few years, many questions have surfaced over numerous claims on fluid milk labels ranging from rbST- free, organic, and conventional milk. Often times these value-added or label claims come with an increased price tag per unit of milk. A recent study conducted by Penn State University and University of Missouri, in conjunction with Monsanto, looked at milk quality, nutritional value, and hormonal differences among organic, rbST-free, and conventional labeled (no rbST- free or organic claim) milk. The study encompassed 334 commercial milk samples from 48 states. Results of this study showed that rbST-free, conventional, and organic milk were compositionally similar in many measures, but slight yet significant differences were shown. Organic labeled milk had decreased levels of IGF-1 which is known as a risk-factor for cancer, especially breast cancer. Previous studies have shown slightly higher IGF-1 in milk from cows administered rbST compared to non treated controls, but no differences were shown in the fluid milk samples in this study. Organic milk has also been shown to contain increased levels of conjugated linoleic acid which has cancer-fighting properties and is found in dairy products and other animal products, but it cannot be produced by the human body. Organic milk contained higher levels of the hormones estrogen and progesterone, while conventional milk has significantly lower bacterial counts than rbST- free and organic milk. Results of this and other studies have shown few and minor differences in milk composition. Although compositional differences are present but minute, price differentials can be substantial. Prices in the study showed rbST-free and organic milk priced $1.00 and $4.00 higher per gallon, respectively. At the local HyVee in Ames, Iowa, a ½ gallon of 2% organically labeled and conventionally labeled milk were $3.69 and $1.44, respectively. People have a choice when it comes to choosing their milk and there are many factors that play into their decision such as emotions, price, nutrition, and safety, but when the milks are virtually the same is the price difference really worth it?

Key Words: rbST-free, organic, conventional milk

150 Raw milk: The controversy continues. S. Stelly*, *Louisiana State University, Baton Rouge*.

Raw milk is defined as milk that is taken straight from the cow that is not pasteurized. It has been said that drinking raw milk could prevent several types of diseases. Among these are heart diseases, kidney diseases, cancer, and lactose intolerance. The argument is that pasteurization destroys nutrients in the milk that helps prevent these diseases. More and more people are starting to believe this and in all actuality it is just not true. The nutritional value of milk and milk products is very much unaffected when pasteurized. In fact the truth is that drinking raw milk can be a great danger in your overall heath. Even though milk and dairy products are important components of a healthy diet, they can be health hazards if consumed unpasteurized because of possible contamination with pathogenic bacteria. It has been documented that numerous food borne illnesses related to unpasteurized milk consumption have occurred since 2005, including outbreaks of salmonellosis, campylobacteriosis, and *E. coli* infections. Since there are advocates of both raw milk and pasteurized milk the controversy over legalizing the sale of raw milk is growing. Understanding the science behind this controversial topic will enable consumers and lawmakers to differentiate fact from fiction when making decisions regarding the legalization of raw milk sales.

Key Words: raw milk, health risks, controversy

151 Human health benefits of bovine colostrum. P. F. Welch*, D. R. Winston, and R. E. James, *Virginia Polytechnic Institute and State University, Blacksburg*.

The dairy cow provides nature's most nearly perfect food. Many products such as cheese, yogurt, and ice cream are derived from milk. Colostrum, either fed to calves or discarded, is generally not considered for human consumption because of the potential for antibiotic residues from dry cow antibiotic therapy. However, interest has increased recently concerning supplementation of human diets with colostrum. Some companies are pursuing colostrum supplementation as another niche market for the dairy industry. Over the past several years demand for supplements derived from colostrum has grown, especially among professional athletes. Colostrum contains insulin-like growth factors I and II (IGF I and II), which have been clinically proven to help increase lean muscle mass and regulate blood sugar and cholesterol levels. Data from the Center for Nutritional Research indicates that bovine colostrum also has beneficial effects when treating gastrointestinal disorders. Colostrum supplements claim to restore the GI tract to optimal functioning while blocking action of pathogens. With all these purported health benefits, colostrum supplementation is gaining popularity with products such as Colostrum D-90, Colostroplex and Colostrum 800, available as tablets, capsules, and/or powders. It may be possible for the dairy industry to capitalize on this niche market for colostrum products and implement strategies on marketing them to athletes and other health food conscious consumers.

Key Words: colostrum, colostrum supplements

152 Importance of conventional dairy products in young adult diets. K. M. Stomack* and E. L. Karcher, *Michigan State University, East Lansing*.

Milk is nature's most perfect food and plays an important role in the diet of young children. Among all the minerals on earth, calcium is one of the most important for humans. Calcium is used by the human body for the growth of bones. This essential mineral is vital for infants as it has been found to stimulate cell growth and maturation of the digestive system (Ebringer et al., 2008). Toddlers obtain calcium more easily from milk than from their bodies and use the fat from milk as a source of energy for growth. By ensuring the body has proper calcium such diseases as osteoporosis can be avoided and proper blood clotting factors can be maintained. Due to its many functions, it is essential to maintain adequate dietary calcium through food sources such as leafy vegetables including broccoli, spinach, and cabbage, and especially dairy products. Recent societal trends towards perceived healthy eating have focused on increasing the amount of rice and soy milk in the diets of infants and children. As a result, there has been an increase in nutritional deficiencies among children given these conventional milk alternatives. The American Academy of Pediatrics has reported the occurrence of nutritional deficiencies in children 17-22 months old who have received milk alternatives (Carvalho et al., 2001). Additional risk may occur when vegan mothers choose to raise their young children with the same dietary beliefs. Dairy is an essential part of a growing child's diet as it

plays key roles in important bodily functions. Therefore, milk should be considered a staple ingredient in the diets of young children.

Key Words: calcium, children, milk

153 Risks associated with raw milk consumption. A. M. Harshbarger*, *The Pennsylvania State University, University Park*.

Milk is handled and processed in a manner that makes it a safe, quality beverage. Before reaching the consumer, it must first pass numerous quality assurance standards. However, people who choose to drink raw milk may be putting themselves at risk for exposure to pathogenic bacteria normally controlled by pasteurization. Milk that has not been pasteurized poses risks for contamination via *Salmonella*, *E. coli*, *Listeria*, and other organisms. A study by Jayarao and Henning showed 12 of 131 farms in South Dakota and Minnesota had positive bulk tank samples for *Campylobacter jejuni*. Additionally, 6% of the tanks contained *Salmonella*. Common sources of bulk tank milk contamination include manure and bedding. Udder health and proper sanitation of milking equipment are also factors. Some areas of the United States have seen an increase in the number of foodborne illnesses linked to raw milk. In Pennsylvania, the first major reported case of illness resulting from unpasteurized milk occurred in 1983. Sixty first grade students were touring a dairy farm as part of a field trip. When it was time for a traditional snack of cookies and raw milk, all but a few of the students became ill as a result of *Campylobacter jejuni*. Some consumers and dairy producers prefer raw milk, even when they understand its associated hazards. Surveys of raw milk drinkers by Rohrbach and Jayarao indicated that 34% of eastern Tennessee citizens and 42% of Pennsylvanians who drink raw milk preferred its taste and convenience. This survey also concluded that many dairy producers who drink their own bulk tank milk are not familiar with the pathogenic bacteria that may be present. Pasteurization makes food borne illnesses resulting from drinking raw milk very preventable. Strict measures have been put into effect by several states to help protect public health. In Pennsylvania, the sale of raw milk is legal only if the producer has a permit from the Pennsylvania Department of Agriculture. However, regulations are not uniform across the nation. It is important that the dairy industry develop an educational plan to inform consumers and dairy producers about the possible risks associated with drinking raw milk.

Key Words: raw milk, foodborne pathogens

154 Defending the US milk supply with a novel bulk milk transportation security system. C. N. Gravatte* and C. D. Thompson, *University of Kentucky, Lexington*.

Increasing concern exists about the safety of US food. The next terrorist attack may be within the food supply, rather than through traditional targets. Of particular concern are bulk foods consumed within days of leaving the farm, especially milk. In light of this, researchers at the University of Kentucky, in conjunction with the University of Louisville, Western Kentucky University and the Kentucky dairy industry, have developed a security system that keeps milk locked up on the truck from farm to processing plant. The traditional security system consists of small, numbered zip ties accompanied by handwritten records. This system is labor and paperwork intensive and is susceptible to human error. The new security system would provide more accountability for the driver because it documents every interaction with the tanker. The system consists of three components: a tank monitoring system (TMS) located on the milk transport tank, a handheld device (computer), and a remote data server. The TMS is probably the most important security feature of the three. It allows entrance into the tank to either collect milk from a producer or deliver milk to a processor. Working in tandem with a keypad user interface, it will document everything that occurs, including opening and closing of the tank. Then, the GPS portion of the system documents where the truck is when it is being opened or closed. This system is designed not only to be a safer alternative to the current milk transportation system but also to help the marketing agency, farmer, and truck driver to keep better records. The handheld device allows the driver to input data about each load as it is collected. They can also keep track of milk weight and temperature. This information is then sent to the remote data server via cell phone. Other users access the server over the Internet and can generate reports about the load of milk. This system not only facilitates a safer milk supply, putting consumers minds at ease, but also opens the door to safer bulk food transportation and, ultimately, a safer food supply.

Key Words: agri-terrorism, milk safety, security

155 On farm pasteurization: Finding a niche market. J. T. Price*, *Clemson University, Clemson, SC*.

As today's farmers continue to face the difficulties of increased fuel costs, feed costs, and low milk prices they are beginning to find alternative ways to turn a profit. Some farmers have begun to market their own on-farm pasteurized products locally as well as to milk coops. Until recently it has been difficult for small dairies (30-200 cows) to survive competing with larger dairies (more than 800 cows); however, the niche market of farmstead production has allowed many farms to continue operating. Farmers in this enterprise are able to produce, process, and market their products on farm. This not only allows potential for increased farm revenue and convenience to farmers, it strengthens relationships between farmers and consumers and provides an opportunity for these farmers to increase consumer awareness. This niche market is based on providing fresh, quality milk, as well as other dairy products, to consumers while eliminating the middle man and enhancing consumer relations as well as revenue. On-farm pasteurization is becoming more common due to a demand from consumers who are now caring more about where their food comes from. Statistics show that approximately 40% percent of consumers are concerned about the origin and processing of the food they consume. Even though there are many advantages to on farm processing there are also a few challenges. These obstacles that farmers would have to overcome include finding a market which consists of customers willing to buy their products, obtaining a milk processing license, finding and purchasing affordable equipment, as well as fulfilling and maintaining sanitation requirements and conditions set by the government. However, through overcoming these obstacles dairy farmers will be able to increase profit through marketing and selling their own products while simultaneously educating consumers about the dairy industry. This new specialty market provides consumers with an opportunity to purchase locally produced, fresh products as well as allowing smaller dairy farms the opportunity to survive the changing times.

Key Words: dairy, farmstead, pasteurization

156 Phosphorus and other nutrient disappearance from plants containing condensed tannins using the mobile nylon bag technique. S. Pagán-Riestra*[1,2], J. P. Muir[1,2], B. D. Lambert[2], L. O. Tedeschi[1], and L. Redmon[3], [1]*Texas A&M University, College Station*, [2]*Texas AgriLife Research, Stephenville, TX*, [3]*Texas AgriLife Extension, College Station, TX*.

A study was designed to evaluate the nutrient disappearance from three Texas browse species containing condensed tannins (CT; *Acacia angustissima* var. *hirta*, *Desmodium paniculatum*, *Smilax bona-nox*, and *Medicago sativa* as control) using the mobile nylon bag technique. Two ruminally or duodenally cannulated steers were fed a basal diet of *Sorghum bicolor* × *S. sudanense* hay. Sixty nylon bags per plant material were incubated in the rumen (24hrs), pepsin/HCl, and duodenum. Twenty bags per plant material were selected to determine the nutrient disappearance at specific incubation sites. The proportion of nutrient that disappeared during rumen, pepsin/HCl, or duodenum incubation differed among plant species and nutrient evaluated (P<0.05) and did not appear to be directly related to relative CT concentrations. *Medicago sativa* had greater nutrient disappearance (P<0.05) for all the nutrients evaluated in every incubation site. Dry matter (DM), inorganic matter (IM), and organic matter (OM) disappearance was greater (P<0.05) during rumen incubation than at other stages for all plants evaluated. Of the plants containing CT evaluated in this study, *A. angustissima* demonstrated the greatest overall disappearance of DM, CP, P, and OM. A greater proportion of *A. angustissima* and *D. paniculatum* crude protein (CP) and phosphorus disappearance (PD) occurred in the duodenum compared to *S. bona-nox* and *M. sativa*. The presence of CT appears to reduce total PD and shift disappearance from the rumen to the duodenum.

Key Words: phosphorus, condensed tannins, mobile nylon bag

157 Effect of feeding supplemental rumen-protected Niacin (Niashure™) on milk yield, and milk composition in early lactation Holstein cows. D. J. Vanderwende*[1], B. A. Hopkins[1], S. M. Emanuele[2], S. Davidson[1], G. W. Smith[1], and L. W. Whitlow[1], [1]*North Carolina State University, Raleigh*, [2]*Balchem Corporation, New Hampton, NY*.

Eighty-six multiparous Holstein cows were assigned to one of three treatments to investigate the effects of 0, 6 and 12 g/d supplemental rumen-protected niacin (Niashure™) from 35 to 142 DIM. Cows received a corn silage based total mixed ration fed *ad libitum* twice daily through individual Calan® feeding stations. At the morning feeding all cows received 21 g/d of a topdress composed of a bentonite carrier blended with treatments of 0, 6, or 12 g/d Niashure™. Feed intakes were recorded daily. Analysis of weekly feed samples composited monthly indicated that diet DM contained 18.3% CP and 21.5% ADF. Milk yields were recorded at each milking (2x/d). Weekly milk samples composited from consecutive a.m. and p.m. milkings were analyzed for fat, protein, urea nitrogen, and lactose. High and low ambient temperatures and humidity levels in the free-stall barn were recorded daily. Skin temperatures were measured at the rear udder attachment five days per week at the p.m. milking using an infrared thermometer. Body weights and body condition scores were measured weekly. Data were analyzed using the mixed procedure of SAS® and significance was declared at $P < 0.05$. There were no significant treatment effects on skin temperatures, body weights, or body condition scores. Milk yield (kg/d), fat (%), protein (%), lactose (%), MUN (mg/dL), and DMI (kg/d) were (38.4, 4.0, 2.9, 4.8, 21.1, 24.9), (40.2, 3.9, 2.8, 4.7, 21.3, 24.9), and (40.0, 4.0, 2.9, 4.8, 21.3, 24.5), for treatments of 0, 6, and 12 g/d Niashure™, respectively, with no significant treatment effects. In comparison to control, Niashure™ supplementation of 12 g/d tended to improve feed efficiency (kg milk / kg DMI) from 1.58 to 1.65 ($P < 0.08$). In comparison to control, supplementation of 6 g/d Niashure™ significantly improved feed efficiency from 1.58 to 1.69 ($P < 0.02$).

Key Words: niacin, dairy, milk

158 Effect of probiotics and yeast culture on rumen development and growth of dairy calves. J. M. Laborde*, C. C. Williams, C. Leonardi, C. F. Hutchison, B. F. Jenny, B. L. Fisher, and A. H. Dolejsiova, *Louisiana State University AgCenter*, *Baton Rouge*.

To determine effects of probiotics and yeast culture on rumen development and growth, 48 Holstein calves were randomly assigned to 1 of 4 treatments which included calf starter containing no additive (C); the yeast culture *Saccharomyces cerevisiae* (YC); the probiotics *Bacillus lichenformis* and *Bacillus subtilis* (P); and yeast culture and probiotics (YCP). Calves were fed treatments from d 2 to 56. Body weights, hip heights and wither heights were measured weekly. Feed and water intake and fecal scores were recorded twice daily. Rumen fluid was collected on d 14, 28, 42, and 56 for analysis of pH, volatile fatty acids (VFA), and ammonia (NH3). Blood was collected on d 28, 42, and 56 for analysis of β-hydroxybutyrate (BHBA). There was a sex*treatment interaction (P < 0.05) for starter intake. Males receiving P consumed less than other calves. Females consuming no additive ate less than males on the same diet. Females consuming YC ate more than males on YC. Calves receiving YC tended (P = 0.06) to eat more than calves not fed YC. Calves consuming P drank less water than all other calves (P < 0.05). Calves consuming YC had higher (P < 0.05) average daily gain (ADG) than calves with no YC. There was a treatment*week interaction for ADG (P < 0.05). Females consuming no additives and males consuming P had lower ADG. There were no differences among treatments for hip and wither height (P > 0.1). Calves consuming YC had higher fecal scores than those with no YC (P < 0.05). However, fecal scores were within normal ranges for healthy calves. There were no differences among treatments for NH3, BHBA, butyrate, and propionate (P > 0.1). Calves consuming P tended (P = 0.08) to have higher total VFA concentrations than calves not consuming P. A significant sex*treatment*week interaction occurred for acetate concentrations (P < 0.05). Calves consuming P had increased acetate, with females showing a greater increase over males. There was a sex*probiotic*week interaction (P < 0.05) for pH. Male calves consuming P had lower rumen pH at d 56 than all other calves. Incorporating YC into starter may result in an increase in growth in neonatal calves.

Key Words: probiotics, yeast culture, calf starter

Dairy Foods: Milk Protein Fractionation Symposium

159 Introduction to milk protein fractionation symposium. L. E. Metzger*, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Recent advances in processing research and membrane technology have allowed for the fractionation of whey proteins directly from milk. The differences in attributes between whey proteins isolated from milk and those isolated from cheese whey are becoming an important factor for dairy protein processors considering this new avenue for fractionating whey proteins. The symposium will cover membrane fractionation technology to produce high purity whey protein concentrates from milk. A detailed comparison of flavor chemistry, sensory properties and functional properties of whey proteins isolated from milk and from cheese whey will be presented. In addition to using membrane technologies to separate whey protein and casein, other emerging technologies have the potential of allowing for the separation of casein and whey protein fractions. This symposium will also present three new research developments: membrane fractionation of milk proteins from whole milk, charged membrane application for whey protein streams and using supercritical carbon dioxide for fractionation of milk proteins. The symposium will provide the latest in research in milk protein fractionation from various dairy research entities in the US and will serve to facilitate discussion of future development in dairy protein fractionation.

Key Words: milk protein, fractionation

160 Global use, opportunities and challenges for dairy proteins. P. Tong*, *Dairy Products Technology Center, California Polytechnic State University*, *San Luis Obispo*.

Several factors can impact the future global use of dairy proteins. For some parts of the world where traditional dairy products are readily available, their motivation to consumer dairy proteins may be quite different than in other regions of the world where availability of milk was limited. In developing and emerging markets, trends of increased urbanization, population growth and affluence will drive future demand for ingredients and foods containing dairy proteins. In some cases, this demand is to enhance the basic nutritional status of its population by incorporation of consuming high quality dairy proteins. As developing countries seek to improve their nutritional status they seek to incorporate more dairy protein into their diet. Here the goal is to introduce dairy proteins into the diet as economically as possible. For such products consistency in performance, availability and cost are very important. In more developed countries where disposable income is high, demonstrating added value of the protein ingredients in food is important. In particular dairy protein ingredients which provide potentially greater health and wellness benefits to food products relative to other food proteins is desired. To improve applicability in food systems, dairy protein based ingredients need to meet the process demands of the food application consistently. Hence, these ingredients need to meet customer specifications and deliver quality attributes over the storage life. Establishing common specifications using common test methods can be challenging as many customers have established many empirical tests that can have a subjective component to their interpretation. Nonetheless the basic nutritional and functional properties of dairy proteins will continue to be in demand. To successfully meet this demand requires matching the customer needs to the ingredient form and insuring dairy proteins consistently delivers value in the final product application.

Key Words: dairy proteins, dairy ingredients, milk proteins

161 Isolation of serum proteins from milk. D. M. Barbano*[1] and J. Zulewska[2], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Warmia and Mazury*, *Olsztyn, Poland*.

Milk is a rich source of organic and inorganic nutrients that can be consumed directly as a beverage, transformed into a range of traditional dairy foods and by-products, or fractionated into a wide range of milk components that can be used as food ingredients. The concept of fractionating milk directly into value-added ingredients has been called milk refining. The 1st step in milk refining became common practice over 100 years ago with the invention of the centrifugal cream separator, which allowed rapid removal of fat from milk. More recently, membrane filtration processes that rapidly separate components of skim milk (without the addition of any chemicals) are being implemented. The most recent of these cutting-edge membrane processes is microfiltration (MF) of skim, which has the capability to directly isolate different groups of proteins (milk caseins versus milk serum proteins) based on their difference in size. A wide variety of membrane materials, geometric designs, system configurations and operating approaches are available. Two major types of MF membranes exist: polymeric and ceramic. Data are just becoming available on these two types of membrane systems. They differ in cost, membrane life, flux, protein separation efficiency, ability to be cleaned, and energy consumption. MF of skim milk produces a filtrate that has some similarities to whey from rennet cheese making, but is not identical in composition, flavor, or functionality. The main component of value in whey and MF permeate is protein. Key differences between MF permeate from skim milk and rennet cheese whey are: cheese whey contains glycomacropeptide, fat, soluble components from starter media, metabolites from starter culture, lactic acid, cellular debris from starter bacteria, residual milk coagulant, and possibly residuals from added color and bleaching agents used in cheese making, while MF permeate does not. These differences may produce differences in flavor, functionality, and value of these two sources of milk soluble proteins.

Key Words: microfiltration, serum proteins, whey

162 Comparison of the functional properties of whey proteins isolated from milk or whey. E. A. Foegeding*[1], J. Zulweska[2], D. M. Barbano[2], M. A. Drake[1], P. J. Luck[1], Y. H. Yong[1], B. Vardhanabhuti[1], and T. Berry[1], [1]*North Carolina State University*, *Raleigh*, [2]*Cornell University*, *Ithaca, NY*.

Cheese whey can be utilized directly or serve as a source for producing protein powders containing 34 – 80% protein (whey protein concentrate, WPC). The functionality of WPC can be influenced by the cheese making process, powder composition and the processes used to make the powders. Whey protein powders could also be produced by removing proteins from milk prior to cheese making. This removes potential functionality-altering processes and compounds associated with cheese making. A comparison of functional properties of whey protein powders was conducted by producing whey protein concentrate from milk (M) or cheese whey (W) containing 34% (WPC34) or 80% (WPC80) at Cornell University and evaluating functional properties at North Carolina State University. Functional properties of solution clarity, solubility, foam formation and gelation were investigated. The most striking difference was in solution clarity, where M-WPC powders produced slightly turbid to clear solutions and those made from whey were opaque. The increased opacity of W-WPC powders suggests that the cheese making process introduced large particles into the whey that became part of the protein powders. Whey protein concentrates made

from milk had greater foaming properties than those produce from whey. As with opacity, this too is most likely related to the presence of particles in the W-WPC's. Particles are known to cause coalescence in foams due to bridging mechanisms. Finally, the M-WPC's produced stronger gels than W-WPC's. Gel strength generally scales as a square function of the network concentration and, since W-WPC's contained protein particles that most likely did not contribute to the gel network, it is logical that they would have lower gel strength. It was shown that whey protein concentrates made from milk have greater functional properties than those made from whey. This is most logically due to a higher concentration of native, non-aggregated protein present in the concentrates made from milk.

Key Words: whey, functionality, protein

163 Comparison of the flavor chemistry and sensory properties of whey proteins isolated from milk and whey. M. A. Drake*[1], D. M. Barbano[2], E. A. Foegeding[1], J. Zulewska[2], and M. Newbold[2], [1]*North Carolina State University, Raleigh,* [2]*Cornell University, Ithaca, NY.*

Nattive whey or serum protein concentrates (SPC) are proteins removed from milk by microfiltration without cheese making. Relative amounts and types of proteins present in SPC and WPC differ; SPC contains no glycomacropeptide. SPC is not exposed to some enzymatic and/or chemical reactions that may lead to off-flavors. Our objectives were to identify and compare composition, flavor, and volatile components of 80% protein SPC and WPC (SPC80, WPC80). SPC80 and WPC80 were manufactured in triplicate with each pair of serum and traditional whey protein manufactured from the same lot of milk and compared to commercial WPC80. Volatile components were extracted by solid phase micro-extraction and solvent extraction followed by solvent assisted flavor evaporation with gas chromatography-mass spectrometry and gas chromatography-olfactometry. Consumer acceptance testing was conducted with 6% protein acidic beverages made with SPC80 and WPC80, as well as commercial WPC80. SPC80 had lower fat and higher pH than pilot plant produced and commercial WPC80 ($p<0.05$). There were few sensory differences between our directly rehydrated SPC80 and WPC80, but their flavor profiles differed from rehydrated commercial WPC80 ($p<0.05$). Our WPC80 had higher concentrations of lipid oxidation products than SPC80, however concentrations in commercial WPC80 were higher than those made in this study ($p<0.05$). Trained panelists found protein-associated flavors in acidic beverages that were not detected in reconstituted neutral pH protein solutions. Protein beverages made with SPC80 were not liked as well as protein beverages made with WPC80 produced in this study or one commercial WPC80 ($p<0.05$). Composition, physical properties and volatile compound composition of SPC80 and WPC80 differed. These differences may cause flavor differences in low pH applications.

Key Words: milk proteins, whey protein, flavor

164 An integrated processing system to produce beta-casein, native whey protein and casein concentrates from whole milk. J. Lucey*[1] and K. Smith[2], [1]*Department of Food Science, University of Wisconsin, Madison,* [2]*Wisconsin Center for Dairy Research, University of Wisconsin, Madison.*

We believe that successful adoption of new milk fractionation schemes by the dairy industry can be achieved if multiple value-added ingredients are created; it is also desirable that no reduced value by-products are generated. In the dairy industry, a barrier to the more widespread use of microfiltration (MF) of milk is the paradigm that skim milk must be the starting raw material (presumably due to concerns over fouling or milk fat damage). For many dairy plants in order to convert all their whole milk (WM) into skim milk would require considerable capital investment and this would add another processing step into any fractionation scheme. We have developed a process to separate beta-casein from milk using polymeric, spiral-wound MF membranes operating at low temperatures. Beta-caseins were then separated from the rest of materials in milk permeate by warming permeate to room temperature where beta-caseins aggregated. The aggregated beta-caseins could then be retained by the MF membrane while native whey proteins passed into the permeate. Casein retentate that was partially depleted of beta-casein has been shown to produce cheese with improved meltability. We developed a process that uses WM as a starting material for MF. We used polymeric, spiral-wound MF membranes instead of ceramic membrane systems. WM has higher viscosity than skim milk, especially at low temperatures, which decreased flux somewhat when operated at low temperatures. Good whey protein permeations rates were observed with WM and no significant loss of flux observed during extended operation in recirculation mode for a 2× concentrated feed. The use of low temperatures results in beta-casein being present in milk permeates and that beta-casein fraction could be removed by the method previously developed for beta-casein purification. This fractionation scheme can use WM to produce beta-casein, native whey and casein concentrate in one processing plant. The operation of our MF system at low temperature may allow the use of raw WM; which could be advantageous in the purification of heat sensitive serum proteins.

Key Words: microfiltration, native whey, casein

165 Charged ultrafiltration membranes for whey protein fractionation. M. Etzel* and S. Bhushan, *University of Wisconsin, Madison.*

Ultrafiltration is widely used to concentrate proteins, but fractionation of one protein from another is much less common. This work examined the use of positively charged membranes to increase the selectivity of ultrafiltration, and allow the fractionation of proteins from cheese whey. By adding a positive charge to ultrafiltration membranes, and adjusting the solution pH, it was possible to permeate proteins having little or no charge, such as glycomacropeptide, and retain proteins having a positive charge. Placing a charge on the membrane increased the selectivity by over 600% compared to using an uncharged membrane. The data were fit using the stagnant film model that relates the observed sieving coefficient to membrane parameters such as the flux, mass transfer coefficient, and membrane Peclet number. The model was a useful tool for data analysis, and for the scale up of membrane separations for whey protein fractionation.

Key Words: ultrafiltration, whey, protein

166 Utilization of supercritical carbon dioxide to produce milk protein fractions. P. M. Tomasula*, L. M. Bonnaillie, and P. X. Qi, *Dairy Processing and Products Research Unit, USDA/ARS/ERRC, Wyndmoor, PA.*

The nutritional, functional and bioactive properties of the individual whey proteins are appreciated by health-conscious consumers, yet few methods have been developed to produce these proteins to satisfy demand. The methods that are available are relatively new technolo-

gies that have not been proven by development research and thus are unfamiliar to food processors. In our laboratory, we have shown that supercritical carbon dioxide (SCO_2) at pressures, P, greater than 7.4 MPa, when injected into solutions containing whey protein isolate or whey protein concentrate is effective for production of enriched fractions of the whey proteins, α-lactalbumin (α-LA) and β-lactoglobulin (β-LG). Fractions containing 70 wt% of α-LA, in solid form, and 95 wt% β-LG in a soluble liquid form uncontaminated with chemical additives have been obtained. We have also produced CO_2-casein, a high calcium-containing casein and other food protein isolates using the process under high pressure conditions in the range from 4.1 MPa to 7.4 MPa. The process is not an extraction process but relies on the production of carbonic acid that results from hydrolysis of solubilized CO_2. Separation of whole protein or the enriched whey fractions is achieved through manipulation of P, temperature, agitation rate, protein concentration, and holding time, all factors which have been shown to affect solvent pH, protein conformation, and yield. A continuous pilot plant process was developed to produce CO_2 casein in kg quantities, and a large-scale process for production of the whey fractions is being designed. Both processes may be integrated to simultaneously produce CO_2-casein and the enriched whey fractions from milk. Processes based on CO_2 separation may be considered sustainable, because much of the CO_2 may be recovered after separation has been achieved. Other advantages are that a relatively concentrated feed stream containing the whey proteins may be processed and post-treatment washing is minimal compared to other methods. This presentation will focus on the casein and whey fractionation processes, as well as some of the properties of the proteins obtained from these processes.

Key Words: CO_2, whey, casein

ADSA Southern Section Symposium: Dairy Replacement Health Challenges in the Southeastern U.S.

167 Advances in colostrum management. S. Godden*[1], S. Wells[1], J . Stabel[2], D. Haines[3], R . Bey[1], J. Fetrow[1], P. Pithua[1], and M. Donahue[1], [1]*University of Minnesota, St. Paul*, [2]*USDA, ARS, National Animal Disease Center, Ames, IA,*, [3]*University of Saskatchewan, Saskatoon, SK, Canada*.

Failure of passive transfer (FPT) continues to affect a significant portion of North American dairy calves, contributing to high preweaning morbidity and mortality rates as well as impaired long-term health and performance. The goal of this presentation is to review key components of a successful colostrum management program with emphasis on recent research findings of practical importance to the industry. A successful colostrum management program will require producers to consistently provide calves with a sufficient volume of clean, high quality colostrum within the first 6 hours of life. Colostrum quality may be improved through the dry cow vaccination program, proper feeding and management of the dry cow, and rapid harvest of colostrum within 6 hours after calving. Use of either a nipple bottle or esophageal tube feeder will provide equal and high levels of passive transfer of immunoglobulin (Ig), provided a large enough volume of colostrum is fed. Microorganisms that may be found in colostrum are of concern because i) pathogenic organisms can cause clinical or subclinical disease and ii) bacteria in colostrum can interfere with passive transfer of colostral Ig, contributing to FPT. Experts recommend that fresh colostrum contain fewer than 100,000 cfu per ml total bacteria count and fewer than 10,000 cfu per ml total coliform count. Methods to reduce colostrum contamination will include careful attention to udder preparation prior colostrum harvest, strict adherence to protocols for sanitation of milking, storage and feeding equipment, and avoiding the pooling of raw colostrum. Bacterial proliferation in stored colostrum can be reduced or minimized by feeding within 1-2 hours of collection, rapid refrigeration (feed within 48 hours) or freezing. Colostrum replacers can also be useful tools, with recent studies demonstrating a lower risk of subclinical Johne's disease in calves originally fed a colostrum replacer vs raw colostrum. If using replacers, producers should feed 150 to 200 g IgG in a product that has been tested for efficacy. Pasteurization of colostrum (60 ° for 60 min.) can reduce pathogen exposure while maintaining colostrum Ig, resulting in enhanced passive transfer of Ig.

Key Words: colostrum, bacteria, calf

168 Strategies to minimize the impact of heat stress on heifer health and performance. J. W. West*, *University of Georgia*, *Tifton*.

Heat stress research has largely focused on the lactating cow because of easily measured parameters such as milk yield and efficiency. Less emphasis has been placed on dairy heifers, either because they are not affected by heat stress (doubtful) or because economic returns to managing for heat stress are less evident. Literature suggests that heifers are impacted by heat stress through slowed growth, impaired immune function or poor reproduction. Data from the southern U. S. and Caribbean regions at latitudes less than 34°N suggests that Holstein females weigh 6 to 10 percent less at birth and average approximately 16 percent lower body weight at maturity than those in more northern latitudes, even when sired by the same bulls (NRC, 1981). Potential explanations include greater maintenance requirements with hot weather, poorer forage quality, and reduced immune function. Is there a physiologic difference in newborns which experience heat stress *in utero*? Heat-stressed ewes and beef cows exhibited reduced uterine blood flow and lower birth weight for newborns. Brains and livers of lambs from heat stressed ewes were smaller, leading to the concern that newborns from heat-stressed mothers may be smaller at birth and less vigorous and lacking the metabolic machinery to thrive following birth. Colostrum from cows exposed to heat stress during late gestation and early lactation may have lower immune globulin content and coupled with the impact of heat stress on newborn calves, mortality losses can be large. Management in heat stress environments should occur at several levels. Environmental modification is crucial for the late gestation cow and for the newborn calf. Maintenance costs are higher reducing potential growth rate for heifers, thus attention to nutrition is necessary to achieve desired rate of gain. Heifer conception rate is typically better than for mature cows; however reproduction efficiency suffers in heifers as well. Good performance in a heifer management program will result from attention to environment, nutrition and health in hot climates.

Key Words: heat stress, dairy heifers, management

169 The impact of genomic selection on A.I. companies, today and tomorrow. K. L. Westaby* and L. H. Kilmer, *Iowa State University*, *Ames*.

Genomic selection may transform the dairy industry by altering the process that A.I. companies use to identify, select, and evaluate new bulls. This advancement in animal genetics involves genotyping animals to ascertain which ones have inherited the best set of alleles responsible for traits desirable to the industry. A.I. companies can use rapid genomic evaluations to genotype more bulls as an initial step to identify those bulls with superior genetics, then progeny test fewer bulls than is done currently. Genomic information is particularly valuable for determining differences among full siblings. Alternatively, A.I. companies now have the option to offer bulls selected from genetic predictions based on genomic information and ancestor performance, without the time consuming process of progeny testing. However, the reliability of these genetic predictions remain to be tested. In the future, the use of genomics can be expanded by selection for traits with low heritability, and testing bulls from families not previously used, to help reduce inbreeding. The positive changes that genomic evaluations have and will continue to make for the A.I. industry are only just being realized. Reliability of genomic estimates will continue to improve as more animals are genotyped, statistical methods are refined, and associations between genotypes and phenotypes are better defined. However, A.I. companies can currently use genomic selection to reduce costs of getting a truly superior new sire into their active line-up, and increase the rate of genetic gain, especially in traits not easily selected for when using parent averages.

Key Words: genomic selection

170 Pre-planning considerations for on-farm dairy processing enterprises. E. A. Chaney*, *University of Kentucky*, *Lexington*.

The current trend toward fewer and larger dairy operations and increasingly volatile milk prices present many challenges for the small dairy business manager. One option that dairy managers searching for a way to maintain a small dairy operation may consider is on-farm processing of a value added dairy product (i.e. cheese, ice cream, or bottled milk). Niche marketing of dairy products, which has increased in recent years, can be a feasible way to maintain family goals and a profitable business simultaneously. The decision to start an on-farm processing business venture should not be taken lightly. Before starting any agribusiness, particularly an on-farm dairy processing enterprise, a considerable amount of thorough research and development must occur. Most existing agribusiness owners started out by going through at least a year of research and travel. Throughout this exploration process, these business managers evaluated the economics of their decision and visited already successful on-site cheese makers, homemade ice cream stores, and milk processing facilities. A complete business plan must be developed before starting an on-farm dairy processing enterprise. Similarly, a comprehensive market research plan should be developed to explore the need and demand for the business and product within the area along with how the business can differentiate itself from potential competitors. With an idea of investment expenditures and projected income from product sales, investment analyses and short and long-term budgeting should be conducted. Local universities, economic development councils, small business management administrations, and the Cooperative Extension Service may be useful resources during this process. On-farm processing facilities are heavily regulated. Consequently, being knowledgeable of and prepared to adhere to all local and regional rules and regulations can help make or break a business. On-farm dairy processing is a hot topic among American dairy farmers. Listening to existing business managers and researching all business and technical considerations will maximize the chances of establishing a successful on-farm processing enterprise.

Key Words: on-farm processing, value added

171 Bovine genomics: Mapping the future of the dairy industry. V. Eubanks*, *Clemson University*, *Clemson, SC*.

Healthy, high producing cows are the foundation of the dairy industry. Although assisted reproductive technologies have made rapid advances in dairy type and production traits, there remains much room for improvement in areas such as milk quality, somatic cell count, productive life, and other economically important traits. Since the initiation of the Bovine Genome Project in 2003 following work on the human genome project, researchers have been granted an additional tool for selecting genetically superior animals. Genomic selection is the process of identifying numerous genetic markers located across an animal's entire genome and using these markers to select elite animals. This bovine genome map can be used to identify more than 40,000 nucleotides on the 30 chromosome pairs. With the help of genome maps, geneticists may now be able to trace valuable traits to individual loci on chromosomes, and then use this knowledge to breed the best individuals. This new technology has enormous potential benefit for the dairy industry. In a world that is currently based on type and production, genomic selection may allow the focus to shift toward health traits such as somatic cell count, reproductive efficiency, and productive life. In addition, the cost of proving bulls may decrease by as much as 92%, and bulls can be proven at a much earlier age, reducing the generation interval and increasing genetic gain. Genomic selection is a very new technology, but as of January 2009 it has become the official standard for genetic evaluations. Genomic selection will be an asset to all facets of the dairy industry by positively influencing the productivity of dairy animals, both cows and sires, as well as enhancing the overall health and longevity of the animals.

Key Words: bovine, genome, dairy

172 The effects of genomic predictions in dairy cattle. R. R. Liskey*, B. G. Cassell, and D. R. Winston, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

The world of dairy cattle genetics is about to change the way producers look at their breeding programs with the new innovation of genomics. In January 2009, the Animal Improvement Programs Laboratory in Beltsville, MD published the first genomic PTA's. Genomic PTA's are created using phenotypic, pedigree, and genotypic data that evaluates the accuracies of traits, increases genetic progress, decreases generation interval, and increases the reliability of records. Currently the genomic data is retrieved with the use of Illumina BovineSNP50 BeadChip and semen samples. The use of the chip enables us to reveal the genetic makeup of an individual at about 50,000 locations out of 3,000,000,000. About 38,000 of those 50,000 locations are used to predict genetic merit for 27 different traits: five yield traits, five for health and fitness, 16 conformation traits, and net merit were computed using genomics. Research (VanRaden, et al, 2009) showed increased reliabilities and decreased

generation intervals with the use of genomics. This work revealed that the reliability using genomic predictions and averaged over all 27 traits increase by 23% compared to reliabilities of parent averages. On average, this increase was equivalent to about 11 additional daughter records. The improvement in accuracy of genetic evaluations at an early age provides distinct economic advantages to genomic breeding programs. Annual genetic gain could be increased by 50% per year through the new technology. The genomic breeding programs also provided a higher discounted profit than a conventional progeny testing program and the costs related to bulls in progeny testing were reduced by 92%. Although this research is still in early phases, the ability to increase efficiency and profitability through the use of genomics shows great potential.

Key Words: genomics, dairy cattle

173 Advanced technology in gender selection: Sexed semen. H. Parkins* and S. Washburn, *North Carolina State University*, *Raleigh*.

Genetic improvements of cattle involve selections made through reproduction; purposely mating individuals possessing favorable traits required to improve overall herd performance. In the 1980s it became possible to sort and sex semen to influence the gender of the offspring, primarily increase the ratio of heifer calves born; this sexing procedure is Fluorescence Activated Cell Sorting (FACS). A pioneer in this field, George E. Seidel, refers to this procedure as Flow Cytometry or Cell Sorting; it requires the use of a Flow Cytometric Sorter System, separating the cells based on DNA content. Female Sperm cells bearing X chromosomes have 4% more DNA than Y-bearing sperm cells. Consequently, X cells pick up a higher content of a fluorescent dye, with no negative effects on living cells. A flow Cytometer works by forcing the cells into little droplets with a vibrator making approximately 70,000-80,000 droplets per minute. A special laser then emits light at a specific wavelength to determine dye content. Results go through a detector and are analyzed by a computer. Droplets are assigned a charge depending on results; X are positive and Y are negative; those with multiple, none or damaged sperm cells do not receive a charge. Cells exit the Cytometer at 80Km/H through a nozzle, and then pass through an electric field where the charged droplets are attracted to opposing charges on opposite sides of the unit; droplets with no charge stay in the center. Three exit streams are formed with X and Y output each at about 20%; unknown or damaged at 60%. Debating issues include small doses of semen and how to make it economically viable for industry use, high cost of a Cytometer, slow rate of sorting, lower fertility, loss of value of Y-bearing sperm cells, and lack of incentive to sort high value bulls. One product (Heifer Plus) currently being marketed has been purported to increase heifer ratio to about 70% at a lower cost than the FACS system. However objective research data are lacking. Recent advances in technology for gender selection have been promising, and more advances will be made as technology advances.

174 Blood pregnancy tests as alternatives to transrectal examinations. N. J. Heim*, *The Pennsylvania State University*, *University Park*.

Low 21-day pregnancy rates are among the largest challenges dairy producers face today. Timely pregnancy diagnosis is key to reducing the inter-service interval. Currently the most widely used method to diagnose pregnancy is transrectal palpation. However, palpation can cause a 2-6% embryonic loss, and this is particularly a problem when palpation occurs before day 35 after insemination. To improve accuracy and timeliness, scientists have developed new technologies, beginning with ultrasonography and followed by blood pregnancy tests. These technologies have benefits over transrectal palpation. In addition, they can be conducted earlier after insemination. BioPRYN® (Pregnancy Ruminant Yes/No; BioTracking LLC) is a commercially available blood test that checks for the presence of pregnancy specific protein-B (PSPB), a protein only produced by the placenta. This technology allows a cow to be checked for pregnancy as early as 30 days after insemination and has an overall 97% accuracy. Test administration does not require a high level of training and is convenient for the producer. Additionally, the blood is tested accurately by participating labs using an enzyme linked immunosorbent assay (ELISA) test. Another blood test is being developed by AspenBio Pharma, Inc. called SurBred™. This is a cow-side test which will determine if a cow is open at days 18-21 after insemination. When a cow is pregnant, specific proteins are increased in her blood during early pregnancy. SurBred™ will test the blood for these specific proteins. This test has potential advantages because it can be performed on the farm and can detect failed inseminations 8-10 days earlier than ultrasonography or BioPRYN®. Blood pregnancy tests provide a safe, accurate and economical management tool for producers to determine pregnancy status earlier and reduce the inter-service interval compared to transrectal examinations.

Key Words: pregnancy, palpation, pregnancy specific protein-B (PSPB)

175 Contracted tendons in calves. M. Reed*, *Louisiana State University*, *Baton Rouge*.

Contracted tendons are the most common congenital abnormality in calves. This condition is not considered directly fatal as it does not interfere with vital organs of the body. The two most commonly affected tendons are the deep digital flexor and the superficial flexor. There is no definitive cause of the syndrome although it is thought that nutrition, intrauterine positioning, and genetics may play a role in the development of this condition. Research has also shown that a manganese deficiency in the dam may cause contracted tendons in the calf. Ingestion of toxic plants such as Lupine alkaloids, locoweed, and poison vetch has also been reported to cause the syndrome. Calf nutrition is equally important in tendon development. Vitamins D and E as well as selenium have been shown to play a key role in muscle and tendon growth in the infantile calf. It is also believed that insufficient room in the uterus for extension and grow of tendons will lead to development of the condition. Autosomal recessive genes have been discovered to cause musculoskeletal defects in infant calves. There are several conditions and diseases that correspond with contracted tendons. The main concern is malnutrition, as calves who cannot walk cannot obtain the nutrients needed for maintenance and growth. Calves may also develop secondary infections from wounds caused by knuckled walking. If calves remain untreated for long periods of time they risk the possibility of tearing the common digital flexor. There are three classifications of the deformity which range from walking on the toes to walking on the dorsal aspect of the lower limb. Treatments for tendon contracture are stretches and exercising, soft splints and plaster cast as well as surgery. Splints are normally used in moderate to severe cases, leaving the toes out to help force the tendon to extend and stretch. Casts are more often used when there is twisting involved as well as the contracture. In conclusion, contracted tendons are a serious condition in calves, but with balanced nutrition and proper treatments it is a correctable problem.

Key Words: contracted tendons, calves, congenital deformity

176 The effects of breeding for increased milk production in dairy cattle on other productive traits. G. A. Carpenter* and E. L. Karcher, *Michigan State University*, *East Lansing*.

The economic model of milk production in the United States gives incentive to dairy farms that produce large amounts of milk. As a result, there is a movement to genetically select cows for superior production. Unfortunately, breeding cattle based on volume of milk produced may affect other traits, such as survival, milk composition, disease, and reproduction. Current research suggests that the stress associated with higher production may lead to increased mortality in these animals. A study by Castillo-Juarex et al. (2000) suggested an adverse correlation between mature equivalent milk and somatic cell score over the entire lactation. Additionally, cows that are genetically superior in milk production are genetically inferior in fertility (Dematawewa and Berger,1998). Although, high production can have antagonistic genetic effects on other productive traits, these effects can be reduced with a combination of breeding selection and sound management practices. Low heritability and repeatability estimates for survival indicate that management can reduce cow mortalities. Moreover, positive error correlations between survival and other traits suggest that producers may be providing better management for high-producing cows than low-producing cows. These management practices may include more meticulous udder preparation and more vigilant estrous detection. Combined, these have the potential to effectively lower the mortality rates for high-producing cows. It can be deduced from these studies that while breeding cattle for increased production can harmfully affect some traits, with proper management, these consequences can be minimized while still achieving a greater profit.

Key Words: breeding, genetics, production

ADSA-SAD (Student Affiliate Division) Undergraduate Competition: Original Research

177 Feeding brown midrib forage sorghum silage and wet corn gluten feed to lactating dairy cows. C. S. Heine*[1], P. J. Kononoff[1], J. F. Pedersen[2], A. G. Geis[1], and A. M. Gehman[1], [1]*University of Nebraska, Lincoln*, [2]*USDA-ARS Grain, Forage, and Bioenergy Research Unit, Lincoln, NE*.

Brown midrib (BMR) forage sorghum contains less lignin, resulting in increased NDF digestibility compared to conventional sorghum. An experiment was conducted to evaluate the effects of BMR sorghum silage in diets containing wet corn gluten feed (WCGF). The objective was to determine the effect of diet on milk production, composition, and total tract digestibility. Twenty Holstein cows weighing 729.8 ± 3.27 kg and averaging 124 ± 29.0 DIM were assigned one of the four dietary treatments: 1) conventional sorghum and 0% WCGF, 2) conventional sorghum and 30% WCGF, 3) BMR sorghum and 0% WCGF, and 4) BMR sorghum and 30% WCGF. The experimental design was a 4 × 4 Latin square in which each cow received each diet during 4 21-d periods. In diets containing no WCGF, 27% DM consisted of sorghum compared to diets containing WCGF, in which 17% DM consisted of sorghum. Ruminal NDF digestibility of sorghum silages was evaluated *in vitro* by incubating approximately 0.3 g of sample in rumen fluid for 48 h. The proportion of NDF digested after 48 h was higher ($P < 0.01$) for the BMR sorghum (53.0 ± 1.7%) compared to the conventional sorghum (39.0 ± 0.78%). Compared to the conventional sorghum, DMI tended ($P = 0.07$) to be higher when cows consumed BMR sorghum silage (24.6 vs. 26.0 ± 1.11 kg/d). In contrast, total tract NDF digestibility was lower when animals consumed diets containing BMR sorghum silage (54.5 vs. 57.0 ± 0.70%). The inclusion of WCGF did not affect DMI or total tract NDF digestibility, and no interactions between silage type and WCGF were observed. Although cows consumed more of the rations containing BMR sorghum silage, no differences were observed in milk production or composition. Similarly, the inclusion of WCGF did not affect milk yield or composition. Across treatments, milk yield averaged 30.5 ± 1.63 kg/d and fat and protein yield averaged 1.08 ± 0.06 kg/d and 0.90 ± 0.05 kg/d respectively. In spite of increased *in vitro* NDF digestibility and DMI, increases in milk production were not observed in cows consuming BMR sorghum silage and no interactions with WCGF were observed.

Key Words: brown midrib, sorghum, wet corn gluten feed

178 Measuring the citrate content in milk, mammary epithelial cells, and blood using capillary electrophoresis. M. J. Howell* and R. Jimenez-Flores, *California Polytechnic State University*, *San Luis Obispo*.

Citrate is an important regulator of calcium in milk and is indirectly related to de novo fatty acid synthesis in milk synthesis by providing NADPH. In this research our objective was to find if there was a correlation between citrate and milk productivity in the two commercial breeds of dairy cows. Levels of citrate were compared in raw milk, mammary epithelial cells, and blood of 12 cows (6 Holstein and 6 Jersey) . Based on productivity records of the Cal Poly Dairy Farm, the cows were classified as high or low producers; they were selected among a herd of 200 cows and chosen at same age and parity. All cows were fed mixed rations and were fed ad libitum. Raw milk was collected by hand, mammary epithelial cells were extracted from the raw milk using Wisteria Fioribunda-A lectin bound to magnetic beads (Dynabeads of 10 micron diameter), and blood was collected via tail vein. Experiments were run in triplicate, and all samples were compared to a standard citrate curve using capillary electrophoresis. While there was a similar trend in citrate content between groups in blood and milk, differences citrate levels were only statistically significant in the blood. Jersey high producing cows had an average of 3.7mM greater concentration of citrate in milk samples compared to low producers of the same breed as well as to the high producers of the Holstein breed, where there was an average of 3.9mM greater concentration of citrate. In blood, the citrate content of Jersey high producing cows was statistically significant when compared with lower producing Jerseys (p=0.078) as well as compared with high producing Holstein cows (p=0.007). Holsteins had no significant difference in citrate levels in the milk or the blood within the breed. Citrate was non-detectible in mammary epithelial cells, as citrate levels in the cells were too low to measure. This data shows there is a difference in citrate concentration between breeds which will have a significant impact on milk composition, like heat stability.

Key Words: citrate, productivity, milk

179 Effects of black hair coat color in neonatal Holstein bull calves. A. J. Krenek*, G. A. Holub, and J. E. Sawyer, *Texas A&M University, College Station*.

The objective of this study was to evaluate if the percent black hair coloring on a Holstein calf influences the rectal temperature (RT), or respiration rate (RR) of the calf. Holstein bull calves < 3 d of age were housed in fiberglass hutches from May 3 to July 8, a total of 56 days. Average Thermal Heat Index (THI) was calculated for each day by averaging the 72 recorded temperatures and RH%. The RT, and RR were taken at 0600 (am) and 1800 hours (pm). RT was taken using a digital thermometer. The RR was taken visually. Free choice water intake was measured in mL. The percent black was calculated using a dot grid on a picture of each side of each calf and determining the percentage of dots of black area and of white area. The two sides were added together and the total percentage determined. On day 51, RT, and, PP was recorded each hour for a full 24 hour period. The percent blackness was divided into three categories based upon standard deviation of percent blackness. Low blackness (LB; < 37.1), medium blackness (MB > 37.1 and < 56.9), and high blackness (HB > 56.9). Calves with MB and HB had decreased am RT than LB respectively (374.92 vs. 374.5 vs. 374.8, P = < .01). Calves with LB had a greater pm RT than the HB (375.3 vs. 375.28, P = < .01) and the calves with MB had the lowest pm RT compared to HB and LB respectively (375.24 vs. 375.28 vs. 375.3, P = < .01). Calves with HB had a greater pm RR than those calves with LB and MB respectively (53.08 vs. 48.68 vs. 52.39 P = < .01). Calves with LB had a greater am RR than those calves with MB (39.50 vs. 39.30 P = < .01). Calves with HB had decreased am RR than calves with MB (39.48 vs. 39.50 P = < .01). Calves with HB had a higher water consumption compared to MB (3611.89 vs. 3482.71 P = < .01). Calves with LB had increased water consumption compared to MB (3572.51 vs. 3482.71 P = < .01). Calves with the MB had the greatest am RT, and am RR than the LB and HB calves. Calves with HB had a greater pm RR, and the largest increase in water consumption than those calves with LB and MB. Calves with LB had a greater am RR, pm RT, and am RR than the HB and MB calves.

Key Words: calves, black

180 The effect of TGF-β1 on cell proliferation in the bovine mammary gland during the dry period. K. Weiss*, L. DeVries, H. Dover, T. Casey, J. Liesman, M. VandeHaar, and K. Plaut, *Michigan State University, East Lansing*.

Transforming growth factor-*beta*1 (TGF-β1) stimulates stromal cell proliferation and inhibits epithelial cell growth in the mammary gland. The role of TGF-β1 during the dry period of dairy cows is unknown. The objective of this study was to determine whether TGF-β1 affects the proliferation of bovine mammary tissue during the dry period. We hypothesized that addition of TGF-β1 to mammary explant cultures would increase stromal cell proliferation and decrease epithelial cell proliferation. Mammary biopsies from seven multigravid Holstein cows were collected at four different time points—275 days lactation, one week dry, three weeks prepartum, and one week prepartum. Biopsied tissue explants were incubated for two hours in Waymouth's media supplemented with insulin, hydrocortisone, 50μM bromodeoxyuridine (BrdU) and either 0ng or 5ng of TGF-β1. Immunohistochemistry was performed on formalin fixed paraffin embedded tissue sections using the Zymed BrdU Staining Kit (Invitrogen, Carlsbad, CA). Images were analyzed using Image Pro Plus software by manually tagging stained and unstained epithelial and stromal cells. At each time point, approximately 2,200 epithelial cells and 1,500 stromal cells were counted. When the study is complete, it's estimated that 10,000 to 15,000 cells of each cell type, epithelial and stromal, will be counted. As expected, the preliminary data revealed an increase in epithelial cell proliferation from 0.2 percent during late lactation to 0.7 percent during one week prepartum (P<0.02). TGF-β1 did not alter the percent of cell proliferation in either the stromal or epithelial cell population, however there was large variability in the response. *This project was supported by National Research Initiative Competitive Grant no. 2006-35206-16719 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: mammary gland, proliferation, transforming growth factor-*beta*1

181 The economic impact of soybean meal products on milk production and components for Holstein dairy cows. J. A. Hartzell*, G. A. Varga, Y.-H. Chung, K. S. Heyler, and V. A. Ishler, *The Pennsylvania State University, University Park*.

Dairy producers are continually challenged with volatility in both milk and commodities markets. Protein sources are the most expensive component of a dairy cow ration, contributing to a majority of the purchased feed costs on dairy farms. Two studies were conducted to evaluate various soybean meal (SBM) products when fed in the lactating cow ration as well as their economic effects. In the first study, ruminal disappearance of six different SBM products were tested. Two of the products evaluated were SoyChoice and Turbomeal. These SBM products are treated by different methods to increase the amount of rumen undegradable protein (RUP) by extracting oil from the soybeans. The methods of treatment include a heat-generated expelling process for Turbomeal and both a heat and mechanical extruding process for SoyChoice. At 12 and 16 hours, ruminal protein disappearance was lower for SoyChoice compared to Turbomeal, and hence a higher RUP percentage. In the second study, SoyChoice was examined for its effects on milk yield and components in 120 Holstein dairy cows. SoyChoice was fed for 17 days at 4% ration DM. Turbomeal served as the control and was fed at 3.6% ration DM. Both rations contained 15% CP and 33% NDF on a DM basis and contained similar nutrient compositions. Individual daily milk yields were recorded and also analyzed weekly for components. The SBM products did not affect milk yields and components as they were similar before and after treatment. The percentages of milk fat and protein for the treatments and control groups were 3.5 and 3.1% and 3.7 and 3.1%, respectively. The treatment group was 6.1% higher for income over feed costs (IOFC) versus the control. Based on the similar results in milk components and yields, the product that was treated with both a heat and mechanical extruding process had a higher IOFC and RUP content. The heat and mechanically extruded product can serve as an adequate protein source in dairy cow rations with added economic advantages and provide a higher source of by-pass protein compared to the product that was treated only with a heat-generated expelling process.

Key Words: rumen undegradable protein sources, income over feed costs

182 Microbial growth in refrigerated colostrum over seven days. M. Beyer* and S. I. Kehoe, *University of Wisconsin, River Falls*.

Passive transfer of immunoglobulins in colostrum is very important for calf health and growth. Using a protocol that allows the calf to receive clean colostrum in under 6 hours is an important factor for overall herd

health. Colostral immune factors are essential for calf health, but it is thought that bacterial contamination of colostrum may negate some of the benefits (Stewart, et al. 2005). The objective of this study was to establish the rate of bacterial growth from contamination (aerobic and coliform) in colostrum stored in a calf bottle over the course of a week. Colostrum samples were collected in sanitized calf bottles at the first milking after parturition. Bottles were then placed in a refrigerator at 0° Celsius after the first sample was plated. Each day samples from the bottle were plated in duplicate using coliform and aerobic Petrifilm plates (Petrifilm, St. Paul, MN) to measure growth in a 24 hour period. Results for aerobic and coliform bacterial growth and titratable acidity by day increased significantly. Results for coliform growth were 927.88, 617.93, 644.45, 761.88, 1029.82, 1858.15, 1255.66 CFU for days 1 through 7, respectively. Results for aerobic growth were 4621, 23084, 20921, 29171, 46769, 46363, 51406 CFU for days 1 through 7, respectively. Titratable acidity resulted in 0.7221, 0.9291, 1.0258, 1.1692, 1.2415, 0.09661% for days 1 through 7, respectively. The findings of this study suggest that there is significant microbial growth in colostrum stored in refrigeration during a period of one week. These results indicate that colostrum should be fed before one week after collection in order to ensure low bacterial contamination for optimal calf health.

Key Words: colostrum, bacteria, calves

183 Postpartum plasma progesterone changes during early lactation in Holsteins, Jerseys and their crosses. S. Sheer*, K. L. Brown, B. G. Cassell, and F. C. Gwazdauskas, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

First lactation cows (n = 147; 35 Holstein-Jerseys (HJ) crosses, 42 Jersey-Holsteins (JH) crosses, 45 Holsteins (HH), and 25 Jerseys (JJ)) were sampled to determine if plasma progesterone differed between breeds. Blood samples were collected weekly postpartum for a 10 wk period. Statistical models (MIXED) evaluated breed, profile, season (cold - November to May; hot - June to October), and breed by season interaction on days open and the slope of change in progesterone to first increase above 1 ng/mL plasma prior to 30 d postpartum. Profile characterized progesterone changes as delayed where progesterone did not increase above a threshold by 70 DIM; early where progesterone increased above a threshold before 28 DIM and did not cycle; normal where progesterone increased above a threshold before 30 DIM and cycled normally; and short, where progesterone increased above a threshold before 30 DIM and declined below the threshold by the next sample. Days open were significantly affected by profile and breed. Days open for HH were longest (152.6 ± 4.5 d), not different for HJ (132.4 ± 4.5 d) and JH (128.2 ± 4.1 d), and JJ (140.5 ± 5.2 d) was different from all except HJ. Cows with a short profile had 33 to 60 d open less than the other groups. There was a breed by season interaction for days open ($P < 0.05$). Slope was affected by breed ($P = 0.0273$), profile ($P < 0.001$), and breed by season interaction ($P = 0.0067$). The HH group had a slope of 0.196 ± 0.023, HJ had a 0.160 ± 0.022 slope, JH had a 0.157 ± 0.020 slope, whereas the JJ slope was 0.229 ± 0.026. The JJ slope was steeper than HJ and JH slopes. Profile of progesterone affected ($P < 0.0001$) slope. A delayed profile had a slope of 0.0024 ± 0.014, early had 0.216 ± 0.017, normal had 0.168 ± 0.018, and short had 0.335 ± 0.061. Only short was not different from early and normal. The delayed slope suggests that there was not an increase in progesterone during the early postpartum period. Breed by season interaction showed a greater slope for JJ in summer and a lower slope in winter than other breed combinations. Breed differences were evident in measures of reproductive efficiency.

Key Words: progesterone

184 Differentiating effects of effective fiber sources on performance of lactating dairy cows. R. A. Starkey*, P. N. Gott, M. L. Eastridge, E. R. Oelker, A. R. Sewell, B. Mathew, and J. L. Firkins, *The Ohio State University*, *Columbus*.

Because of high feed costs and limited availability of some forage sources, alternative effective fiber sources are being considered. The objective of this study was to compare the feeding of corn silage as the sole forage versus feeding corn silage with alfalfa hay, wheat straw, and corn stover to lactating dairy cows. A 5x5 Latin square design was used with 5 multiparous cannulated Holstein cows (122 ± 62 DIM). Diets were: 1) CS = corn silage as sole forage source, 2) ALF = corn silage and 11.5% alfalfa hay, 3) STW-5 = corn silage and 5% straw, 4) STW-10 = corn silage and 10% straw, and 5) STV = corn silage and 5.5% corn stover (without cobs). Diets were formulated for similar concentrations of CP, NFC, and 18% forage NDF, except for STW-10 with 23% forage NDF. Diets were fed for 3 wk, and samples were collected during the last week of each period. Period 4 was extended 9 d because one cow had a displaced abomasum at the beginning of the period. The DMI was lowest for STW-10 (28.6, 28.9, 30.5, 26.7, and 28.6 kg/d for CS, ALF, STW-5, STW-10 and STV, respectively; $P < 0.05$). The BW (734 kg) and BCS (3.18; 1 to 5 scale) were similar. Milk (35.6 kg/d), milk fat (3.56%), milk protein (2.87%), and MUN (17.4 mg/dl) also were similar. The different forage sources resulted in similar total tract digestibilities of OM (76.9%) and NDF (63.5%). Rumen pH (6.12), acetate:propionate (3.10), and ruminal concentrations of total VFA, acetate, propionate, butyrate, and valerate were similar. Concentrations of isovalerate ($P < 0.01$) and isobutyrate ($P < 0.10$) were highest for STW-10 compared to the other diets, and isovalerate was also lower ($P < 0.10$) for ALF than for STW-5 and STV. Feeding the higher level of straw may have caused more rumen fill and thus reduced DMI, which would likely lower milk yield in a longer study. Feeding similar forage NDF concentrations using corn, alfalfa hay, and wheat straw can result in similar animal performance and ruminal fermentation with adequate formulation of NFC and total NDF.

Key Words: corn stover, straw, effective fiber

185 The effects of betaine on free choice water intake and vital signs related to heat stress of neonatal Holstein bull calves. J. L. Clark*, G. A. Holub, and J. E. Sawyer, *Texas A&M University*, *College Station*.

A study evaluating the effects of Betaine (BET) added to milk replacer on free choice water intake and vital signs related to heat stress was conducted with Holstein calves <3 days in age (n=44; mean BW = 42.28 ± 3 kg). The study was conducted in College Station, Texas beginning on May 13 and ended July 8 (d=56). BET, is reported to be used by the animal as an osmlyte which can help maintain cell volume and fluid balance. Calves were housed in fiberglass hutches with free choice water and commercially available starter feed. BET (2g/d, 96% BET) was added at time of mixing to the .9 Kg of commercially available milk replacer (25% CP; 20% CF). Calves were randomly assigned to BET treatment or control groups. Free choice water intake was measured daily in mls. Starter intake was measured daily in Kgs. Vital signs were measured daily at 0600 h (AM) and 1800 h (PM). Vital signs included Respiration Rate (RR), Pulse Rate (PR), and Rectal Temperature (RT). RR was obtained visually. PR was obtained by digital palpation of the jugular vein and RT was taken with digital thermometer. Water intake in BET calves was greater than control calves (3818.24 and 3528.78; P<.0273). Significant differences in vital signs included RR AM and RR PM. BET calves had a trend toward lowered AM RR (39.03 vs 39.77, P>0.0540); however, PM RR of BET calves was greater than control

calves (52.21 vs 50.72, P>0.0491). In all, calves fed BET consumed more water then control calves, and BET calves had greater RR in the hottest part of the day then control calves.

Key Words: betaine, calves, osmlyte

186 Producer assessment of dairy extension programming in Kentucky. R. A. Russell* and J. M. Bewley, *University of Kentucky*, *Lexington*.

The Kentucky dairy industry is challenged by a shrinking number of dairy farms, an aging farmer population, per cow milk production levels well below the national average, and competition from more progressive dairy industries in neighboring states. To assess opportunities to address these issues through extension programming, a survey was distributed to all licensed milk producers in Kentucky. Two hundred and twenty-nine producers responded to the survey. Within this survey, a series of questions were asked about off-farm meeting attendance. With regard to frequency of off-farm meeting attendance, 1.8% indicated they attended meetings twice per month, 3.5% attended monthly, 12.8% attended quarterly, 29.1% attended twice per year, 25.1% attended annually, and 27.7% indicated they never attended meetings. The top three reasons selected for not attending more meetings were (1) not enough time (62.0%), (2) meetings held at the wrong time of day (37.0%) and (3) meetings not held at a convenient location (32.9%). Producers reported that the most effective methods for extension to communicate with them were (1) printed farm magazines (81.0% of respondents), (2) agricultural newspapers (77.4%) and (3) printed newsletters from a county agriculture agent (75.7%). Respondents indicated that the most important management topics for extension programming (with mean response calculated using the following numeric values: not important-1; important-3, very important-5) were (1) mastitis and milk quality (4.35 ± 1.05), (2) animal well-being (4.05 ± 1.14), (3) disease prevention and vaccinations (4.01 ± 1.06), (4) cow comfort (3.97 ± 1.09) and (5) disease treatment (3.95 ± 1.10). Dairy producers prioritized extension program areas (with mean response calculated using the following numeric values: low-1; medium-3, high-5) as follows: (1) providing written and printed information for producers (3.96 ± 1.31), (2) conducting local and regional extension programs (3.74 ± 1.33) and (3) on-farm planning and troubleshooting (3.66 ± 1.37). These results provide invaluable insight for future dairy-related Cooperative Extension Service programming efforts.

Key Words: survey, dairy extension, needs assessment

187 Performance of weanling goats when fed a mixed concentrate with dried distillers grains compared to a pelleted concentrate. J. Popowski*[1], M. Raeth-Knight[1], T. Walsh[2], J. Linn[1], and R. Larson[2], [1]*University of Minnesota*, *St. Paul*, [2]*Hubbard Feeds*, *Mankato, MN*.

The primary objective was to compare intake, growth, and carcass characteristics of weanling goats when fed a mixed concentrate with dried distillers grains (DDG) or a pelleted concentrate. The secondary objective was to determine the impact of corn processing in a mixed concentrate on goat performance and carcass characteristics. Two groups of 45 weanling dairy crossbred wether goats were randomly assigned to 1 of 3 dietary treatments. Treatments were 1) pelleted concentrate (CON); 2) mixed concentrate using whole corn (MWC); or 3) mixed concentrate using cracked corn (MCC). The CON treatment contained (as-fed basis): corn (43.3%), wheat middlings (30.0%), alfalfa meal (10.0%), soybean hulls (7.5%), soybean meal (4.9%) and vitamins and minerals (4.3%). Mixed concentrate treatments included (as-fed basis): corn (61.5%), DDG (18.5%), protein/fiber pellet (15.0%) and a molasses trace mineral mix (5.0%). Goats were housed in pens with five goats per pen for 56 d (6 pens per treatment). Treatment diets and water were fed free choice daily and hay was limit fed at 0.23 kg (as-fed)/head/d. Feed offered was recorded daily and refusals were weighed 3 d each week. Body condition score and live carcass evaluation were determined d 1, 28 and 56. Body weights were taken every two weeks. Using three pens per treatment, two goats from each pen (total 18 goats) were harvested for carcass evaluation 3 d after study completion. Concentrate intake and average daily gain was 0.13 kg/d and 0.02 kg/d higher, respectively for goats fed a pelleted compared to a mixed concentrate. Processing corn for mixed diets slightly improved concentrate intake (0.07 kg/d) but had no impact on body weight gain.

Table 1.

	Trt[1]			C[2]	C[2]
	CON	MWC	MCC	1	2
DM Intake, kg/d					
Total	1.13	0.96	1.04	<0.01	<0.01
Concentrate	0.92	0.76	0.83	<0.01	<0.01
ADG, kg/d	0.17	0.15	0.15	0.03	0.74

[1]Treatments: CON= pelleted concentrate; MWC = mixed concentrate using whole corn; MCC = mixed concentrate using cracked corn. [2]Contrast: 1 = CON vs. MWC and MCC; 2 = MWC vs. MCC.

Key Words: goat concentrate, dried distillers grains

188 The effects of in-vivo derived trophoblastic vesicles on corpus luteum lifespan and serum progesterone concentrations in dairy cattle. E. R. Waggoner*, J. L. Fain, and J. R. Gibbons, *Clemson University*, *Clemson, SC*.

Embryo transfer is a technique used with success in the dairy industry, however freezing embryos for future transfer compromises quality and reduces conception rates. One proposed method of increasing pregnancy rates with frozen embryos is through the utilization of trophoblastic vesicles (TV). Trophoblastic vesicles, formed from the outer, trophoblastic cells surrounding an elongating embryo, secrete bovine interferon tau; the hormone presumed responsible for maternal recognition of pregnancy. It is hypothesized that intrauterine transfer of TVs in normally cycling cows will prevent lysis of the corpus luteum (CL); extending its lifespan and maintaining higher progesterone levels to potentially enhance the opportunity for pregnancy establishment. The current research aims to study the effects of TVs on CL lifespan and serum progesterone (P4) concentrations in dairy cattle. This study consisted of mature, lactating Holstein cows (n=8) and breeding-age Holstein heifers (n=12). Trophoblastic vesicles were generated through embryo collection of superovulated donors 14 days post insemination. After collection, inner cell masses were removed and embryos were sectioned, with segments allowed to incubate 24 hours before freezing. All transfer recipients were synchronized using CIDRs and prostaglandin $F_{2\alpha}$ injections. In-vivo derived, frozen/thawed TVs, ranging from 0.6 to 1.0 mm in diameter were transferred on day seven to uterine horns ipsilateral the CL of half the animals in each group (n=10) using standard embryo transfer procedures. Utilizing the same technique the remaining cattle received sham transfers of phosphate buffered saline. Blood samples were collected daily through the estrous cycle for each animal and assayed for P4 concentrations. Beginning at day seven, ultrasonography

was used to map corpus luteum development until return to estrus. No difference in estrous cycle length was observed between the two groups ($P > 0.05$), indicating trophoblastic vesicle lifespan may be limited to 14-20 days and therefore does not significantly delay luteolysis when transferred on day seven of the estrous cycle.

Key Words: trophoblastic vesicle, P4, dairy

Animal Health: Immunity and Swine Health

189 Pea dietary fiber for adhesion and excretion of enterotoxigenic *E. coli* K88 to prevent intestinal colonization. P. M. Becker*, P. G. van Wikselaar, A. J. M. Jansman, and J. van der Meulen, *Animal Sciences Group of Wageningen UR, Lelystad, the Netherlands*.

Enterotoxigenic *Escherichia coli* (ETEC) expressing K88 (F4) fimbriae are associated with post-weaning diarrhea in piglets. Dietary components as well as feed additives can interfere with the colonization of the porcine intestine by ETEC. Digestion resistant fibers, for example, can competitively inhibit the adherence of ETEC to host intestinal tissues. Grain legumes such as peas or faba beans are alternative plant protein sources to soybeans in animal feed that can be cultivated in temperate climates. In fact, these crops are not only rich in protein, but also contain starch and fiber. The aim of this study was to test the binding capacity for ETEC O149:K91:K88ac (LT+/STb+) of pea (*Pisum sativum*, cv. Attika) and faba bean (*Vicia faba*, cv. Divine), and of different fractions of these grain legumes obtained before and after *in vitro* digestion. All products were milled to a particle size of less than 1 mm. *In vitro* digestion was performed using pepsin and pancreatin. Adhesion of ETEC K88 to the pea and bean materials was determined in a microplate-based binding assay. When comparing the raw products, pea hulls, pea inner fiber, whole pea, pea starch and pea protein scored higher in terms of adhesion of ETEC K88 than faba bean starch, whole faba bean, faba bean protein and faba bean hulls. Pea hulls proved even superior to a commercial yeast cell wall product in terms of the binding capacity for ETEC K88. After *in vitro* digestion, the binding capacity for ETEC K88 remained preserved in washed digestion remnants of both pea hulls and whole pea, indicating the potential of these products to offer alternative adhesion sites for ETEC K88 to host receptors in the piglet small intestine.

Key Words: anti-adhesion, *E. coli* K88, grain legumes

190 Health benefits of yeast derivates: in vitro and in vivo investigation. A. Ganner* and G. Schatzmayr, *BIOMIN Research Center, Tulln, Lower Austria, Austria*.

Yeasts have been used for fermentation and baking as well as for health aids throughout the history. In animal nutrition yeast products have been discussed as replacements of preventive antibiotics and as health promoting feed additives for over 20 years. Yeast products which are primarily promoted on the market are cell walls, beta-glucans, nucleotides and autolysed yeast. According to literature, yeast cell walls can prevent colonization of the intestinal tract by pathogens (binding of pathogens trough mannose-specific type I fimbriae); β-glucan and nucleotide products are described as immune stimulants by activating phaogocytic cells, but little research has been conducted regarding specific pathogen binding capabilities. Therefore, in vitro pathogen binding assays and immunological assays were conducted with subsequent in vivo feeding trials to gain more profound knowledge on health benefits of yeast products. The pathogen binding capacity of yeast cell wall was investigated with microplate-based assays by measuring the OD as growth parameter of adhering bacteria. Several *E. coli* and *Salmonella* strains adhered to a particular cell wall product with an amount between 1000 and 1000000 CFU/mg. As immunological parameters the nitric oxygen-production of a chicken macrophage cell line (HD11) stimulated with yeast nucleotides and yeast beta-glucans was analyzed. Production of NO was enhanced up to 100% relative to the positive control (LPS *E. coli* 0127). In an ex vivo trial with piglets fed yeast beta glucan in concentrations of 250 and 500 mg/kg, beneficial effects on lymphocyte viability and an increase of IL-18 could be demonstrated, however, animal performance was not affected. In an in vivo trial, broilers received yeast cell wall at a concentration of 2kg/T. Body weight was improved with statistical differences ($P<0.05$) compared to the control (+10%) and mortality reduced (-2%), also FCR (-5.8%) was improved to 35 days of age. In vitro and in vivo results suggest that yeast derivates are promising health and growth promoters for animal husbandry.

Key Words: yeast, pathogens, immunology

191 Use of *Saccharomyces cerevisiae* fermentation product during *Salmonella* infection in weaned pigs. K. L. Price*, H. R. Totty, H. B. Lee, M. D. Utt, M. A. Ponder, and J. Escobar, *Virginia Polytechnic Institute and State University, Blacksburg*.

Fermented yeast products are rich in mannanoligosaccharides, β-glucans, and other compounds that may optimize gut health and immunity, which can translate into better growth performance and a lower risk of food borne pathogens. The objective of this study was to quantify the effects of *Saccharomyces cerevisiae* fermentation product (Original XPC, Diamond V Mills, Inc., Cedar Rapids, IA) inclusion in nursery diets on pig performance before, during, and after an oral challenge with *Salmonella*. Pigs (n=10/treatment) were weaned at 21 d of age, blocked by BW and randomly assigned to treatments. The experimental design was a complete randomized design in a 2×2 factorial treatment arrangement consisting of diet (control or 0.2% XPC) and inoculation (broth or *Salmonella*). Pigs were fed a 3-phase nursery diet (0-7 d, 7-21 d, and 21-35 d) with ad libitum access to water and feed. On d 14, pigs were orally inoculated with 1×10^9 CFU of *Salmonella enterica* serovar Typhimurium or sterile broth. From d 17-20, all pigs were treated with an antibiotic (10 mg/kg BW i.m. ceftiofur). Growth performance was measured during pre-inoculation (PRE; 0-14 d), SICK (14-21 d), and post-inoculation (POST; 21-35 d) intervals after weaning. Rectal temperature (RT), BW, and ADG were measured weekly and daily during SICK. Diet had no effect on BW, ADG or RT during any period (P = 0.12 to 0.95) or frequency of *Salmonella* shedding in feces (P = 0.14 to 1.00) during SICK. Pigs inoculated with *Salmonella* had decreased ADG and BW, and elevated RT during SICK ($P < 0.001$). Furthermore, fecal CFU (log transformed) was correlated with ADG ($r = -0.50$, $P < 0.001$) and RT ($r = 0.63$, $P < 0.001$) during SICK. During POST, an interaction between diet and inoculation ($P = 0.009$) on ADG indicated that pigs infected with *Salmonella* grew better while consuming Original XPC compared to the control diet. The addition of XPC to the diets of weaning pigs can result in greater compensatory gains after infection with *Salmonella* than pigs fed conventional nursery diets.

Key Words: pig, *Salmonella* challenge, *Saccharomyces cerevisiae* fermentation product

192 Effects of feeding OmniGen-AF on neutrophil-mediated killing of *Archanobacterium pyogenes*. A. Rowson*, Y.-Q. Wang, S. B. Puntenney, and N. E. Forsberg, *OmniGen Research*, *Corvallis, OR*.

Arcanobacterium pyogenes is a filamentous gram-positive bacterium formerly classified as a fungus. It is a widely distributed inhabitant of mucus membranes and can infect animals following a precipitating injury. Economically important diseases in dairy cattle associated with A. pyogenes infection include mastitis, metritis and abortion. The organism is associated with liver abscesses in feedlot cattle. OmniGen-AF is a commercially-available feed additive which has been widely adopted within the US dairy industry. Recent studies (Wang et al., 2007, 2009) have shown that OmniGen-AF increases markers of immunity. Unpublished studies have also shown that neutrophils isolated from animals fed this product have enhanced ability to kill pathogens including Streptococcus uberis and Escherichia coli. The goal of this study was to determine whether neutrophils of OmniGen-AF-fed animals exhibited enhanced killing of A. pyogenes. Male CD rats (ca. 250 g, 8 per treatment) were assigned to a control ration or the same ration containing 0.5% (w/w) OmniGen-AF (Prince Agri Products, Quincy, IL). Animals were maintained on rations for 14 days after which they were anesthetized with xylazine and acepromazine and blood (10 ml) was taken via cardiac puncture. Neutrophils were prepared via Percoll gradient centrifugation. A. pyogenes was recovered from a clinical case of bovine metritis and cultured to known density. Neutrophils and A. pyogenes were combined in a ratio of 1:30 for 2 hr after which ability of A. pyogenes to metabolize MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) to formazin was assessed as an index of A. pyogenes viability. Formazin concentration was assessed spectrophotometrically. Addition of OmniGen-AF caused a significant ($P<0.05$) 45% reduction in viability of A. pyogenes. This implies that one of the neutrophil killing mechanisms (NET formation, phagocytosis or ROS generation) was enhanced by feeding rats the product for 14 d. Field studies have shown that OmniGen-AF reduces incidence of metritis in dairy cattle. A possible mechanism for this may be via enhanced neutrophil-mediated killing of A. pyogenes.

Key Words: OmniGen-AF, metritis, neutrophil killing

193 Influence of an *in vivo* endotoxin challenge on *ex vivo* phagocytic and oxidative burst capacities of bovine neutrophils. M. A. Ballou*[1], L. E. Hulbert[2], L. R. Schwertner[1], J. A. Carroll[2], L. C. Caldwell[3,4], R. C. Vann[5], T. H. Welsh Jr.[3], and R. D. Randel[4], [1]*Texas Tech University*, *Lubbock*, [2]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*, [3]*Texas AgriLife Research, Texas A&M System*, *College Station*, [4]*Texas A&M System*, *Overton*, [5]*MAFES, Mississippi State University*, *Raymond*.

Neutrophils promote health by reducing the early growth of invading pathogens. The objective of this study was to elucidate the temporal effects of an endotoxin (lipopolysaccharide; LPS) challenge on neutrophil function. Brahman heifers (186.1±11.8 kg; n=6) were challenged with LPS (0.25 μg IV/kg BW). Immediately before and at 1, 2, 4, 6 and 24 h relative to challenge, peripheral blood samples were collected to analyze phagocytic and oxidative burst capacities of neutrophils following 15–min or 60–min incubation periods with pre–opsonized *Mannheimia haemolytica*. Data are presented as the percentage and mean fluorescence intensity (MFI) of neutrophils phagocytizing or undergoing an oxidative burst. In addition, overall indices of phagocytosis and oxidative burst were calculated as the percentage of neutrophils multiplied by their respective MFI. The percentage as well as the MFI of phagocytizing neutrophils increased ($P < 0.001$) following the LPS challenge. Therefore, the phagocytic index increased ($P < 0.001$), peaking at 1 and 2 h for the 15– and 60–min incubations, respectively. Within 24 h the phagocytic index returned to baseline for the 15–min incubation, but there was a tendency ($P < 0.06$) for the phagocytic index to remain elevated for the 60–min incubation, reflecting an increased ($P < 0.01$) percentage of phagoycytizing neutrophils. The percentage of neutrophils producing an oxidative burst increased ($P < 0.001$), but only in the neutrophils incubated for 15–min. The MFI of the neutrophils producing an oxidative burst decreased ($P < 0.001$) rapidly for both incubation times and remained suppressed 24 h after the challenge. These data indicate that an LPS challenge stimulates the phagocytic capacity of neutrophils. However, despite more early-responding neutrophils undergoing an oxidative burst, the MFI and overall oxidative burst index are suppressed and remain so 24 h following an LPS challenge. The suppressed oxidative burst capacity may compromise the ability of neutrophils to control the growth of pathogens; alternatively, it may be a compensatory mechanism limiting excessive pathology.

Key Words: bovine, endotoxin, neutrophil

194 Influence of an *in vivo* corticotropin–releasing hormone (CRH) challenge on *ex vivo* phagocytic and oxidative burst capacities of bovine neutrophils. M. A. Ballou*[1], L. E. Hulbert[2], L. R. Schwertner[1], J. A. Carroll[2], L. C. Caldwell[3,4], R. C. Vann[5], T. H. Welsh Jr.[3], and R. D. Randel[4], [1]*Texas Tech University*, *Lubbock*, [2]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*, [3]*Texas A&M System*, *College Station*, [4]*Texas A&M System*, *Overton*, [5]*MAFES, Mississippi State University*, *Raymond*.

Various stressors are linked in the etiology of disease states. The adverse actions of pathogens are limited by the ability of neutrophils to phagocytize and neutralize them. The objective of this study was to elucidate the temporal effects of an exogenous CRH challenge on neutrophil function. Brahman heifers (193.2±9.4 kg; n=6) were challenged with an intravenous bolus of bCRH (0.5 μg/kg BW). Immediately before (baseline) and at 1, 2, 4, 6 and 24 h relative to the challenge peripheral blood samples were collected to analyze phagocytic and oxidative burst capacities of neutrophils following 15–min or 60–min incubation periods with pre–opsonized *Mannheimia haemolytica*. Data are presented as the percentage and mean fluorescence intensity (MFI) of neutrophils phagocytizing or undergoing an oxidative burst. In addition, overall indices of phagocytosis and oxidative burst capacities were calculated as the percentage of neutrophils multiplied by their respective MFI. The percentage of neutrophils phagocytizing at the 15–min incubation was rapidly suppressed following the CRH challenge, but within 24 h values were not different from baseline. Neutrophils incubated for 60–min were initially suppressed, but compensated with more phagocytizing neutrophils 2 h after the challenge and within 4 h there was no difference relative to baseline. Mean fluorescence intensities of phagocytizing neutrophils were less responsive to the CRH challenge. The percentage of neutrophils producing an oxidative burst was suppressed at the 15–min incubation reaching the nadir at 2 h and returning to baseline at 6 h after the challenge. However, the MFI and the oxidative burst capacity index of neutrophils producing an oxidative burst for both incubation times decreased rapidly and remained suppressed 24 h after the challenge. These data indicate that both phagocytosis and oxidative burst capacities of neutrophils are suppressed by an *in vivo* administration of CRH. Diminished neutrophil capacities concurrent with or subsequent to a stressful event may contribute to increased susceptibility to pathogens.

Key Words: bovine, neutrophil, stress

195 Bovine adipose tissue depot inflammatory gene expression responsiveness to lipopolysaccharide (LPS) in vitro. M. Mukesh, D. E. Graugnard*, M. Bionaz, J. K. Drackley, and J. J. Loor, *University of Illinois*, *Urbana*.

In addition to its fundamental role as energy storage depot, studies with non-ruminants have reported a strong pro-inflammatory potential of adipose tissue. The transcriptional response of adipose tissue with respect to its immune responsiveness in dairy cows remains poorly characterized. Thus, we sought to examine mRNA expression and responsiveness of subcutaneous (SUBQ) and mesenteric (MES) adipose tissue from non-pregnant dairy cows to a short-term (2 h) in vitro LPS challenge (20 μg/mL). mRNA abundance of tumor necrosis factor-α (TNF), interleukin-6 (IL6), serum amyloid A1 (SAA1), toll-like receptor 4 (TLR4), monocyte chemoattractant protein-1 (MCP-1 or CCL2), RANTES/chemokine C-C motif ligand 5 (CCL5), and the lipogenic transcription regulator Lipin 1 (LPIN1) were analyzed using quantitative PCR. Tissue samples were collected at slaughter from 5 non-pregnant/non-lactating Holstein cows fed a diet containing 1.61 Mcal/kg NE_L for 8 wk. Basal (prior to LPS challenge) mRNA abundance of SAA1, CCL5, and LPIN1 was ca. 5-, 1.4-, and 3-fold, respectively, greater ($P \leq 0.07$) in MES than SUBQ. Regardless of depot site, LPS increased ($P \leq 0.06$) mRNA abundance of TNF, IL6, and CCL5. We also observed tendencies (interaction $P \leq 0.09$) for increased expression of CCL2 and IL6 primarily due to LPS in MES. Overall, data suggest that mesenteric adipose tissue has greater lipogenic and immune-response potential than subcutaneous adipose. Results provided initial evidence that adipose depots of dairy cows are immune-responsive and capable of synthesizing pro-inflammatory cytokines and chemokines rapidly when exposed to inflammatory conditions that can arise from a pathogenic insult (e.g., mastitis) or normally as it occurs during the onset of parturition.

Key Words: acute phase response, inflammation

196 Genotypic profiling of enterococci isolated from bovine origin. B. A. Stewart*[1], T. H. Yang[1], J. S. Hogan[2], and C. S. Petersson-Wolfe[1], [1]*Virginia Tech, Blacksburg*, [2]*The Ohio State University, Ohio Agricultural Research and Development Center, Wooster*.

The objective of the current study was to test enterococci isolated from milk, bedding and feed samples for the presence of genes related to virulence, the ability to form biofilm and resistance to a variety of commonly used antibiotics. A collection of 390 environmental streptococci and enterococci isolates were identified using standard bacteriology techniques as described by the National Mastitis Council and confirmed using the API 20 STREP test. A total of 164 of the 390 isolates were identified as enterococci using the *tuf* gene to distinguish from other environmental streptococci. Of the 164 isolates determined to be enterococci, the API 20 STREP test inaccurately identified 12 (7.3%) isolates as other environmental streptococci. Standard PCR procedures were used to detect the following virulence genes; *esp, efaAfs, gelE, efaAfm, agg, ace* and *fsr*. A total of 47 of the 164 isolates had at least 1 of the 7 tested virulence genes within the genome. The most virulence genes any isolate contained was 5 of the 7 that were tested. The majority of those isolates containing 5 virulence genes were *Enterococcus faecalis*, based on API identification. Only 2 of the tested isolates displayed the ability to form biofilm based on the published optical density cut-off value of 0.1. Furthermore, wide ranges in antibiotic sensitivity profiles were observed. A greater understanding of the genetic makeup of enterococci from bovine origin will provide knowledge regarding the pathogenesis of these bacteria and may lead to novel therapeutic options.

Key Words: *Enterococcus* spp., mastitis, virulence factors

197 Protective effect of polysaccharide produced by *Enterobacter cloacae* Z0206 on cyclophosphamide-induced suppression of immune functions in mice. M. Jin*, Y. Wang, X. Yang, C. Xu, and Z. Lu, *Institute of Feed Science, Zhejiang University*, *Hangzhou, Zhejiang Province, China*.

Polysaccharides are a complex group of important biological molecules known to enhance the immune functions. The objective of this experiment was to investigate the immunomodulatory effects of polysaccharide (EPS-1) produced by *Enterobacter cloacae* Z0206 on immunosuppressed mice. A total of 40 ICR male mice (18 ± 2g) were randomly allocated to four treatments of ten each. Three immunosuppressed groups were administered by gavage once daily with EPS-1 (0, 200 and 400 mg/kg body weight (B.W.)) for 14 days, and cyclophosphamide (CP) was given intraperitoneally at 50 mg/kg B.W. on the 12th day. The control mice received same volume of normal saline. Immune organ index, splenic lymphocyte proliferation induced by concanavalin (ConA) and lipopolysaccharide (LPS), and serum hemolysin concentration were detected in these animals. CP, as expected, showed suppressive effects on immune functions of mice. Polysaccharide treatment itself produced no toxicity and showed protection in CP-treated animals. Results showed that ESP-1 (Treatment with 200 and 400 mg/kg B.W.) significantly ($P<0.05$) increased spleen and thymus index in CP-treated animals. Moreover, EPS-1 (400 mg/kg B.W.) increased LPS-induced splenic lymphocytes proliferation ($P<0.05$) and serum hemolysin concentration ($P<0.05$) respectively compared with CP-treated animals alone. Together, this data implied that EPS-1 produced by *Enterobacter cloacae* Z0206 could provide protection against CP-induced immunosuppression in mouse model and it may act as potent immunomodulatory agent.

Key Words: polysaccharide, *Enterobacter cloacae*, immunomodulation

198 Effects of recombine porcine Lactoferrin–N on growth performance and immune function of weanling piglets. L. Yifan, H. Feifei, X. Yonggang, and W. Yizhen*, *Zhejiang University*, *Hangzhou, Zhejiang, China*.

A total of ninety weanling piglets (Duroc×Landrace×Yorkshire) at an average initial body weight of 8.0±0.23 kg were used in a 15–d growth experiment to investigate the effect of recombine porcine Lactoferrin–N (rPLFN) on growth performance and immune function. The pigs were allocated on the basis of bodyweight and litter to 3 treatments in a randomized complete block design. The dietary treatments were:control group (basal diet), antibiotics group (basal+100 mg/kg aureomycin), and rPLFN group (basal diet+50 mg/kg rPLFN). There were 3 replicated pens per treatment, and pigs were grouped with 10 pigs per pen. Six pigs, randomly selected from each treatment (2 pigs/pen), were slaughtered for serum and spleen samples on d 15. Results showed that supplementation with 50mg/kg rPLFN improved growth performance, significantly increased the average daily gain (ADG) by 31.67% ($P\leq0.01$),decreased the feed efficiency (F/G) by 11.22% ($P\leq0.05$) and the diarrhea by 66.25% ($P\leq0.01$). Adding 50mg/kg rPLFN to base diet increased concanavalin A(ConA)–and lipopolysaccharide (LPS)–induced spleen lymphocyte proliferation by 9.40% ($P\leq0.05$) and 7.70% ($P\leq0.05$) respectively on d 15 as compared with the control group. 50mg/kg rPLFN supplementation enhanced serum IgG by 28.34% ($P\leq0.05$), IgA by 7.10% ($P\leq0.05$), IgM by 12.47% ($P\leq0.05$), complement 3 (C3) by 7.10% ($P\leq0.05$) , complement 4 (C4) by 15.22% ($P\leq0.05$), IL-2 by 40.81% ($P\leq0.01$), IL-18 by 41.06% ($P\leq0.01$) relative to the control group on d 15. Compared with the control group, supplemental with 100mg/kg aureomycin also increased ADG, the ConA-and LPS-induced spleen lymphocyte

proliferation, serum IgG, IgA, IgM,C3,C4 ($P \leq 0.05$), and increased IL-2,IL-18 ($P \leq 0.01$), decreased F/G and diarrhea ($P \leq 0.05$), while there was no significant difference between rPLFN group and antibiotics group. These results imply that rPLFN would be used as an additive to improve growth performance and immune functions of weanling pigs. This would seem to be a good method for defending weanling piglets from infections and weanling stress.

Key Words: recombine porcine Lactoferrin-N(rPLFN), growth performance, immune function

199 Effects of α-ketoglutarate on mucosal morphology and function of small intestine in piglets. Q. Hu, Y. Hou*, B. Ding, H. Zhu, Y. Liu, M. Wang, and H. Xiao, *Hubei key Laboratory of Animal Nutrition and Feed Science, Wuhan Polytechnic University*, *Wuhan, Hubei, P. R. China*.

Three experiments were conducted to evaluate the effects of dietary supplementation of α - ketoglutarate (AKG) on mucosal morphology and function of small intestine in piglets. Both the experiment 1 and experiment 2 included 32 piglets, and they were weaned at 21 ± 2 days and randomly allotted to 4 treatment groups with dietary supplementation of AKG at 0, 0.5%, 1.0% and 2.0% respectively. On the 14th day of the experiment, the piglets were infused 10% D-xylose solution at 1 ml per kg of body weight, after 60 minutes, blood samples were collected from anterior vena cava, the concentration of D-xylose and activity of diamine oxidase and the content of endotoxin in plasma were determined. In the experiment 3, twelve piglets were weaned at 21 ± 2 days and randomly divided into 2 treatment groups, one group was fed with basal diet and the other were fed with basal diet +1.0% AKG. On the 14th day, all pigs were sacrificed to observe the mucosal morphology. The small intestine was cut off three 5 cm segments at distal duodenum, mid-jejunum and mid-ileum. The segments were processed, embedded, and stained to make tissue sections, the villus height (VH) and the associated crypt depth (CD) were measured, and then the ratio of villus height to crypt depth (VH/CD) were calculated. Differences among groups were analyzed by one-way analysis of variance and subsequent Duncan's multiple range test. The results showed that, in the groups of 1.0% AKG, crypt depth and activities of diamine oxidase were decreased ($P < 0.10$), VH/CD was increased; compared to 0% group, in the groups of 1.0% AKG, the contents of endotoxin were decreased by 33.41% ($P < 0.05$), and plasma D-xylose contents were increased by 21.02% ($P < 0.05$). These results indicated that dietary supplementation of AKG could improve histological morphology and function of the small intestine of piglets and dietary supplementation of 1.0% AKG was better relatively.

Key Words: α-ketoglutarate, small Intestine, piglet

Breeding and Genetics: Whole Genome Selection - The New Frontier?

200 National and international genomic evaluations for dairy cattle. P. M. VanRaden*[1] and P. G. Sullivan[2], [1]*USDA Animal Improvement Programs Laboratory*, *Beltsville, MD*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*.

Genomic evaluations are rapidly replacing traditional evaluation systems used for dairy cattle selection. More than 35,000 dairy cattle worldwide have been genotyped for 50,000 markers. Reliabilities of 60-70% for young genotyped animals are now possible as compared to 35% for parent average. Gains depend on numbers of genotypes and are much less for Jerseys or Brown Swiss than for the large North American Holstein population. Accurate blending of genomic and non-genomic information is important because many animals are not genotyped. In U.S. evaluations, extra information from genotyped parents is transferred to non-genotyped descendants using the same formulas that adjust traditional evaluations for foreign parent data. Propagation from genotyped progeny to non-genotyped parents is more difficult because the extra information from genotyped progeny should not exceed the direct gain from genotyping the parent. Genomic information may be transferred across countries using simple conversion equations or by modifying multi-trait across-country evaluation (MACE) to account for correlated residuals and to account for genomic rather than pedigree relationships when deregressing national evaluations. In traditional MACE, residuals are independent because each daughter is measured in only one country. In genomic MACE, residuals may be correlated for two reasons: 1) multiple evaluation centers may include the same genomic and phenotypic data in national estimates of marker effects, and 2) genomic predictions act as repeated measures of the same portion of genetic merit rather than independent measures of total merit, especially for major gene marker(s) and low-density SNP panels. Marker effects in the U.S. and Canada are highly correlated because both countries share the same genomic data and include traditional MACE evaluations as input to their genomic equations. Residual correlations can be approximated using daughter equivalents from genomics as a fraction of the total in each country and proportions of common bulls shared. Economies of scale in genomics promote cooperation across country borders.

Key Words: genomic evaluation, MACE, SNP

201 Beef cattle industry structure: Implications for whole genome selection. A. Van Eenennaam*, *University of California*, *Davis*.

The breed diversity, lack of vertical-integration, and segmentation of the beef cattle industry present unique challenges for the implementation of whole genome selection. Under the current model of genetic improvement, the costs involved in phenotyping and objectively ranking breeding animals are mostly incurred by the seedstock sector in partnership with breed associations. Record-keeping focuses on traits that are of importance to bull-buyers who understandably select on traits that directly impact their profitability. However, downstream segments of the beef industry (feeder, processor, retailer) each have their own set of economically relevant traits, and market failure means breeders and cow-calf producers receive little or no reward for including traits that are of importance to these segments (e.g. tenderness) in their selection decisions. The promise of genomic selection to improve traits that are currently intractable (feedlot health, feed efficiency, eating experience) will require the development of training populations with appropriate phenotypes. Research suggests that the development of accurate genomic prediction equations will require training populations of thousands of phenotyped and genotyped animals. Developing these populations will be expensive and require increased collaboration between industry segments. Additionally, marketing systems will have to begin to appropriately reward the costs associated with the incorporation of new traits into breeding and cattle evaluation programs. Finally, genomic prediction equations will need to be validated in populations raised in different environments and made up of various breed combinations. These variables have frustrated the validation of the first generation of

DNA-marker tests for quantitative traits in beef cattle. If the scientific validation of this approach shows that it is able to consistently deliver accurate genetic merit estimates for young beef sires, producer education and integration of genomic data into national cattle evaluation will be requisite for the ultimate adoption of whole genome selection.

Key Words: beef cattle, genomic selection, industry structure

202 Utilization of next generation sequencing technologies for development of a high-density pig SNP genotyping platform. R. P. M. A. Crooijmans*[1], M. A. M. Groenen[1], and L. B. Schook[2], [1]*Wageningen University, Wageningen, the Netherlands*, [2]*University of Illinois, Urbana*.

The Illumina Genome Analyzer (Solexa) and Roche 454 FLX 'next generation' sequencing platforms were identify porcine SNPs from diverse commercial breeds. The combined approach permitted increased sequence depth and longer 454 reads to obtain adjacent SNP sequence information to design the primers for the genotyping assay. Considering that only approximately 70% of the pig genome had been sequenced at the time of SNP discovery and beadchip design, the utilization of the longer 454 reads further allowed coverage of the genome at the same SNP density as for the remaining 30% not sequenced or assembled. The only caveat in this approach is the fact that because no information was available regarding the position of these SNPs, it was not possible to predict even SNP distribution. Thus, to maximize SNP spacing, the position of such SNPs on the porcine genome was predicted based on the human-porcine comparative map and end sequences of BACs present on the highly robust BAC contig map. Mapping results on build 8 of the pig genome clearly underscored the success of this approach. The importance of this strategy can be extended to other species where the reference genome and the genomic resources are less developed and/or for which there is no genome sequence available. The number of new porcine SNPs identified in this study exceeded 375,000, which demonstrated that the identification of large numbers of novel SNPs is now feasible in a highly efficient manner. The overall confidence of the SNPs identified by this approach using the porcine SNP60 beadchip demonstrated > 95% of the predicted SNPs were validated. These SNPs were subsequently used to design an Illumina iSelect pig DNA chip (60,000 SNPs). This Illumina iSelect chip was used to SNP genotype global wild boar (35 samples from Europe and Asia) and ten European, North American and Asian domesticated breeds. The average heterozygosity and MAF ranged from 21.6 to 31 and 0.15 to 0.23 respectively for Western breeds, from 14.3 to 17.3 and 0.08 to 0.19 respectively for Chinese breeds, and from 8 to 17.6 and 0.09 to 0.24 for global Wild boar populations. Considering that the breeds used for the discovery of these SNPs included the four main breeds used in pig production (Duroc, Pietrain, Landrace and Large White) as well as the wild boar, the ancestor of all modern pig breeds, it is anticipated that the porcine SNP60 beadchip will be highly efficient to be used for genomic selection by the pig breeding industry.

203 Bioinformatics requirements to apply whole genome prediction in livestock. D. Garrick*, *Iowa State University*, *Ames.*

The traditional method of evaluation adjusts records for non-genetic effects then combines adjusted deviations on the individual of interest and its relatives. The emphasis attributed to various relatives is dictated by their covariance, derived from pedigree information based on expected identity by descent. The prediction has three potential sources, the collective knowledge of its parents genetic merit, the individuals own information relative to its contemporaries, and the average merit of any offspring, adjusted for the merit of mates. Individuals without their own or progeny information can only be estimated from the average merit of their parents and reliability (r^2) cannot exceed 0.5. Whole genome prediction involves tracking inheritance of chromosome regions to infer identity by descent and thereby derive genetic covariances between members of the population. A consequence of this approach is that merits of relatives other than parents and progeny can directly influence the evaluation of a young selection candidate so that it can depart from parent average before individual or progeny information is collected, increasing reliability above the 0.5 threshold. The application of whole genome prediction requires a bioinformatics system to store, access and analyze genotypes, phenotypes and relationships. One computational approach directly uses genotypes to construct the variance-covariance matrix using knowledge of the appropriate emphasis that should be attributed to each chromosomal region. That information can be obtained from prior Bayesian analyses known as training, that estimates the genetic variance of each region, or equivalently, estimates the effect associated with each marker. In circumstances whereby the marked genomic regions collectively account for less than 100% additive variation, predictions can be improved by accounting for covariation between relatives due to residual polygenic effects, not captured by genomic relationships. Prediction of genomic and residual polygenic contributions can be undertaken jointly, or in separate analyses with results subsequently combined into single predictions of merit.

Key Words: genomic analysis, genetic evaluation, Bayesian analysis

Companion Animals: Dietary Supplements in Companion & Exotic Animal Nutrition - Use, Regulations & Safety

204 Navigating the FDA's regulation of animal feed "supplements". J. B. Murphy*, *U.S. Food and Drug Administration's Center for Veterinary Medicine, Rockville, MD*.

The Center for Veterinary Medicine (CVM) is the branch of the U.S. Food and Drug Administration (FDA) that is responsible for the regulation of products (food, drugs, and devices) intended for animals, which includes both livestock and pet animals. The use of food products for both humans and animals is governed by the provisions of the Federal Food, Drug and Cosmetic Act (FFDCA). CVM regulates two classes of orally ingested products intended for animals: food or drugs. The Dietary Supplement Health and Education Act (DSHEA) created a third class of products for humans, the dietary supplements. In 1996, FDA determined that DSHEA does not apply to animals and that the use of the term "dietary supplement" and associated labeling practices are not permitted for animal products. Therefore, depending on the intended use, an animal "supplement" is considered either a food or drug under the FFDCA. The evolution of the pet product market over the past several years has led to an exponential increase in the number of pet supplements available for consumers. Many of these products contain ingredients, claims, and labeling practices that are associated with human dietary supplements that are not permitted for animal products. In addition, CVM is concerned about the inclusion of dietary supplement-type substances, such as herbs and their extracts in pet products. Many of

the substances that are suitable for human supplements are not permitted for use in pet food and may cause adverse effects in animals. Ingredients that are acceptable for use in an animal feed product are approved food additives (FA), substances that are generally recognized as safe (GRAS) for an intended use, and ingredients that are defined in the *Official Publication* (OP) of the Association of American Feed Control Officials (AAFCO). The process for establishing a new FA or GRAS substance is defined in federal regulations, and that for defining new AAFCO ingredients can be found in the AAFCO OP. CVM is responsible for reviewing FA and GRAS substances and serves as the scientific reviewer for AAFCO ingredients.

Key Words: regulation, pet food, supplement

205 Safety of Dietary Supplements for Horses, Dogs and Cats – New NRC Publication. G. L. Czarnecki-Maulden*, *Nestle Purina Research, St Louis, MO*.

Evaluating the safety of inherently safe compounds and complex ingredients can be challenging, particularly in the absence of traditional toxicology studies. At the request of the FDA, the National Research Council (NRC) convened a committee to evaluate the safety of lutein, garlic and evening primrose oil for dogs, cats and horses. After compiling and studying the information available the committee's conclusions were published in a National Research Council publication (Safety of Dietary Supplements for Horses, Dogs, and Cats, 2009). One objective of the committee was to examine factors to consider when assessing safety of supplements. Extrinsic factors, such as growing and processing conditions, and intrinsic factors, such as presence of antinutritive factors, can affect dietary supplement safety. Supplements can be given in purified form. However, they are also fed as intact ingredients further complicating safety evaluation. Physiological differences between species must be considered when evaluating data obtained from other species. Likewise, physiological state can affect supplement safety. The committee assessed the strength of data obtained from various types of published and nonpublished studies and gave guidelines to follow when evaluating studies. Few traditional toxicology studies had been published for these three supplements. Therefore, data was also obtained from a number of non-traditional sources including efficacy studies, case reports, and historical use documentation. After evaluating all available information, the committee concluded that there was insufficient data to determine No Observed Adverse Effect Levels (NOAEL) or Safe Upper Limits (SUL) for the three supplements. The committee defined an alternate term, Presumed Safe Intake (PSI) as, "amounts that will not impair animal health or production efficiency". With the exception of garlic for cats, PSI levels were estimated for each of the supplements and animal species. The PSI's estimated by the committee for horses, dogs and cats, respectively were lutein: 8.3, 1.8 and 7.2, evening primrose oil: 400, 424 and 391, and garlic (as dried garlic powder): 90 and 56 mg/kg bw/day.

Key Words: safety, dog, cat

206 The big "S" supplementation in exotic animal diets. N. A. Irlbeck*, *Colorado State University, Fort Collins, CO*.

Modern day zoos are living museums preserving animal species that would not otherwise survive in today's world. Many mammals, reptiles, birds, fishes and invertebrates no longer live in natural habitats and more are threatened with extinction. In order to maintain health and the ability to propagate, dietary nutrient requirements must be provided. Until the world of exotic animal nutrition reaches the level of expertise found in domestic animals supplementation is dietary essential! But as in all supplementation issues, there is a more complex reality. Researchers are able to evaluate nutrient requirements in domestic animals for each physiological status with feeding trials. In exotic species this is seldom feasible due to limited animal numbers, management issues, lack of dietary information, and diversity of dietary strategies (herbivores, carnivores and omnivores). Public scrutiny often complicates the ability to feed efficiently because of viewing needs. Representative domestic animal models can be used as starting point for nutrient requirements for some exotics (i.e., horse for rhino, elephant and wild equids; goats for smaller antelope species). Evaluation of "natural" diets provides data to feed exotics. Domestic foodstuffs are used to mimic nutrients in wild diets. Development of exotic animal diets is in its infancy and often they are not available or are expensive. Ultimately a combination of feeds must be fed to meet dietary needs and supplementation becomes a reality. With the diversity of animal species and non-traditional diets, limitations of dietary foodstuffs must be considered. Frozen raw fish require thiamine supplementation. Feeding invertebrates like crickets and mealworms requires supplemental calcium. Animals from similar families but from different parts of the world must be fed differently. New world primates need vitamin D3 supplementation and old world primates do not. Browsers need low starch diets and higher vitamin E supplementation than grazers. Exotic animal nutrition is incredibly complex and each nutrition issue needs to be approached with a problem-solving attitude when determining which supplement is to be fed and when.

Key Words: exotics, supplementation, nutrition

207 From arthritis to zinc deficiency, veterinarians are increasingly recommending pet supplements. P. Brown*, *Nutri-Vet LLC, Boise, ID*.

While consumers have always connected sound nutrition with the long-term health of their animals, pet owners are now going beyond the blind acceptance that pet foods provide "everything" needed for a full and long life and are seeking out supplements capable of optimizing their pets' life. As veterinarians have increased their appreciation of the roles that supplements play in certain physiological dysfunctions and come to better understand the potential negative side effects of drugs, the use of pet supplements in veterinary practices has increased dramatically. Pet owner demand for pet supplements is certainly growing. According to Packaged Facts, spending on supplements and functional treats is expected to hit $1.7 billion by 2012. The National Animal Supplement Council (NASC) reports that pet supplements have grown sales 15 percent annually since 2000 and are now a $1.3 billion business. Some manufacturers are seeing increases of 35-40% from the introduction of veterinary formulated "condition-specific" supplements. The Simmons Research Bureau reported that approximately 17% of dog or cat owners routinely give their pets supplements. The trend in pet dietary supplements is shifting away from general wellness formulations such as multi-vitamin and mineral formulations and toward age-related, condition-specific products that address health issues. Pet supplements that support joint health and skin and coat maintenance are most commonly recommended. Now there are products that address specific conditions such as cataracts, memory loss, liver health, and even behavioral disorders associated with household stress or separation anxiety. There are indeed thousands of circumstances where pet supplements are helpful to the veterinarian's clients. Most owners learn about supplements

through friends, retail stores, internet and media advertisements, but, unfortunately, this information may be incomplete or biased. The judicious use of pet supplements have provided veterinarians an emerging segment that helps address client demand and promote animal health and well being.

Key Words: pet supplements

208 Who are we, what do we do and how can we help? W. Bookout*, *National Animal Supplement Council, Valley Center, CA*.

The National Animal Supplement Council was founded in 2002 in response to the lack of a legal category for dietary supplements for companion animals and initiatives to remove them from the US marketplace. Over 100 companies now belong to NASC. In 1994, the Dietary Supplement Health and Education Act created a specific legal category for these products under the Federal Food, Drug and Cosmetic Act that allowed their marketing for human use. The agency responsible for the regulation of animal food and drugs is the FDA's Center for Veterinary Medicine. CVM works closely with the states through regulatory associations like AAFCO. In 1996, CVM published a notice explaining why DSHEA does not apply to animals. This ruling gives products marketed for animals that are similar to human dietary supplements only two possible legal categories under US law: animal feed or drugs. If a product on the market is not approved as an animal drug or contains unapproved feed ingredients, it may be deemed an adulterated drug or feed, and subject to regulatory action. NASC had three options to address this issue: 1) file legal action challenging the ruling that DSHEA does not apply to animals; 2) introduce new legislation; or 3) engage regulatory agencies at the state and federal levels to identify key metrics for responsible industry conduct, thereby allowing products to be marketed under regulatory discretion in the near term while establishing the foundation for a long-term solution. We clearly believe the last approach is in the best interest of all stakeholders. To support this goal, NASC implemented: a comprehensive adverse event reporting system (NAERS); labeling guidelines; scientific review for ingredient risk; an independent mandatory audit program for member companies; guidance for labeling claims; and other requirements suggested by CVM and AAFCO including proposed cGMP guidelines. We have a productive working relationship with US regulatory agencies and are currently working with organizations in other countries as they address similar issues in their markets.

Key Words: companion animals, regulatory, dietary supplements

Food Safety

209 *Clostridium difficile* in cattle and swine. R. Harvey*, *FFSRU, ARS, USDA, College Station, TX*.

There are some implications that human disease from *Clostridium difficile* (Cd) may originate from animals or meat. The objective of this study was to determine the prevalence of Cd among different age and production groups of swine in a vertically integrated swine operation in Texas in 2006, and to compare our isolates to those originating from humans, meat, and other animals. Cultivation of Cd was performed utilizing enrichment/concentration techniques and restrictive media. We recovered 131 Cd isolates from 1008 swine fecal samples with the majority (72%) of isolates occurring in nursing piglets. Decreased prevalence was observed in grower/finisher swine (11.5%) and pork trim (3.0%). Isolates were tested for resistance to 11 commonly used antibiotics. Molecular characterization demonstrated that 127/131 of the isolates were positive for toxins A and B genes, were positive for binary toxin, possessed a 39 bp gene deletion, and were of toxinotype V. These results compare favorably to our non-clinical human isolates (toxinotype V), but differ from clinical isolates of human hospitals in which most are the more virulent toxinotype III. Our swine isolates appear to be genetically similar to each other and have similar antibiotic resistance patterns to isolates from cattle which tend to be of toxinotype V. When sampling meat, we recovered 4 Cd isolates from pork trim, and 1 each from pork chorizo, ground turkey, and pork sausage, but not ground beef. All 7 were toxinotype V. This is in contrast to isolates from ground beef and veal in which the majority have been toxinotype III. Our isolates tended to be less resistant to antibiotics than human clinical isolates. In this study, Cd primarily originated from nursing piglets, but not in grower/finisher swine. If Cd were to be considered food related, then a relatively low prevalence in late production and the predominance of toxinotype V (a less virulent strain of Cd), suggest a low food safety risk. Our results do not appear to implicate Cd as food-vectored.

Key Words: *Clostridium difficile*, cattle, swine

210 Optimising fluorescence of feces as a real-time solution for the detection of fecal contamination on carcasses. M. R. F. Lee*[1], V. J. Theoblad[1], M. K. Theodorou[1], A. Veberg Dahl[2], F. Lundby[2], and J.-P. Wold[2], [1]*Aberystwyth University, Wales, UK*, [2]*Nofima Mat, Ås, Norway*.

In most abattoirs carcasses are checked by `eye' and washed with chemical sprays or dissected to remove areas contaminated with feces or digesta contents. Unfortunately small areas of contamination are seldom visible to the naked eye and may harbour millions of potentially pathogenic bacteria. The `VerifEYE ®' system uses ultra-violet imaging to detect chlorophyll and its fluorescent degradation products in feces. Not surprisingly animals offered fresh forage have a greater concentration of fluorescent compounds in their feces than animals offered conserved forages and concentrate based diets. Consequently the accuracy of the `VerifEYE ®' detection system can vary as it depends on the nature of the animal′s diet and this may explain the poor uptake of the technology by the industry. We have investigated the use of five different markers to be added to the diet in a pre-slaughter feed in an attempt to provide a stable level of fluorescence in the feces. Ten Cheviot sheep were offered a concentrate and barley straw diet and split into five treatment groups during a duplicate changeover 5 × 5 Latin square design where each period lasted 2 weeks. Four of the groups received a different marker at a rate of 1 g/d for the second week of each experimental period. The last group received no supplement and was used as the control. At the end of each period feces were collected and analysed for fluorescent compounds and intensity of the fluorescence. There were no differences in fecal concentration of the markers or their derivates 3.1 ± 0.15 and 7.2 ± 0.37 mg/g DM, respectively. Each of the markers significantly increased the fluorescence intensity of the feces over the control. The use of markers in pre-slaughter diets would thus improve the accuracy of fecal detection as a result of greater fluorescence and pin pointing the excitation wavelengths of the marker to help with visualisation. Further work is being continued to identify the most suitable marker and feeding regime.

Key Words: fecal contamination, fluorescence markers, pathogenic bacteria

211 Influence of serum prolactin concentrations on fecal shedding of *E. coli* O157:H7 in cattle. R. L. Farrow*, T. S. Edrington, K. M. MacKinnon, R. C. Anderson, and D. J. Nisbet, *USDA - ARS, College Station, TX.*

Previous research in our laboratory demonstrated hormones known to respond to changing day length can influence fecal shedding of *E. coli* O157:H7 in cattle. Continuing with this research, we examined the effect of serum prolactin concentrations on fecal shedding of *E. coli* O157:H7 and cellular immune response. 2–Bromo–α–ergocryptine methanesulfonate salt (BROMO) a dopamine agonist and sulpiride a D–2 dopamine receptor blocker were administered to decrease and increase prolactin levels, respectively. Fifteen Holstein steers experimentally infected with *E. coli* O157:H7 were randomly assigned to receive BROMO (0.05 mg/kg BW), sulpiride (0.05 mg/kg BW) or control (ethanol) via s.c. injection, twice daily. Fecal samples were collected daily and shedding of *E. coli* O157:H7 was determined via an immunomagnetic separation technique. Blood samples were collected via jugular venipuncture for analysis of serum prolactin concentrations and circulating neutrophils were isolated from peripheral blood on d 7 and 14 and degranulation and oxidative burst (OB) assays conducted. When examined over the 14-d experimental period, BROMO decreased ($P = 0.0001$) the percentage of cattle shedding *E. coli* O157:H7 (56% vs. 25.33% for control and BROMO treatments, respectively) while sulpiride had no effect ($P > 0.10$). BROMO decreased ($P < 0.0001$) serum prolactin concentrations, while sulpiride injections had no effect ($P > 0.10$). Oxidative burst by neutrophils for BROMO vs. control showed no significant difference on d 7, however, on d 14 OB by neutrophils tended to be higher for BROMO vs. controls ($P = 0.08$). Serum prolactin concentrations tended to be negatively correlated with OB ($P = 0.09$). No significant differences were observed for degranulation in BROMO vs. control on either d 7 or 14. These results support our hypothesis that hormones influenced by day length are responsible for the seasonality of *E. coli* O157:H7.

Key Words: *E. coli* O157:H7, beef cattle, seasonal shedding

212 Oral delivery systems for encapsulating bacteriophage targeted at *E. coli* O157:H7. K. Stanford*[1], T. P. Stephens[1], T. A. McAllister[2], D. Niu[1,3], and R. P. Johnson[4], [1]*Alberta Agriculture and Rural Development, Lethbridge, AB, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [3]*Dalian University of Technology, Dalian, China*, [4]*Public Health Agency of Canada, Guelph, ON, Canada*.

Bacteriophages (PHAGE) are natural predators of *E. coli* O157:H7 in feedlot cattle and their environment. As PHAGE are inactivated at low pH, protection against gastric acidity may enhance efficacy of orally-administered PHAGE. *In vitro*, polymer encapsulation effectively protected 4 spray-dried PHAGE (wV8, rV5, wV7 and wV11) from acid digestion and a mean of 2.70×10^9 PFU was recovered across PHAGE types after 20 min exposure to pH 2.8. Twenty-four steers were administered 10^{10} CFU of naladixic acid-resistant *E. coli* O157:H7 (NalO157) on D0 and housed in 6 pens of 4 animals. Two pens served as CONTROL (NalO157 inoculation only) and remaining animals received 10^9 PFU of polymer-encapsulated PHAGE on d-1, 1, 3,6 and 8. Two pens received PHAGE orally in a gelatin capsule using a starch carrier (BOLUS) while the remaining 2 pens received PHAGE top-dressed on barley silage in the feed bunk (FEED). A daily 150g sample of FEED was retained to verify PHAGE titre using a standard plaque assay. Fecal shedding of *E. coli* O157:H7 was monitored for 10 wk by collection of fecal grab and hide swab samples from individual animals and via collection of fecal pats, feed and water in environment. Acceptable viability of mixed PHAGE was found in BOLUS and FEED treatments, averaging 1.82 and 1.50×10^9 PFU, respectively. However, treatment with PHAGE did not reduce numbers of animals shedding NalO157 compared to CONTROL, although duration of shedding was reduced by 14 d in BOLUS as compared to CONTROL animals. This study developed 2 successful delivery systems for PHAGE, but a better understanding of PHAGE-*E. coli* O157:H7 ecology is required to make PHAGE therapy a viable mitigation strategy in the feedlot.

Key Words: bacteriophage, *E. coli* O157:H7, cattle

213 Effects of Aviplus® on *E. coli* O157:H7 in pure culture and in mixed ruminal culture fermentations. T.R. Callaway*[1], E. Grilli[2], M. R. Messina[2], and A. Piva[2], [1]*Food and Feed Safety Research Unit, Agricultural Research Service, USDA, College Station, TX*, [2]*DIMORFIPA, University of Bologna, Bologna, Italy*.

Foodborne pathogenic bacteria can be harbored in the gut of food animals and transmitted to humans through the food supply, through water supplies or animal contact. Populations of the pathogenic bacteria E. coli O157:H7 can be affected by changes in the native flora of the intestinal tract. Organic acid products have been suggested for use as non-antibiotic modifiers of the gastrointestinal fermentation of animals. However, the impact of these acids on the overall microbial ecology of the intestinal tract remains unknown. Therefore, this study was designed to examine the effects of these acids on populations of the foodborne pathogen, Escherichia coli O157:H7. Pure cultures 3×10^5 CFU/ml of E. coli O157:H7 were added to tubes that contained Aviplus® added at 0, 0.1, 1, 2, 5, and 10% (w/v; n = 3). Aviplus® did not affect ($P > 0.1$) the growth rate or final populations of E. coli O157:H7 in pure culture, indicating that Aviplus® does not directly kill this pathogen at levels similar to those found in the intestinal tract. Ruminal fluid was collected from cows fed concentrate and placed in in vitro buffers. E. coli O157:H7 was added to in vitro ruminal fermentation, respectively, that contained Aviplus® at concentrations of 0, 1, 2, 5, and 10% (w/v; n = 2) and were incubated for 24 h. Aviplus addition did not affect ($P > 0.1$) populations of E. coli O157:H7 in the ruminal fluid. The ruminal A:P ratios were reduced ($P < 0.07$) by Aviplus® treatment. Organic acid products, such as Aviplus®, can alter the intestinal microbial ecology and impact animal productivity and health, however in vitro it does not appear that Aviplus® has an impact on populations of tested foodborne pathogenic bacteria inoculated at relatively high initial populations.

Key Words: Aviplus, food safety, fermentation

214 Control of *E. coli* O157:H7 in corn silage with inoculants under anaerobic and aerobic conditions. A. F. Pedroso[1,2], A. T. Adesogan[2], O. C. M. Queiroz*[2], and S. K. Williams[2], [1]*Brazilian Agricultural Research Corporation, Embrapa Cattle-Southeast, Sao Carlos, Sao Paulo, Brazil*, [2]*Department of Animal Sciences, Institute of Food and Agricultural Sciences, University of Florida, Gainesville*.

The aim was to determine if bacterial inoculants could eliminate *E. coli* O157:H7 (ECOL) in contaminated corn silages and if inoculants transferred antibacterial activity to silages. Chopped corn forage was ensiled in triplicate after treatment with:1) distilled water (control); 2) 5 x 105 cfu/g of ECOL (EC); 3) EC and 1 x 106 cfu/g of *Pediococcus pentosaceus* and *Propionibacterium freudenreichii* (EC+BII); 4) EC and 1 x 106 cfu/g of *Lactobacillus buchneri* (LB; EC+LB); 5) EC and 1 x 106 cfu/g of LB and *P. pentosaceus* (EC+B500). Silos were opened after 3, 7, 31, and 82 d and analyzed for pH and ECOL counts as well

as VFA, lactate, and aerobic stability on d 82. By d 3, all silages had pH was <4 (SE=0.33; p=1) and pH did not increase subsequently; therefore ECOL was not detected in any silage. The Kirby-Bauer disc diffusion test showed that all pure cultures of inoculants had pH-independent antibacterial activity against ECOL but inoculated silages did not, suggesting that ECOL elimination was mediated by pH reduction. Inoculation with LB resulted in less lactate (SE=0.31; p<0.05), more acetate (SE=0.35; p<0.05), and greater aerobic stability (SE=7.1; p<0.05) versus control. Day-82 silages were reinoculated with EC at silo opening (immediate) or after 144 h of exposure (delay) and ECOL were enumerated 24 h later. All immediately reinoculated silages had low pH values (<4) and no ECOL 24 h later. Control, EC, and EC+BII silages reinoculated after the delay had relatively high pH values (4.71, 5.67, and 6.03) (SE=0.74; p<0.05) and ECOL counts (2.87, 6.73, and 6.87 log cfu/g) (SE=1.4; p<0.05), whereas those treated with LB had low pH values (<4) and undetectable (EC+B500) or low ECOL counts (1.96, cfu/g; EC+LB). Inoculants did not enhance elimination of ECOL during ensiling, but *L. buchneri inoculants* increased stability and eliminated or inhibited ECOL in aerobically exposed silages.

Key Words: *E. coli* O157:H7, inoculant, silage

215 Characterization of antimicrobial-resistant *Escherichia coli* from samples collected throughout processing of feedlot cattle at a commercial abattoir. T. W. Alexander*[1], G. D. Inglis[1], L. J. Yanke[1], E. Topp[2], and T. A. McAllister[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*, [2]*Agriculture and Agri-Food Canada, London, Ontario, Canada*.

This study investigated antimicrobial-resistant *Escherichia coli* from samples throughout abattoir processing of feedlot cattle fed diets containing chlortetracycline plus sulfamethazine (AS700) or no antimicrobials (control). For each treatment, samples analyzed were: 1) feces collected at the feedlot (N=30); 2) hides after euthinization (N=15); 3) carcasses after evisceration and after 24 h in the chiller (N=15 for both); 4) ground beef stored for 1 and 8 d (N=15 for both); 5) digesta and mucosa from nine sections of the lower digestive tract (N=5 for each); 6) environmental abattoir samples (N=10); 7) air samples during slaughter (N=15). Generic, ampicillin (AREC)-, and tetracycline (TREC)-resistant *E. coli* were isolated on MacConkey agar or MacConkey agar containing ampicillin or tetracycline. All animals harboured AREC and TREC. Compared to control animals, the number of AREC (26.5% vs. 7.9%) and TREC (50.9% vs. 12.6%) were greater in feces from AS700 treated animals (P < 0.05) but were similar between hide, digesta and mucosa samples. Generic *E. coli*, AREC and TREC were detected from carcasses after evisceration and after 24 h in the chiller and d1- and d8-ground beef samples. Generic *E. coli* were isolated from all air samples. Resistant *E. coli* were isolated from the abattoir environment after slaughter of both groups of animals. Susceptibilities to 11 antimicrobials and pulsed field gel electrophoresis (PFGE) analyses were conducted on 362 AREC and TREC isolates across all samples. Twenty-five antibiogram profiles were detected. Most (28.2%) AREC were multi-resistant to ampicillin, streptomycin, and tetracycline while TREC (53.5%) were mainly resistant to tetracycline. From PFGE, 11 and 26 genotypes were detected amongst AREC and TREC respectively. Generally, isolates from meat and environmental samples had genetic backgrounds similar to isolates from animal tissue, digesta, or hide samples. These data indicate that antimicrobial-resistant *E. coli* from feedlot cattle can contaminate meat products at the slaughter plant and enter the food chain.

Key Words: antimicrobial resistance, abattoir, *Escherichia coli*

216 Screening of class IIa bacteriocin-producing lactic acid bacteria from Chinese traditional fermented food by PCR based method. H. Yi, L. Zhang*, Y. Tuo, X. Han, and M. Du, *Harbin Institute of Technology, Harbin, Heilongjiang, China*.

Class IIa bacteriocins of lactic acid bacteria are by far the most investigated and have been considered as one of the most interesting and potential groups of antimicrobial peptides for use in food preservation. There are abundant and various traditional fermented foods in China, which are likely to be valuable database containing class IIa bacteriocin-producing LAB. However, how to screen the desirable LAB rapidly from the complex fermented food ecosystem presents challenge. Therefore, development of rapid and reliable method for screening of microbes producing class IIa bacteriocins from potential organisms holds the key to the discovery of new and applicable class IIa bacteriocins. A method based on colony-PCR was developed and applied to screen class IIa bacteriocin-producing bacteria from 43 traditional fermented products (18 raw milk or yoghurt samples, 15 koumiss and 10 fermented vegetables samples) collected from specific ecological localities (Qinghai, Gansu, Sinkiang, Tibet) throughout the northwestern China. Results showed that 6 of 275 isolates gave rise to PCR fragments. Fragments of 3 kb can be detected with strain SB31 and Q5, while 3.4 kb with strain J20, J23 and 3.8 kb with strain M18 and X20 were obtained. The discrepancy of the amplicons size suggests that the size of peptide between bacterioncin and histidine kinase exists strain-specific. Amplicons of 332 bp (with strain M18 and X20), 412 bp (with strain SB31 and Q5), 428 bp (with strain J20 and J23) indicate the presence of pediocin, enterocin, plantaricin, respectively. This assay showed agreement with the conventional well-diffusion method. It offers several advantages over the existing methods in terms of rapidity, simplicity and accuracy, which make it a promising alternative to the conventional protocols. In addition, isolates of LAB from natural niches with the plateaus climate in the northwestern China could not only preserve the native microbes, but also eventually be an important resource for the development of novel starter cultures as well as food biopreservatives.

Key Words: class IIa bacteriocin, lactic acid bacteria, screen

217 *Salmonella* infection and immune response in finishing pigs. M. H. Rostagno*, S. D. Eicher, and D. C. Lay, *USDA, ARS, Livestock Behavior Research Unit, West Lafayette, IN*.

Finishing pigs infected with *Salmonella* pose food safety risks by carrying the pathogen into abattoirs. A study was conducted to determine the dynamic of *Salmonella* infection in finishing pigs, and immunological alterations that occur in *Salmonella*-carrier pigs, by longitudinally comparing infected to non-infected pigs. Pigs (n=24) were individually inoculated with *Salmonella* Typhimurium. Fecal and blood samples were collected from each pig, and 3 pigs were randomly selected and euthanized to collect additional samples (spleen, liver, mesenteric lymph node, ileum, and cecum) on days 1, 2, 7, 14, 21, 28, 35, and 42 post-inoculation (p.i.). A control group (n=15) of non-infected pigs was maintained for comparison by sampling at 1, 2, 7, 14, and 21 days. No inoculated animal showed any clinical sign of infection. Bacteriological data revealed that all inoculated pigs started shedding *Salmonella* within 24 h p.i., and persistently shed the bacteria up to the end of the study. Ileal and cecal content samples were all positive throughout the study. Mesenteric lymph nodes were also positive during the entire study and at the same level as intestinal content samples. All samples contained 3-4 logs (cfu/g) of *Salmonella* at 24 h p.i., and 4-5 logs (cfu/g) of *Salmonella* up to 4 wk p.i. Interestingly, levels of *Salmonella* dropped markedly (P<0.05) in all samples at 5 wk p.i., being detectable only by enrichment.

The number of peripheral blood monocytes tended to be less in infected pigs, with no difference between groups for other white blood cell measures. Tumor necrosis factor-Î± was greater (P<0.05) in infected pigs: 1) in the mesenteric lymph nodes by 48 h p.i.; 2) at 24 h and 3 wk p.i. in the ileum; and 3) in the cecum and spleen by 3 wk p.i. Interleukin-12, IL-1 and its antagonist, and a porcine specific antimicrobial peptide RNA expression in tissues changed over time, but were not different between groups. Immune data demonstrate that site specific immune changes occurred first, followed by more peripheral responses. These results will enable us to develop and plan the application of intervention strategies that will contribute to increase pork safety.

Key Words: swine, salmonella, food safety

Graduate Student Paper Competition-CSAS Oral Competition: CSAS Graduate Student Competition 2

218 The effect of animal location during transit on heart rate of pigs transported to slaughter using two vehicle types. J. A. Correa*[1], H. Gonyou[2], R. Bergeron[3], S. Torrey[4], T. Crowe[5], T. Widowski[3], J. P. Laforest[1], C. Dewey[3], N. Lewis[6], and L. Faucitano[4], [1]*Laval University, Quebec, QC, Canada*, [2]*Prairie Swine Centre, Saskatoon, SK, Canada*, [3]*University of Guelph, Guelp, ON, Canada*, [4]*Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada*, [5]*University of Saskatchewan, Saskatoon, SK, Canada*, [6]*University of Manitoba, Winnipeg, MB, Canada*.

The objective of this study was to assess the effect of the location in the vehicle on heart rate of pigs during transport. A total of 1,597 crossbred pigs (BW:124.2±7.9kg) were transported over 6 weeks (February-March 2008) from a commercial growing-finishing unit to a slaughter plant (2 h journey time) using two types of vehicles, a three-deck pot-belly trailer with internal ramps to upper and lower levels (PB; 181 pigs per week in 8 experimental compartments; 0.41 m2/pig) and a double-decker hydraulic truck without internal ramps (DD; 85 pigs per week in 4 compartments; 0.40 m2/pig). A sub-population of 252 pigs (PB: 28 pigs/week; DD: 14 pigs/week) was equipped with heart rate monitors (Polar Electro Canada) and randomly distributed through the selected compartments in both vehicles. Heart rate was recorded at 5 sec intervals and averaged over the following events: loading (L), wait before departure from the farm (W), transport (T) and unloading (U). Heart rate data were analyzed using the mixed model procedure in SAS, with the pig as the experimental unit. In the DD truck, independently of the deck position, a higher (P<0.05) heart rate was recorded during T in pigs located in the rear compartments (127.4±2.9 beats/min) of the vehicle compared to those loaded in the front ones (118.9±2.9 beats/min). No difference in heart rate was found between these locations in the PB trailer. In the PB trailer, pigs located on the upper deck showed higher (P<0.05) heart rate during W (165.8±3.2 beats/min) compared to those loaded in the middle (158.6±3.5 beats/min) and lower (157.3±4.0 beats/min) decks. During U, pigs from the upper (172.1±4.3 beats/min) and lower (171.1±4.9 beats/min) decks showed higher (P< 0.01) heart rates than pigs from the middle deck (163.6±4.3 beats/min). Overall, the heart rate of pigs during transport can be affected by their position in the vehicle.

Key Words: pigs, transport, heart rate

219 Utilization of electrolytes to encourage early feed and water consumption in weanlings. A. K. Gigiel*, N. J. Lewis, and M. L. Connor, *University of Manitoba, Winnipeg, MB, Canada*.

Three trials were conducted to determine the best management strategy for providing electrolytes to weanlings. Each trial used 90 piglets (19±1d) in a repeated measures design with a 2×5 factorial arrangement of treatments. Piglets were weaned for 12 or 0h and transported (<1h) to an offsite research facility. Trials 1 and 2 were done to determine the effects of providing electrolytes for different durations (T1) and at different concentrations (T2) on feed intake (FI) and growth rate. In T1, electrolytes (Vetoquinol, QC, Canada) were provided at the label dose of 60ml/940ml of water for 0, 6, 12, 18 or 24h on d1–d3. In T2, electrolytes were given *ad lib* at 100, 75, 25, 50 or 12.5% of the label dose on d1–d3. Trial 3 (T3) was done to determine the optimum number of days that electrolytes should be made available in order to maintain piglet weight and encourage FI. Electrolytes, at the label dose, or water (control) were given *ad lib* on d1, d1 and d2, d1–d3, or d1 and d3. All piglets had water *ad lib* from d4–d14. Piglets were weighed daily on d0–d7 and on d14, and FI was recorded daily to d4. ADG was calculated using d7 and d14 weights. Data was analyzed using PROC Mixed. In T1, on d7 percent weight change from d0 (%Wt) was significantly higher in the groups that received electrolytes for 12h and 18h than in the 24h group (9.2±1.65, 10.0±1.59 vs. 6.2±1.56%; *P*=0.04), but FI on d4 was higher in the 12h group than in the 18h and 24h groups (300.1±29.49 vs. 184.2±29.26, 209.8±27.47g/d; *P*=0.07). In T2, on d14%Wt was significantly higher in the 25% concentration group than in the 75% group (56.4±5.53 vs. 39.0±5.53%; *P*<0.05), and ADG was higher in the 25% group than in the 50, 75 and 100% groups (0.4±0.05 vs. 0.3±0.05, 0.3±0.05, 0.3±0.05g/d; *P*<0.10). In T3, there were no differences after d3 in %WT, FI or ADG. The data suggests that weanlings benefit from electrolytes at lower concentrations (<100%) for a shorter time period (<24h/d) than currently recommended. A subsequent experiment will focus on verifying the best combination of electrolyte concentration and total duration of treatment.

Key Words: piglet, electrolyte treatment, performance

220 Identification of single nucleotide polymorphisms influencing feed efficiency and performance in multi-breed beef cattle using a candidate gene approach. M. K. Abo-Ismail*[1], M. J. Kelly[1], E. J. Squires[1], K. C. Swanson[1], J. D. Nkrumah[2], and S. P. Miller[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Igenity Livestock Production Business Unit, Merial Ltd., Duluth, GA*.

Mutations in genes involved in biological processes associated with economically important traits are candidates which can be targeted for QTL detection to facilitate marker assisted selection. Therefore, the objectives of this study were to identify new SNPs in nine genes involved in digestive function and metabolic processes associated with feed efficiency and to examine the discovered SNPs for associations with feed efficiency and performance. An in silico study was conducted to discover SNPs in the candidate genes. Briefly, expressed sequence tags (ESTs) were acquired from the gene bank NCBI, and then ESTs were aligned using DNA sequence assembly software Sequencher. Single nucleotide polymorphisms, change in the sequence of amino acids, and the position of each SNP were detected. Animals (993) were genotyped for selected SNP (43) with 23 SNP identified as real (not fixed).

A univariate mixed-inheritance animal model was fit in ASREML to evaluate the association of phenotypes with either genotypes or allele substitution effects. Phenotypes included daily dry matter intake (DMI), ADG, midpoint metabolic weight (MMW), residual feed intake (RFI) and feed conversion ratio (F:G) on 660 genotyped crossbred bulls, steers and heifers fed through the University of Guelph feedlot with measured feed intake. Average breed contributions were Angus (41%), Charolais (23%), Piedmontese (11%), Simmental (8%), and Limousin (1%). SNP1 within Pancreatic Anionic Trypsinogen and SNP2 within Cholecystokinin receptor β genes influencing digestive function and satiety were associated with residual feed intake (P<0.01). Allele substitution effects for SNP1 and SNP2 were associated with a decrease of 0.197 ±0.075 (P<0.01) and 0.176±0.088 (P<0.05) kg RFI, and 0.188±0.10 (P<0.059) and 0.229±0.12 (P<0.073) kg in DMI, respectively. Substitution of SNP1 was associated with increased ADG (0.0408±0.025 kg, P=0.105). Further research will identify additional SNP, validate these results in other populations and elucidate the biological mechanism underpinning these discoveries.

Key Words: candidate genes, feed efficiency, beef cattle

221 Heritability estimates of reproductive, growth and carcass traits of tropical pigs: A meta-analysis. E. C. Akanno*, F. S. Schenkel, V. M. Quinton, R. M. Friendship, and J. A. B. Robinson, *University of Guelph*, *Guelph, ON, Canada*.

Export of pig germplasm (live animals or semen) from Europe and North America into the tropics for the improvement of indigenous populations has been going on for over five decades. Breeding program design for the tropics requires knowledge of genetic parameters for economically important traits determined under tropical conditions. A literature review found a total of 350 heritability (h^2) estimates for 37 traits across 85 papers published from 1972 to 2008, covering tropical Africa, Southeast Asia, the Caribbean and Latin America. There were as many h^2 estimates for litter as growth traits, but far fewer for other traits relating to reproduction and carcass merit. A meta-analysis was conducted on all of the assembled papers. The weighted mean h^2 across these studies for reproductive, growth and carcass traits was 0.06, 0.23 and 0.61 for indigenous breeds and 0.08, 0.30 and 0.50 for exotic breeds, respectively. Weighted least-squares analyses of the h^2 estimates were performed by fitting breed (indigenous or exotic), region of tropics, data origin (field or experimental), estimation method and time of recording for each trait as appropriate for the data available. Breed, region, data origin, estimation method and time of recording were found to be significant ($P < 0.05$) for at least one of the traits analysed. These results indicate the relevance of having local, population-specific genetic parameter estimates for the tropics. When estimates are not available for a specific tropical pig population, the weighted mean h^2 estimates from the current study are recommended for use. Where estimates within a population are available, but not reliable enough, they could be combined with the weighted literature average. A simple rule would be to weight each, the local estimate and the pooled mean, by the inverse of its corresponding squared error.

Key Words: heritability, economic traits, tropical pigs

222 Seasonal based genetic regulation of reproductive traits in a male turkey line. L. A. Case*[1], M. J. Kelly[1], S. P. Miller[1], and B. J. Wood[2], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Hybrid Turkeys*, *Kitchener, ON, Canada*.

Environment can affect the genes contributing to phenotypic performance resulting in a genotype by environment (GxE) interaction. The objective of this study was to investigate the expression of potential GxE interactions for turkey reproductive traits. Seasonal re-ranking of turkey reproductive performance was indicative of a GxE for egg production, fertility, and hatchability. The genetic correlation between the traits expressed in the winter and summer season was used to quantify the strength of the GxE. Pure male line large white turkeys from a primary breeder hatched between 1990 and 2008 were used in the study. Egg number was expressed as the percentage of days with an egg produced between 210 and 420 days of age, fertility represented the proportion of hatched eggs that contained a fertile embryo and hatchability was the percent of fertile eggs that produced a live bird. ASREML was used to estimate variance components and heritability. The heritability of (h^2) of egg production was 0.32 with the phenotypic (σ^2_p) and genetic (σ^2_g) variance, 118.3 and 38.35 percent days with egg produced^2, respectively. The h^2, σ^2_p and σ^2_g estimates for fertility were 0.08, 576.9%^{2} and 48.43%^{2} . The hatchability h^2, σ^2_p and σ^2_g estimates were 0.15, 582.2%^{2} and 90.01%^{2}. Best linear unbiased prediction (BLUP) was used to calculate estimated breeding values (EBVs) using variance component estimates. EBVS fluctuated annually and resultantly egg number, fertility and hatchability were evaluated as two traits, summer and winter lay in a bivariate model. The correlation between the seasonal traits was lower than unity ($r_{egg\ production}$=0.86, $r_{fertility}$=0.19, $r_{hatchability}$=0.68) suggesting a GxE interaction. Egg production, fertility, and hatchability in turkeys could be considered as two distinct traits in an animal model with traits based on season of lay. By considering independent genetic contribution to reproductive phenotypes based on season of lay, the accuracy of prediction of estimated breeding values by genetic evaluation models could be increased.

Key Words: genotype by environment interaction, reproduction, heritability

223 Effects of feeding solid feed on ruminal pH and expression of genes involved in ketogenesis in dairy calves during weaning transition. A. H. Laarman* and M. Oba, *University of Alberta*, *Edmonton, AB, Canada*.

The objective of this study was to determine the effects of feeding solid feed on rumen pH and the expression of genes involved in ketogenesis in ruminal epitheila. Eight two-week old Holstein calves (44.4 ± 4.0 kg) were blocked by BW, and assigned to either a diet of only milk replacer (MR: 22% CP and 17% fat) or MR and a commercial calf starter containing 23% CP (MR+S). Calf starter was fed ad libitum, and the MR calves was fed extra milk replacer to maintain metabolizable energy intake between calves within blocks. When a calf consumed 680 g of starter feed for 3 consecutive days, a small ruminant rumen pH-measuring device (20.6 mm diameter, 138 mm length, mass 245 g) was inserted orally to measure rumen pH continuously. Three days later, blood was sampled for glucose analysis and calves were slaughtered (51.1 ± 6.7 days old), then ruminal epithelia was harvested from the ventral sac. Statistical analysis was conducted using the Fit model procedure of JMP with fixed effects of block and treatment. Average daily gain for MR and MR+S was 0.58 ± 0.04 and 0.70 ± 0.04 g/d, respectively ($P < 0.11$); plasma glucose concentration at slaughter was not different between treatments, averaged at 117.1 mg/dL. Daily mean ruminal pH was 6.03 ± 0.13 for MR+S and 6.41 ± 0.10 for MR ($P = 0.13$). Relative mRNA abundance of Acetyl-CoA acyltransferase 1 (ACAT-1) was 47% lower for MR+S compared to MR ($P < 0.05$), even though total RNA content was similar ($P = 0.34$). Abundance of HMGS-1 mRNA was positively

related to plasma glucose levels (r = 0.82; $P < 0.05$). While HMG-CoA lyase (HMGL) mRNA abundance was unaffected by treatment, it was positively correlated to the duration of time ruminal pH was less than 5.8 (r = 0.81; $P < 0.05$). These results suggest that feeding solid feed to dairy calves during weaning transition may decrease expression of genes involved in ketogenesis in ruminal epithelia.

Key Words: rumen pH, ketogenesis, calf development

224 The threonine requirement in sows increases in late gestation. C. L. Levesque*[1], S. Moehn[1], P. B. Pencharz[2], and R. O. Ball[1], [1]*Swine Research and Technology Centre, University of Alberta, Edmonton, AB, Canada*, [2]*Sick Children's Hospital, University of Toronto, Toronto, ON, Canada*.

The NRC (1998) assumes a constant requirement for amino acids (AA) in gestation; however, metabolic focus changes from maternal tissue gain in early gestation (EG) to fetal and mammary tissue growth in late gestation (LG). This change in metabolic focus may affect the requirement for AA in EG and LG. The threonine (THR) requirement of second parity sows in EG and LG was determined using the indicator amino acid oxidation technique. A basal corn diet was formulated at 60% of NRC (1998) THR requirement based on BW, expected maternal gain and litter size. Each sow was fed six levels of dietary THR and daily THR intake ranged from 4.9 to 16.1 g•d^{-1}. [1-^{13}C]phenylalanine (PHE) was given orally in 8 1/2-hourly meals as an indicator AA and expired ^{13}CO2 was quantified. Plasma PHE enrichment was used to calculate protein turnover. A nonlinear Mixed model was used to determine the THR requirement for each period. Sow BW gain and reproductive performance were similar to commercial standards. Sows responded differently to THR intake in early and late gestation. The THR requirement was 6.0 g•d^{-1} (R^2=0.59) in EG and 13.6 g•d^{-1} (R^2=0.56) in LG. In EG, protein synthesis increased (R^2=0.79) and PHE oxidation (R^2=0.84) decreased at THR intakes below requirement. In LG, protein synthesis (R^2=0.41) and PHE oxidation (R^2=0.40) responded linearly to increasing daily THR intake. Total protein breakdown (p=0.27, 44.1 ± 2.2 vs 46.2 ± 2.3 g•d^{-1}, respectively) and PHE flux (p=0.12, 57.0 ± 2.5 vs 60.0 ± 2.6 g•d^{-1}, respectively) were not different between EG and LG. However, protein breakdown (p= 0.001, 0.25 ± 0.01 vs 0.22 ± 0.01 g•kg $^{-1}$ BW, respectively) and PHE flux (p= 0.001, 0.32 ± 0.01 vs 0.28 ± 0.01 g•kg^{-1}BW, respectively) as a proportion of BW were greater in EG than LG. The THR requirement in LG is greater than in EG. Feeding sow diets with constant levels of AA throughout gestation results in overfeeding AA in EG and underfeeding AA in LG. *Support: AB Pork, ON Pork, AB Livestock Industry Development Fund, ACAAF, Ajinomoto Heartland.*

Key Words: threonine, gestation, requirement

225 Energy and amino acid utilization in expeller-extracted canola meal fed to growing pigs. T. A. Woyengo*, E. Kiarie, and C. M. Nyachoti, *University of Manitoba, Winnipeg, MB, Canada*.

Two experiments were conducted to determine the nutritive value of expeller-pressed canola meal (EECM) for growing pigs. In Exp. 1, 6 ileal-cannulated barrows (average initial BW = 26.8 kg) were fed 3 diets in a replicated 3 × 3 Latin square design to determine standardised ileal digestible content (SIDC) of AA. The 3 diets included a cornstarch-based diet with either solvent extracted canola meal (SECM) or EECM as a sole source of protein, and a low casein cornstarch-based diet, which was used to estimate endogenous AA losses for determining SIDC of AA. In Exp. 2, 18 intact barrows (average initial BW = 25.9 kg) were fed 3 diets in a completely randomized design (6 pigs per diet) to determine total tract digestible nutrient content of EECM. The diets included a basal corn-based diet or the basal with corn replaced by 350 g/kg of SECM or EECM; the basal diet was used for determining total tract digestible nutrients by the difference method. The EECM used in both experiments was obtained from Associated Proteins, Ste. Agathe, MB. The SECM, which is commonly used in formulation swine diets, was fed in both experiments for comparison with EECM. The SECM and EECM were similar in CP content (41.8 vs 41.4%). The EECM was, however, slightly higher in ether extract (5.89 vs 5.54%), and lower in NDF content (23.8 vs 29.9%) than SECM. The EECM had also a higher content of all the AA except Met, Cys and Ser by approximately 6.6%; Met and Cys were higher in SECM, whereas Ser was similar between the 2 meals. The EECM compared with SECM had higher ($P < 0.1$) SIDC of Lys (16.38 vs 14.55 g/kg DM). The SIDC of all the remaining AA except Met were also higher ($P < 0.1$) for EECM than for SECM by a mean of 13.4%; the SIDC of Met was similar between the 2 meals. The EECM compared with SECM had higher ($P < 0.01$) DE (4107 vs 3790 kcal/kg) value. The results show that the EECM used in the current study had higher digestible AA and energy contents than the SECM, and hence it may be a better source of protein and energy for growing pigs than the latter.

Key Words: canola meal, nutritive value, pigs

226 Calcium chloride and sodium nitrate as nutritional means to overcome the reduction in performance of pigs fed high potassium diets. J. Guimaraes*, D. Wey, C. Zhu, and C. F .M de Lange, *University of Guelph, Guelph, ON, Canada*.

Co-products from the bio-fuel and food industries are used increasingly as inexpensive pig feed ingredients. However, high dietary potassium (K) levels in co-product based diets contribute to reduced growth performance in pigs and abnormalities in kidney histology. This study was conducted to investigate the addition of calcium chloride ($CaCl_2$) or sodium nitrate ($NaNO_3$) to pig diets as means to overcome the negative effects of feeding 1.4% K containing diets. $CaCl_2$ has been used to manipulate dietary electrolyte balances while $NaNO_3$ has been shown to increase loss of potassium in man. Forty eight purebred Yorkshire pigs (average initial BW 22.8 kg; 2 gilts and 2 barrows per pen) were fed one of the following diets over a 4 week period: (1) Control (standard corn and SBM based diets; 0.7% K in diet), (2) diet K_2CO_3 (control with added 1.15% K_2CO_3; 1.4% K in diet; previously shown to mimic effect of a 1.4% K containing diet with 20% and 6% diet dry matter from whey permeate and corn steep water, respectively), (3) diet $NaNO_3$ (diet K_2CO_3 with 0.4% $NaNO_3$), and (4) diet $CaCl_2$ (diet K_2CO_3 with 0.76% $CaCl_2$). Pigs had free access to feed and water. Data were exposed to analyses of variance using GLM of SAS with treatment as the only source of variation; treatment means were compared using orthogonal contrasts. Diet did not influence feed intake or BW gain ($P>0.10$). Feed to gain (SEM=0.08, n= three pens per treatment) for Control (1.77) was better than the mean of the other treatments (P=0.04). Diets $NaNO_3$(1.91) and $CaCl_2$(1.79) yielded better feed:gain than diet K_2CO_3 (2.10; P=0.02). Hot carcass weight, carcass lean yield and loin color did not differ among treatments ($P>0.10$). Subjective histology observations suggest that the most kidney damage was present with diet $NaNO_3$, followed by diet K_2CO_3; diet $CaCl_2$ appeared to alleviate the kidney damage and was comparable to Control. These dietary interventions may allow

for increased co-product usage in pig diets and reduce the reliance on traditional feed ingredients, such as corn.

Key Words: pigs, electrolyte balance, co-products

227 Protein turnover and heat production of sows varies at day 30, 45 and 105 of gestation. R. S. Samuel*[1], S. Moehn[1], P. B. Pencharz[2], and R. O. Ball[1,2], [1]*Swine Research and Technology Centre, University of Alberta, Edmonton, AB, Canada*, [2]*Research Institute, Hospital for Sick Children, Toronto, ON, Canada*.

As gestation progresses, an increasing part of the nutrients and energy consumed by sows are used for growth of the conceptus. However, sows are typically fed restrictively and inadequate allowance may be made for changing requirement during gestation. The objective of this experiment was to determine energy and leucine balance of sows in early-, mid-, and late-gestation. Gravid 2nd parity sows (n=5) were fed 2.4 ± 0.1 kg of a barley-wheat-SBM diet of 12.5 MJ ME/kg, 0.65% total lysine, and 15% crude protein twice daily throughout gestation. Heat production, by indirect calorimetry, was determined simultaneously with leucine kinetics, by primed-constant IV infusion of L-[1-^{13}C]leucine (1.0 mg•kg^{-1}•h^{-1}) over 24 h. All measurements were made at d 30, 45, and 105 of gestation. The effect of "day" was assessed using mixed model analysis (SAS 2002) with individual animals as a random variable. Significance was taken at $P < 0.05$; a tendency at $P < 0.1$. Leucine flux, appearance from breakdown, and incorporation into protein were greater ($P<0.001$) on d 45 than on d 30 or 105 of gestation. At constant feed intake, protein gain was lower ($P<0.05$) on d 45 than (137.6 g/d) than on d 30 (167.6 g/d) or 105 (164.1 g/d). Energy balance (i.e. intake over maintenance) was greater ($P<0.01$) on d 45 (6.1 MJ/d) than on d 30 (3.7 MJ/d) or d 105 (1.4 MJ/d) of gestation. This greater energy balance allowed lipid deposition only on d 45 where the respiratory quotient (RQ) was greater than 1, indicating lipogenesis. The RQ was not different than 1 on d 30 and 105. Energy intake (30.5 ± 0.9 MJ/d) was not significantly different from HP (29.1 ± 1.5 MJ/d) on day 105. Therefore, sows needed to mobilize body lipid to support fetal growth. These results indicate that after regaining body protein lost in a preceding gestation and lactation, sows deposit lipid during mid-gestation. Feeding a constant daily amount of feed does not provide sufficient energy in late gestation.

Key Words: energy, protein, gestation

228 Prediction of DE content of common ingredients in grower pigs using an in vitro digestibility technique. P. R. Regmi*[1], N. S. Ferguson[2], A. Pharazyn[2], L. F. Wang[1], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*Nutreco Canada, Guelph, ON, Canada*.

Energy value of feed ingredients can vary widely due to changes in energy digestibility. Prediction of variation in DE value among and within ingredients is important to determine the energy value of ingredients and to balance feed formulations. Previously, a 2-d in vitro digestibility technique, involving subsequent digestion of ground samples in pepsin (2 h), pancreatin (6 h), and Viscozyme, a fiber-digesting enzyme complex (18 h), was used to predict DE content of feed samples in swine. The objective of this study was to test the accuracy of the in vitro technique to predict the variation in DE content across common ingredients (corn, wheat, barley, field pea, soybean meal, corn DDGS, canola meal, and wheat millrun) and within ingredients (wheat and canola meal) in swine. The range of ADF and CP contents (in DM) were, respectively, 3.0 to 16.9 and 9.6 to 52.1% among ingredients, 3.3 to 6.2 and 11.2 to 20.8% among batches of wheat, and 15.2 to 18.1 and 36.2 to 41.3% among batches of canola meal. In vivo DE value was determined using barrows (n = 48) in complete randomized design and ranged among ingredients, within wheat, and within canola meal from 1.82 to 3.18, 3.36 to 3.81, and 3.01 to 3.18 Mcal/kg of DM, respectively. Similarly, in vitro DE value among ingredients, within wheat, and within canola meal ranged from 2.71 to 4.08, 3.50 to 3.94, and 2.96 to 3.33 Mcal/kg of DM, respectively. The relationship of in vitro and in vivo DE values was strong across ingredients ($R^2 = 0.86$, $Y = 1.02 X — 0.13$) and within wheat ($R^2 = 0.78$, $Y = 0.92 X + 0.20$), but was poor within canola meal ($R^2 = 0.05$). Higher ADF and ash (6.7 to 8.6%) contents possibly caused discrepancies between in vivo and vitro digestion, and a narrow range of DE content might have contributed to the poor relationship between in vivo and vitro DE values in canola meal. The in vitro technique can be used to estimate the variation in DE content among common ingredients and within wheat; however, the technique needs to be improved to predict DE content within canola meal.

Key Words: digestible energy, pig, in vitro digestibility

Meat Science and Muscle Biology: Symposium: Balancing Live Cattle Performance and Beef Quality

229 Growth technologies: Performance benefits and quality considerations. J. D. Tatum*, *Colorado State University, Fort Collins*.

Growth enhancement is unquestionably one of the most effective management tools currently available to beef producers for adding value to cattle. Growth-enhancement technologies have been used for more than 50 yr in US beef production systems to improve cattle performance and reduce per-unit cost of beef. In today's commercial cattle feeding industry, most cattle produced in conventional finishing systems receive 1 or 2 growth-promoting (estrogenic, androgenic, or combination) implants. Moreover, growing numbers of implanted feedlot cattle also are fed 1 of 2 recently approved beta adrenergic agonists (BAA) during the final few wk of finishing. Growth enhancement in successive stages of finishing using implants and BAA produces additive, beneficial effects on rate and efficiency of gain and substantially increases pay-weight, thereby improving economic returns to the feeding enterprise. In a 2007 analysis conducted by Iowa State University economists, estimates of value added to feedlot cattle by a) implanting and b) supplementing implanted cattle with BAA were $71 and $15/animal, respectively. Within the past 2 decades, however, development and subsequent adoption of growth-enhancement products with ever-increasing potency have intensified concerns in the packing, retail, and foodservice sectors of the beef industry about potential adverse effects of growth enhancement on beef quality characteristics. Growth-enhancement programs designed to maximize cattle performance have been shown to reduce deposition of intramuscular fat, increase beef toughness, and decrease consumer acceptability. In addition, aggressive growth enhancement can increase frequencies of heavyweight carcasses and over-sized beef cuts. When growth-enhancement programs, cattle types, and marketing targets are properly matched, use of growth technologies can facilitate efficient production of beef without substantially reducing product quality.

Key Words: growth technologies, beef, quality

230 Production systems to optimize growth and beef quality. I. Rush*, *University of Nebraska, Lincoln*.

Cattle producers have many options in utilizing available resources for economical production of high quality beef. Cattle performance must be optimized to assure the economical production of the animal to harvest, however ultimately the industry must produce a high quality product that is readily acceptable to the consumer with high market value. Economic analysis of various production systems consider input costs such as grazed forages, harvested feeds (grain, by-product feeds and forages) and non-feed costs. Efficiency of production, which is often associated with high performance, is one of the most important parameters in determining the most profitable or the least cost production system. Many data sets show that production parameters post weaning are 2-3 times more important than the value of the carcass when sold on an average grid basis. Often carcass weight was a large factor in determining the lowest breakeven. This may have sent the wrong market signal and has often overlooked the importance of the quality of the product. We know that when considering the entire production system many factors may affect the quality of the ultimate beef product. These include genetic traits, nutrient flow to the fetus in the uterus, level of antibodies received from colostrum in early life, level of nutrition of the calf in early life, age of calf when harvested, temperament of animal, lifetime health of the calf, level and timing of growth promotants, feeding management and conditions plus other factors. Three areas of the production systems that affect a large range of the use of these resources are: 1) early weaning and placing the calf on a high concentrate diet (2) normal weaning and then placing on finishing diets and (3) normal weaning however growing the calf on forages (often grazed) and placing them on a finishing diet at a heavier weight. All segments of the industry must work together to assure the production of the highest quality economical product. In order for the industry to stay competitive in the animal protein market, low cost systems must be evaluated however high quality beef must be a part of the overall decision process in any beef production system.

Key Words: systems, beef, quality

231 Cellular differentiation: Muscle growth and marbling. B. J. Johnson*, K. Y. Chung, and S. L. Parr, *Texas Tech University, Lubbock*.

Exogenous growth-enhancing compounds have been used to improve growth rate and efficiency in meat animals for over a half century. In cattle, these compounds enhance efficiency of growth by preferentially stimulating skeletal muscle growth at the expense of adipose tissue accretion. Consequently, these growth-enhancing compounds have been shown to reduce intramuscular fat (marbling) in beef cattle compared to nonimplanted cattle. Concurrent administration of trenbolone acetate (TBA) and estradiol-17β (E2) has shown to increase carcass protein accumulation 8 to 10% in yearling steers. Muscle satellite cells isolated from steers implanted with TBA/E2 had a shorter lag phase in culture compared to satellite cells isolated from nonimplanted steers. Collectively, these data indicate that activation, increased proliferation, and subsequent fusion of satellite cells in the muscle of implanted cattle may be an important mechanism by which anabolic steroids enhance skeletal muscle hypertrophy. These cellular events may in part be responsible for the negative effects observed with the use of these compounds in terms of marbling development in beef cattle. Markers of adipogenic differentiation are also affected by TBA/E2. Specifically, PPARγ and SCD mRNA levels, were lower in biopsy samples ($P < 0.06$) of TBA/E2 implanted steers compared to nonimplanted steers. In adipose tissue, an enzyme important for energy balance, AMPKα, may also be affected by anabolic steroids. These data indicate that in adipose tissue compared to skeletal muscle, anabolic steroids may have opposite effects on cellular growth and differentiation. This inverse relationship may contribute to changes in beef quality.

Key Words: adipose tissue, anabolic steroids, skeletal muscle

232 Managing genetic antagonisms between economically important beef production traits and marbling. R. L. Weaber[1] and R. M. Enns*[2], [1]*University of Missouri, Columbia*, [2]*Colorado State University, Fort Collins*.

As the beef complex has become more consumer focused with more cattle individually priced through value-based marketing systems, seedstock and commercial producers have been motivated to place more selection pressure on carcass traits by downstream industry partners. A number of grid pricing systems exist that substantially reward cattle that grade average Choice or better and meet other production specifications for branded beef programs. Economic incentives and the publicity surrounding branded programs have raised industry awareness of the value of carcass merit. Additional motivation for selection to improve end-product quality and consistency comes from the 2000 National Beef Quality Audit which identified insufficient marbling and inappropriate USDA Quality Grade mix as beef attributes that needed improvement. A wide range of carcass traits have been shown to be moderately to highly heritable and lowly to moderately correlated with production traits such as cow body condition score, direct and maternal weaning weight. Many breed association sponsored genetic evaluation systems now include carcass traits and several breed organizations utilize ultrasound indicator traits of carcass merit in a multiple trait genetic evaluation. Considerably more selection pressure is placed on carcass traits today, by a wider range of seedstock and commercial producers, than ever before. Genetic regression and a selection index architecture was used to investigate the potential correlated responses and economic consequences to selection for increased marbling. Predicted genetic changes in correlated traits were small in magnitude for all traits included in the breeding objective and for their indicator traits even when considerable selection pressure was placed on marbling score. Changes in net merit value for an integrated production system that retains ownership through harvest and produces its own replacement females were also small in magnitude. These small changes in net merit may be reflective of the lower economic importance of changes in marbling relative to other traits in the index including cow longevity and fertility.

Key Words: beef cattle, marbling, selection

233 Maternal obesity affects adipogenesis and myogenesis in fetal sheep muscle at late gestation. X. Yan*, W. Xu, J. F. Tong, J. X. Zhao, M. J. Zhu, S. P. Ford, and M. Du, *University of Wyoming, Laramie*.

During fetal development, both muscle cells and adipocytes are derived from mesenchymal stem cells. Enhancing adipogenesis in fetal muscle increases intramuscular adipocytes which enhances marbling in offspring animals. Using pregnant sheep as a model, the objective of this study was to investigate the impact of maternal overnutrition on adipogenesis in fetal skeletal muscle at late gestation when skeletal muscle matures in sheep. Non pregnant ewes were randomly assigned to a control (Con, 100% of NRC recommendations, n=5) or obesogenic (OB, 150% of NRC, n=5) diet from 60 days before to 135 days after conception, when fetal Lateral and Medial Gastrocnemius, Soleus and semitendinosus (St) muscle were collected and weighed. The St muscle was used for

histochemical and biochemical analyses. At the end of the treatment, both maternal body weight (90.4 ± 7.7 kg vs. 107.6 ± 7.1 kg, $p < 0.05$) and body condition score (6.1 ± 0.4 vs. 8.5 ± 0.4, $p < 0.05$) were higher in OB than Con groups. Intriguingly, there was no significant difference in fetal body weight (5205.7 ± 282.9 g vs. 5113.4 ± 283.2 g) as well as St muscle weight (8.7 ± 0.3 g vs. 8.2 ± 0.5 g) between these two groups. Fetal St muscle from OB mothers contained more large adipocytes, with the total relative area of fat cells increased by 26.3 ± 3.4% ($P < 0.05$). Corresponding to that, the number of muscle cells in a certain area was decreased by 11.6 ± 1.7% ($P < 0.05$) in OB fetal St muscle, as well as a decreased average diameter by 11.1 ± 3.7% ($p<0.05$). OB enhanced the expression of peroxisome proliferator-activated receptor γ (PPARγ) and Preadipocyte factor-1 (Pref-1) in fetal muscle by 23.8 ± 3.9% ($P < 0.05$) and 14.0 ± 5.7% ($P=0.09$), indicating enhanced adipogenesis. The protein content of Glut 1 and Glut 4 was decreased by 22.1 ± 4.8% and 13.9 ± 1.3% in OB fetal muscle respectively ($P < 0.05$). In conclusion, maternal over-nutrition during fetal stage dramatically increases the number and size of intramuscular adipocytes, which will provide sites for intramuscular fat accumulation in offspring, and could effectively improve marbling and quality grade of the resulting carcasses.

Key Words: adipogenesis, fetus, marbling

Nonruminant Nutrition: Improving the Nutritional Value of Alternative Feed Ingredients

234 Carbohydrates in alternative feed ingredients. B. M. Vester Boler and G. C. Fahey Jr.*, *University of Illinois, Urbana*.

With the fluctuating prices of commodity ingredients fed to livestock, poultry, and companion animals, alternative feed ingredients are of interest as partial substitutes for more traditional ingredients used in animal diets. Many of these alternative ingredients have carbohydrate concentrations and profiles different from those of traditional ingredients. Indeed, greater proportions of fermentable carbohydrates (i.e., dietary fibers) often are found. Popular alternative ingredients include corn co-products (e.g., distillers dried grains, distillers dried grains with solubles, corn germ, corn germ meal, corn gluten feed, corn gluten meal, corn bran), legumes (e.g., peas, soybean hulls), wheat middlings, canola meal, sunflower meal, and even grains other than corn (e.g., barley, oats, rice, sorghum, wheat) and co-products from the bakery industry (e.g., bakery by-product meal). Good analytical techniques exist for the measurement of all categories of carbohydrates, but for these values to be meaningful, further characterization of carbohydrates is needed that emphasizes their nutritional/physiological relevance for a particular animal species. Starch, hydrolyzable carbohydrates, rapidly and slowly fermentable carbohydrates, non-starch polysaccharides, total dietary fiber, and detergent fibers are carbohydrate fractions affecting select aspects of animal metabolism such as nutrient intake and digestion, glycemic response, immune response, and gut microbiota modulation. Most contain multiple carbohydrate moieties, and various analytical techniques exist for their quantification. To fully appreciate the importance of carbohydrates in alternative feed ingredients, integration of information related to chemical composition, analytical methodology, and nutritional/physiological outcomes must occur.

Key Words: carbohydrates, alternative feeds, nutrition

235 Mycotoxins in alternative ingredients. T. K. Smith*, *University of Guelph, Guelph, ON, Canada*.

Mycotoxins are metabolites produced by fungi (molds) that can infest crops pre-harvest and can continue to flourish under sub-optimal storage conditions. Grains with a high moisture content are particularly unstable and prone to mold proliferation and possible mycotoxin production. Excess rainfall at harvest and at key periods during the growing season can be a major promoter of mycotoxin contamination of feedstuffs. The most significant species of mycotoxin-producing fungi that have an impact on livestock production would include *Aspergillus* and *Fusarium*. The most significant mycotoxin produced by *Aspergillus* fungi are the aflatoxins and these are most commonly found in tropical and semi-tropical climates. The *Fusarium* mycotoxins include the trichothecenes such as deoxynivalenol (DON, vomitoxin), zearalenone and the fumonisins. The major economic cost of feed-borne mycotoxins is immunosuppression. This results in lingering herd health problems, animals that do not respond to medication and failure of vaccination programs. Other more specific symptoms of mycotoxicoses include behavioral changes arising from altered brain neurochemistry including loss of appetite, loss of muscle coordination and lethargy; impaired reproduction and gastrointestinal tract pathology resulting in reduced efficiency of nutrient absorption. Recent increases in fuel ethanol production have diverted feed grains away from the animal industries. This has increased the price and reduced availability of traditional feedstuffs while alternative feed ingredients such as distillers dried grains and corn and wheat gluten by-products have become more attractively priced and more available. Such products, however, have an increased likelihood of mycotoxin contamination. The use of alternataive feed ingredients, therefore, requires increased monitoring for mycotoxin contamination.

Key Words: alternative ingredients, mycotoxins, immunosuppression

236 Anti-nutritional compounds and other limitations to the use of alternative feed ingredients. H. H. Stein*, *University of Illinois, Urbana*.

Alternative feed ingredients that are used in the swine industry may be categorized in 4 groups: 1) Intact ingredients such as field peas, canola seeds, barley, wheat, and oats; 2) Processed ingredients that are by-products from other industries such as distillers dried grains with solubles (DDGS), high protein distillers dried grains, corn gluten meal, hominy feed, corn gluten meal, corn germ, wheat middlings, soybean hulls, alfalfa meal, canola meal, de-hulled sunflower meal, cotton seed meal, glycerol, and liquid whey; 3) Off-spec products from other industries such as pet food, cookies, bread, etc, and 4) Left-overs from other industries such as outdated bread, out dated milk, left-over chocolate, etc. Anti nutritional compounds may be present in some of these ingredients such as gossypol in cottonseed products, glycosinolates in canola products, tannins in field peas, alkaloids in lupins, and mycotoxins in many cereal grains and by-products of grains. However, these anti-nutritional compounds can usually be managed and in most cases, they do not represent major limitations to the use of alternative feed ingredients, although there are exceptions to this rule. Many alternative feed ingredients, especially from the group of processed ingredients, contain relatively large concentrations of dietary fiber, which on many occasions limits the inclusion rate of these ingredients in diets fed to swine. This is true in particular for ingredients such as alfalfa meal and soybean hulls. Undesirable characteristics of the carcass of pigs fed alternative ingredients may also limit the inclusion rate of ingredients such as DDGS with high concentrations of unsaturated fatty acids.

Another major limitation to the inclusion rate of alternative ingredients is variability in the concentration and digestibility of the nutrients in the ingredient. This concern limits the inclusion rate of many ingredients in group 3) and 4), and the ingredients in these groups are usually only attractive if some guarantees for consistency can be obtained from the supplier of the ingredients.

Key Words: alternative ingredients, anti-nutritional compounds, pigs

237 Phytase and NSP-degrading enzymes for alternative feed ingredients. R. T. Zijlstra*[1], E. Beltranena[1,2], C. M. Nyachoti[3], and S. W. Kim[4], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*Alberta Agriculture and Rural Development, Edmonton, AB, Canada*, [3]*University of Manitoba, Winnipeg, MB, Canada*, [4]*North Carolina State University, Raleigh*.

Co-products from cereal and oilseed crops processed for food, biofuel, or bio-industrial purposes are attractive feed ingredients to manage feed costs per unit of gain in swine. These alternative feed ingredients may contain more phytate and non-starch polysaccharide (NSP) than traditionally measured in cereal grains that may limit nutrient digestibility or feed intake. Supplemental feed enzymes combined with feed processing technologies and advanced feed quality evaluation techniques are important components of a strategy to mitigate risks of high dietary inclusion of co-products. Supplemental enzymes have been studied for decades in combination with cereal grains; however, more recently, specific efforts have started to apply enzyme technology to co-products. Some important considerations are: a) the substrate for the enzyme must be the main limitation for digestibility of the nutrient of interest, b) effects of enzyme must be clarified for the co-product vs. the rest of the diet, and c) processing technology may affect the content and functional characteristics of phytate and NSP in the co-product. Thus, analysis of phytate and NSP content should be part of feed quality evaluation. Generally, phytase improves P digestibility and its effects on energy and AA digestibility are variable depending on trial conditions. Generally, NSP-degrading enzymes improve energy digestibility and their effects on AA and P digestibility are variable depending on trial conditions. Due to the altered nutrient flow through the intestinal tract, supplemental enzymes may also alter nutrient availability to intestinal microbes, and hence alter microbial populations. Application of enzyme technology combined with modern feed processing and feed quality evaluation technologies may provide the pig with additional energy, AA, and P resulting in cost-effective, predictable growth performance and carcass quality.

Key Words: alternative feedstuff, enzyme, pig

Physiology and Endocrinology: Dairy Cattle Reproduction

238 Effect of PRID administered 5-12 days post-insemination on progesterone levels and pregnancy risk in previously inseminated dairy cows. S. J. Scott*, K. E. Leslie, R. B. Walsh, J. S. Walton, and S. J. LeBlanc, *University of Guelph, Guelph, ON, Canada*.

Progesterone (P_4) concentration in the days following AI is one important factor in maintenance of the developing conceptus. The effects of a Progesterone-Releasing Intravaginal Device (PRID) inserted between 5 – 12 d after AI and removed 7 d later on serum P_4 concentrations and risk of pregnancy were studied in 671 lactating dairy cattle on 8 farms in Ontario. Cows were visited weekly and randomly assigned to receive PRID or PID (Placebo Intravaginal Device). Serum P_4 was measured at insertion and removal of the device. At insertion P_4 levels were similar between treatment groups (2.9 ± 1.7 ng/ml). The probability of pregnancy to the AI immediately before device insertion was not significantly different in PRID (36%) and PID (38%) treated cows, or between cows enrolled 5 - 8 and 9 - 12 days post-AI (P=0.8). Cows that received PRID had higher serum P_4 at device removal than controls (4.8 vs. 4.3 ng/ml, P=0.04, accounting for P_4 at insertion). Yet, change in P_4 concentration was only significant in cows that received PRID 9 - 12 days post-AI (3.7 versus 3.1 ng/ml in PRID and controls, respectively, P=0.05). Use of Ovsynch had confounding effects. Cows bred off natural heat detection (HD; n = 427) were 1.5 times more likely to become pregnant to that breeding than cows bred with Ovsynch (n = 234) (P=0.03). Cows bred on Ovsynch had 0.52 ng/ml less P_4 upon device removal (P=0.03), compared to cows bred on HD. BCS recorded at the time of enrolment was not significantly different between treatment groups (2.75 ± 0.3). There was no association of BCS with probability of pregnancy or P_4 at device removal, and no interaction of BCS with the effect of PRID. Average milk yield (41.2 ± 7 kgs) was positively associated with the probability of pregnancy (P=0.05). There was no interaction of milk yield with the effect of PRID. Under the conditions of this study administration of a P_4 device post-insemination increased circulating P_4 but was not associated with pregnancy to the preceding AI.

Key Words: PRID, progesterone, pregnancy

239 Plasma hormones and energy metabolites in postpartum lactating (L) and nonlactating (NL) Holstein cows that either conceived or failed to conceive at first insemination. A. N. Brauch*[1], J. C. Green[1], J. P. Meyer[1], A. M. Williams[1], C. S. Okamura[1], P. Taube[2], L. Goetze[2], and M. C. Lucy[1], [1]*University of Missouri-Columbia, Columbia*, [2]*Pfizer Animal Health, New York, NY*.

Lactation affects circulating concentrations of metabolic hormones involved in nutrient partitioning for milk synthesis. The objective was to examine hormones and energy metabolites in dairy cows that were either L or NL and either conceived [pregnant (P)] or failed to conceive [not pregnant (NP)] at first insemination. Primiparous Holstein cows were assigned to one of two treatments after calving [L (n=23) or NL (n=20), dried off immediately]. Blood was collected thrice weekly for 60 d postpartum. Cows were treated with Presynch-Ovsynch and inseminated with frozen semen from a single ejaculate. The interval to first insemination (61 ± 1 d) was similar for L and NL cows that were either P (n=16 L; n=11 NL) or NP (n=7 L; n=9 NL) at first insemination. The L cows averaged 30.4 ± 0.8 kg milk/d at 60 d postpartum. There was an effect of lactation on plasma growth hormone (GH) concentrations (P<0.01) because L cows had greater GH when compared with NL cows (14.9 ± 1.8 vs. 6.8 ± 1.8 ng/mL, respectively). Insulin-like growth factor 1 (IGF1) concentrations were affected by both lactation (P<0.001) and status (P<0.02). L cows had lesser IGF1 than NL cows and, regardless of treatment, NP cows had lesser IGF1 than P cows (L cows: 104.7 ± 12.3 and 125.2 ± 7.8 ng/mL for NP and P; NL cows: 167.4 ± 10.2 and 195.9 ± 9.3 ng/mL for NP and P). There was an effect of lactation (P<0.001) and a status by day interaction (P<0.01) for plasma glucose. L cows had lesser glucose compared with NL cows (65.7 ± 0.9 and 77.4 ± 0.8 mg/dL for L and NL, respectively). Plasma glucose was greater in P cows than NP cows during d 0 to 30 (72.6 ± 0.4 and 68.9 ± 0.5 mg/dL for P and NP cows) but was similar thereafter (d 31 to 60; 72.5 ± 0.3 and 72.2 ± 0.4 mg/dL for P and NP cows). L cows had greater (P<0.01) plasma non-esterified fatty acid (NEFA) than NL cows (436.6

± 32.3 vs. 188.6 ± 30.7 µEq/L, respectively). Plasma NEFA were similar (P>0.10) for P and NP cows. Overall, lactation affected hormone and metabolite concentrations that were associated with pregnancy at first insemination in both L and NL cows.

Key Words: lactation, hormone, metabolite

240 Effect of lactation on plasma progesterone concentrations and early embryonic development in Holstein cows. J. C. Green*[1], J. P. Meyer[1], A. M. Williams[1], A. N. Brauch[1], C. S. Okamura[1], P. Taube[2], L. Goetze[2], and M. C. Lucy[1], [1]*University of Missouri, Columbia*, [2]*Pfizer Animal Health, New York, NY*.

Progesterone is stimulatory to embryonic development and its blood concentrations may be decreased by greater metabolic activity in lactating cows. The objective was to determine if the physiological state of lactation affects plasma progesterone concentrations and embryonic growth from d 28 to 42 of pregnancy in Holstein dairy cows. Primiparous cows were assigned to one of two treatments immediately after calving [lactating (L; n=22) and non-lactating (NL; dried off immediately after calving; n=19)]. Blood was collected thrice weekly. Cows were treated with Presynch-Ovsynch and artificially inseminated with semen from a single ejaculate. Cows that did not conceive to first insemination were re-inseminated until they became pregnant. Pregnant cows were slaughtered on 28 (n = 6 L and 7 NL), 35 (n = 8 L and 6 NL), or 42 (n = 8 L and 6 NL) d after insemination and tissues were collected and weighed. The interval to first insemination, services per conception, and days open were similar for L and NL cows. There was no effect (P>0.10) of treatment (i.e., lactation) on blood progesterone concentrations during the first, second, or third (after insemination) postpartum luteal phases. Weight of the CL increased with successive d of pregnancy (6.0 ± 0.7, 7.6 ± 0.7, and 8.4 ± 0.6 g; 28, 35, and 42 d, respectively; P<0.05) but there was no effect of treatment on CL weight (P>0.10). There was an effect of treatment (P<0.06) and d of pregnancy (P<0.001) on fetal weight because fetuses grew during pregnancy and NL cows had heavier fetuses than L cows (0.1 ± 0.1, 0.8 ± 0.1, and 2.0 ± 0.1 g vs. 0.1 ± 0.1, 0.6 ± 0.1 and 1.6 ± 0.1 g for NL vs. L on d 28, 35, and 42, respectively). Likewise, there was an effect of treatment (P<0.01) and d of pregnancy (P<0.001) on placental weight because placenta were heavier on successive d of pregnancy and NL cows had heavier placenta than L cows (1.2 ± 1.6, 13.2 ± 2.2, 25.0 ± 1.6 g vs. 1.1 ± 2.2, 8.1 ± 1.7, 16.8 ± 1.5 g for NL vs. L on d 28, 35, and 42, respectively). The conclusions were that there was no effect of lactation on plasma progesterone but lactation reduced the weights of the fetus and placenta.

Key Words: lactation, progesterone, embryo

241 Effects of resynchronization programs on fertility, progesterone and PAGs after insemination. I. M. Thompson*[1], R. L. A. Cerri[1], I. H. Kim[2], J. A. Green[3], J. E. P. Santos[1], and W. W. Thatcher[1], [1]*University of Florida, Gainesville*, [2]*Chungbuk National University, South Korea*, [3]*University of Missouri, Columbia*.

Objectives were to develop a Timed (T) AI resynchronization platform to improve pregnancy (P) rate and to evaluate responses of progesterone (P4) and P associated glycoproteins (PAGs) in lactating cows. Cows (n=1578) were presynchronized with 2 injections of PGF2Î± given 14 d apart at 42±3 d postpartum followed by Ovsynch (GnRH, 7 d PGF2Î±, 56 h GnRH, 16 h TAI [d 0]). The Treatment (TRT) group received a CIDR from d 18 to 25, GnRH at d 25, d 32 ultrasound P diagnosis and non-pregnant (NP) cows received PGF2Î±., GnRH 56h after and TAI 16 h later (d 35). The Control (CON) group was diagnosed for P at d 32 and NP cows received GnRH, d 39 PGF2Î±, GnRH 56 h after, and TAI 16 h later (d 42). P was re-confirmed at d 60. Blood for analyses of P4 and PAGs was taken every 2 d from d 18-30 in 100 cows and continued weekly to d 60 of P (n=43). P rates at d 32 (45.8%, n=814; 45.9%; n=764) and P losses at d 60 (6.7% and 4.0%) did not differ for TRT and CON, respectively. Second service P rates (36%, n=441 and 39.5% n=412) and P losses (6.3% and 6.7%) did not differ for TRT and CON. Days non-pregnant for pregnant and NP cows for 2 TAI were less for TRT (120.7 < 124.9 d P < 0.01). Plasma P4 was greater (P < 0.01) for pregnant TRT cows (18-60 d; 6.6 > 5.3 ng/ml), and P4 at d18 was greater (P < 0.03) for pregnant than NP cows (5.3 > 4.3 ng/ml). Plasma PAGs in P were lower (P < 0.01) for TRT on d 39 (2.8 < 4.1 ng/ml) and 46 (1.34 < 3 ng/ml). Cows pregnant at d 32 that had P loss by d 60 (n=7) had lower (P < 0.05) PAGs at d 30 than pregnant cows (n=36) until d 60 (2.9 < 5 ng/ml). PAGs at d 30 (> 0.33ng/ml) were predictive of d 32 P diagnosis (Sensitivity 100%, Specificity 90.6%). In conclusion, TRT and CON protocols had comparable P rates for first and second TAI services, but P occurred 4 d earlier in TRT. CIDR and/or GnRH increased P4 during pregnancy. Dynamics of PAGs were indicative of pregnancy status and pregnancy loss.

Key Words: resynchronization, progesterone, PAGs

242 Fertility after timed artificial insemination in lactating dairy cows resynchronized using Double–Ovsynch or standard Ovsynch. J. O. Giordano*[1], M. C. Wiltbank[1], S. Bas[1], A. P. Cunha[1], R. A. Pawlisch[2], J. N. Guenther[1], and P. M. Fricke[1], [1]*Department of Dairy Science, University of Wisconsin, Madison*, [2]*Brodhead Veterinary Clinic, Brodhead, WI*.

Our objective was to assess if using Double–Ovsynch (DO, Pre–Resynch, GnRH–7d–$PGF_{2\alpha}$–3d–GnRH, 7d later Breeding–Resynch, GnRH–7d–$PGF_{2\alpha}$–56h–GnRH–16h–TAI) to resynchronize ovulation for second and subsequent TAI may increase pregnancies per AI (P/AI) compared to Standard Ovsynch (OV, GnRH–7d–$PGF_{2\alpha}$–56h–GnRH–16h–TAI). Cows at various DIM and prior services were blocked by parity and were randomly assigned to either DO or OV for resynchronization of ovulation and TAI. All DO cows received the 1st GnRH injection of Pre–Resynch 22 d after TAI, and cows (*n*=962) diagnosed not pregnant using transrectal ultrasonography 29 d after TAI continued the protocol. All OV cows received GnRH 32 d after TAI, and cows (*n*=956) diagnosed not pregnant using transrectal palpation 39 d after TAI continued the protocol. In a subgroup of cows from each treatment, the proportion of cows with a corpus luteum (CL) at the 1st GnRH injection of Breeding–Resynch and OV and ovulation to the last GnRH injection before TAI was assessed using transrectal ultrasonography. Pregnancy diagnosis was performed for all cows in both treatment groups by ultrasonography at 29 d and transrectal palpation at 74 d after TAI. Overall, P/AI 29 d after TAI was not affected by parity (*P*=0.58) and was greater for DO compared to OV cows [38.5% (370/962) vs. 30.0% (287/956), *P*<0.0001]. Pregnancy loss from 29 to 74 d after TAI was not affected by parity (*P*=0.55) and did not differ (*P*=0.22) between treatments [DO, 13.9% (50/359) vs. OV, 17.5% (49/280)]. Proportion of cows with a CL at the 1st GnRH injection of Breeding–Resynch and OV was greater for DO than OV cows [85.4% (373/437) vs. 68.9% (314/456); *P*<0.0001]. Ovulation to the GnRH injection before TAI was similar between treatments [DO, 90.0% (251/279) vs. OV, 87.5% (238/272); *P*=0.36]. We conclude that Double–Ovsynch increased fertility of lactating cows compared to a Standard

Ovsynch protocol when used for resynchronization of ovulation. *Supported by Hatch project WIS01171*

Key Words: Double–Ovsynch, resynchronization

243 Effect of parity on pedometer activity at estrus in dairy cows. S. J. Caldwell and G. E. Mann*, *Division of Animal Sciences, School of Biosciences, University of Nottingham*, *Sutton Bonington Campus, Loughborough, UK*.

The increase in walking activity seen around estrus in cows has led to the use of pedometers as an estrous detection aid. While the increase in activity is clearly established, results on the effect of age or parity are less clear with studies reporting both increases and decreases in activity with increasing age or parity. The aim of this study was to determine the effect of parity on pedometer activity in Holstein Friesian cows in an automatic milking system and housed throughout lactation. All animals were maintained within the University of Nottingham commercial dairy unit in a free stall system with free access to robotic milking machines Cows were fed an ad lib total mixed ration with additional concentrates supplied at milking according to yield. Each cow was fitted with a pedometer and activity data downloaded at each milking. Data was analyzed over a four year period from a total of 59 cows in which data was available three successive lactations for each cow (lactation 1 - 3, n=25; lactation 2 - 4, n=18; lactation 3 - 5, n=16). For each cow, a mean value for peak pedometer activity at all estruses was determined over each successive lactation. Peak pedometer activity (steps per hour) at estrus was highest during 1st lactation (331±20) and declined during 2nd (273±16; P<0.05) and 3rd (233±10; P<0.01) lactations. No further decline was seen during 4th (215±13) or 5th (211±32) lactation. There was no significant effect of year of study on pedometer activity (P>0.4). These results indicate a decrease in pedometer activity at estrus over earlier lactations that stabilizes in older cows. The magnitude of this decline is of importance in determining the level of activity that constitutes an estrous episode in cows of different ages.

Key Words: cow, estrus, pedometer

244 Effect of body condition score on milk yield, milk composition and reproductive competence during the service period of Holstein-Friesian dairy cattle. T. J. Hole[2] and J. K. Margerison*[1], [1]*Massey University*, *Palmerston North, New Zealand*, [2]*Plymouth University*, *Seale Hayne, Newton Abbot, UK*.

The aim of this experiment was to compare the effect of body condition score and body condition change on milk yield, milk composition, postpartum interval to insemination, ovarian activity and conception rate. This experiment was completed using 90 multiparous Holstein-Friesian cows in the same management system over the serving period at Butland Farm, Dorset, UK. There was no significant effect of body condition change at 50 pp on mean condition score (1 to 5), L 2.46, S 2.36, G 2.47 (sem 0.078), milk yield at first service (kg/d), L 40.9, S 44.1, G 42.9 (sem 1.02), milk fat yield at first service (kg/d), L 2.01, S 2.16, G 2.04 (sem 0.077), or third service (kg/d), L 1.37, S 1.66, G 1.60 (sem 0.082), milk protein yield at first service (kg/d), L 1.23, S 1.26, G 1.31 (sem 0.027) or second service (kg/d), L 1.10, S 1.26, G 1.20 (sem 0.026). Milk yield at second service was significantly different between body condition change groups (kg/d), L 34.5, S 41.3, G 39.3 (sem 0.96), P<0.05, and third service (kg/d), L 27.7, S 39.5, G 37.5 (sem 1.55) P<0.05, milk fat at second service(kg/d), L 1.53, S 1.88, G 1.92 (sem 0.053) P<0.05 and milk protein at third service (kg/d), L 1.37, S 1.70, G 1.60 (sem 0.082) P<0.05. Body condition change groups were not significant different in PP interval to first service (d), L 66.9, S 59.6, G58.9, (sem 2.13), PP interval to second service (d), L 106.0, S 88.2, G 85.4, (sem 3.06), PP interval to third service (d), L 120.3, S 116.2, G 116.5 (sem 4.31), all inter-service intervals (d), L 36.1, S 36.1, G 27.5 (sem 1.93), PP interval to conception (d), L 85.2, S 76.3, G 84.0 (sem 4.43) and services per conception (no.), L 1.73, S 1.25, G 2.00 (sem 0.127), Body condition score per se had no significant effect on milk production, milk composition and reproduction. Body condition loss at 50 d pp had a negative effect on milk yield, milk composition and reproduction.

Key Words: reproduction, body condition, milk production

245 Effects of nutrient restriction on ghrelin secretion and cyclicity in dairy heifers. M. E. Field*, S. E. Cossel, S. L. Marion, J. B. Wheelock, S. R. Hartman, M. D. O'Brien, T. R. Bilby, R. P. Rhoads, R. J. Collier, P. B. Hoyer, and M. L. Rhoads, *University of Arizona*, *Tucson*.

Circulating ghrelin (GHR) concentrations are affected by plane of nutrition and may be involved in signaling metabolic status to the reproductive tract. Objectives were to measure daily and peri-prandial plasma GHR concentrations during chronic undernutrition and correlate these changes with dynamic changes in ovarian structures and steroid hormone concentrations. Following an acclimation period (3 wk), Holstein heifers (n=12; 338.0 ± 7.8 kg) were fed ad libitum (WF; n=6) or restricted to 50% of ad libitum intake (UF; n=6) for 7 wk. Body condition scores (BCS) were recorded during wk 1 and 10 and weekly measurements were obtained for: ovarian follicular and luteal development, body weights, plasma GHR and plasma progesterone. Plasma GHR concentrations were also measured during a peri-prandial sampling window (every 15 min between 0500 and 0900, feed was given at 0700) in wk 10 of the experiment. Weekly GHR concentrations were greater in UF than WF heifers (264.9 ± 34.3 vs. 108.3 ± 31.4 pg/ml, respectively; $P < 0.05$). During the sampling window, plasma GHR concentrations fluctuated over time ($P < 0.01$) suggesting an effect of feeding. During the sampling window GHR concentrations tended to be greater in UF than WF heifers (119.9 ± 21.5 vs. 64.8 ± 19.6 pg/ml, respectively; $P < 0.09$). Plasma GHR concentrations and change in BCS were negatively correlated (R^2=0.39; $P < 0.01$) in that heifers that lost the most BCS had the highest concentrations of circulating GHR. Two of the UF heifers (33% of the group) became anestrus by wk 6 of the experiment. Plasma GHR concentrations, however, were not correlated with plasma progesterone or ovarian measurements. In summary, circulating GHR concentrations increased in Holstein heifers during chronic negative energy balance induced by underfeeding. One third of the heifers with elevated plasma GHR concentrations became anestrus although no direct correlations between circulating GHR concentrations and reproductive parameters were detected.

Key Words: ghrelin, dairy

246 The effect of GnRH and an opioid antagonist on pregnancy rate of repeat breeding Holstein dairy cows. V. O. Fuentes*, A. Bernal-Canseco, and P. I. Fuentes-Castro, *Centro Universitario de los Altos*.

The objective of this study was to observe the effect of GnRH and naloxone in repeat breeder Holstein dairy cows. In a double blind study 45 repeat breeder Holstein cows were selected from a large dairy

cooperative farm of the highlands of the occident of Mexico. All cows presented a history of repeat breeding, and further more, during palpation the presence of an ovaryan cyst was detected. Divided at random in three groups of 15 cows. Group one was treated with 100 µg GnRH im on the oestrus day of insemination. Group 2 was treated with naloxone, 5 mg im at 12 hour intervals for three consecutive days, treatment commenced since one day before insemination. Group 3 was used as a control injected with 5 ml im of saline solution at 12 hour intervals for three consecutive days, injections commenced since one day before estrual insemination. Cows were inseminated twice (12 h apart) according to the AM-PM rule and pregnancy was confirmed by rectal palpation between 12 and 18 weecks after the last insemination. Pregnancy rates in GnRH treated repeat breeder cows was 56%, while pregancy rate in naloxone treated cows was 89% ($p< 0.01$) and control cows showed a 20% pregancy rate. There was a significant correlation betweein progesterone levels and pregancy rate in all groups. It was concluded that opioids participate significantly in the expression of estrous behaviour and ovulation in repeat breeder Holstein cows.

Key Words: GnRH, naloxone, dairy

247 Use of OVSYNCH and alternative protocols to synchronize estrus and ovulation in dairy cows managed in a seasonal grass-based system. M. M. Herlihy*[1,2], M. A. Crowe[2], M. G. Diskin[3], and S. T. Butler[1], [1]*Teagasc Moorepark DPRC, Fermoy, Co. Cork, Ireland*, [2]*SAFVM, University College Dublin, Ireland*, [3]*Teagasc, APRC, Athenry, Co. Galway, Ireland*.

Lactating dairy cows (n=1,623) were enrolled in a study to evaluate estrus/ovulation synchronization protocols. Cows in each herd (n=8) were divided into 3 groups based on days in milk (DIM) at mating start date (MSD): Group 1, 2 and 3 animals were ≥42, 21-41 and 0-20 DIM at MSD. At 10 d before MSD Group 1 animals were sorted by parity and calving date and randomly assigned to: 1) d -10 GnRH (10 µg i.m. Buserelin) and CIDR insert (1.38 g P4); d -3 $PGF_{2\alpha}$ (25 mg i.m. dinoprost); d -2 CIDR out and AI at observed estrus (CIDR_OBS); 2) same as CIDR_OBS, but GnRH 36 h after CIDR out and TAI (timed AI) 18 h later (CIDR_TAI); 3) same as CIDR_TAI, but no CIDR (OVSYNCH) or 4) Untreated Controls (CTL). The efficiency of each protocol was assessed by measuring plasma P4 on d 0 and 11 (<1ng/mL = low; ≥1ng/mL = high). The numbers of visible corpora lutea and follicles per cow were counted by ultrasound before assignment to treatment. Treatment facilitated estrus/TAI on day 0 (MSD), day 21 and day 42 for Group 1, 2 and 3. The proportion of cows with low P4 on d 0 was similar (0.99, 0.99, and 0.97 for CIDR_OBS, CIDR_TAI and OVSYNCH). The proportion of cows with elevated P4 on d 11 was highest ($P < 0.001$) for CIDR_TAI (0.88, 0.97, and 0.89 for CIDR_OBS, CIDR_TAI and OVSYNCH). Treatment affected ($P < 0.05$) conception rate to first service (CRFS) (53.7, 49.4, 42.6 and 49.3% for CIDR_OBS, CIDR_TAI, OVSYNCH and CTL). CRFS was greater ($P < 0.001$) for cows with a CL at the time of treatment than for those that did not (53 vs. 44%). Calving to service interval was shorter ($P < 0.001$) for CIDR_TAI and OVSYNCH compared with CIDR_OBS and CTL. Calving to conception interval was 8 days shorter ($P < 0.01$) for CIDR_TAI compared with CTL (76 vs. 84 days). Estrus and ovulation synchronization protocols were effective at achieving earlier first service and conception in grass-based seasonal calving dairy herds.

Key Words: estrus synchronization, TAI, dairy cow

Ruminant Nutrition: Feedlot, Byproduct Feeds

248 Effects of ruminally degradable N in diets containing wet corn distillers grains and steam-flaked corn on feedlot cattle performance and carcass characteristics. C. H. Ponce*[1], M. S. Brown[1], N. A. Cole[2], C. L. Maxwell[1], and J. C. Silva[1], [1]*Feedlot Research Group, West Texas A&M University, Canyon*, [2]*USDA ARS Conservation and Production Research Laboratory, Bushland, TX*.

Assessment of degradable N needs in diets containing wet corn distillers grains with solubles (WCDGS) is needed to aid the cattle industry in managing feed costs. Yearling steers (n = 525; initial weight = 373 +/- 13 kg) were housed in 54 pens (9 to 10 steers/pen) and received treatments in a 2 x 3 + 1 factorial. Factors included WCDGS (15 or 30% of DM) and non-protein N (NPN; 0, 1.5, or 3.0% of DM) from urea. The control diet without WCDGS contained 3.0% NPN (1.06% urea) and cottonseed meal. Steers were fed twice daily for 129 d and WCDGS was obtained three times/week from a local plant. Final shrunk BW was less ($P < 0.02$) for 30% WCDGS than for the control or 15% WCDGS. Overall DMI was not different ($P > 0.31$) between the control diet and 15 or 30% WCDGS, but overall DMI increased linearly ($P = 0.04$) as NPN increased. Overall ADG and gain efficiency were affected by both WCDGS and NPN (interaction, $P < 0.12$). Overall ADG for steers fed 15% WCDGS was greater for 1.5 and 3.0% NPN than for 0% NPN ($P < 0.07$, quadratic); however, ADG was not influenced by NPN for 30% WCDGS. Overall ADG was not different between the control and 15% WCDGS, but ADG was lower ($P < 0.02$) for 30% than for 15% WCDGS. Overall gain efficiency among steers fed 15% WCDGS was greatest for 1.5% NPN and least for those fed 0% ($P < 0.07$, quadratic), whereas gain efficiency decreased linearly ($P < 0.09$) as NPN increased in 30% WCDGS diets. No interactions between WCDGS and NPN were evident for carcass traits. Dressing percent was greater ($P < 0.01$) for the control diet than for 15% or 30% WCDGS (65.1, 64.2, and 63.9% for control, 15% WCDGS, and 30% WCDGS, respectively). Hot carcass weight was not different between the control and 15% WCDGS ($P = 0.44$), whereas carcass weight was less for 30% WCDGS than for 15% WCDGS ($P < 0.01$). Other carcass measurements were not different among treatments. Data suggest that optimum performance occurs between 1.5 and 3.0% NPN when diets contain 15% WCDGS, and with 1.5% NPN or less when diets contain 30% WCDGS.

Key Words: protein, beef cattle, byproduct feeds

249 Evaluation of lighter density fraction from dried distillers grains with solubles as a feedstuff for ruminants. J.M. Greene*[1], R. Srinivasan[2], and B.J. Rude[1], [1]*Animal and Dairy Sciences, Mississippi State University, Starkville*, [2]*Agricultural and Biological Engineering, Mississippi State University, Starkville*.

A novel combination of sieving and air classification has been developed to separate dried distillers grains with solubles (DDGS) into different fractions based upon density and size. The lighter fractions have greater fiber than the original DDGS. The objective of this trial was to evaluate the lighter fraction of DDGS as a possible feedstuff for cattle diets. Angus and Hereford (n = 12; 238 ± 5.74 kg) steers were randomly

assigned to three treatment groups to evaluate the lighter fraction resulting from DDGS separation using the elusieve process. Each treatment group received diets consisting of either the lighter fraction of DDGS (L), a DDGS based diet (D), or a control diet (C). After a 14 day diet adaptation, steers were placed in metabolism crates for 10 days and allowed ad-libitum access to feed and water. The first 3 days were used for adaptation to the crates followed by 7 days of data collection. During the data collection period, feed offered, orts, and fecal and urinary output were recorded and sampled (5%) to determine nutrient digestibility and crude protein retention. Dry matter intake was greater (P = 0.0394) for steers consuming C (6.5 kg/d) compared to those consuming L (4.3 kg/d) with steers consuming D being intermediate (6.0 kg/d). Crude protein digestibility was greatest (P = 0.0008) for the steers consuming L (78%) with steers fed D (72%) digesting more CP than C (63%). Protein retention did not differ (P = 0.2452) among treatments ranging between 254 and 424 g/d. Fat digestibility was greatest (P = 0.0036) for steers consuming the L and D diets (69 and 71%, respectively) compared to those consuming C (53%). Digestibilities of dry matter (ranged between 65 and 72%), OM (ranged between 66 and 72%), ash (ranged between 59 and 66%), NDF (ranged between 54 and 62%), ADF (ranged between 51 and 57%), hemicellulose (ranged between 55 and 68%), crude fiber (ranged between 55 and 65%) and energy (ranged between 66 and 72%) did not differ (P > 0.05) among treatments. These data suggest that the lighter fraction of DDGS can be effectively fed to cattle without adversely affecting digestibility.

Key Words: distillers grains, digestibility, beef cattle

250 Effects of grain processing method and use of dried corn distillers grains on beef carcass composition, heterocyclic amine concentration and fatty acid profiles of lean and lipid portions. P. L. Black*[1], G. L. Parsons[1], M. K. Shelor[1], M. E. Dikeman[1], K. K. Karges[2], M. L. Gibson[2], J. S. Smith[1], and J. S. Drouillard[1], [1]*Kansas State University*, *Manhattan*, [2]*Dakota Gold Research Association*, *Sioux Falls, SD*.

Carcass composition and fatty acid profiles were analyzed from separated 9th-10th-11th rib sections of crossbred heifers (n=689, 302 ± 65 kg initial BW) fed finishing diets of steam-flaked corn (SFC), dry-rolled corn (DRC), and dried corn distiller's grains with solubles (DDG). The study was a randomized complete block design with a 2 x 2 factorial arrangement of treatments. The SFC based diets contained 0 or 25% DDG and 0 or 25% DRC. Heifers were individually weighed and blocked into heavy and light groups. Within block, heifers were assigned randomly to pens containing 25 animals each. Heifers were fed once daily *ad libitum*, and heavy and light weight blocks were harvested after 137 and 157 d, respectively. Four heifers were randomly selected from each of 24 pens (3 pens per treatment at each harvest point). Three heifers were removed due to excessive trimming of the carcass. 9-10-11th rib sections were removed from one side of the selected carcasses after a 24-h chill and physically separated into lean, fat, and bone as described by Hankins and Howe (1946). Separated portions of lean and fat were evaluated by proximate analyses and for fatty acid profiles. Steaks were used to determine concentrations of heterocyclic amines after cooking at 204°C. Diet had no affect on concentrations of heterocyclic amines in cooked steaks (P>0.15). There were no differences among treatments in the separable portions of lean, fat, and bone; or percentages of protein, moisture, and ether extract (P>0.10). In the fatty acid triglyceride portion, oleic acid decreased while proportions of stearic and linoleic acids increased (P<0.05) in response to feeding DDG. Diet had little impact on fatty acids within the phospholipid fraction. DDG and DRC can be added to SFC diets with little impact on composition of the carcass.

Key Words: carcass composition, distiller's grains, feedlot cattle

251 Optimal roughage level in finishing diets containing combinations of flaked corn and dried distiller's grains with solubles. K. A. Miller*, M. K. Shelor, G. L. Parsons, and J. S. Drouillard, *Kansas State University*, *Manhattan*.

Flaked corn finishing diets containing dried distillers grains with solubles (DDGS) were fed to crossbred heifers (n=298, initial BW=336 kg) to determine optimal concentration of alfalfa hay as the source of roughage. Cattle were stratified by weight and allotted, within strata, to 20 dirt-surfaced pens with 15 animals per pen. Diets consisted of steam-flaked corn (density = 0.36 kg/L) with 25% DDGS, 8% corn steep liquor, and ground alfalfa hay at 3, 6, 9, 12, or 15% of diet DM (4 pens per level of alfalfa hay). Monensin, tylosin, and melengestrol acetate were fed at the rates of 300, 90, and 0.5 mg/animal daily. Cattle were fed once daily ad libitum for 126 days and then transported to a commercial abattoir for harvest. Carcass data were collected following a 24-h chill. Heifers fed 3, 6, 9, 12, and 15% alfalfa had DMI of 10.69, 11.06, 11.25, 11.85, and 11.52 kg/d, respectively (linear P<0.01, quadratic P<0.05). Gain efficiencies were not impacted (linear, P=0.19; quadratic, P = 0.82) by roughage level (0.144, 0.144, 0.143, 0.140, 0.140, for 3, 6, 9, 12, and 15% alfalfa, respectively). Hot carcass weight tended to increase with increasing level of roughage (336.0, 339.8, 342.1, 345.3, 341.6 kg for 3, 6, 9, 12, and15% roughage, respectively; linear effect, P=0.087). Carcass-adjusted ADG was increased by 7.7% for heifers fed 12% roughage compared to those fed 3% roughage. Yield grade increased linearly (P<0.05) as percent alfalfa in the diet increased. There was a tendency for a quadratic effect of alfalfa hay level on deposition of intramuscular fat (P = 0.06), with 9% alfalfa yielding the most marbling. The percentages of carcasses grading USDA Choice or better were 59, 67, 63, 55, and 49 for cattle fed 3, 6, 9, 12, and 15% roughage, respectively (linear, P = 0.15, quadratic, P = 0.23). Performance and carcass characteristics of heifers may be influenced by dietary roughage level when distiller's grains are fed in combination with steam-flaked corn.

Key Words: distiller's grains, steam flaked corn, roughage

252 The effect of corn or sorghum dried distillers grains + solubles on growth performance and carcass characteristics of beef steers. K. M. Wood*[1], H. Salim[1], P. L. McEwen[2], I. B. Mandell[1], S. P. Miller[1], and K. C. Swanson[1], [1]*Department of Animal and Poultry Science, University of Guelph*, *Guelph, ON, Canada*, [2]*Ridgetown Campus, University of Guelph*, *Ridgetown, ON, Canada*.

Sixty crossbred steers (Angus X; n=36 and Charolais X; n=24) were used in a randomized complete block design to investigate the effects of feeding corn or sorghum dried distiller′s grains in growing and finishing rations on growth performance and carcass traits. Steers were randomly assigned to one of three dietary treatments, used in both feeding periods: a Control ration containing soybean meal (n =20;CON), a ration containing 20% (DM basis) corn dried distiller′s grains + solubles (n=20;CDDGS) and a ration containing 20% (DM basis) sorghum dried distiller′s grain + solubles (n=20;SDDGS). Steers were fed a corn silage (CS) based grower ration (~75% CS) for 56 d and then switched to a high grain finisher ration (15% CS). Intakes were measured using Insentec (n=48) and Calan gate (n=12) feeding systems. Animals were weighed and ultrasounded for backfat and rib eye area (REA) every 28 d and slaughtered at an estimated backfat of 10 mm. Data were analyzed using PROC GLM in SAS; the model included the effects of block (barn), breed and dietary treatment and P < 0.05 was used to indicate significance. Dietary treatment did not affect DM intake in the growing phase, although ADG was lower for SDDGS vs. CON (P=0.008) and CDDGS (P=0.02). This resulted in a

lower gain:feed in the growing phase for SDDGS vs. CON (P=0.07) and CDDGS (P=0.04). In the finishing phase, inclusion of corn or sorghum DDGS did not affect ADG, DM intake or gain:feed. Total trial ADG was 1.56 kg d^{-1}±0.04 for CON, 1.54 kg d^{-1}±0.04 for CDDGS, and 1.51 kg d^{-1}±0.04 for SDDGS and did not differ between treatments. However, fewer days on feed were required for SDDGS to reach the target backfat for slaughter than CDDGS (P=0.03) and CON (P=0.05). There was no difference between treatments for final weight (P>0.60) and hot carcass weight (P>0.57), when days on feed was included as a covariate in the model. These results indicate that sorghum dried distiller′s grain can be included at 20% inclusion level, similar to corn distiller′s grains, in grower and finisher rations, without negatively influencing overall growth or carcass traits.

Key Words: distiller's grains, steers, sorghum

253 Effect of feeding fiber from wet corn gluten feed and silage in diets containing 30% modified wet distillers grains plus solubles on feedlot cattle performance and nitrogen mass balance. A. R. Rich*, M. K. Luebbe, G. E. Erickson, T. J. Klopfenstein, and J. R. Benton, *University of Nebraska*, *Lincoln*.

Ninety-six calves (307 ± 7 kg) were stratified by BW, and assigned randomly to 12 pens to evaluate the effects of feeding fiber from wet corn gluten feed (WCGF) and corn silage in diets containing 30% modified wet distillers grains plus solubles (MDGS) on steer performance, manure N removed, and N lost via volatilization. Steers were fed for 178 d from November to May. Dietary treatments consisted of either 30% MDGS, 65% corn, and 5% supplement (DGS), or a diet with 30% MDGS, 30% WCGF, 15% corn silage, and 5% supplement with the WCGF and silage replacing corn (DGS+CGF). Nitrogen excretion was determined by the difference between N intake and individual steer N retention. Total N lost was calculated by subtracting manure and runoff N from excreted N. Dry matter intake (P=0.01) and ADG (P=0.01) were less for the steers fed the DGS treatment, while G:F was similar (P=0.63) to steers fed the DGS+CGF treatment. Likewise, HCW (P=0.02) and fat depth (P=0.08) were lower for the DGS diet. Nitrogen intake was greater (P<0.01) for the steers fed DGS+CGF (53.7kg) than for steers fed DGS (41.1kg). Nitrogen retention was greater (P=0.01) for the DGS+CGF treatment than for the DGS treatment (due to greater ADG). Nitrogen excretion was also greater (P<0.01) for the DGS+CGF treatment (47.8kg) than the DGS treatment (35.8kg). Manure N was greater (P=0.03) for the DGS+CGF treatment (16.2kg) compared to the DGS treatment (10.8kg). However, N runoff was not different (P=0.98) between treatments. The amount of N lost was greater (P=0.01) for the DGS+CGF treatment (31.1kg) than for the DGS treatment (24.5kg) but the percent loss (percent of excreted N) was not different (P=0.50) between treatments. Feeding wet corn gluten feed and corn silage with distillers grains increased N excretion which increased N in manure and the amount lost; however, % loss was unaffected compared to feeding distillers grains alone.

Key Words: cattle, fiber, nitrogen

254 Effects on ruminal pH, hydrogen sulfide concentration, and feed intake when using wet distillers grains with solubles to adapt cattle to finishing diets compared to forage. K. M. Rolfe*, G. E. Erickson, T. J. Klopfenstein, and J. T. Vasconcelos, *Department of Animal Science, University of Nebraska*, *Lincoln*.

Eight ruminally fistulated steers (348 ± 34 kg) were used to determine effects of using wet distillers grains with solubles (WDGS) when adapting cattle to a finishing diet. Steers were assigned randomly to one of two adaptation systems: 1) alfalfa hay decreased from 45% to 7.5% inclusion and dry-rolled corn increased while 5% supplement and 35% WDGS were constant (CON) and 2) WDGS decreased from 87.5% to 35% inclusion and dry-rolled corn increased while 5% supplement and 7.5% alfalfa were constant (TRT). Four, 7-d adaptation diets (step 1 to 4) were fed within each adaptation system followed by 7 d on a common finishing diet (52.5% dry-rolled corn, 35% WDGS, 7.5% alfalfa hay, and 5% supplement; DM basis). Ruminal pH and DMI were monitored continuously with wireless submersible pH probes and feed bunks suspended from load cells. On the last day of each step, ruminal H_2S was measured 8 and 23 h post feeding. In step 1, no differences in ruminal pH were observed; however, TRT steers had lower DMI (P < 0.01) than CON steers. In step 2, steers on TRT had lower DMI (P = 0.01), lower average pH (P = 0.03) and greater H_2S (P = 0.08). In step 3, TRT steers had lower DMI (P = 0.06) compared to CON steers, while average pH was lower in TRT steers during steps 3 (P = 0.01) and 4 (P = 0.04). No differences in DMI, pH, or H_2S were observed between TRT and CON steers on the finishing diet (P > 0.19). No drastic decreases in DMI or ruminal pH (SD similar to CON) were observed in steers adapted with TRT, with lowest average pH (5.36) on the finishing diet. Steers on TRT had greater H_2S during steps 1 and 2, with the greatest concentration being 28.4 μmol/mL, but based on previous research and visual appraisal, sulfur was not a problem. Adapting cattle to finishing diets with WDGS may lower DMI and pH, but appeared to adapt cattle to corn since no differences were observed on the finishing diet.

Key Words: grain adaptation, steer, wet distillers grains plus solubles

255 High sulfur content in distillers grains alters ruminal fermentation and diet digestibility by beef steers. S. Uwituze*[1], M. K. Shelor[1], G. L. Parsons[1], K. K. Karges[2], M. L. Gibson[2], L. C. Hollis[1], and J. S. Drouillard[1], [1]*Kansas State University*, *Manhattan*, [2]*Dakota Gold Research Assn*, *Sioux Falls, SD*.

Twelve ruminally cannulated Angus cross steers were used to evaluate ruminal fermentation characteristics and diet digestibility when 30% (DM basis) dried corn distiller's grains with solubles (DDGS) containing normal or elevated levels of dietary sulfur were incorporated into finishing diets containing steam-flaked corn (SFC) or dry-rolled corn (DRC). The study was a randomized incomplete block design with a 2 × 2 factorial arrangement of treatments. Factors consisted of dietary sulfur concentration (0.42% and 0.65% of DM; LS and HS, respectively), and grain processing method (steam-flaked or dry-rolled corn; SFC and DRC, respectively). HS was achieved by spiking the basal diets with sulfuric acid. Steers were randomly assigned to diet and individual, slatted-floor pens equipped with individual feed bunks and water fountains that allowed access to feed and clean water ad libitum. Two 15-d experimental periods were used, each consisting of a 12-d diet adaptation phase and a 3-d sample collection phase. Samples were collected at 2-h intervals post feeding during the collection phase. Ruminal pH was measured immediately after sampling. Concentrations of ruminal ammonia, and VFA were determined. Fecal samples were composited by animal and used to determine total tract digestibility of DM, OM, NDF, CP, starch, and ether extract. One animal became ill during the experiment and was removed from all analyses. HS tended to decrease DM intake (P = 0.08), but increased ruminal pH and apparent total tract digestibility of DM and ether extract (P < 0.05). HS increased ruminal ammonia and decreased total VFA and propionate concentrations (P < 0.01). These effects were more exaggerated in cattle fed DRC (interaction, P < 0.01). Concentrations of lactate and butyrate also

were decreased by HS (P < 0.01). High sulfur levels may have negative consequences for ruminal fermentation.

Key Words: digestibility, sulfur, distiller's grains

256 High sulfur content in distillers grains with solubles may be deleterious to performance and carcass quality of finishing steers. S. Uwituze*[1], M. K. Shelor[1], G. L. Parsons[1], K. K. Karges[2], M. L. Gibson[2], L. C. Hollis[1], and J. S. Drouillard[1], [1]*Kansas State University, Manhattan*, [2]*Dakota Gold Research Assn, Sioux Falls, SD*.

Crossbred yearling steers (n = 76; 410 ± 2.7 kg BW) were used in a finishing trial to evaluate effects of sulfur content in dried distiller's grains with solubles (DDGS) on growth performance and carcass characteristics of finishing steers. The study was a randomized complete block design with a 2 × 2 factorial arrangement of treatments. Factors consisted of dietary sulfur concentration (0.42% and 0.65% of DM; LS and HS, respectively), and grain processing method (steam-flaked or dry-rolled corn; SFC and DRC, respectively). HS was achieved by spiking the basal diets with sulfuric acid. All diets included 30% DDGS (DM basis). Steers were blocked by weight and randomly assigned within block to treatments. Cattle were housed in individual, concrete-surfaced, partially enclosed pens equipped with feed bunks and water fountains. Steers were fed ad libitum amounts of their respective diets at approximately 0800 h each day. Steers were harvested on d 140. No interactions between grain processing method and sulfur level were observed. Steers fed diets with HS had 8.9% lower DMI (P < 0.001); 12.9% poorer ADG (P = 0.006); 4.3% lighter final BW (P = 0.006); and tended (P = 0.13) to have poorer G:F compared to steers fed diets with LS. Cattle fed HS yielded 4.3% lighter HCW (P = 0.006) and had 16.2% less KPH fat (P = 0.009) compared to steers fed LS. Steers fed HS had lower (P = 0.05) percentage of liver abscesses compared to steers fed diets containing LS and lower yield grades (P = 0.04) than their counterparts fed diets containing LS. There were no differences among treatments with respect to dressing percentage; 12th-rib back fat; REA; or USDA quality grades. Grain type had no effect (P > 0.15). Feeding distiller's grains which are high in dietary sulfur may decrease DMI and compromise growth performance and carcass characteristics of feedlot cattle.

Key Words: distiller's grains, grain processing, sulfur

257 Evaluation of feedlot and carcass performance of steers fed different levels of ECORN™, a potential new feed product from ethanol plants. C. M. Godsey-Williams*[1], G. E. Erickson[1], T. J. Klopfenstein[1], M. Greenquist[2], P. Guiroy[2], C. Ibanez[2], and J. Kazin[3], [1]*University of Nebraska, Lincoln*, [2]*Cargill Inc., Wayzata, MN*, [3]*Renessen LLC., Wayzata, MN*.

The objective of this study was to evaluate the use of ECORN™ (ECORN), a corn-based by–product from the production of ethanol and food grade corn oil, as a replacement to dry–rolled corn (DRC) in feedlot finishing diets containing wet distillers grains plus solubles (WDGS) or wet corn gluten feed (WCGF). One–hundred twenty individually–fed crossbred yearling steers (372 ±17 kg) were blocked by initial BW and assigned randomly to one of eight treatments (15 steers/treatment) in a 2x4 factorial design. Diets were formulated to contain 30% WDGS or WCGF and either 0, 20, 40, or 60% ECORN (DM basis). The diets were formulated to replace DRC with ECORN at an equal proportion of DM and all diets contained 5% corn stalks and 5% dry supplement. The ECORN product contains 10.9% CP, 1.5% fat, 0.1% S, and 17.4% NDF. Steers were fed 153 d. As the level of ECORN increased from 0 to 60% diet DM, DMI increased quadratically (P=0.04) with 20 and 40% inclusion having similar DMI (P>0.10). As ECORN increased in the diet, G:F (0.139, 0.144, 0.131, and 0.140) responded cubically (P=0.02) while ADG (1.37, 1.43, 1.33, 1.33) was unaffected (P>0.21). Linear decreases in marbling score, fat depth, and calculated yield grade were observed with increased ECORN inclusion (P<0.01); whereas, LM area responded cubically (P<0.01). Steers fed WDGS had lower DMI and greater G:F versus steers fed WCGF (P<0.02), with carcass characteristics unaffected by by-product type (P>0.17). Results of this study would suggest replacing DRC with ECORN at 20% of the diet DM would optimize G:F and offer a feeding value equal to 118% the relative value of corn. However, no difference in ADG or G:F between the 0 and 60% ECORN suggests ECORN may replace corn in diets containing WDGS or WCGF. Further research to explain decreases in marbling score, fat depth, and yield grade (with no affect on HCW) should be considered.

Key Words: finishing cattle, fractionation, wet distillers grains

Ruminant Nutrition: Forage Digestibility Estimates; Obtaining and Applying Meaningful Values

258 Opportunities and challenges in determining forage digestibility values. R. Ward*, *Cumberland Valley Analytical Services, Hagerstown, MD*.

In the last ten years, the use of NDF digestibility (NDFD) has evolved from strictly a research evaluation to a common commercially available value provided by forage laboratories. Cumberland Valley Analytical Services (CVAS) recorded requests for NDF digestibility values in excess of 820 in 2000; 13,200 in 2004; and 39,500 in 2008. Despite the wide acceptance and use of NDF digestibility values, there remain significant questions as to the appropriate use of this information for forage evaluation and nutritional modeling systems. There are no standard procedures for NDF digestibility and most systems reference a procedure by Tilley and Terry from 1963. Values generated by laboratories vary widely, and later time points have been advocated for consistency but do little more than define an asymptotic value. Reported NDFD values and associated estimates of rate are only relevant within procedures, and even then have questionable relationship to animal models. NDF digestibility values generated by a system will be dependent on drying method, grinder type and grind size, inoculum source, buffer, and type of containment system. NDF digestibility systems that generate relevant values will 1) exhibit consistency over time, 2) generate repeatability within run, 3) be sufficiently sensitive to define differences between forages, and 4) be robust across commercial laboratory settings. These objectives are critical to a laboratory providing information of value and are necessary points to be understood by users of this information.

Key Words: NDF digestibility

259 Do in vitro digestibility data have value in dairy cattle nutrition? W. P. Weiss*, *Ohio State University*, *Wooster*.

The use of ruminal in vitro (IV) digestion to evaluate feeds was first reported in the early 1900's, but for numerous reasons IV digestibility did not gain widespread use until the early 1960's when Tilley and Terry published their two-stage IV method. In vitro digestibility of forages using that method were correlated, but not equivalent, to in vivo digestibility when ruminants (most of the experiments used sheep) were fed all forage diets. The next major change in the IV method was the modification developed by Van Soest that replaced pepsin digestion with neutral detergent extraction. Several modifications have been made, but incubating a feed in rumen fluid-buffer mixture for 24 to 48 h followed by the NDF assay is the basic method used today. The question that needs to be addressed is, what do we as dairy nutritionists do with IV values? In vitro digestibility has been used to estimate energy (e.g., NEL) in feeds, although data evaluating whether this actually works are limited. Indeed, recent publications show a poor relationship between IV NDF digestibility and in vivo NDF digestibility in lactating cows fed mixed diets. Experiments are needed to determine if certain IV methods (e.g., 24 vs. 30 h incubation, donor cow diets, etc.) are better at estimating in vivo digestibility. In vitro NDF digestibility also has been used as an index of DMI by lactating cows. Within studies (meaning the IV assays were probably conducted concurrently on the different forages), cows fed diets based on forages with lower IV NDF digestibility usually have lower DMI than cows fed forages with higher digestibility. This relationship has only been shown to exist when comparisons are made within forage type (e.g., within corn silages or within alfalfa). For IV data to have greater utility for estimating relative DMI, lab results must be consistent across time so that a forage being fed today can be compared with a forage that will be available for feeding and sampling next month. Experiments with cows should either be conducted concurrently or precede studies designed to standardize this assay so that the standardized values actually have utility in diet formulation.

Key Words: in vitro, fiber digestibility, intake

260 Obtaining and applying meaningful forage digestibility estimates: Forage-fed beef. E. S. Vanzant* and J. W. Lehmkuhler, *University of Kentucky*, *Lexington*.

Knowledge of forage quality is of tantamount importance for proper nutritional management of beef cows and growing calves. Forage digestibility is generally considered to be a very useful integrated measurement of forage quality. Our discussion will examine issues associated with obtaining and applying meaningful estimates of forage digestibility in forage-based beef cattle operations. We will begin by defining what is meant by "meaningful" when applied to forage digestibility analysis. Results from sensitivity analysis using the NRC (1996) model provide us with a basis for determining desirable levels of accuracy and precision in our estimates. This information will allow us to address the ramifications of errors in digestibility estimates with a focus on both animal performance and economic implications. Next, we will address current practices by presenting results from a survey of university research and extension personnel as well as commercial forage analysis laboratories. Survey results will illustrate the current range in practices associated with each step in the forage analysis process, including sampling methodologies, laboratory procedures, and application of results. Finally, to determine the need for further improvements in the acquisition and utilization of forage digestibility estimates, we will evaluate the current practices in light of our definition of "meaningful forage analysis".

Key Words: forage, digestibility

261 Addressing fiber digestibility in low-forage diets. N. DiLorenzo and M. L. Galyean*, *Department of Animal and Food Sciences, Texas Tech University*, *Lubbock*.

To optimize efficiency of production and cost of gain, inclusion of fiber in finishing diets is typically decreased to the minimum necessary to maintain a healthy rumen and to maximize NEg intake. From an energetic standpoint, the contribution of the fiber fraction in typical feedlot diets with low inclusion of high-fiber coproducts is likely not greater than 4% of the total DE/kg of dietary DM. The energy contribution depends largely on the extent of fiber digestibility, which is influenced by grain source and processing, as well as roughage concentration, source, and processing. Measuring NDF digestibility is challenging with high-grain diets because of the interference with starch in the analytical method. Thus, ADF digestibility (ADFd) is often reported in the literature to assess the digestibility of the fiber fraction in low-roughage diets. Ruminal ADFd seems to be less in steam-flaked corn-based diets (SFC) than in dry-rolled corn-based diets (DRC), perhaps reflecting the decreased ruminal pH for SFC vs. DRC, with associated negative effects on ruminal cellulolysis. A meta-analysis of literature data with high-concentrate diets revealed no relationship between dietary ether extract (% of DM) and ruminal (P = 0.30) or total tract (P = 0.53) ADFd, but a tendency (P = 0.09) was noted for a linear decrease in ruminal ADFd with increasing ADF from the roughage portion of the diet (rADF). No relationship (P = 0.67) was noted, however, between rADF and total tract ADFd, indicating that postruminal digestion of fiber might compensate for decreased ruminal ADFd. A previously conducted meta-analysis indicated a positive linear relationship (r^2 = 0.96) between dietary NDF and DMI by beef cattle fed diets ranging from 7.5 to 35.3% NDF. Thus, the effects of rADF on ruminal ADFd might be mediated by an increased DMI with increasing roughage concentration and associated effects on rate of passage and mean retention time of fiber. Research is needed to characterize the fiber fractions in various high-fiber coproducts, as well as their effects on rate of passage, intake, and ruminal fermentation.

Key Words: acid detergent fiber, high-concentrate diet, ruminal and total tract digestion

262 Attempting to apply meaningful forage values and digestibility estimates in commercial feedlot diets. T. M. Peters*, S. P. Montgomery, and S. J. Bierman, *Corn Belt Livestock Services*, *Rock Falls, IL*.

The practice of adding forage to feedlot diets benefits the rumen environment by decreasing the risk of digestive disorders. Research shows that adding increasing forage amounts to high energy, starch-based finishing diets often increases DMI of cattle but may decrease ADG and G:F. On a NE basis, forages are typically the most costly of ingredients, thus nutritionists often include forage at minimal concentrations in finishing diets. Research has demonstrated that forages can be substituted for one another based upon their NDF concentration. Therefore, forages containing increased NDF concentrations can potentially be included in finishing diets at lower concentrations, ultimately providing finishing diets with greater NE values while preventing digestive disorders. However, forage particle size may affect forage effective NDF value and should be considered when formulating finishing diets. Forage particle size, length, as well as type are often subjective quantifications assigned by different nutritionists. Data indicate that the degree of forage processing may have little effect on growth performance if NDF is similar among processing methods. Nutritionists often question if this statement is accurate, when associated with differing grain processing methods and (or) grain by-product inclusion. Survey data indicate fiber

analysis methods used by feedlot nutritionists consist of crude fiber, NDF, ADF or that no fiber analysis is used. Nutritionists continue to apply different criterion and personal biases when assigning dietary fiber levels and forage types in finishing diets. Reasons for differing forage levels in finishing diets among nutritionists appears to be based upon environmental conditions, cattle type or management ability among feedlots. Particle separation of forage has been used to measure effective fiber concentrations in finishing diets. Methods to better evaluate NDF level and forage digestibility in finishing diets should continue to be evaluated and reported.

Key Words: digestibility, feedlot diets, forage

Swine Species

263 Birth weight implications for reproductive parameters in boars. F. R. C. L. Almeida*[1], A. L. N. Alvarenga[1], G. R. Foxcroft[2], and H. Chiarini-Garcia[1], [1]*Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brazil*, [2]*University of Alberta*, *Edmonton, Alberta, Canada*.

Selection for prolificacy appears to have created an imbalance between the number of conceptuses surviving to the post-implantation period and uterine capacity. These animals show characteristics of Intra-Uterine Growth Restriction (IUGR) due to a great competition among fetuses for nutrients and oxygen, resulting in lighter fetuses at term. The effects of IUGR on testes development have not been demonstrated so far. Newborn male pigs (n = 6; DanBred X PIC terminal line), born to 4th - 6th parity sows and in litters of 10 to 15 pigs, were identified as falling into two birth weight groups: high (HW: range 1.8 to 2.2 kg) and low (LW: range 0.8 to 1.2 kg). They were castrated at 7 days post-partum for evaluation of testicular morphological characteristics. Evidence of IUGR on testis development was analyzed by comparing the mean numbers of gonocytes and Sertoli cells present in twenty cross sections of testicular cords per testis chosen at random. Data were analyzed as a fully randomized design and the comparison between means was performed by t-test. LW offspring had lighter testes and lower gonadossomatic index (GSI = testes wt/body wt x 100) compared to their HW counterparts. Moreover, the numbers of gonocytes and Sertoli cells per testicular cord were also lower in LW piglets (Table 1). These results show that light weight animals have smaller and less developed testes relative to body weight. As Sertoli cell number established before puberty determines adult testes size and sperm production, light birth weight boars may have lower reproductive performance. We gratefully acknowledge Fapemig and CNPq for funding this work. Reproductive characteristics in low (LW) and high (HW) birth weight boars born to multiparous sows and into litters of 10 to 15 pigs ($P < 0.0001$ for all parameters)

Table 1.

Parameters	LW	HW	SEM
Birth wt (kg)	1.17	2.02	0.014
Weight at d7 (kg)	2.03	3.30	0.029
Mean testicular weight (g)	0.44	0.97	0.014
GSI (birth)	0.038	0.048	0.0007
GSI (castration)	0.021	0.029	0.0004
Gonocyte / testicular cord	0.870	1.580	0.090
Sertoli cell/ testicular cord	19.22	22.36	0.419

Key Words: testes, sertoli cells, gonocytes

264 Effect of ambient temperature and light intensity on reproduction in mature gilts. D. Canaday*, B. Yantis, A. Visconti, J. Salak-Johnson, and R. Knox, *University of Illinois, Champaign-Urbana*.

The effect of variation in the environment for sows housed in crates on animal reproduction and well-being is uncertain. The objectives of this study were to determine whether differences in temperature and lighting would have a detrimental impact on fertility measures for gilts housed in crates. In replicate one, thirty-six mature cyclic gilts were synchronized with Matrix. At last Matrix feeding (LMF), gilts were assigned by age and weight in a 3 x 2 factorial treatment design to an ambient room temperature (HOT: 30°C, THERMAL NEUTRAL [TN]: 20°C, COLD: 16°C) and lighting intensity at pig level (DIM: 40 Lux, BRIGHT: 350 Lux). Estrous detection and real-time ultrasound (RTU) were performed daily from LMF until ovulation to determine onset of estrus and assess follicle growth and ovulation, respectively. For all gilts, AI occurred at onset of estrus and 24-h later. Measurements of feed intake, body temperature and weight occurred weekly. All gilts were sacrificed on day 30 and reproductive tracts evaluated for ovarian status, pregnancy and litter characteristics. Data were analyzed in SAS using Proc Mixed for the effect of temperature and lighting on response variables. Our preliminary results showed no significant effect of temperature and lighting, nor any interaction, on expression of estrus (100%), LMF to estrus (130 h), duration of estrus (58 h), gilts ovulating (100%), number of corpora lutea (17 ± 3.5), pregnancy rate (97%), litter size (14.0 ± 3.8), fetal weight (2.3 g) or fetal length (26.6 mm). Measures of within litter variation for fetal weight (0.32 ± 0.1 g) and length (1.1 ± 0.4 mm) also did not differ. Rectal temperature (38.4 ± 0.73°C) and daily feed intake (2.7 kg) did not differ among treatments. Initial body weights were not different (141.8 ± 1.8 kg), but weight gain during the treatment period was affected ($P < 0.01$) by temperature (COLD: 25.1; TN: 29.6; and HOT: 30.0 kg). These preliminary results suggest that wide temperature and lighting levels may have little effect on reproduction during breeding and early gestation in gilts housed in gestation crates.

Key Words: housing, reproduction, temperature

265 Cloning and expression of porcine lactoferrin N– lobe gene in *Pichia methanolica* and effects of recombine protein on growth performance of weanling piglets. F. Han*, Y. Xie, Y. Liu, Y. Gao, and Y. Wang, *Institution of Feed Science, Zhejiang university*, *Hangzhou, Zhejiang, China*.

The porcine lactoferrin N–lobe (PLF–N) gene was cloned from mammary gland cells of lactating sows, inserted into the recombinant plasmid pGEM–3Z–PLF–N and sequenced. This analysis indicated that the cloned gene sequence is 1038bp in length and is 99% identical to the published sequence (Gene bank L77887). PLF–N was amplified using two new primers with the template pGEM–3Z–PLF–N and cloned into pMET–B, subsequently was linearized and transformed into PMAD11 competent cells by eletroporation. Ade^+ (Mut^s) recombinants were selected by PCR and Mut phenotype determination. SDS–PAGE and western blot results showed that PLF–N was extracellularly expressed in *Pichia methanolica* successfully. The yeast powder containing 10 g/kg

PLF–N were produced by recombinant strain fermentation, fermentation fluid filtration and spay drying methods. Then a total of 90 crossed–bred (Duroc×Landrace×Yorkshire) weanling piglets were used in a 15 days growth experiment to investigate the effect of yeast powder containing 10g/kg PLF–N on growth performance. The piglets were allocated on the basis of weight and litter to 3 dietary treatments in a randomized complete block design. There were three replicate pens per treatment and piglets were grouped with 50 g/kg general yeast powder (control group), basal diet supplemented with 50 g/kg yeast powder containing 10 g/kg PLF–N (PLF–N group), basal diet supplemented with 50 g/kg general yeast powder and 100 mg/kg chlortetracycine (antibiotics group) respectively. Supplementation with 50 g/kg yeast powder conaining 10 g/kg PLF–N significantly increased the ADG by 31.67% ($p<0.01$), decreased the F/G by 11.22% ($p<0.05$) and diarrhea rates by 66.25% ($p<0.01$), respectively as compared with the control group. Compared with antibiotic group, there were no significant difference of ADG, F/G and diarrhea rates were observed when 50 mg/kg yeast powder containing 10 g/kg PLF–N was supplied in diet.

Key Words: porcine lactoferrin N–lobe, *Pichia methanolica*, grow performance

266 Influence of seasonality of the growing-finishing period on carcass characteristics of heavy barrows and gilts. M. A. Latorre*[1], S. Calvo[1], and L. Ariño[2], [1]*Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain*, [2]*Integraciones Porcinas SL, Teruel, Spain*.

A trial was conducted to study the influence of gender (barrows; gilts) and seasonality of the growing-finishing period (S: summer; W: winter) on carcass quality of Duroc × (Landrace × Large White) pigs. A total of forty animals were slaughtered at 131 kg BW (239 ± 3 d old for S pigs and 228 ± 3 d old for W pigs). The farm was located at 715 m altitude in North-Eastern Spain (40.87° North latitude and -0.1° West longitude). The average temperature in S period was 20.5°C (range 14.2-33.7°C) and in W period was 7.4°C (range 1.5-16.5°C). All the animals fed commercial corn, barley, wheat, and soybean meal diets that contained 9.20 MJ NE/kg, 16.9% CP and 1.00% total lys from 20 to 70 kg BW, and 9.75 MJ NE/kg, 14.4% CP and 0.86% total lys from 70 to 130 kg BW. Each treatment was replicated ten times and the experimental unit was the pig. No significant interaction between gender and seasonality was detected. Carcasses from barrows were shorter ($P<0.01$) but tended ($P<0.10$) to be fatter at the level of *gluteus medius* muscle (26.8 vs. 24.3 mm) and to show lighter loins (6.7 vs. 7.2 kg) and hams (27.1 vs. 28.5 kg) than carcasses from gilts. The S pigs had thinner fat depth over the *gluteus medius* muscle (23.7 vs. 27.3 mm; $P<0.01$) and longer ($P<0.10$) and narrower ($P<0.05$) hams than W pigs. The S pigs had heavier shoulders ($P<0.01$) and loins ($P<0.05$) than W pigs but the weight of hams was similar. Consequently, higher total trimmed cut yield (shoulder+ham+loin) was detected in S pigs (47.4 vs. 45.3%; $P<0.001$) than in W pigs due to the higher ($P<0.001$) proportion of shoulders (15.6 vs. 14.1%) and loins (6.6 vs. 6.0%). It is concluded that the differences between barrows and gilts were scarce and any effect of seasonality was independent of gender. Under Spanish natural-environment conditions and at 131 kg of slaughter weight, the S pigs were 11 d older but had better carcass quality than W pigs because of the higher yield of primal trimmed lean cuts.

Key Words: seasonality, carcass quality, pigs

267 Artificial sweeteners enhance the capacity of the swine small intestine to absorb glucose. A. Moran*[1], D. Arora[1], M. Al-Rammahi[1], D. Batchelor[1], E. Coulter[1], N. Jones[1], C. Ionescu[2], D. Bravo[2], and S. Shirazi-Beechey[1], [1]*Department of Veterinary Preclinical Sciences, University of Liverpool, Liverpool, UK*, [2]*Pancosma SA, Geneva, Switzerland*.

Weaning piglets at the age of 3-4 weeks has major consequences for their digestive functions. Strategies have been developed with the aim of counteracting post-weaning problems and to stimulate feed intake and growth. Inclusion of artificial sweeteners in the piglet's diet is a common practice. It was assumed that artificial sweeteners increase palatability and hence increased food intake. However, recent findings that artificial sweeteners may enhance the capacity of the gut to absorb carbohydrates have important implications for the nutrition of piglets and avoidance of post-weaning digestive problems. In this study we weaned 4 groups of 28 day old piglets to isocaloric diets containing 35.9% or 60.3% digestible carbohydrate, or 43% digestible carbohydrate with or without sucram. The animals were maintained on these diets for 3 days and had access to water at all times. At the end of the experimental period piglets were sacrificed by giving intravenous pentobarbitone (Approved by the UK Home Office under schedule 1). Intestinal tissue samples were either fixed or frozen in liquid nitrogen for further analysis. We show that there is a 3-4 fold enhancement ($p=0.004$) in SGLT1 expression and glucose absorptive capacity in the intestine of piglets maintained on a 60.3% carbohydrate diet compared to piglets fed 35.9% carbohydrate. Furthermore, addition of sucram to the 43% carbohydrate - containing diet increased SGLT1 expression and glucose absorptive rates 4.5-fold ($p=0.0063$) more over the diet without sucram. These finding has important implications in feed formulation and management. Statistical analyses were performed using Student's t-test.

Key Words: intestine, artificial sweetener, glucose absorption

268 Changes in expression of swine intestinal Na^+/glucose cotransporter in response to increased dietary carbohydrates. A. Moran*[1], M. Al-Rammahi[1], D. Arora[1], D. Batchelor[1], E. Coulter[1], N. Jones[1], C. Ionescu[2], D. Bravo[2], and S. Shirazi-Beechey[1], [1]*Department of Veterinary Preclinical Sciences, University of Liverpool, Liverpool, UK*, [2]*Pancosma SA, Geneva, Switzerland*.

Absorption of glucose in the intestine is accomplished by the Na^+/glucose cotransporter, SGLT1. It has been shown that SGLT1 expression is upregulated in response to increased dietary carbohydrates in a number of mammalian species. However, very little information is available on the regulation of swine intestinal SGLT1 by dietary carbohydrates. In order to assess the response of intestinal glucose transport to increased dietary carbohydrates, 28d old piglets of both sexes were weaned to isocaloric diets containing either 7%, 35.9%, 43%, or 60.3% digestible carbohydrates. The animals were maintained on these diets for 3d and had access to water at all times. At the end of the experimental period, piglets were sacrificed by giving intravenous pentobarbitone (Approved by the UK Home Office under schedule 1). Intestinal tissue samples were either fixed or frozen in liquid nitrogen and used for further analyses. Our data indicate that SGLT1 expression at the level of mRNA, protein and function remains the same when piglets are maintained on diets containing either 7%, 35.9% or 43% digestible carbohydrates. However, there was a 4-fold increase ($p=0.004$) in SGLT1 expression and glucose absorptive capacity in animals maintained on a 60.3% carbohydrate - containing diet. This increase was manifested in SGLT1 expression in all villus enterocytes, and was independent of any changes in total area for absorption. We conclude that there is a basal level of

SGLT1 expression in the intestine capable of absorbing dietary glucose. However this pathway becomes limited and is upregulated in response to high concentrations of dietary carbohydrate, i.e. 60.3%. This finding has important implications for the nutrition of pigs, in particular during the post-weaning period. Statistical analyses were performed using Student's t-test.

Key Words: intestine, SGLT1, dietary carbohydrate

269 Individual piglet birth weight, sow parity, gestation length, number of fully formed pigs and within litter birth weight variation affect incidence of stillborns. J. S. Fix*[1], J. W. Holl[2], W. O. Herring[2], and M. T. See[1], [1]*North Carolina State University, Raleigh*, [2]*Smithfield Premium Genetics Group, Rose Hill, NC*.

Litters (n = 463) from commercial Large White × Landrace sows bred to Duroc boars were used to evaluate the effect of sow parity, number of fully formed pigs (FFP) (stillborns + born alive), gestation length, standard deviation of individual piglet birth weight (SD) and individual piglet birth weight (IBW) on incidence of stillborn pigs. All FFP (born alive: n = 5747; stillborns: n = 513) were weighed and individually identified within 24 h of birth. No sows were induced to farrow during the study. The model to evaluate incidence of stillborns in a litter (SB) included fixed effect of sow parity; covariates of linear and quadratic effects for gestation length and FFP. The model to evaluate effect of IBW on likelihood of a piglet being stillborn included fixed effects of sex and sow parity; covariates of IBW, gestation length (linear and quadratic) and FFP (linear and quadratic). For both analyses parity was divided into three groups (group 1 = parities 1, 2, 3; group 2 = parities 4, 5; group 3 = parities > 6). Groups were selected based on comparison of LS means. Descriptive statistics (min, max, mean): IBW (0.29, 2.77, 1.41 kg), gestation length (108, 119, 114.5 d), FFP (4, 20, 13.4 pigs) and SB (0, 15, 1.1 pigs). Number of SB differed ($P < 0.01$) between parity groups (group 1: 0.83±0.09; group 2: 1.23±0.14; group 3: 2.03±0.18). Quadratic relationships for gestation length (0.056 and -12.76; $P < 0.01$) and FFP (0.024 and -0.439; $P < 0.01$) with SB were observed. Number of SB reached a minimum at 114-115 d of gestation and 9-10 FFP, respectively. A 100 g increase ($P = 0.05$) in SD resulted in 0.15 pig increase in SB. Mean litter birth weight did not affect SB. As IBW decreased the odds of a piglet being stillborn increased (odds ratio: 0.13; $P < 0.01$). Both short (< 113 d) and long (> 115 d) gestation lengths had greater numbers of stillborn pigs. Incidence of stillborns was greatest in small litters (FFP < 8) and large litters (FFP > 11). Litters with greater variation in piglet birth weight had increased stillborns. Pigs with lower birth weights were more likely to be stillborns.

Key Words: stillborn, birth weight, pigs

270 New DFM product (Bacillus) improves performance of grower/finisher swine. I. Knap and B. T. Lund*, *Chr. Hansen, Hoersholm, Denmark*.

Bacillus spores are ideal as DFM due to thermostability and consistent performance. As the spores enter the small intestine of the pig, the spores attach to the mucus layer and start germination. The vegetative Bacillus cells grow and multiply in the mucus layer. The probiotic effect of Bacillus is due to its immune stimulation, production of metabolites and pathogen exclusion. The research objective was to identify new improved DFM. A new strategy was been implemented to select for fast outgrowth Bacillus spores at a high bile salt level and at the same time with increased production of metabolites. The first product based on this concept has been developed for grower/finisher swine. The outgrowth of the improved Bacillus spores at both 0.4 mM bile salt and 0.6 mM bile salt was increased by a factor two (in-vitro data) and the expression of metabolites was increased by a factor of 5 (in-vitro data). In the feeding study, with two treatment (control and control plus DSM) 9 pigs per pen, 12 replicate pens per treatment. Pelleted corn-soy diets were fed in 4 phases of 21, 32, 28 and 24-d each. Starting weight were approx. 57 lbs. The effect of the new improved DFM product in barrows showed a significant lower ($P<0.05$) FCR (-4.1%) most pronounced in the late feeding phase (-8.9%) and with a reduced back fat content compared to the control group. Growth rate were 2.223 lb/day in the treated group. No significant effects were seen in gilts. This research proves a new strategy for identifying spore based products. In the future several new high performing DFM products can be developed by this method.

Key Words: Bacillus, DFM, swine

271 Cholecystokinin excited and sensitized porcine gastric mechanoreceptors responding to distension. W. L. Grovum*, W. R. Ellison, and W. W. Bignell, *Department of Biomedical Sciences, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada*.

The purpose of the present work was to use pigs as a model for humans to learn how to manipulate gastrointestinal neural mechanisms to suppress hunger (decrease snacking) or hasten satiety (decrease meal size). Cholecystokinin (CCK-8) excited and sensitized mechanoreceptors sensing gastric distension in rats and it depressed food intakes in rats, pigs, humans and other species but the physiological significance of these data keeps being raised. This question was addressed in 22 Yorkshire pigs (29 to 64 kg) anesthetized with sodium pentobarbital. Fluid secretion from the pancreas, and pressures on fluid filled balloons in the gallbladder and duodenum were measured. Single fiber activity in the vagus nerve originating from gastric mechanoreceptors was increased stepwise by distension alone (0, 250, 500, 750 and 1000 ml air in a gastric balloon) and by intravenous CCK-8 alone (0, 0.06, 0.24, 1 and 4 μg/kg) ($P\leq0.001$ in both cases). All combinations of these treatments were also tested. The threshold CCK-8 doses for exciting the receptors in the absence of distension and for sensitizing them to distension were similar to those for increasing small intestinal contractions, pancreatic secretion and gallbladder tone. Since the latter 2 were used to define CCK as a hormone, it now appears that controlling small intestinal motility, gastric mechanoreceptor activity and ingestive behavior may also be physiological functions of CCK in the pig.

Key Words: appetite, pigs, cholecystokinin

Tuesday, July 14, 2009
POSTER PRESENTATIONS

Animal Health: Mastitis and Associated Microbiology

T1 Natural autoantibodies in milk and their role in the development of mastitis in dairy cows. A. T. M. Van Knegsel*, G. De Vries Reilingh, A. Lammers, B. Kemp, and H. K. Parmentier, *Adaptation Physiology Group, Wageningen Institute of Animal Sciences, Wageningen University*, *Wageningen, the Netherlands*.

Natural antibodies (NAbs) are antigen-binding immunoglobulins present in non-immunized individuals. They can be considered as humoral part of the innate immune system. Two types of NAb are distinguished. *Overt* NAb (which plasma concentrations rise with age) are readily detected towards exogenous antigens. *Cryptic* NAb bind autoantigens in short temporal intervals. They are suggested to clear intracellular proteins upon their leakage from necrotic cells and regulate inflammatory processes. In cows, overt NAb concentrations in plasma and milk were related to parity, energy balance and diet composition. The objective of the current study was to detect cryptic NAb in cow milk, and relate them to somatic cell count (SCC) and the incidence of mastitis. Milk samples were collected weekly from cows (n=96) from calving till week 9 postpartum (pp) and analyzed for fat, protein, SCC, and NAb to autoproteins (myosin, thyroglobulin, transferrin). NAb titers are expressed as the ^{2}log values of the highest dilution giving a positive reaction. Data are expressed as MEANS ± SEM. Repeated observations were analyzed in a mixed model. Cows produced 40.3 (±0.3) kg of milk with 3.20 (±0.01) % protein, 4.00 (±0.02) % fat, and a SCC of 150 (±16)×10^3/ml. NAb binding myosin (5.66 ± 0.06), thyroglobulin (4.85 ± 0.06), and transferrin (5.76 ± 0.07) were found in milk. Week pp affected (P≤0.05) NAb titers binding thyroglobulin and transferrin. Clinical mastitis incidence (9%) tended to be related to NAb binding myosin (P=0.06) and transferrin (P=0.08), while NAb binding thyroglobulin tended to be related to SCC (P=0.09).This study demonstrates the presence of cryptic NAbs in cow milk, and shows trends for a relation between enhanced cryptic NAb concentrations and mammary inflammatory processes, as indicated by SCC and mastitis. Future studies should confirm these trends and shed light on the exact role of cryptic NAb in cow milk.

Key Words: somatic cell count, natural antibodies, early lactation

T2 Psoriasin expression in bovine udder is induced by *E. coli* infection. P. Regenhard*[1], W. Petzl[2], H. Zerbe[2], and H. Sauerwein[1], [1]*Institute of Animal Science*, *Bonn, NRW, Germany*, [2]*Clinic for Ruminants*, *Munich, Bavaria, Germany*.

Human psoriasin (S100A7) has originally been described as a member of the family of S100 calcium-binding proteins and is overexpressed in patients suffering from psoriasis. The bovine homolog was first identified as a cow-derived respiratory allergen. Human psoriasin as well as the bovine homolog exhibit antibacterial activity especially against *Escherichia coli*. During *E. coli*-mastitis, the host defense status is a cardinal factor influencing systemic disease severity and outcome of the disease. Because of its antibacterial properties psoriasin might be an evolutionary ancient component of innate immunity in the udder. *Escherichia coli*-mastitis is a common problem in dairy cattle, and bovine psoriasin was found to exhibit antimicrobial activity against *E. coli*. We therefore examined by immunoblotting whether and in which localisation the bovine protein is expressed in the mammary gland, and whether this expression is inducible by infection with *E. coli*. To obtain an antiserum, rabbits were immunised with recombinant bovine psoriasin. Six German Holstein cows in their first lactation (26 to 30 months of age, 3 to 5 months in milk) were used; 4 of them were intramammarily infected with 500 CFU of an *E. coli* strain isolated from udder secretions of a cow with clinical mastitis, 2 cows served as control animals and received no treatment. All challenged cows developed clinical mastitis after 12 h. After 24 h, the cows were slaughtered and samples were collected from 3 different localisations of the quarters. Psoriasin expression was limited to the teat cistern of the *E. coli*- infected cows, but was absent in the teat cistern of the non-infected cows and in the parenchyma of both groups, whereas the expression on udder skin was demonstrated in both infected and non-infected cows. Psoriasin thus appears to be a part of the local host defense mechanisms in the udder and seems to be inducible by infection with *E. coli*.

Key Words: antimicrobial peptides, mastitis, psoriasin

T3 Innate immune responses in dairy cows and study of a promising candidate: Osteopontin. K. Alain[1,3], N. A. Karrow[3], C. Thibault[1], M. Lessard[1], and N. Bissonnette*[1,3], [1]*Dairy and Swine Research and Development Center, Agriculture and Agri-Food Canada*, *Sherbrooke, Québec, Canada*, [2]*Université de Sherbrooke*, *Sherbrooke, Québec, Canada*, [3]*University of Guelph*, *Guelph, Ontario, Canada*.

Mastitis is the most important disease in dairy cows and the main cause of economic losses for producers. Search for genes involved in innate immune response and their genetic variants is highly appropriate to identify markers associated with resistance to mastitis. Genetic selection of bulls using those markers associated with innate immunity will result in cows with greater resistance to mastitis, thereby reducing antibiotic use. Following the discovery of a key gene involved in immune response, we evaluated the genetic potential of the osteopontin gene as a candidate for the selection of animals with greater natural resistance to mammary gland infection. The use of the subtractive hybridization technique on cDNA libraries of milk cells from cows infected with *Escherichia coli* revealed an abundant transcript expressed early during infection, namely osteopontin. The search for DNA polymorphisms (SNP) for this *SPP1* gene was conducted by comparing bulls with extreme estimated breeding value (EBV) for the somatic cell count (SCC), an indicator of mammary gland health. Amplification of genomic regions including the promoter and the seven exons was performed and used to identify four SNPs: *SPP1c. 1301G>A*, *SPP1c. 1251C>T*, *SPP1c. 430G>A*, and *SPP1c.*41A>C*. A population consisting of 578 Holstein bulls divided into 26 families (10–60 offsprings per bull-sire family) was genotyped. The study presents the EBVs for the SCC health trait in relation to the different SNP and their associated haplotypes in Canadian Holstein bovines. Results show that *1301G>A* had an impact on the SCC value ($p < 0.001$). The SNP **41A>C* affected the SCC ($p < 0.01$), as demonstrated by allelic substitution ($p < 0.05$). Haplotype analysis did not provide any statistically valid results, however, owing

to a low proportion of certain alleles in the population under study. In addition, certain SNP and their locations (promoter and 3′–untranslated regions) potentiate the genetic impact (EBV) of this candidate gene for the SCC trait. Because the SCC is directly related to mastitis, these DNA polymorphisms could affect mastitis resistance.

Key Words: osteopontin, DNA polymorphisms, innate immunity

T4 Expression of Toll like receptor 4 on bovine neutrophils is not dependent on transcriptional activation. M. Worku*, A. Morris, H. Mukthar, and N. Mikiashvilli, *North Carolina A&T State University*, *Greensboro*.

Endotoxin released from the cell wall of Gram negative bacteria is associated with the pathogenesis of mastitis caused by Escherichia coli (E. coli). The objective of this study was to evaluate the effect of smooth (S) and rough (R) forms of lipopolysaccharide (LPS) on the expression of Toll-like receptor 4(TLR4) in bovine blood neutrophils. Isolated neutrophils (10^7 cells/mL) from three Holstein Friesian cows were treated with E. coli LPS serotype O111:B4 smooth (S) or rough (Rd) forms. Reverse transcriptase PCR was done using primers specific for TLR-4. Flow cytometry was used to assess cell surface expression of TLR-4. Analysis of variance was performed to determine the differences between the groups. No mRNA was detected for TLR-4. Exposure to LPS induced increased cell surface expression of TLR-4. The percentage of total neutrophils binding the monoclonal antibody to TLR-4 was significantly increased on treatment with both S and R forms of LPS ($P < 0.05$) compared to the PBS control. Mean binding increased from 13.57±1.51 in PBS to 24.42±2.61 in Rd treated and 24.41±4.57 in O111:B4 treated neutrophils. No significant difference was observed in the level of TLR-4 expression between treatments with S and R forms of LPS or the PBS-treated control ($P>0.05$). Enhanced TLR-4 activity from exposure to LPS in bovine neutrophils was not dependent on transcriptional activation as evidenced by lack of mRNA induction. Increased cell surface TLR4 may be the result of recruitment of TLR4 from an intracellular pool to the bovine neutrophil cell membrane in response to LPS exposure. This mechanism has implications for the immediacy of the innate immune response to LPS from Gram negative organisms.

Key Words: neutrohphil, TLR4, mastitis

T5 Comparison of in vivo and in vitro mammary cell expression of selected inflammatory genes in response to α-linolenic acid. P. Rezamand*, B. P. Hatch, K. Parnell, K. M. Hunt, J. E. Williams, W. Price, and M. A. McGuire, *University of Idaho*, *Moscow*.

Specific fatty acids (FA) such as α-linolenic acid (ALA: 18:3 ω3) affect immunity. One such effect is modulation of inflammatory responses. The objective of this study was to compare in vivo and in vitro effects of ALA on bovine mammary cell expression of selected inflammatory genes. In an in vivo experiment, canola meal (18:1 ω9) was replaced with camelina (camelina sativa) meal (24.4% ALA) at 0, 3, 6, and 9% (DM basis) to provide rations with incremental concentrations of ALA. Primiparous Holstein cows in mid-lactation (n=18) were randomly assigned to a treatment sequence in a 4×4 Latin square design. Periods lasted 16 d with milk samples collected during the final 2 d of each period. Milk cells (MC) were harvested for RNA extraction, from which cDNA was synthesized. Quantitative PCR analysis demonstrated that expression of pro-inflammatory TNF- α in MC was linearly reduced (up to 40%) as dietary ALA increased ($P<0.01$). No significant differences were detected among treatments in gene expression of IL-1β, intra-cellular adhesion molecule (ICAM)-1 or IL-6 in MC. In vitro, bovine mammary epithelial cells (Mac-T) were grown in DMEM containing 10% FBS. Cells were then sub-cultured in a medium void of FBS, to which incremental concentrations (up to 90 μM) of ALA: BSA (FA-free) solution were added and cells were collected at specific time-points over 48 h. Although expression of IL-1β and ICAM-1(6 h) mRNA were increased, that of IL-6 was reduced (time × dose $P=0.001$) by ALA. Whereas mRNA expression of IL-8 was reduced by 50% when treated with ALA up to 20 μM, treatment with 90 μM ALA up-regulated IL-8 mRNA expression. More notably, mRNA expression of TNF-α was reduced by 55% when cells were exposed to 60 μM of ALA (48 h; $P<0.01$), similar to MC obtained from cows fed rations containing increased levels of ALA. Overall, ALA regulated expression of some of the major pro-inflammatory markers in MC and Mac-T cells but responses were not identical.

Key Words: dairy, inflammatory marker, α-linolenic acid

T6 Development of a multiplex-PCR detection assay for simultaneous identification of the major pathogens causing mastitis in dairy milk. B. Cressier*[1,2], C. Thibault[1], and N. Bissonnette[1,2], [1]*Dairy and Swine Research and Development Center, Agriculture and Agri-Food Canada*, *Sherbrooke, Québec, Canada*, [2]*Université de Sherbrooke*, *Sherbrooke, Québec, Canada*.

Mastitis remains the major disease affecting the dairy industry worldwide. Microbiological methods remain the "gold standard" for mastitis pathogen detection in Canada. Introducing a molecular detection system would reduce the delays to identify the causative pathogen and allow proceeding with the adequate veterinary treatment. A molecular approach would speed up the detection process and must show unambiguous results with an improved sensitivity. To detect specie-specific genes, one predilection technique relies on multiplex-PCR to amplify multiple loci each localized to a specific pathogen's genomic DNA. In this study, we challenged this method for detecting in milk the major mastitis causing bacteria in a single PCR reaction: *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Mycoplasma bovis*, *Streptococcus uberis*, *Str. agalactiae*, and *Str. dysgalactiae*. Specific DNA primers have been designed for each species and tested for optimal sensitivity and specificity. Because each specific primer is labelled with a different fluorescent dye, the analysis of multiple fragment length by capillary electrophoresis is a suitable system for detecting simultaneous multiple pathogen loci with improved sensitivity provided by the fluorescent signal. To challenge the molecular detection assay, we optimized an extraction assay for isolation of bacterial genomic DNA from milk. The extraction assay proposed is convenient for all detected species and greatly reduces the presence of PCR inhibitors inherent to milk. The sample is clarified using a chelator, milk pellet is washed, and a chelating resin is introduced before perfoming the boiling DNA extraction. This method provides a simple, efficient and inexpensive detection assay, which can be easily amenable into a high-throughput scheme using 96- or 384-well plaques. This development opens up possibilities for the functional integration of both extraction and detection of mastitis pathogens in milk of dairy herd using a high-throughput automated screening system.

Key Words: mastitis, pathogen detection, multiplex-PCR

T7 Microbiology results of milk samples from California dairies received between 1999 and 2008. D. F. Resende*, K. Glenn, J. S. Cullor, and R. G. S. Bruno, *University of California-Davis*, *Tulare*.

The objective of this study was to determine prevalence and temporal distribution of bovine mastitis pathogens isolated from milk samples received in the Milk Quality Laboratory at the Veterinary Medicine Teaching and Research Center – UC Davis between 1999 and 2008. Records evaluated on this study included individual cow milk samples obtained from clinical and subclinical mastitis cases and milk samples collected during mastitis screening programs. Samples were cultured according to the National Mastitis Council guidelines and results were classified as negative or positive for bacterial growth and then evaluated for specific pathogens. Contaminated samples were defined based on the presence of more than two environmental pathogens identified in the same plate. Presence of contagious microorganisms was considered positive for determined pathogen disregarding the numbers of other environmental pathogens isolated in the same plate. Data were evaluated based on annual and seasonal trends of major mastitis pathogens. A total of 370,748 milk samples were received between January of 1999 and December of 2008, with the majority of the samples being delivered on the winter season (n=98,815). Multiple mastitis pathogens were isolated from 64.2% of the samples (n=237,968), and among these positive samples Environmental *Staphylococcus* spp were the most prevalent (44.8%) followed by Coliforms (33.5%), Environmental *Streptococcus* spp(14.8%), *Bacillus* spp (10.4%), Coagulase-negative *Staphylococcus* (5.6%), *Staphylococcus aureus* (5.6%) and *Streptococcus agalactiae* (0.1%). Contaminated samples accounted for 8.8% of positives samples being more prevalent during winter seasons ($P<0.05$). Environmental *Streptococcus* was the only species consistently more prevalent in the winter compared to other seasons in all years and *S. agalactiae* was the least prevalent ranging from 0.01% to 0.28%. There was no annual or seasonal trend for isolation of contagious microorganisms. In conclusion, environmental were more prevalent than contagious mastitis pathogens in all years of this study and milk samples submitted during the winter had higher risk to be contaminated.

Key Words: dairy cows, mastitis, milk samples

T8 Prototheca mastitis outbreak investigation in lactating Jersey cows. A. G. Kenyon*, D. F. Resende, K. Glenn, R. Moeller, and R. G. S. Bruno, *University of California - Davis*, *Tulare*.

A mastitis outbreak was investigated in a 2700 Jersey cow dairy in California from March through September 2008. The only change reported in the dairy was the replacement of rubber with silicon based milk liners in the milk equipment (March 2008) and adjustment of parlor setting for the new liners. Mastitis was defined as abnormal milk with or without udder or systemic changes. Epidemiological investigation started in July 2008 when milk samples from all mastitis cases and monthly string sample were submitted for microbiological analysis at the Milk Quality Laboratory, VMTRC – UC Davis. Plates were incubated at 37° C and evaluated at 24 and 48h after incubation. Isolated pathogens were identified according to laboratory guidelines and *Prototheca zoopfi* was identified by gram stain and then by the API 20C system. Four animals with a record of chronic mastitis and lack of response to any mastitis therapy had milk samples collected and their mammary glands submitted for histopathology. String milk sample were collected once monthly to monitor mastitis pathogen in the herd. Examination of the parlor under the new settings identified pulsators overheating and some of them melting. Baseline data (BL) of the herd were retrieved retrospectively from the months prior to the mastitis outbreak. Epidemiological investigation revealed a point source type of outbreak with recurrent infection. Mastitis incidence rate increased from 1% (BL) to 7% (July 2008) after the new parlor settings and incidence of repeated cases of mastitis also increased from 0.7% (BL) to 2.6% after March 2008. Milk sample collected from the 4 chronic cases had a pure growth of *Prototheca zoopfi*. Histopathology of the udders identified a chronic mastitis with numerous fungal organisms present in alveoli, intralobular ducts and the interstial connective tissue. The presence of *Prototheca* in the string samples were observed in 75% of pens during the peak of the outbreak and has been decreased to 12% after recommended changes. The recommendations consisted of selective culling of affected animals, replacement of silicon to rubber based liners, and readjusting the parlor setting to the new liners.

Key Words: Jersey cows, mastitis, Prototheca zoopfi

T9 Comparison of 16S rRNA gene sequence analysis with aerobic milk culture for the identification of potential bacterial etiologies of bovine clinical mastitis. J. R. Wenz*, T. E. Besser, L. K. Fox, and Y. Zhang, *Washington State University*, *Pullman*.

A preliminary study was performed to evaluate the potential use of 16S rRNA gene sequence analysis (16S) to better understand the ecology of bacteria in the milk of the bovine mammary gland with clinical mastitis (CM). Aerobic bacterial culture of milk is the standard method to identify the etiology of CM. Bacteriologically negative (BN) aerobic milk cultures have been reported as high as 40%. Furthermore, numerous CM cases fail to respond to therapy as would be predicted by milk culture results. Anaerobic bacteria have been identified in cases of CM but have been generally ignored. Taken together this suggests that pathogens not identified by standard aerobic milk culture may be involved in the pathogenesis of CM in dairy cattle. Milk from 17 cows with CM in a single quarter and known milk culture results were chosen for this study. Milk (2 ml) was centrifuged, DNA was extracted from the pellet and the V3 region of the small ribosomal subunit was amplified using PCR primers broadly complementary to eubacterial conserved sequences, and cloned. Five to 10 clones from each milk sample were sequenced. Two to 7 different bacterial clones were identified in the majority of samples. The 16S analysis was concordant with the milk culture result for 8/12 (67%) samples, though most 16S results included bacteria other than those found on milk culture, some of which were anaerobes. Predominant bacteria observed in 5 BN milk samples included *Pseudomonas* spp., *Bacteroides* spp., *S. aureus* and *S. dysgalactiae*. This preliminary work needs to be furthered by a study including control milk samples from contralateral, unaffected quarters as well as anaerobic and mycoplasma cultures for better interpretation of 16S results. Nonetheless, these results suggest a more complex bacterial ecology in cases of bovine CM than is indicated by aerobic milk culture. Furthermore, CM cases with a BN milk culture result may be caused by a heterogeneous population of bacteria, including Gram negative and positive organisms and anaerobes.

Key Words: clinical mastitis, dairy cattle, 16S rRNA

T10 Effect of year period on mastitis prevalence and routine procedures characteristics of milking in Culiacán, Sinaloa. M. Valdez*, M. A. Luque, L. Almeida, J. Rodríguez, F. T. Olivas, and D. C. Ochoa, *Investigación y Transferencia de Tecnología para Rumiantes, Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México*.

The objective of present new work was to know the effect of year period on mastitis prevalence and to characterize the routine procedures of milking in dairy herds of Culiacan, Sinaloa, Mexico. Total cows analyzed in the year were 976 with 3,904 quarters, in 8 representative herds randomly selected. The work was realized of September 2007 to June 2008, taking like representative year periods different environmental conditions, September month (it warms up and humid, 28.95 °C t and 78% RH); January (fresh, 19.05 °C t, 70% RH); and June (it warms up and dry, 29.65 °C, 60% RH). The health of each quarter was determined with the California Mastitis Test (CMT). The routine practices of milking in each herd were characterized taking 10 minutes from video with hidden camera, udder preparation, teats disinfection before and after milking, milking unit positioning, and over milking occurrence was analyzed. Traces result level was considered not affected, the proportion of negative quarters to CMT was 67.88% without differences (P>0.05) between year periods, corresponding 64.68, 69.26 and 69.69% to September, January and June, respectively. The proportion of positive quarters to CMT was 28.42% without differences (P>0.05) between year periods, corresponding 31.74, 26.89 and 26.63% to September, January and June, respectively. The fibrous quarters proportion was 3.70%. Udder preparation is not adapted one, teats disinfection before milking is not realized, in 50% herds use teat sealant, milking unit positioning is not advisable one, and the over milking is frequent. One concludes that the mastitis prevalence is elevated and is not affected by the year period, because the routine procedures of milking are not adapted.

Key Words: mastitis, prevalence, milking

T11 Effects of *Mangifera indica* peel extracts on *Staphylococcus aureus* mammary infections. S. Stella and D. Tedesco*, *University of Milan, VSA Dep.*, *Milan, Italy*.

In our previous trial, lower *Staphylococcus aureus* mammary infections was evidenced in milk obtained from dairy cow treated with Mangifera indica peel (personal communication). To verify this important effect, we performed an in vitro trial to evaluate the activity of Mangifera indica peel water and ethanol extracts on *Staphylococcus aureus* by agar gel dilution method. One g of each tested extract (water and ethanol) was solubilised in distilled water (10 mL) and sterilized by filtration. One mL aliquots of each solution were inoculated into fluid trypticase soy agar (100 mL) at 45°C. Then the inoculated media were plated into Petri dishes. *Staphylococcus aureus* suspensions (10^2 and 10^3 CFU/mL) were spread on the surface of the media and the plates were incubated aerobically at 37°C for 48 hours. After the incubation period, the number and the size of colonies in the extract-containing and extract-free plates were compared. *S. aureus* colonies were observed by optical microscope Olympus BX41 (12.5X); images were acquired by Image ProPlus software (Media Cybernetics Inc.). The diameter of at least 30 colonies for each medium was measured. The test also included plates containing only the culture medium and the culture medium plus ethanol, in order to obtain a control of the solvent antimicrobial effect. *S. aureus* strains were considered susceptible in case of complete growth inhibition (bactericidal effect) or when colonies were smaller than colonies in control plates (bacteriostatic effect). *S. aureus* strains were considered resistant when the number and size of colonies didn't change compared to the control plates Our results showed an efficient bacteriostatic action due to all Mangifera indica extracts tested: sizes of the tested colonies were smaller than in control (Table 1). The extract effects are following reported according to their efficacy: - Mangifera indica ethanol extract 1 mg/mL - Mangifera indica water extract (0.5 mg/mL) + ethanol extract (0.5 mg/mL) - Mangifera indica water extract 1 mg/mL. In conclusion treatment with this natural wastes extracts can reduce mammary infection.

Table 1. Bacteriostatic effect of Mangifera indica peel extracts on *S. aureus*

Blank (TSA)	Water extract	Ethanol extract	Mixed W/Et extract
2109,5 +/- 228,1	1549,2 +/- 189,2	1188,5 +/- 54,9	1477,0 +/-54,6

S. aureus colony size (µm, mean +/- st. dev.)

Key Words: *Staphylococcus aureus*, Mangifera indica peel extracts, mammary infections

T12 Effects of OmniGen-AF on mammary mucosal responses to an *Escherichia coli* challenge. Y.-Q. Wang*, A. Rowson, N. E. Forsberg, and S. B. Puntenney, *OmniGen Research*, *Corvallis, OR*.

Previous studies (Wang et al., 2007, 2009) have shown that feeding OmniGen-AF to animals increases blood-borne markers of immunity. The goal of this study was to examine effects of feeding OmniGen-AF on the mammary mucosal response during a pathogen challenge. A murine model of bovine mastitis was used. Twenty-four timed pregnant CD1 mice were assigned to three treatments: 1) negative control, 2) positive control and 3) OmniGen-AF-fed. Negative control animals were fed a control diet. At d10 of lactation, they were anesthetized and both L4 and R4 mammary glands infused with sterile PBS. Positive control animals were fed the same diet but infused with 50 colony forming units (CFU) of a bovine clinical isolate of Escherichia coli. The final group of animals was fed OmniGen-AF (0.5% w/w) for 14 d prior to the infusion of 50 CFU of E. coli into the L4 and R4 mammary glands. Infection was allowed to progress for 24 h after which animals were euthanized (ca. d10 of lactation) and whole mammary samples were recovered and RNA isolated using Trizol reagent. Concentrations of mRNAs encoding myeloperoxidase (MPO), major histocompatibility complex 2 class II (MHC), macrophage inflammatory protein (MIP) and beta-actin were assessed using either Sybr green or TaqMan-based quantitative PCR assays. Beta-actin was used as a housekeeping gene to standardize mRNA concentrations. Mammary concentrations of MPO and MHC mRNAs were elevated significantly (P<0.05) in OmniGen-AF-fed animals. MIP mRNA was unaffected by treatment (P>0.05). Enhanced mammary MPO mRNA implies that neutrophil infiltration into infected tissue was increased. An increase in mammary MHC mRNA implies that antigen presentation was enhanced by provision of OmniGen-AF in the diet. Wada et al (2008) reported that OmniGen-AF reduced incidence of mastitis in dairy cattle. Possible mechanisms may include enhanced neutrophil infiltration into infected mammary tissue and enhanced antigen presentation in mammary antigen presenting cells.

Key Words: OmniGen-AF, mastitis, mucosal immunity

T13 Decision-making for early postpartum subclinical mastitis. V. E. Cabrera*, J. Pantoja, P. Ruegg, and G. Shook, *University of Wisconsin*, *Madison*.

A decision tree model was developed to study the economic outcomes of testing and treating early postpartum cows for subclinical mastitis. The model evaluates sequential decisions that determine economic outcomes based on a 305-d lactation. Logistic regression models were used to predict positive and negative results of 2 diagnostic tests: quarter

somatic cell count (SCC) or California Mastitis Test (CMT). The tests were used to detect intramammary infection (IMI) for different DIM (2 to 8), parity statuses (heifer or cow), and a defined SCC threshold. Producer decisions for each cow included (1) test or no test, (2) if test is pursued, what type of test (CMT or SCC), and (3) a final decision: cull, segregate, administer antibiotics, or take no action. Each intermediate or final node of the model was associated with an economic outcome that the decision tree used to find the economically optimal pathway. The cost of subclinical mastitis was assessed as the aggregation of five factors: (1) milk loss, (2) milk premium loss, (3) premature culling, (4) clinical flare-ups, and (5) transmission to herd mates. These costs were a function of the lactation curve, milk price, defined SCC threshold, livestock prices, and a defined prevalence of contagious mastitis pathogens. Preliminary results indicate, in general, the selection of CMT and no action for negative cows. Seems that the administration of antibiotics could be a feasible option for positive cows, especially when a cow is in first parity (increased rate of cure), milk from a treated cow is used for heifer feeding, and the prevalence of contagious pathogens is high. The cost of mastitis under an optimal policy would vary between $142 to $225 per cow per 305-d lactation, and depend strongly on mastitis prevalence, SCC threshold, milk price, milk production level of cow, and parity.

Key Words: decision tree, mastitis cost, mastitis economic impact

T14 Effects of CpG ODN adjuvant on the immune responses elicited by a quadrovalent mastitis vaccine in dairy cows. S.-C. Lee[1] and J.-W. Lee*[2], [1]*Graduate Institute of Animal Vaccine Technology, National Pingtung University of Science and Technology*, *Neipu, Pingtung, Taiwan*, [2]*Department of Tropical Agriculture and International Cooperation, National Pingtung University of Science and Technology*, *Neipu, Pingtung, Taiwan*.

Staphylococcus aureus (*S. aureus*) and *Escherichia coli* (*E. coli*) remain to be common pathogens inducing bovine mastitis worldwide. Prevention of mastitis by using vaccines has not been very successful. Accumulated lines of evidence indicated that the efficacy of a vaccine can be enhanced by using bacterial DNA, or synthetic CpG oligodeoxynucleotides (ODNs), as the adjuvant. In the present study, a quadrovalent mastitis vaccine, containing formalin inactivated three strains of *S. aurues* (T5, T8, and smith compact) and *E. coli* J5, was formulated with or without a sequence of CpG ODNs that has been shown to be immunostimulatory to bovine cells. Eighteen healthy dairy cows were randomly assigned to three groups and received (1) the control (Freund's incomplete adjuvant, FIA, alone, n=6), (2) Vaccine + FIA (n=6), and (3) Vaccine + FIA + CpG (n=6). Serum antibodies specific to the four strains of bacteria and the expression of cytokines, including interferon-gamma (IFN-γ) and IL-4, in peripheral blood mononuclear cells (PBMC) in response to killed bacteria were analyzed by real-time PCR. In comparison with the control, titers of serum antibody specific to the three *S. aureus* strains were significantly ($p < 0.05$) increased. Addition of CpG ODNs into the vaccine did not enhance the production of antibodies. However, PBMC from cows immunized with CpG ODNs as the adjuvant had a significantly increased expression of IFN-γ (11 v.s. 4 folds) and decreased expression of IL-4 (2 v.s 10 folds) at the transcriptional level. Results indicated that inclusion of CpG ODNs as the adjuvant in an inactivated mastitis vaccine can enhance Th1 type immune responses, which might be beneficial to the elimination of bacteria by phagocytes.

Key Words: vaccine, CpG, mastitis

T15 Intramammary glucocorticoid treatment during LPS-induced mastitis. O. Wellnitz, M. Saudenowa, and R. M. Bruckmaier*, *University of Bern, Vetsuisse Faculty, Veterinary Physiology*, *Bern, Switzerland*.

Therapeutically used glucocorticoids have dose-dependent effects on the immune system. Glucocorticoids such as prednisolone (Pred) are traditionally added to antibiotic intramammary injectors aiming to support the cure of the inflamed mammary gland. The goal of the study was to evaluate the effects of Pred at the dosage commonly used in intramammary injectors on the immune system of the mammary gland and to evaluate the influence of Pred on the mammary immune response to E. coli lipopolysaccharide (LPS) stimulation. Five healthy lactating dairy cows with quarter somatic cell counts (SCC) below 120×10^3 cells/mL were intramammarily infused with either Pred (10 mg), LPS (100 μg), Pred+LPS, or saline solution (9 g/l) in one out of four quarters, respectively. Udders were completely emptied by machine milking every 12 h. SCC of each quarter, tumor necrosis factor alpha (TNF) in milk, and lactate dehydrogenase (LDH) in milk were measured at 0, 3, 6, 9, 12, 24, and 36 h. mRNA expression of TNF, interleukin (IL)-1beta, IL-8, IL-10, and lactoferrin (LF) were measured in milk cells at 0, 12, 24, and 36 h using qRT-PCR. Differences between treatments were considered significant if $P<0.05$. SCC increased in LPS stimulated quarters independent of Pred within 6 h until the end of the experiment. TNF milk concentrations increased immediately after LPS stimulation independent of Pred lasting until the 12 h milking. Milk LDH was elevated at the 9 h sample in the LPS quarters and at the 12 to 36 h samples in the LPS+Pred quarters. SCC, TNF, and LDH remained unchanged in the control quarters and in the Pred treated quarters. mRNA expression of TNF, IL-1beta, IL-8, IL-10, and LF increased in LPS treated quarters independent of the presence of Pred. No changes in mRNA expression of these factors in milk cells were observed in controls and Pred treated quarters. In conclusion, stimulation of udder quarters with LPS had a pronounced effect on the mammary immune response. The investigated parameters responded to LPS as typically expected. Based on the measured parameters no immune modulating effects of Pred were observed in healthy udder quarters despite a slightly delayed LDH response.

Key Words: prednisolone, mammary immunity, cow

Breeding and Genetics: Dairy Cattle Breeding II and Rabbit Breeding

T16 Ketosis – Managable by breeding strategies? F. Rehbock[1], G. Freyer[2], F. Klug[3], and N. Vukasinovic*[4], [1]*Landesforschungsanstalt für Landwirtschaft und Fischerei M-V, Institut für Tierproduktion*, *Dummerstorf, Germany*, [2]*FBN, Unit Genetics and Biometry*, *Dummerstorf, Germany*, [3]*Alexandrastr. 4*, *Graal-Müritz, Germany*, [4]*Newsham Choice Genetics, STL Research Center*, *Chesterfield, MO*.

Improving health and fertility is an economic prerequisite for increasing longevity and life performance in dairy cows. According to the literature, ketosis has been reported to be the cause for 9 to 26% reduction

in milk yield, 26 to 37% shorter productive life, and 27 to 46% increase in fertility problems. Ketosis can be a trigger for other diseases as well as an accompanying disease. Generally, it has been assumed that this metabolic disorder occurs in cows in the second lactation and upwards. However, recent studies indicated an increased rate of ketosis in the first lactating cows, which can be explained by their most negative energy balance in the early lactation, caused by intensive selection on high milk yield in the first lactation. This relation will be studied further. Previous studies found high genetic variability and a significant differentiation among offspring groups regarding ketosis incidence. That suggests that ketosis could be managed by breeding. Simulation studies showed that considering milk protein percentage in the selection index aimed at an optimum combination of yield and content traits let to a significant reduction of ketosis rate in the offspring. Sires with high breeding values (BV) for protein percentages had also a better BV for general health and an increased length of productive life. Further, metabolic and endocrine parameters were not related to energy balance and should not be used for selection purposes. On the other hand, selection for increased feed intake leads to reduction in energy deficit and thus indirectly to reduced rate of ketosis.

Key Words: ketosis, health, functional traits

T17 Genetic parameters and breeding values estimated under heterogeneous variances of two groups for type records of Holstein cows in Japan. T. Baba*[1], Y. Masuda[1], Y. Goto[2], and M. Suzuki[1], [1]*Obihiro University of A and VM*, *Obihiro, Japan*, [2]*The Holstein Cattle Association of Japan, Hokkaido branch*, *Sapporo, Japan*.

Type records in Japan are obtained from progeny test (PT) and herd enrollment for type (HE). However, farms participate in PT are selected randomly from those farms that provide milk records to the Hokkaido Dairy Milk Recording and Testing Association, but on the other hand, HE are voluntary. The objectives of this study were to estimate genetic parameters and breeding values for type traits when assuming that residual variances of its two groups are heterogeneous.Type traits and pedigree information of 705,453 animals were obtained. PT and HE of animals were 157,544 and 147,772, respectively. Genetic parameter and breeding value for two groups were estimated on assuming that only residual variances were difference (Model 1). And, as compared with results of Model 1, estimated values were obtained when their heterogeneity wasn't taken into account (Model 2). Breeding values for type traits were calculated from variance components obtained in Model 1 and 2. Breeding values estimated in Model 1 also assumed that residual variance are heterogeneous. Spearman's rank correlation coffecients of breeding values obtained from Model 1 and 2 were calculated.In examining the results in Model 1, we found that the residual variances estimated for type traits in PT were larger than in HE. Therefore, heritabilities in HE were higher values except in front teat placement. Heritabilities in Model 2 were likely to be mostly intermediate values between PT and HE. Correlations of breeding values between Model 1 and 2 were 0.999 in all traits for both sire and cow. For the top of breeding values in Model 2, there was little variability in correlations in cows and sires and when there was it was greater in cows. Therefore this result indicated that heterogeneity of residual variance in two groups didn't need to be assumed for sires.

Key Words: genetic parameter, breeding value, heterogeneous variance

T18 Estimation of genetic parameters for maturity of lactation using a test day model in Japanese Holsteins. Y. Masuda* and M. Suzuki, *Obihiro University of Agriculture and Veterinary Medicine*, *Obihiro, Japan*.

Test day milk yield for dairy cattle was affected by within-lactation and age (i.e., lactation curve and maturity of lactation). The straightforward approach to account for the contribution of maturity to additive genetic effects is to include the random regressions on age in the models. The objective of this study was to estimate genetic parameters for maturity of milk production by using a test day model with additive genetic curve over the life of Holsteins in Japan. Data included 1,011,634 test day records with first five lactations from 39,954 cows calving between 1985 and 2005. A single trait model was employed which contained random regressions both on days in milk (lactation curves) and on age at testing (curves for maturity). Permanent environmental effect was modeled as maturity curves and lactation curves common to all parities, while the additive genetic effect was only considered as a curve of maturity. Third order Legendre polynomials were fitted to animal genetic effects and two permanent environmental effects. Covariance components were estimated via Gibbs Sampling with GIBBS3F90 program. Heritability estimates of test day milk yield ranged from 0.20 to 0.25. Heritability of maturity rate was 0.09 when maturity rate was defined as the difference in total milk production from a cow 50-55 mo old and 30-35 mo-old cow. The model applied in this study provides a genetic curve for maturity for each cow. This approach needs lower computational demands for prediction of gentic maturity rate compared to multiple-parity random regression models.

Key Words: maturity, random regression, test day model

T19 Bayesian analysis of random regression using B-splines to model test-day milk yield of Holstein cattle. A. B. Bignardi*[1,3], L. El Faro[2], G. J. M. Rosa[3], F. F. Silva[3,4], V. L. Cardoso[2], P. F. Machado[5], and L. G. Albuquerque[1], [1]*Universidade Estadual Paulista*, *Jaboticabal, São Paulo, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios*, *Ribeirão Preto, São Paulo, Brazil*, [3]*University of Wisconsin*, *Madison*, [4]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [5]*Universidade de São Paulo*, *Piracicaba, São Paulo, Brazil*.

A total of 152,145 weekly test-day milk yield records from 7,317 first lactations of Holstein cows distributed across 93 herds in southeastern Brazil were analyzed. Test-day milk yields were classified into 44 weekly classes of days in milk (DIM). The contemporary groups were defined as herd-year-week of test-day. The model included direct additive genetic, permanent environmental and residual effects as random, and fixed effects of contemporary group and age of cow at calving as covariable. Mean trends were modeled by a cubic regression on orthogonal polynomials of DIM, and additive genetic and permanent environmental effects were estimated using B-splines. Residual variances were modeled by step function with 6 variance classes. A total of 12 models, considering different combinations of linear, quadratic and cubic B-splines and up to six knots, were considered. Estimates of (co) variance components were obtained using Bayesian inference, assuming flat bounded priors, and employing a Gibbs sampling algorithm as implemented in the program RRGIBBS. A single chain with 400,000 samples was run for each model, discarding the first 10,000 samples as burn-in period. Models were compared by residual mean square error (MSE) as well as by a weighted (by number of days in interval) average of estimates of residual variances (RES). Results indicated a better fit for the model employing cubic B-splines to both random effects, with knots at 1, 10, 19, 26, 35 and 44 weeks (78 parameters). For this model,

the heritability estimates were higher in the 1st week and between the 29th and 36th weeks, varying from 0.21 (3rd week) to 0.42 (1st week). Genetic correlation estimates between adjacent controls were high and close to one, and became smaller as the distance between controls increased. Negative genetic correlation estimates were observed between the 1st and the 6th weeks onwards and between the 2nd and 15th weeks onwards controls. Results indicated that a random regression model fitting basis functions of cubic B-splines is well suited to model the dynamic of milk yield over the lactation period.

Key Words: Bayesian, B-splines, test-day

T20 Study on genetic evaluation for linear type traits in Holstein cows. D.-H. Lee[1], S.-H. Oh*[2], and N. C. Whitley[2], [1]*Hankyong National University, Ansung, Gyeonggi, South Korea*, [2]*North Carolina A&T State University, Greensboro*.

The objective of this study was to determine better methods to evaluate genetic performance of individual animals with linear type traits of dairy cows, especially focusing on comparative traits, and to estimate actual data for genetic variances. Data used in this study was collected from 118,290 Holstein dairy cows between the years of 2000 and 2004 by Korea Animal Improvement Association (KAIA). Only data of more than five tested cows by Herd-Appraisal date and of individuals having more than ten daughters were included to increase the reliability of the data analyses. Outliers were removed and the records of individuals having one or both of parents were included in the analyses. The data used in the analysis is a total of 30,204 records of the selected traits, which was collected from 26,701 individuals having pedigree information. Herd-Appraisal date, year of age, lactation stage (grouped by month), and time lagged for milking were assumed as fixed effects on the model. Animal additive genetic effects considering pedigree relationship, and residual errors were assumed with random effects. Year of age at appraisal date was classified from one to nine years of age, assigning the value of nine years of age for animals that were greater than or equal to nine years of age. Five comparative traits were investigated in this study, general stature composite (GSC), dairy capacity composite (DCC), body size composite (BSC), foot and leg composite (FLC), and udder composite (UDC). In the present study, the greatest breeding values for GSC were estimated for Canada with the breeding values for USA lines increasing for 10 years starting in 1989 but tending to the decrease after that until 2004. For DCC, the breeding values for USA and Canadian lines showed similar patterns until 1999, after which the breeding values for the USA lines declined sharply. For BSC, Korea, Canada and USA data followed similar trends, but the breeding values of the USA decreased starting in 1999. In the US, selection indexes were based primarily on milk yield traits until methods for evaluating other traits began to emerge.

Key Words: Holstein, linear type traits, genetic evaluation

T21 Comparison of Swiss and New Zealand cows in a pasture-based milk production system. P. Kunz*, V. Piccand, and P. Thomet, *Swiss College of Agriculture, 3052 Zollikofen, Bern, Switzerland*.

The high yielding dairy cow which is widespread in Switzerland is not suited to a production system based on roughage and very little concentrates. Investigations in Ireland and New Zealand have shown that the New Zealand Holstein Friesian population is well adapted to a pasture-based milk production system with seasonal calving. For this reason 72 pregnant Holstein Friesian heifers with at least two generations of New Zealand ancestry were imported from Ireland in 2006 and placed on twelve dairy farms in Switzerland. The objective was to investigate over 3 years (2007 - 2010) the attributes of cows adapted to a roughage-based seasonal production system under Swiss conditions. The amount of feed over one year was composed of 65 - 70% grazed pasture, 20 - 25% conserved roughage and at most 300 kg of concentrates. For comparison, pairs of Swiss and New Zealand (HF-NZ) cows were established with similar age (±6 months) and calving date (± 35 days) on the twelve farms. The Swiss cows consisted of 14 Brown Swiss (BS), 13 Fleckvieh (FV) and 18 Holstein Friesian (HF-CH) breeds. Body weight (BW) in the first lactation was higher in Swiss than in NZ cows (BS: 494 kg, HF-NZ: 472 kg; FV: 560 kg, HF-NZ: 473 kg, HF-CH: 572 kg, HF-NZ: 483 kg). Milk yield was higher in HF-CH (5441 kg energy corrected milk (ECM)) than in HF-NZ (4818 kg ECM) cows, but lower in FV (5027 kg ECM) than in HF-NZ (5508 kg ECM) and in BS (4366 kgECM) than in HF-NZ (5047 kg ECM) cows. Efficiency (kg ECM/kg metabolic BW) was higher in HF-NZ (49.9) compared to BS (41.7) and higher in HF-NZ (54.3) compared to FV (43.8) but similar between HF-NZ (46.9) and HF-CH (46.7). The results show advantages for NZ compared to BS and FV cows but there are also individual Swiss cows with similar attributes. Additional variables are currently being analysed, which will hopefully help to achieve the aim of finding the key attributes of cows adapted to a pasture-based seasonal production system.

Key Words: lactating cows, breed, pasture

T22 Udder health traits as related to economic losses in Friesian cattle. H. G. El Awady[1] and E. Z. M. Oudah*[2], [1]*Kafr El Sheikh University, Kafr ElSheikh, Egypt*, [2]*Mansoura University, Mansoura, Egypt*.

A total number of 4752 lactation records of Friesian cows from 2000 to 2005 were used to determine the relationship between somatic cell count (SCC), udder health traits (UHS) and economic losses in milk production. Studied traits were milk yield traits {i.e., 305-milk yield, (MY), fat yield (FY) and protein yield (PY)} and udder health traits {i.e. SCC, mastitis (MAST) and udder quarter infection (UDQI)}. Least square analysis was used to estimate the fixed effects of month and year of calving, parity and stage of lactation on different studied traits. Data were analyzed using Multi-trait Derivative Free Restricted Maximum Likelihood to estimate the genetic parameters. The effects of SCC, MAST and UDQI on milk traits were also studied. Unadjusted means of MY, FY, PY and SCC were 3936, 121, 90 kg and 453,000 cells/ml, respectively. All fixed effects were significantly ($P<0.01$) affect all traits except the effects of month of calving on both FY and PY was not significant. The SCC, MAST, UHS and UQI increased during winter and summer than spring and autumn. Additionally, SCC and MAST noticeably increased with advancing in parities. Increasing SCC from 300,000 to 3000,000 cells/ml increased UDQI from 5.5 to 23.2%. Losses in monthly and lactationally milk yields per cow ranged from 14 to 89 and from 105 to 921 kg, respectively. Losses in monthly and lactationally milk yields per cow ranged from 14 to 89 and from 105 to 921 kg, respectively. Losses in monthly and lactationally milk yields return per cow at the same level of SCC ranged from 24.5 to 155.75 LE and from 50.8 to 1612 LE, respectively. Heritability estimates of MY, FY, PY, SCC, MAST, UHS, UDQI were 0.31, 0.33, 0.35, 0.14, 0.23, 0.13, and 0.09, respectively. All milk production traits phenotypically and genetically correlated negatively with SCC, MAST and UDQI. It could be concluded that the SCC can be used as a perfect tool for UHS and milk quality. The use of SCC thresholds for parities and stages of lactation to detect intra-mammary infection improve quality parameters over a fixed threshold of 200,000 cell/ml.

Key Words: udder health, genetic parameters, dairy cattle

T23 Comparing random regression models to analyse first lactation daily milk yield data in Murrah buffaloes by Bayesian inference. F. C. Breda Mello*[1], L. G. de Albuquerque[3], R. F. Euclydes[2], H. Tonhati[3], and A. B. Bignardi[3], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [3]*Faculdade de Ciências Agrárias e Veterinária / Universidade Estadual Paulista*, *Jaboticabal, São Paulo, Brazil*.

Random regression models were used to estimate genetic parameters for test day milk yield in buffaloes using Bayesian inference. Data comprised 17,935 test-day milk records from 1,433 buffaloes. Different orders of fit of the Legendre orthogonal polynomials (LP) for the regression of random effects were considered. The term LP(ij) was adopted, where i and j indicate the order of fit for additive genetic and permanent environmental effects, respectively. All twelve models included fixed effects of contemporary group, milking number and age of buffaloes as covariate. In addition, residual variances were considered to be heterogeneous with six classes of variances. Models were compared based on residual mean square (MSR) errors and estimates of genetic parameters. The models LP46, LP56 and LP67 presented the smaller MSR estimates. The three models differed little in the partition of phenotypic variance into genetic, permanent environmental and residual variance. The differences in the heritability estimates between models were detected at the beginning (0.34 and 0.45) and at the end of lactation (0.40 and 0.50). Ignoring heritabilities for milk yield in the first and final weeks of lactation, the estimates ranged from 0.19 to 0.30, which was highest between week 9 and week 19. In general, models LP46, LP56 and LP67 yielded similar estimates of the genetic parameters, though, models LP67 and LP56 resulted in a higher degree of interdependence between additive genetic and permanent environmental random regression coefficients. This finding might explain the difficulty in convergence to distribution stationary observed when processing the analyses with these models. In addition, LP56 and LP67 yielded negative genetic correlations between the initial and mid-lactation (after week 9). The results indicated that a model using fourth- and sixth-order polynomials for additive genetic and permanent environmental effects, respectively, was appropriate to describe the changes in variances that occur along the buffalo lactation curve.

Key Words: Bayesian inference, buffaloes, milk yield

T24 Genetic parameters estimation for milk yield of buffaloes Murrah breed using parametric functions. F. C. Breda*[1], R. F. Euclydes[2], L. G. de Albuquerque[3], H. Tonhati[3], and A. B. Bignardi[3], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Univesidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [3]*Faculdade de Ciências Agrárias e Veterinária/ Universidade Estadual Paulista*, *Jaboticabal, São Paulo, Brazil*.

The objective of this study was to evaluate random regression models, which used different parametric functions and residuals variances classes for describing the milk production genetic variation of buffaloes, through genetic parameters estimates and broad range of model comparison criteria. Twenty seven random regression models were used to adjust 17,935 test day milk records of 1,433 buffaloes. The models include fixed effects of contemporary group, milking number and age of buffaloes as covariable. The additive genetic and permanent environmental effects were modeled through random regression models, using Wilmink and Ali and Schaeffer functions and Legendre orthogonal polynomial. Models were compared by Akaike's information criterion (AIC), Bayesian information criterion (BIC), Log likelihood function, information theoretic measure of model complexity (ICOMP), weighted residual variance (VRP) and an index that considered all model comparison criteria mentioned. The Ali and Schaeffer function (AS) presented better values of LMV, VRP and ICOMP to the model with 42 residuals variances classes (ASHE42); AIC and index for model with 17 residuals variances classes (ASHE17); and BIC for model that considered homogeneous residual variance (ASHO). However, ASHE42 didn't differ of ASHE17 for the likelihood test. Additionally, the additive genetic and permanent environmental variances and correlation produced by ASHE17 and ASHO were similar, not justifying the use of models more parameters to describe the changes in variances that occur along the lactation curve. Heritability estimates ranged from 0.18 to 0.31 and were higher at the week 8 to 17, indicating larger genetic variability in this period. The genetic correlation among test days were positive and decreased with the increase in lag between tests, except at the initial weeks. Random regression models were efficient in describing the milk production genetic variation, except at the beginning and at the end of the lactation. The ASHO is recommended to model the test day milk yield of Murrah buffaloes, in genetic evaluation programs.

Key Words: buffaloes, milk yield, random regression

T25 Estimation of heritability of monthly test day milk yield at different calving seasons in Holsteins of Khorasan province of Iran. R. Lotfi*[1], H. Farhangfar[2], and A. Shoorideh[3], [1]*Tarbiat Modares University*, *Tehran, Iran*, [2]*Birjand University*, *Birjand, Iran*, [3]*Jihade Agriculture of Razavi Khorasan*, *Mashhad, Iran*.

In this study, a total of 58513 monthly test day milk yields belonging to 13045 Iranian first lactation Holsteins during 2003-2008 and distributed in 113 herds were used to estimate heritability of monthly test day milk yield at different calving seasons. A test day repeatability animal model including fixed effects of herd-year of calving-stage of lactation (HYS), Holstein gene (linear covariable), age at calving (linear covariable) and also direct additive genetic and permanent environment random effects were used. Restricted maximum likelihood (REML) estimates of genetic and environmental variances were estimated for different calving seasons by DFREML software. The heritability estimates of monthly test day milk yield for different calving seasons of spring, summer, autumn and winter were found to be 0.16, 0.20, 0.23 and 0.09 respectively. Heritability estimates were highest for fall calvers followed by summer, spring and winter calvers. Different heritability estimates for calving seasons found in the present study indicate that additive genetic as well as environmental variations vary over the calving seasons suggesting that a greater genetic gain could be achieved over the generations as the genetic selection of candidates animals is practiced based upon the performance records of fall calvers.

Key Words: calving seasons, heritability, environment variation

T26 Genetic characteristics of energy balance for Iranian primiparous Holsteins using a fixed regression test day model. H. Farhangfar*[1], R. Lotfi[2], and M. H. Fathi Nasri[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Tarbiat Modares University*, *Tehran, Iran*.

A fixed regression test day animal model was used to estimate genetic and environmental variance components of energy balance for Iranian primiparous Holsteins. The data set comprised a total of 51,402 monthly test day (thrice a day milking) milk yields, fat and protein percentages collected from 7111 first lactation cows calved between 2003 and 2008 in 113 herds distributed over the Khorasan province of Iran. Energy

balance for individual months of lactation was estimated based upon a multiple regression model proposed by Friggens et al. (J. Dairy Sci, 2007, 90:5453-5467). In the data set, total number of sires and dams were 642 and 6117 respectively. Furthermore, average monthly test day milk yield, fat and protein percentage were 30.7 kg, 3.29% and 3.12% respectively. The overall mean monthly test day energy balance was found to be 21.3 MJ/d over the course of the lactation. In the model, herd-year-season of calving- stage of lactation was included as a contemporary fixed environmental effect. Moreover, linear covariates of Holstein genes, age at calving, milk yield, fat and protein percentages were taken into account. The cow number was also included in the model to account for direct additive genetic as well as permanent environmental random effects. DMU package was applied for genetic analysis of energy balance. The results showed that direct additive genetic, permanent and temporary (residual) variance components for energy balance were 3067, 687 and 74607 (MJ/d)2 respectively. Heritability and repeatability of the trait were found to be approximately 0.039 and 0.047 respectively indicating that a very low potential genetic variation is available for energy balance to be genetically improved by candidate's selection in the population.

Key Words: energy balance, genetic parameters, Iranian Holstein

T27 Estimation of genetic correlations among peak milk yield, energy balance and age at first calving for Iranian Holstein heifers. H. Farhangfar*[1], R. Lotfi[2], and M. H. Fathi Nasri[1], [1]*Birjand University, Birjand, Iran*, [2]*Tarbiat Modares University, Tehran, Iran*.

This study aimed to estimate genetic relationships among milk yield at peak time, energy balance and first calving age for Iranian first lactation Holstein cows. A total of 6994 records obtained from 6994 heifers calved between 2003 and 2008 was used. All milk records were thrice a day milking samples collected from 112 herds distributed over the Khorasan province of Iran. Energy balance for individual cows was estimated based upon a multiple regression model proposed by Friggens et al. (J. Dairy Sci., 2007, 90:5453-5467). In the data set, total number of sires and dams were 640 and 6028 respectively. In the data set, average milk yield, energy balance and first calving age were 32.28 kg, -316.45 MJ/d and 26.08 month respectively. A multivariate animal model was used to estimate variance and covariance components for genetic and environmental random effects through restricted maximum likelihood statistical method implemented in DMU package. In the model, herd-year-season of calving (as a contemporary fixed environmental effect) and linear covariate of Holstein genes were included. The cow number was also included in the model to account for direct additive genetic random effect. Heritability estimates of milk yield at peak time, energy balance and first calving age were 0.107, 0.008 and 0.047 respectively. At genetic level, peak milk yield was negatively correlated with energy balance (-0.68) and first calving age (-0.21). Genetic correlation between energy balance and first calving age was 0.83. Although peak milk yield had a negative environmental correlation with energy balance (-0.45) it was positively correlated with age at first calving (0.09). A negative environmental correlation (-0.05) was found between energy balance and first calving age.

Key Words: genetic correlation, energy balance, Iranian Holstein

T28 Mixed model analyzing of some environmental factors affecting average lactation somatic cell score in Iranian Holstein heifers. H. Farhangfar*[1], A. Abedini[1], K. Shojaeian[2], and M. H. Fathi Nasri[1], [1]*Birjand University, Birjand, Iran*, [2]*Zabol University, Zabol, Iran*.

To study the effects of some environmental factors affecting somatic cell score, a total of 13977 records from Iranian Holstein heifers (three times a day milking) was used. The number of cows, sires and dams were 13977, 871 and 12882 respectively. The records were collected from 183 herds between 2002 and 2006. The trait was defined as the average lactation somatic cell score (ALSCS) for individual cows. The somatic cell score was expressed as loge-transformed somatic cell count (logeSCC) from monthly test days measured in 1000 cells/ml. Mean ALSCS in the data file was 4.48. The data were subsequently analyzed by a mixed linear model. In the model, herd, year and season of calving, age at first calving and Holstein gene percentage (as linear covariates) and interaction between age and calving season were included as fixed environmental effects. Sire and the interaction between herd and sire random effects were also fitted in the model. Mixed procedure of SAS software was applied to fit the model. The results showed that herd and year of calving significantly ($P<0.01$) affected the ALSCS. The trait was not significantly affected by the Holstein gene percentage and two-way interaction terms included in the model. Although season of calving was found to be statistically a non-significant factor on the trait, Tukey-Kramer adjustment paired comparisons applied in the model revealed that spring and summer calvers had a significant ($P<0.01$) higher level of ALSCS than that of cows calving in fall and winter seasons. No significant differences were found between spring and summer and between fall and winter calvers. Restricted maximum likelihood estimates of sire, herd*sire and residual variance components for ALSCS were 0.011, 0.045 and 0.587 respectively indicating that a small genetic variation was available for the ALSCS.

Key Words: somatic cell score, Iranian Holstein, mixed model

T29 Genetic association between male fertility and prolificacy after artificial insemination with semen subjected to limited screening. L. L. Tusell*[1], R. Rekaya[2], M. López-Bejar[3], M. García-Tomás[1], O. Rafel[1], J. Ramon[1], and M. Piles[1], [1]*Unitat de Cunicultura, IRTA, Barcelona, Spain*, [2]*University of Georgia, Athens*, [3]*UAB, Barcelona, Spain*.

The aim of the study was to estimate the (co)variance components for male fertility (F), defined as success or failure of artificial insemination (AI) and male prolificacy (TB), defined as number of total born per litter, in a rabbit population selected for growth rate. Semen from 248 males was used to generate a total of 6,613 doses to inseminate 2,293 crossbred females applied 24 h after collection. Ejaculates were rejected only if individual motility was lower than 2 (from 0 to 5 scale), or if they had urine. A bivariate longitudinal mixed model for F and TB was assumed. Systematic effects included: concentration, building, batch-technician, physiological status of the female, and buck-age. Unrelated female, non-additive genetic plus permanent environmental effects of male, permanent environmental effect of male and day of AI, male additive genetic effect, and the residual term were included as random effects. Missing TB was predicted by data augmentation and Gibbs sampling was used for inference. The mean (s.d.) of the marginal posterior distribution for heritability was 0.12 (0.05) and 0.11 (0.04) for male F and TB, respectively, and the genetic correlation was very high 0.97 (0.05). Therefore, TB in prolific species could be considered as another measure of fertility. Under these conditions of AI, the additive genetic variation was higher than when natural mating or AI without any storage period was performed in rabbit, or after AI in other spe-

cies. The random effect of male and day of AI was the most important for both traits, being 25.3% and 10.3% of the phenotypic variance for F and TB, respectively. This effect encompasses the strong source of variation that every ejaculate is subjected to during the handling of the male doses when AI is performed.

Key Words: fertility, prolificacy, (co)variance

T30 Breeding values of fat and protein content in inbred and outbred cows. J. Bezdicek*[1], J. Subrt[1], R. Filipcik[2], and J. Riha[1], [1]*Agrovyzkum Rapotin Ltd., Rapotin, Czech Republic*, [2]*MZLU v Brne, Brno, Czech Republic*.

The aim of this study was to explore the effect of inbreeding depression on production in holstein cows. Production (in kg of fat and protein) was presented in the form of breeding values. The data included holstein cows (253,286) calved in the years 1990-2006 at farms in the Czech Republic. For proper comparison each inbred cow was assigned to at least one outbred equal (2.063 equals in sum). Inbred cows with their outbred equals were matched on characteristics such as identical sire, first calving interval occurrence on the same farm, first calving occurring in the same year and period (±2 months) and dam reaching the same breeding value of milk production. The goal was to make doublets of inbred and outbred cows which were very similar in terms of origin (the same sire, dam with similar breeding value) and which would also produce under the same conditions and time. Inbred cows and their matched outbred equals were subsequently divided according to the inbreeding coefficient of inbred cows into three groups (F_X=1.25%, F_X=2.0-3.125%, F_X=4.0-12.5%). The data were analysed using PROC GLM of SAS. Both the observed milk components showed significant decrease in breeding value when the level of inbreeding was higher. Compared to their coevals, inbred cows showed lower breeding values. Within the observed groups (F_X=1.25%, F_X=2.0-3.125% and F_X =4.0-12.5%) the average breeding value of inbred cows (and their coevals) was, in kg of protein 4.76 (5.32); 4.36 (5.24); 3.20 (7.19) kg. A similar tendency was also apparent in the breeding value of inbred cows (coevals) in kg of fat 4.17 (4.89); 4.42 (4.72) a 3.42 (7.11). These summaries show clearly not only a decrease in kg of fat and protein connected to increased level of inbreeding but also lower values reached by inbred cows compared to their coevals. In this study we have shown a decrease in breeding values of kg of fat and kg of protein in inbred cows compared to their noninbred coevals. When the coefficient $F_X$was high (4.0-12.5), the decrease was significant or highly significant.

Key Words: inbreeding, Holstein, protein

T31 Genetic correlations of dry matter intake with fat corrected milk yield, body weight, and body condition score in eleven commercial tie-stall dairy farms. S. M. Hall*[1], C. D. Dechow[1], J. M. Daubert[1], M. D. Dekleva[1], J. W. Blum[2], G. A. Varga[1], C. R. Baumrucker[1], and W. Liu[1], [1]*Pennsylvania State University, University Park*, [2]*University of Bern, Bern, Switzerland*.

The objective of this study was to estimate genetic correlations of dry matter intake (DMI), with fat corrected milk yield (FCM), body weight (BW), and body condition score (BCS) in commercial tie-stall dairy farms. Dry matter intake, BW and BCS were recorded within 7 days of monthly DHI milk testing on 11 Pennsylvania dairy farms. In order to minimize disruption to the farm feeding routine, herd managers were instructed to distribute feed evenly for all cows. Any feed subsequently moved to or taken from a cow was recorded by the research technician, and all feed refusals were weighed the following morning. Records from cows more than 280 days in milk or in greater than fifth parity were removed. A total of 1,158 daily DMI, 1,790 BCS and 984 BW observations from 587 cows were available for analysis. Fat corrected milk was retrieved from all prior lactation for cows in second lactation or greater, resulting in 42,931 daily FCM observations. Total DMI, total FCM, average BW, and average BCS for the first 280 days of lactation were derived with solutions estimated with a 4-trait random regression model. Total lactation traits were then analyzed with a 4-trait animal model in ASREML. The mean total DMI for the first 280 days was 6,031 kg, whereas mean FCM was 9,718 kg. Mean BW and BCS were 674 kg and 2.94, respectively. Heritability estimates ranged from 0.12 for BCS and DMI to 0.33 for BW. Dry matter intake was genetically correlated with more FCM (0.74), higher BW (0.66) and higher BCS (0.38). Standard errors for the genetic correlations were high, ranging from 0.37 (FCM and BW) to 0.58 (BCS). Phenotypic correlations of DMI with FCM (0.32), BW (0.30) and BCS (0.07) were all positive. Feed intake can be measured in commercial tie-stalls with sufficient accuracy to estimate genetic parameters for DMI. Dry matter intake was genetically correlated with higher FCM and BW.

Key Words: feed intake, heritability, genetic correlation

T32 Phenotypic and genotypic variation of bovine immune responses in Cohort dairy herds across Canada. K. A. Thompson*[1], N. Karrow[1], K. Leslie[1], M. Quinton[1], F. Miglior[2], and B. A. Mallard[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Canadian Dairy Network, Guelph, ON, Canada*.

Infectious diseases contribute to substantial economic loss in the dairy industry with human and animal health implications. The immune system is a tightly genetically regulated system that largely controls response to infectious disease. Including estimated breeding values (EBV) of immune response (IR) traits in a selection index has the potential to improve inherent animal health. Cows and pigs classified as high IR (HIR) in University of Guelph research herds had increased responses to commercial vaccines, and other health and production benefits. Cows ranked as HIR in a large US commercial dairy herd had lower disease scores (Hernandez, 2008 PhD thesis, University of Guelph, DeLapaz, 2008 MSc thesis, University of Florida). The objective this study is to evaluate antibody-mediated (AMIR) and cell-mediated IR (CMIR) in 58 commercial herds across Canada to determine effects on health and performance. This will provide novel insight into IR phenotypes on a national scale to confirm results of a single herd. In collaboration with the Canadian Bovine Mastitis Network and National Cohort of Dairy Herds 690 Holsteins were systematically immunized with both a type 1 and a type 2 antigen to stimulate AMIR and CMIR, respectively. To classify cows as high (H) or low (L) responders, serum antibody was measured by ELISA. Skin-fold thickness measurements were taken to evaluate delayed-type hypersensitivity (DTH), a measure of CMIR. Genomic analysis will be performed to determine genetic profiles associated with these diverse IR phenotypes. National health and production records are available for correlation with IR. Preliminary results show measurable differences in AMIR and CMIR between cows, herds, and provinces, making it possible to identify H and L responders. Identifying H and L responders (phenotypically and by EBV) and genetic profiles of these phenotypes may make it feasible to include IR in breeding indices to improve health.

Key Words: immune response, breeding, genetics

T33 Study on genetic parameters of conception rate and heat detection rate of NY Holsteins. C. Huang[1], S. Tsuruta*[1], I. Misztal[1], and T. J. Lawlor[2], [1]*University of Georgia*, *Athens*, [2]*Holstein Association USA Inc.*, *Brattleboro, VT*.

The purpose of this study was to estimate genetic parameters of heat detection (HD), conception rate (CR) and days open (DO). Because HD is not observed directly, two indirect measures of HD were created: HD1=minimum [21/service interval (SI), 1] and HD2=[0 if SI>21; 1 if SI≤21]. Field data were obtained from DRMS, Raleigh, NC and included milk and service records of NY Holsteins. Edits included only farms with herd-year size >50 and with approximately even daily insemination pattern; the last step was to eliminate herds using timed AI. The final data set included 115,405 cows with 244,967 service records from 1999 to 2003. Traits considered were CR as the binary outcome of each insemination, DO as the interval of calving date to last service date with limits of 21-250d, and the 2 indirect HD measures. Traits analyzed in the bivariate model were one of CR and DO and one of HD1 or HD2. Effects included in the model were DIM, season, milk yield, age at calving, AI status as fixed effects, herd-year, service sire, additive sire, and cow's permanent environment as random effects. The heritability estimates of CR, DO, HD1 and HD2 were 3.6-4.1%, 3.2%, 1-1.6% and 3.5-3.8%, respectively. The estimated genetic correlations were -0.73 (CR, HD1), -0.40 (DO, HD1), -0.26 (CR, HD2), and -0.14 (DO, HD2). The different sign of correlation was expected with CR and DO because the correlation between these traits is strongly negative. Previous studies on DO, CR, HD1 and HD2 using simulated data indicated large variability of estimated correlations between fertility and heat detection measures as a function of missing data and treatment of censoring and that the most accurate estimates were between CR and HD1. Further model refinements are necessary for unambiguous determination of the sign of the genetic correlation between the CR and HD.

Key Words: conception rate, days open, heat detection

T34 Beta-casein enhancer (BCE) and evolutionarily conserved region 3 (ECR3) polymorphisms are associated with milk composition and management traits in dairy cattle. G. Rincon[1], M. Rijnkels[2], A. Islas[1], and J. F. Medrano*[1], [1]*University of California*, *Davis*, [2]*USDA/ ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine*, *Houston, TX*.

The bovine casein gene locus is located on BTA6 and comprises four genes: CSN1S1,CSN2, CSN1S2 and CSN3. In addition to the casein genes, there are five physically linked genes and a number of non-coding conserved regions that may play a role in regulation of gene expression. Beta-casein enhancer (BCE) and evolutionarily conserved region 3 (ECR3) are potential regulatory regions located in the casein gene cluster that are present in most species. In the present study we resequenced BCE and ECR3 genomic regions in a sample of 8 Brown Swiss, 8 Holstein and 8 Jersey cows that were unrelated in a three generation pedigree. Three SNPs were found in the BCE region (SNP_20586, SNP_20752, SNP_20827) and two SNPs were found in the ECR3 region (SNP_9109, SNP_9518). The SNPs were genotyped and tested for associations with milk production and management traits in 800 Holstein bulls from the UC Davis archival collection and 300 Holstein cows from farms in the California Central Valley. Bull PTA values were obtained from the USDA Animal Improvement Programs Laboratory (Beltsville, MD). Milk composition analysis was performed to obtain phenotypes in the cow population. The association analysis was developed using the SNP Variation Suite from Helixtree to test allelic associations with phenotypic variables. Significant results ($p<0.01$; FDR<0.05) were observed for SNP_20752 in the bull population for milk yield, protein yield, productive life and somatic cell score PTA traits. The same SNP was also significantly associated with protein and casein percentages in the cow population. SNP_20586 and SNP_9109 were associated with PTA protein percentage in bulls. These results emphasize the importance of SNP variation in the BCE and ECR3 regions in relation to milk production and management traits in dairy cattle. To provide support to this finding, we are examining if different genotypes for BCE and ECR3 have an association with gene expression differences in the casein locus.

Key Words: casein cluster, milk production, management traits

T35 Comparison of superovulation, embryo recovery, and embryo transfers in lactating dairy cows and heifers. M. B. Gordon*, T. Pretheeban, and R. Rajamahendran, *University of British Columbia*, *Vancouver, BC, Canada*.

While reproductive performance in lactating dairy cows have dramatically decreased, fertility in dairy heifers still remains high. Some factors which may contribute to poor fertility include: poor oviductal and uterine environments, altered follicular dynamics and oocyte quality, reduced corpus luteum function and increased embryo mortality. The objectives of this study were to compare heifers to 2nd and 3rd parity cows with respects to response to superovulation and embryo recovery, and compare the uterine environment by comparing pregnancy data following the transfer of embryos collected from heifers to recipient heifers and 2nd and 3rd parity cows. Beginning 10 to 11 days after synchronization of estrus, standard superovulation treatment was carried out on 2nd and 3rd parity lactating dairy cows (n=23) and virgin heifers (n=32), with subsequent non-surgical embryo recovery 6 to 7 d after a timed double insemination (a.m. and p.m.). Heifers had a significantly higher response to superovulation treatment as indicated by the number of corpus lutea present on the day of embryo recovery (11.6 ± 1.0 vs. 5.8 ± 1.2; P=0.0007). The average number of viable embryos recovered from animals was 7.1 ± 0.9 and 2.7 ± 1.1 (P=0.002) for heifers and cows, respectively. Heifers also had significantly higher progesterone concentrations on an individual CL basis than cows on day 4 (3.82 ± 1.08 vs. 0.43 ± 1.23 ng/mL; P=0.05) and day 6 (3.11 ± 0.57 vs. 0.90 ± 0.65 ng/mL; P=0.02) post-insemination. Recipient animals were estrus synchronized for subsequent embryo implantation 6 to 7 days after estrus. Of the animals that were prepared for implantation, 63% of parity cows (n=27) and 60% of the heifers (n=35) were at the proper stage of the estrous cycle to receive embryos. Pregnancy rates of cows and heifers were 53.3% and 52.4%, respectively. This study suggests that heifers may ovulate superior viable embryos, and may produce better functional corpus lutea in the first 6 days after estrus, as indicated by high progesterone concentrations.

Key Words: superovulation, embryo transfer, fertility

T36 Effect of sexed semen on conception rate for Holsteins in the United States. H. D. Norman and J. L. Hutchison*, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Effect of sexed-semen breedings on conception rate was investigated using US Holstein field data from January 2006 through October 2008. Sexed-semen breeding status was determined by a National Association of Animal Breeders' 500-series marketing code or by individual breeding information in a cow or heifer reproduction record from a dairy records processing center. Marketing-code 514 was not identified as sexed semen

because that technology is a gender-bias semen that results in only 10% more female births than semen that has not been sex sorted. Sexed-semen breedings resulted in 91% female offspring. Only breedings with confirmed outcomes were included: 1,190,587 heifer breedings (of which 119,920 were sexed-semen breedings) and 9,835,105 cow breedings (of which 106,393 were sexed-semen breeding). Overall mean conception rates for sexed-semen breedings was 44% for heifers (compared with 57% for conventional semen) and 26% for cows (compared with 30% for conventional semen). For heifers, 80% of sexed-semen breedings were first breedings; 16%, second breedings; and 3%, third breedings, with conception rates of 45, 39, and 35%, respectively. For cows, 43% of sexed-semen breedings were during first lactation and 28% during second. For first-lactation cows, 51% of sexed-semen breedings were first breedings; 23%, second breedings; and 12%, third breedings, with conception rates of 29, 27, and 25%, respectively. For second-lactation cows, 47% of sexed-semen breedings were first breedings; 25%, second breedings; and 13%, third breedings, with a mean conception rate of 26% for the first 3 breedings. For bulls with >300 breedings, correlations between sire conception rates from sexed and conventional semen were 0.19 for heifer breedings (67 bulls) and 0.49 for cow matings (51 bulls). Corresponding correlations for bulls with >800 breedings were 0.32 (31 bulls) and 0.78 (15 bulls).

Key Words: sexed semen, conception rate, Holstein

T37 Derivation of factors to estimate daily fat, protein, and somatic cell score from one milking of cows milked twice daily. M. M. Schutz*[1], J. M. Bewley[2], and H. D. Norman[3], [1]*Purdue University, West Lafayette, IN*, [2]*University of Kentucky, Lexington*, [3]*USDA-ARS, Beltsville, MD*.

The objective was to derive factors to predict daily fat (F) and protein (P) yield and somatic cell score (SCS) when milk is sampled once per d for cows milked twice per d. Milk samples were collected for each milking on test-day by Dairy Herd Improvement personnel from herds recording milking times and milk weights automatically. Following edits, 2190 records of 1869 first lactation (L1) cows and 3363 records of 2931 later lactation (L2) cows in 25 2x herds remained. Factors currently in use to adjust single milking F and P for milking interval (MINT) were applied. No adjustments are currently in use for SCS. Also, 3 methods were compared to estimate factors or equations to predict daily F, P, and SCS. Factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (24 intervals in 2 parities) [Method 1] or as the sum of the ratios of daily yield to partial daily yield for each cow-day divided by the number of cow-days within parity-MINT class [Method 2]. Resulting factors from both methods were smoothed, applied to data, and residuals were regressed on days in milk (DIM). Regression equations (n=112) were also developed within parity-MINT-DIM classes (2x7x8) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for am and pm milking for each trait in L1 and L2. Method 3 resulted in consistently stronger correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for all components in both milkings in L1 and L2. Method 3 resulted in rMSE of 0.12 (F, L1), 0.17 (F, L2), 0.07 (P, L1), and 0.10 (P, L2) kg for am milkings; compared to rMSE of 0.15, 0.20, 0.08, and 0.11 kg from current factors for the same traits in L1 and L2. Differences in rMSE were similar for F and P for the pm milkings and for SCS for both milkings. Work is ongoing to determine whether equations from Method 3 will allow accurate estimation of daily milk, F, P, and SCS when applied to other herds.

Key Words: milking interval, adjustment factor, milking frequency

T38 Best prediction of lactation yields accounting for regional and seasonal differences. J. B. Cole and D. J. Null*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

In the United States, lactation yields are calculated using best prediction (BP), a method in which test day (TD) data are compared to breed- and parity-specific herd lactation curves that do not account for differences among regions of the country or seasons of calving. This may result in biased estimates of lactation yields. Data from 5,345,621 lactations of 348,123 Holstein cows with lactation lengths between 250 d and 500 d, records made in a single herd, at least _ve reported TD, and twice-daily milking were extracted from the national dairy database (NDDB). Herds were assigned to one of six regions of the country, individual lactations were assigned to three-month seasons of calving, and lactation curves for milk and fat yield were estimated by parity group (first versus later) for regions, seasons, and seasons within regions. The resulting curves were added to the BP software and tested against a validation dataset of 891,809 lactation records from 400,000 Holstein cows sampled at random from the NDDB. Mature equivalent (ME) milk and fat yields were calculated using the standard curves and the new curves. Differences between 305-d ME yields were calculated and tested for significance. Yields calculated using 50-d intervals from 50 to 250 DIM and using all TD to 500 DIM allowed comparisons of predictions for records in progress (RIP). Differences in ME milk ranged from 0 to 51 kg and were slightly larger for first- than later-parity cows, but were not significant ($P > 0.05$) in any case. Fat yields also did not differ significantly. Correlations of projected yields for 50-d intervals with yields using all TD data were similar across analyses. Differences among predictions averaged 57 kg lower for the new curves than for the standard curves using TD in the first 50 DIM, decreasing to 20 kg as TD from subsequent 50-d intervals were added. Complete lactation yields were similar for all curves, but projected yields for RIP were slightly more accurate when adjusted for regional and seasonal differences.

Key Words: best prediction, milk yield, regional effects

T39 Trends in international flow of Holstein genes. R. L. Powell*, J. R. Wright, and H. D. Norman, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Holstein genes spread from Europe to much of the world through live cattle more than 100 yr ago. By the advent of artificial insemination, selection emphasis in North America had led to a specialized dairy strain that was in demand internationally. From 1995, genetic evaluations through Interbull more accurately identified the best bulls across countries. Many of the same bulls were used in many countries, particularly to sire sons for progeny testing, so a number of countries had bulls worthy of international consideration. Data from over 100,000 Holstein bulls and 27 countries in the January 2009 Interbull evaluation were used to examine changes over birth years in the direction of gene flow by examining the country of AI bulls' sires. Birth years ranged from 1986 to 2003. Percentage of bulls having a foreign sire was surprisingly steady, being 56% in 1986 and 55% in 2003, after a high of 65% for 1995 to 1997. Through 1991, nearly all AI bulls progeny tested in France, Germany, Italy, and The Netherlands were sired by bulls from other countries. For bulls from those countries born in 2003, 49 to 87% were by foreign sires. Although the United States used fewer foreign sires of sons, that portion has been about 25% for bulls born this decade. The United States provided the most foreign sires of sons every year, as high as 86%, with Canada second in most years; the two together contributed 56 to 97%. The "hot bulls" syndrome is evident from the dramatic changes in country of foreign sires from one

year to year. The Netherlands had not accounted for more than 4% of foreign sires until 12% in 1999 followed by 24, 18, and dropping to 5%. Frequency of German sires went from 1% in 2000 to 12% in 2001 while Italian sires went from 1% in 2001 to 14% in 2002. Sourcing of sires is a dynamic situation with the proportion of sires from a given country rapidly changing. The constant is that foreign sires produce the majority of Holstein bulls progeny tested. The portion of foreign sires has not shown much trend, but certainly the accuracy with which sires are chosen has improved.

Key Words: sires of sons, Interbull, genetics

T40 Holstein, Jersey and its cross affects fatty acid composition under grazing conditions. R. A. Palladino[1], F. Buckley[2], J. J. Murphy[2], R. Prendiville[1,2], and D. A. Kenny*[1], [1]*University College Dublin, Belfield, Dublin 4, Ireland*, [2]*Teagasc, Moorepark Dairy Research Centre, Fermoy, Co. Cork, Ireland*.

Dietary n-3 polyunsaturated fatty acids (PUFA) and conjugated linoleic acid (CLA) have beneficial properties for human health. Dairy cow breed affects PUFA concentration in milk but most work to-date has been conducted under TMR based systems. Additionally, there is little information about the cow breed and heterosis on concentrations of milk PUFA. The objective of this study was to compare milk FA concentration of two dairy cow breeds (Holstein and Jersey) and their F1 hybrid managed under a grazing system. Eighty-one spring-calving dairy cows (27 cows per treatment) were managed under a predominantly perennial ryegrass pasture during two experimental periods (June and July). Milk yield, fat, protein, lactose and fatty acids (FA) were recorded once a week during each period. Milk FA were analyzed by gas chromatography. Data were analyzed by ANOVA. Cow was used as random effect. Statistical model was $Y_{ij} = \mu + breed_i + period_j + breed_i \times period_j + error_{ij}$. No interaction was found for any of the variables studied over the two periods. Holstein cows had the highest milk yield, Jersey the lowest with the crossbred animals intermediate (P<0.01). Milk fat and protein were highest for Jersey, lowest for Holstein and the crossbred animals intermediate (P<0.01). Holstein had higher n3:n6 ratio (P<0.05), C18:2 n6, and the Ã¢Ë†â€ 9 desaturase index (P<0.01). Milk CLA also tended to be higher in Holstein (Table 1). Under the grazing conditions employed here, Holstein dairy cows produced more milk with a higher content of CLA, probably due to the higher mammary gland Ã¢Ë†â€ 9 desaturase enzyme activity observed. No evidence for any heterotic effects on milk related variables measured was found from this study.

Table 1. Effect of breed on milk FA composition

FA (g/kg of Total FA)	Holstein	Jersey	H x J	SED[1]	Significance[2]
t-11 C18:1 (VA)	44.4	45.2	38.4	3.95	NS
C18:2	5.9[a]	4.7[b]	4.6[b]	0.38	**
CLA	17.8	15.3	14.7	1.36	†
C18:3	6.6	6.0	6.6	0.35	NS
n3:n6	0.77[b]	0.99[a]	1.01[a]	0.100	*
Δ9 desaturase index[3]	0.09[a]	0.08[b]	0.08[b]	0.004	**

[a, b]Means within a row with different superscripts differ (P<0.05); [1]Standard error of the difference; [2]NS = not significant; † = P<0.10; * = P<0.05; ** = P<0.01; [3]C14:1/(C14:0 + C14:1).

Key Words: fatty acids, dairy breeds, conjugated linoleic acid

T41 Logistic analysis of some environmental factors affecting multiple birth performance of Iranian indigenous goats. H. Farhangfar*[1], Y. Shamshirgaran[2], M. Esfandiari[3], and M. H. Fathi Nasri[1], [1]*Birjand University, Birjand, Iran*, [2]*Ferdowsi University of Mashhad, Mashhad, Iran*, [3]*Agricultural Jihad Organisation, Birjand, Iran*.

To study the effects of some environmental factors influencing multiple birth performance of Iranian indigenous goats a total of 815 records collected from 2000 to 2007 was used. All data were obtained from a breeding flock of Cashmere indigenous goat in southern Khorasan province of Iran. The number of kids and dams in the whole data set was 815 and 405 respectively. In the data, single birth was coded as 1 and the litter size greater than one was set to 2. A logistic regression model was subsequently used to analyze the multiple birth performance of the population. In the model, fixed environmental factors of year of kidding (2000-2007), number of kidding (kidding 1, 2, 3 and 4), and kid sex (male and female) along with linear covariate of kid weight at birth (2.11 kg, SD=0.44 kg) were included. The model was fit using logistic procedure of SAS software. The results showed that the number of kids born was significantly (P<0.01) influenced by all the factors considered in the model. Point estimation of odds ratio for the birth weight was found to be 0.077 indicating that the ewes with heavier kids tend to have more probability for the multiple birth. Taking account of female sex as the reference level, the odds ratio for male kid was 1.853 showing that ewes with multiple birth performance are expected to have a greater number of male progeny. The results found in this study also revealed that multiple birth probability was greater for the ewes kidding at the third time, followed by the fourth and second times than that of the first-kidding ewes.

Key Words: Iranian indigenous goat, multiple births, logistic analysis

T42 A neural networks approach for prediction fertility in rabbit using semen quality parameters. L. L. Tusell*[1], R. Rekaya[2], M. López-Bejar[3], M. García-Tomás[1], C. Andreu[3], O. Rafel[1], J. Ramon[1], and M. Piles[1], [1]*Unitat de Cunicultura, IRTA, Barcelona, Spain*, [2]*University of Georgia, Athens*, [3]*UAB, Barcelona, Spain*.

Several statistical techniques based on linear and nonlinear regression have been used to relate seminal quality with fertility showing limited predictability power. In this study, a Neural Networks approach is proposed to predict fertility based on seminal quality parameters. A total of 107 ejaculates from 27 bucks were used for insemination at two different dose concentration (10 and 40 millions of spermatozoa per mL) 24 h after collection. Ejaculates were rejected only if individual motility was lower than 2 (from 0 to 5 scale), or if they had urine. A feed-forward network with one hidden layer was used in the context of a multi layers feed-forward networks. Randomly, 79 records were used for the training process and the remaining 28 records were used for the validation step. Concentration of the ejaculate, individual motility, percentage of viable spermatozoa, acrosome-reacted spermatozoa, spermatozoa with morphological abnormalities of head, neck-midpiece and tail and spermatozoa with cytoplasmic droplet, age of the male and dose concentration were used as input nodes. An extra input node with fixed value equal to one was added. The hidden layer had 4 nodes. Fertility, defined as % kindling rate, was the only output of the network. Weights were updated after all the observations in the training set were presented to the network. A 100,000 iterations were performed with a learning rate of 0.45. The back propagation algorithm was used to optimize the network weights during the training process. The network approach performed reasonable well in predicting the kindling rate. In fact, the correlation

between the observed and the predicted values using the training and the validation sets were 0.71 and 0.53, respectively.

Key Words: neural network, fertility, semen quality

Dairy Foods: Dairy Foods Processing/Cheese/Dairy Micro

T43 Understanding and controlling flavor and color development resulting from non-thermal browning (NTB) in cheese. A. Lopez-Hernandez*, N. Van Epps, and S. A. Rankin, *University of Wisconsin, Madison*.

Under certain conditions, some cheeses brown (i.e. parmesan, gouda) during the course of aging yielding concomitant changes in flavor and color. Very little definitive science exists to describe, define or control the reaction chemistry of non-thermal browning (NTB) in cheese from either the flavor or pigmentation perspective. There is a number of suggested pathways that attempt to explain these changes. Such pathways involve factors such as redox potential, available oxygen, the presence of α–dicarbonyl compounds, amino acid type and concentration, Mn^{2+} ions, and microbial tyrosinase activity. However, NTB still exists in the industry with no clear means of understanding or controlling its development. The aim of the present study was to define the chemical structures of flavorants and pigments generated through non-thermal browning mechanisms in cheese as an aid to understand and control its development. Our results showed that the pigments are stable to air exposure and soluble in some non-polar solvents, such as pentane and pentane-methylene chloride (2:1 v/v). The UV-Visible spectra of the extracts showed maximum absorption peaks at 400 and 450 nm. Volatile characterization revealed compounds specific to brown cheeses including lactones, ketones and pyran derivatives. The relative abundance of the compounds was found to be higher in those cheeses where browning and more intense aroma was more evident. Parallel studies in a cheese model systems demonstrated that α–dicarbonyls specific to fermentation showed little effect on the development of brown color. Extensive heat treatment of the cheese milk source also showed little effect on the development of brown pigmentation.

Key Words: non thermal browning, parmesan, maillard reaction

T44 Transcriptomic analysis of Camembert cheese fungal activity. C. Viel*, F. Boileau, A. Thériault, and S. Labrie, *Département des sciences des aliments et de nutrition, Centre de recherche en sciences et technologie du lait (STELA), Institut des neutraceutiques et des aliments fonctionnels (INAF), Université Laval, Québec, QC, Canada*.

Camembert cheeses are dynamic microbial ecosystems that evolve during ripening. The overall metabolic activity of the microbiota largely determines the quality of the cheeses. However, little is known about the genes expressed by the surface microbiota. We studied the transcriptome of a ready-to-eat Camembert cheese to gain a better understanding of the major activities of the fungi responsible for rind formation. Samples were collected from the rind of a Camembert cheese, inoculated on selective media, and three isolates were microbiologically characterized and further identified as *Penicillium camemberti*, *Geotrichum candidum*, and *Debaryomyces hansenii* by rDNA sequencing. High quality total RNA was obtained from the same rind and was analyzed by RT-PCR using a Bioanalyzer 2100. Specific primers revealed that the three species could be amplified from total RNA. mRNA was purified from the total RNA and retro-transcribed. A cDNA library was constructed. The sequence of the clones were compared to those in public databases. Putative gene functions were attributed as follows: 26% were involved in metabolism, 20% in translation, 10% in cell signaling, 4% in survival (defense, stress, and repair), 4% in ion transport, 4% in transcription, 2% in apotosis, 2% in cell transport, and 3% in other functions, while 25% had unknown functions. The results of the present study will help guide the selection of biomarker genes that can be used to monitor fungal activities during cheese ripening.

Key Words: transcriptome, fungi, camembert

T45 Comparison of Hispanic cheeses from US and country of origin manufacturers. L. A. Jimenez-Maroto[1], A. Lopez-Hernandez*[1], B. Maldonado[2], and S. A. Rankin[1], [1]*University of Wisconsin, Madison*, [2]*Tecnológico de Monterrey, Campus Querétaro, Querétaro, México*.

There is anecdotal information that US-made Hispanic cheeses are criticized by Hispanic consumers for not being authentic compared to cheeses made in their countries of origin. In order to determine what characteristics define the authenticity of Hispanic cheeses several assessments were conducted including microbial testing, sensory profiles, chemical composition, and functional character. Commercial samples of three different types of Hispanic cheeses (fresh, pasta filata, aged) were acquired from domestic (n=44) and country of origin (n=40) manufacturers from three regions (Mexico, Central America, Caribbean). Proximate analysis was conducted using standard methods. A modified melt-flow apparatus was used to ascertain the melt character. Quantitative descriptive analyses (QDA) of cheese flavor, texture, and appearance were conducted by trained panelists (n=13) and the results analyzed using principal component analysis (PCA) and canonical analysis. Consumer panels comparing US and Mexican samples were conducted for each of the cheese types studied. None of the samples tested positive for the presence of food pathogens. Country of origin cheeses had higher moisture and pH, lower salt, similar lipid and protein content. Some of the non-US cheese products contained non-dairy ingredients, such as vegetable oils. Melt character of fresh and aged cheeses showed significant differences between domestic and country of origin samples, while pasta filata cheeses showed no significant differences. There were significant differences in salt, bitter, buttery, cowy, milkfat, oxidized, unclean and rancid flavor attributes. Consumer panels showed that Mexican consumers similarly rated US-made cheeses as highly authentic when compared to the Mexican-made samples. These results provide insight into the characteristics that define the authenticity of the Hispanic cheeses analyzed. Knowledge of these characteristics will aid U.S. manufacturers to produce a Hispanic cheese with more authentic qualities that will satisfy the demands of their Hispanic consumers.

Key Words: Hispanic cheese, sensory profile, melt character

T46 Partitioning of omega-3 fatty acids in Cheddar cheese curd and whey. C. Brothersen*, D. J. McMahon, and B. Pettee, *Western Dairy Center, Utah State University, Logan*.

Full-fat Cheddar cheese was made with milk fortified with omega-3 fatty acids and the partitioning of omega-3 fatty acids into the curd

and whey was determined. Omega-3 fatty acids from both animal and plant sources in both encapsulated and free oil were used. The omega-3 fatty acid preparations were incorporated into the milk by the following methods: 1) mixing the encapsulated powder in the milk, 2) mixing oil in the milk, 3) mixing oil in cream, 4) homogenizing oil in milk, and 5) homogenizing oil in the cream. With the homogenization treatments, the homogenized milk and cream constituted ten percent of the fat in the cheese milk. Also, encapsulated omega-3 fatty acid preparations, from animal and plant sources, were added to stirred and milled curd during dry salting, and the omega-3 content of the pressed curd was determined. The recovery of omega-3 fatty acids from the animal source, averaged over all treatments was 90.5%, and was significantly higher ($\alpha\# = 0.05$) than that of the plant source at 80.3%. The average recoveries of omega-3 fatty acids from the homogenization treatments were 90.3% and 92.8% for treatments 4 and 5 respectively, and were not significantly ($\alpha\# = 0.05$) different. There was a significant difference in the average recovery of omega-3 fatty acids in curd from the homogenized treatments compared to that of the non-homogenized treatments, which were 80.2%, 79.0% and 82.8% for treatments 1-3 respectively. The recovery in the curd form the non-homogenized treatments were not significantly different from each other. When the encapsulated form of omega-3 fatty acids were added to the cheese curd during salting, the average recovery for the animal and plant sources, were significantly ($\alpha\# = 0.05$) different at 99.4% and 91.1% respectively. The average recovery of omega-3 fatty acids in the milled curd was 94.4%, and was not significantly different from that of the milled curd at 96.1%. Therefore, the most efficient method of fortifying Cheddar cheese with omega-3 fatty acids, is adding the encapsulated powder to the curd during salting.

Key Words: cheese, omega-3, fortification

T47 Microbiological quality of raw milk utilized for small scale artisan cheese production. D. J. D'Amico* and C. W. Donnelly, *University of Vermont*, *Burlington*.

This study evaluated the overall milk quality and prevalence of four target pathogens in raw milk used for small scale artisan cheesemaking and examined specific farm characteristics and practices and their effect on bacterial and somatic cell counts. Raw milk samples were collected weekly from 21 artisan cheese operations (6 organic), manufacturing raw milk cheese from cow (12), goat (5), or sheep (4) milk during the summer of 2008. Individual samples were examined for standard plate (SPC) coliform (CC), and somatic cell counts (SCC). Samples were also screened for *Listeria* spp., *Staphylococcus aureus*, *Salmonella* spp., and *Escherichia coli* O157:H7 by direct plating and PCR. Overall, 86% of samples had SPC <10,000 cfu/mL, with 42% <1000 cfu/mL. Additionally, 68% of samples tested were within pasteurized milk standards for coliform bacteria under the Pasteurized Milk Ordinance (PMO) at <10 cfu/mL. SPC and CC did not differ significantly between species. Similarly, method of sample delivery (shipped or pick up), farm type (organic or conventional) and duration of milking (year round or seasonal) did not have significant affects on farm aggregated mean SPC, CC or SCC. Strong positive correlations were observed between herd size and mean SPC and between SPC and CC as well as SCC when data from all species was combined. Although cows milk SCCs were significantly lower than those of goats and sheep, 98%, 71%, and 92% of cow, sheep, and goat milk samples were within the limits of the PMO for SCC, respectively. Fourteen of the 21 farms (67%) were positive for *S. aureus*, detected in 38% of samples at an average level of 20 cfu/mL. Neither *L. monocytogenes*, *E. coli* O157:H7 or *Salmonella* spp. were detected or recovered from any of the 101 samples tested. Our results indicate that most raw milk intended for small scale artisan cheesemaking was of high microbiological quality with no detectable target pathogens despite the repeat sampling of farms. These data will also help inform risk assessments which evaluate the microbiological safety of artisan and farmstead cheeses, particularly those manufactured from raw milk.

Key Words: raw milk, cheese, pathogen

T48 Effect of anhydrous milk fat, milk fat globular membrane and corn oil as the fat source in the AIN93 diet on the fecal microbiota in Fisher 344 rats. R. E. Ward*[1], D. Snow[1], R. Jimenez-Flores[2], and K. J. Hintze[1], [1]*Nutrition, Dietetics and Food Sciences, Utah State University*, *Logan*, [2]*Dairy Products Technology Center, Department of Agriculture, California Polytechnic State University*, *San Luis Obispo*.

The milk fat globular membrane (MFGM) is a complex biopolymer of membrane lipids (phospholipids, sphingolipids, plasmalogens, gangliosides) and glycoproteins which coats fat globules in fresh milk. It is hypothesized that this material may contain beneficial bioactive properties, but few studies have been conducted in this area. During butter production, substantial amounts of MFGM are produced by disruption of the native fat globule, and MFGM may be recovered from the buttermilk for use as an ingredient. To better understand potential benefits of MFGM, we conducted a feeding study comparing MFGM as a dietary fat source to anhydrous milk fat (AMF) and corn oil (CO) in Fisher 344 rats. MFGM was isolated from buttermilk and proximate, mineral and comprehensive lipid analyses were conducted. MFGM was subsequently incorporated into the AIN-93 rodent diet as the sole fat source. Between the experimental diets, there was no significant effect on consumption or weight gain, and MRI analysis of whole animals indicated no significant effect on body fat (13.6% CO, 14.4% AMF, 14.1% MFGM). Fecal samples were collected from each group (n=3) and subjected to comprehensive fecal microbiota profiling using a novel pyrosequencing method. On average, 1,920 sequences were identified in each fecal sample, totaling 526 unique isolates. At the phylum level, 62% of the sequences identified were Bacteroidetes, 29% were Firmicutes, and 5% were Verrucomicrobia. Animals fed AMF had the most diversity in their fecal microbiota, which was significantly different than the MFGM and control diets at the 95% confidence level.

Key Words: globule, membrane, microbiota

T49 Beneficial effects of bovine colostrum acid protein on bone properties of ovariectomized rats. M. Du*[1], L. Zhang[1], Z. Mu[2], H. Yi[1], and X. Han[1], [1]*Harbin Institute of Technology*, *Harbin, Heilongjiang, China*, [2]*Inner Mongolia Agricultural University*, *Hohhot, Inner Mongolia, China*.

Many reports have shown that bovine basic protein components, bovine colostrum and extracts of bovine colostrum have positive effects on bone growth of humans, such as increasing bone mineral density (BMD) and promoting calcium absorption. However, the effects of bovine colostrum acid protein components (BCAP) on properties of bone have not been reported. This study investigated the effect of BCAP on the prevention of bone loss in ovariectomized (OVX) rats. Forty-eight 3-month old female Sprague-Dawley rats were ovariectomized and another 12 rats underwent a sham operation (Sham). The OVX rats were randomly separated into four groups, i.e., OVX control, OVX low-dose (2 mg/d), OVX medium-dose (10 mg/d) and OVX high-dose (50 mg/d),

and were gavaged with BCAP once per day for 12 weeks. The effects of BCAP on bone mineral content (BMC), BMD, microarchitecture and biomechanical properties were determined. We found that BCAP increased the BMC and BMD of the femur. Moreover, BCAP acted in a dose-dependent manner. Observation of the distal femur by scanning electron microscope and mechanical testing further confirmed the positive effects of BCAP on bone properties. We conclude that BCAP (2~50 mg/d) could prevent osteoporosis caused by bone loss owing to estrogen reduction in OVX rats.

Key Words: biomechanical property, histomorphometry, bone mineral density

T50 Comparison of commercially available RNA extraction methods for effective bacterial RNA isolation from milk. S. Secchi[1], A. Serrano[2], P. García-Nogales[1], S. Gutiérrez[3], and A. Arís*[2], [1]*Applied Research using OMICS Sciences*, *Barcelona, Spain*, [2]*Institut de Recerca i Tecnologia Agroalimentàries*, *Barcelona, Spain*, [3]*Centre de Recerca i Investigació de Catalunya*, *Barcelona, Spain*.

The objective of this study was to compare four commercially–available RNA extraction kits for the purification of bacterial RNA isolated from culture and milk samples: the RNeasy Protect (Qiagen), the NucliSENS miniMAG (Biomerieux), the TRIzol (Invitrogen) and the RiboPure (Ambion). We compared the efficiency in terms of quantity and quality of extracted RNA for two bacteria species, a gram negative *Escherichia coli* and a gram positive *Staphylococcus aureus*. Strains were grown on culture media and all RNA extractions were performed from 1mL of culture at the middle log phase point (OD_{550}=0.5) with or without UHT milk. The amount of colony forming units at OD_{550}=0.5 was determined for both strains as $1.4x10^8$ and $2.8x10^8$cfuxmL^{-1} for *E.coli* and *S.aureus*. RNA extraction was performed by triplicate and quantified by OD_{260}. Yield differences among the kits and between milk and culture medium were submitted to ANOVA analysis. RNA purity and integrity was analyzed using the Experion Automated Electrophoresis system (Bio-Rad). Obtained RNA yields indicated no significant differences between milk or milk-free RNA extractions either for *E.coli* or *S.aureus* although there was a tendency (*P*=0.0873) with *S.aureus* and the Biomerieux kit for greater RNA extraction from milk than from culture (30.75 µg versus 7.85 µg respectively). Biomerieux and Qiagen kits produced the best yield results from all *S.aureus* samples, and the Ambion kit resulted in the lowest amounts (0.36 µg per extraction). For *E.coli*, the Qiagen kit provided the greatest RNA yield in culture media and milk (25.26 and 38.86 µg respectively). The greatest RNA purity was obtained in all cases with the Qiagen kit. The results obtained indicate that the Qiagen kit is the most suitable commercial method for RNA extraction from culture and milk samples of *E.coli* and *S.aureus* under the conditions described in this study.

Key Words: RNA extraction, bacteria, milk

T51 Effect of carbon dioxide on microbial growth in refrigerated raw milk. P. C. B. Vianna and M. L. Gigante*, *State University of Campinas*, *Campinas, SP, Brazil*.

UHT milk represents 74% of the fluid milk consumption in Brazil and the main problem that can affect its quality is age gelation, probably caused by indigenous enzymes and extracellular enzymes produced by psychrotrophic bacteria during the refrigerated storage of raw milk. The objective of this work was to evaluate the impact of carbon dioxide (CO_2) addition and the storage temperature on the microbial growth in refrigerated raw milk. Raw milk was divided into two portions: control milk (without CO_2 addition) and treated milk (added of CO_2 until pH 6.2). Each portion was subdivided in 300 ml glass bottles fitted with metal lids and stored at 4±1°C and 7±1°C. Samples were daily analyzed to standard plate count (SPC), psychrotrophic bacteria count and *Pseudomonas* spp. count. Analyses were performed until SPC had reached 7.5×10^5 ufc/ml, which corresponds to the microbiological standard for raw milk established by the Brazilian legislation. Split-split-plot design was used and the complete experiment was replicated two times. The treatments effects on SPC were evaluated by multivariate variance analysis. Gompertz model was used to evaluate the treatments effects on the development of psychrotrophic bacteria and *Pseudomonas* spp. by lag phase, growth rate and generation time parameters. CO_2 addition, temperature and storage time significantly affected the raw milk shelf life. Milk with CO_2 stored at 4°C took approximately 14 days to reach the SPC legal upper limit for raw milk, while milk without CO_2 took 12 days. Samples stored at 7°C took 8 and 6 days, with and without CO_2 addition, respectively. Independent of the storage temperature, CO_2 extended the lag phase, increased the generation time and decreased the growth rate of psychrotrophic bacteria and *Pseudomonas* spp. The addition of CO_2 effectively increased the shelf life and delayed the bacteria growth in raw milk and could be used to prevent quality problems in dairy products caused by extracellular enzymes produced mainly by psychrotrophic bacteria.

Key Words: carbon dioxide, milk shelf life, psychrotrophic bacteria

T52 Expression profile analysis of intestinal cells effected by *Lactobacillus acidophilus* NCFM. M. Wang[1], G. Zhang[1], L. Yao[1], Y. Zhou[1], L. Han[1], and Y. Jiang*[1,2], [1]*Key Lab of Dairy Science, Ministry of Education, Northeast Agricultural University*, *Harbin, China*, [2]*National Dairy Engineering & Technical Research Center, Northeast Agricultural University*, *Harbin, China*.

Lactic acid bacteria are a flock of microorganism which can make host cells healthy. However, further insights into the mechanism of action are needed to understand the rationale of their use. The objective of this study was to investigate the effect of *Lactobacillus acidophilus* NCFM, with the excellent biological characteristics and health function, on the gene expression profile of the human intestinal tract cell line Caco-2 by gene expression profile chip. Caco-2 cells were treated with *Lactobacillus acidophilus* NCFM (3×10^8cfu/ml) for 2h. The total RNA of them was extracted. Hybridization with gene expression profile chip was performed. The image scanning and data analysis were performed subsequently. The partial results of hybridization were validated by real time RT-PCR. The data showed that the expression levels of 508 genes were altered as compared with the control 473 of them were up-regulated, and 35 were down-regulated after *Lactobacillus acidophilus* NCFM treated Caco-2 cells. It was supposed that many genes in Caco-2 cells were induced, so that *Lactobacillus acidophilus* NCFM could play a part in immune response, antioxidant activity, bioadhesion, cholesterol absorption and so on. Four striking differential expression genes CCL2, PTX3, CXCR4 and TNFRSF9 which involved immune regulation system were validated by real time RT-PCR. And the results of real time RT-PCR showed the same expression trend as in gene chip. The differential expression genes in Caco-2 cell during the effect with *Lactobacillus acidophilus* NCFM can be found by gene expression profile chip. These genes in this study were likely to reveal the beneficial function and mechanism of this probiotic strain. *This work was supported by the Innovative Research Team Program of*

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Key Words: *Lactobacillus acidophilus* NCFM, Caco-2 cells, gene chip

T53 Development of a Multiplex-PCR detection assay for simultaneous identification of the major mastitis causing pathogens in dairy milk. B. Cressier*[1], C. Thibault[2], and N. Bissonnette[1,2], [1]*Université de Sherbrooke, Sherbrooke, QC, Canada*, [2]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*.

Mastitis still remains the major disease affecting the dairy industry worldwide. Microbiological methods are still thought to be the gold standard for mastitis pathogen detection in Canada. Instead, using a molecular detection system would reduce the delays to identify the causative pathogen and allow proceeding with the adequate veterinary treatment. A molecular detection technique would show unambiguous results with an improved sensitivity. To detect species-specific genes, one predilection approach relies on Multiplex-PCR to amplify multiple loci each localized to a specific pathogen's genomic DNA. In this study, we challenged this method for detecting in milk the major mastitis causing bacteria in a single PCR reaction: *Staphylococcus aureus, Escherichia coli, Klebsiella pneumoniae, Mycoplasma bovis, Streptococcus uberis, Str. agalactiae, Str. dysgalactiae*. Gene specific DNA primers have been designed for each species and tested for optimal sensitivity and specificity and for the absence of primer-dimers generated by cross-reaction in a PCR reaction. The primers used are 5′-labeled with different fluorescent dyes allowing improved sensitivity by fragment analysis through a capillary electrophoresis system (Genetic Analyser). To challenge the molecular detection assay, we optimized an extraction assay for isolation of bacterial genomic DNA. The extraction assay proposed is convenient for all species and also greatly reduces carry over of milk component which could greatly inhibit molecular detection: The milk sample is clarified using a chelator, centrifuged and washed before a chelating resin is used to resuspend and boil the bacterial pellet. This technique has the benefit of being simple, quick and inexpensive; it can also be easily integrated into a high throughput scheme using 96 or 384-well plaques. Therefore, this extraction and detection protocol is then transposable for screening dairy cattle herds regularly and detecting mastitis pathogens preventively.

Key Words: mastitis, pathogen detection, multiplex PCR

T54 Nisin-inducible expression of recombinant peptides in dairy lactic acid bacteria. J. A. Renye and G. A. Somkuti*, *USDA-Agricultural Research Service, Wyndmoor, PA*.

In *Pediococcus acidilactici* a four gene operon (*papA-D*) controls expression of pediocin, a class IIa bacteriocin with antilisterial activity. Previously we confirmed that this operon functions in *Streptococcus thermophilus* and *Lactococcus lactis* and that expression could be tightly regulated using a nisin-inducible promoter. In this study, nisin-induced expression of the pediocin operon was tested in *Lactobacillus casei* C2. The vector pRSNPed was electrotransformed into *L. casei* and the presence of the plasmid was confirmed by PCR amplification of a DNA fragment containing the *nisA* promoter and *papA/B* (0.8 kb). The *L. casei* transformants produced pediocin and inhibited the growth of *Listeria monocytogenes* Scott A; however, pediocin expression was not tightly regulated as observed in *S. thermophilus* and *L. lactis*. In the absence of nisin 1,600 arbitrary units (AU) ml^{-1} of pediocin were produced, equaling the level of production observed in *L. lactis* and surpassing the level observed in *S. thermophilus* (400 AU ml^{-1}) following nisin induction. When induced with nisin, the level of production by *L. casei* increased to 3,200 AU ml^{-1} and resulted in the inhibition of a nisin-resisitant strain of *L. monocytogenes (NR30)*, which remained resistant to supernatants of the *L. lactis* and *S. thermophilus* transformants. In addition, the expression vector pRSNAHP was constructed, to test the nisin-inducible promoter for the overexpression of a recombinant *pap* operon with the pediocin structural gene replaced with a synthetic gene for a milk-derived antihypertensive (AH) peptide. The operon was designed so that the recombinant peptide would be fused in frame with the pediocin leader peptide to allow for secretion of the AH peptide. After the electrotransformation into *S. thermophilus*, *L. lactis* and *L. casei*, the presence of pRSAHP was confirmed by PCR amplification of a 0.3 kb DNA fragment containing the AH peptide gene and *papA/B*. Results of research currently in progress indicate that the *nisA* promoter may be used to regulate the expression and secretion of recombinant peptides fused to the pediocin leader peptide.

Key Words: LAB, pediocin, antihypertensive peptide

T55 Growth-promoting activities of bovine and caprine caseinomacropeptide. G. Robitaille*, R. Ioannoni, and C. Jolicoeur, *Food Research and Development Centre, Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada*.

Caseinomacropeptide (CMP), is a 7 kDa polypeptide fragment released from κ-casein during chymosin-induced renneting of milk. Up to 50% bovine CMP (bCMP) were O-glycosylated. The extent of O-glycosylation of caprine CMP (cCMP) reaches less than 30%. N-acetyl and N-glycolyl neuraminic acid are the terminal sugars of oligosaccharides in goat specie in a proportion of 1:1, whereas N-acetyl neuraminic acid is the only amino sugar found on oligosaccharidic side chains linked to bCMP. In this study we analysed the effect of the addition of whole CMP, non-glycosylated CMP (aglyco-CMP), and glycosylated CMP (GMP) on the growth rate of 3 strains of probiotics: *L. rhamnosus* RW-9595, *L. plantarum* 299V, and *B. thermphiles* ssp *infantis* RBL 67. bCMP and cCMP preparations were fractioned by ion exchange chromatography to obtain aglyco-CMP and GMP having > 3.5 moles neuraminic acid / mole of GMP. Growth-promoting activities of CMP, aglyco-CMP, GMP, and bovine β-lactoglobulin were conducted in the basal medium described by Morishita et al. (1981) for lactobacilli, using turbidometric microplate assay under microaerophilic conditions. Supplementation of the growing medium with 0.5 to 2 mg/ml of bCMP and cCMP stimulated bacterial growth of *L. rhamnosus* RW-9595 and *B. thermphiles* ssp *infantis* RBL 67 ($P < 0.05$), compared to the medium without addition or the one supplemented with β-lactoglobulin. The growth rate improvement was related to the origin of the CMP ($P < 0.05$), about 1.3 and 1.1 times for bCMP and cCMP respectively, and was dose dependent. The addition of CMP to growth medium did not enhance *L. plantarum* 299V growth rate ($P > 0.1$) indicating that the growth-promoting effect of CMP was species specific. The growth-promoting activities of aglyco-CMP and GMP from bovine and caprine origin towards *L. rhamnosus* RW-9595 and *B. thermphiles* ssp *infantis* RBL 67 were similar ($P > 0.1$) suggesting that neither the presence of oligasaccharidic side chains nor the type of the neuraminic acid derivate was essential factors for the growth promoting activity of CMP.

Key Words: caseinomacropeptide, probiotic, bacterial growth

T56 Study of the genetic diversity of *Geotrichum candidum*. I. Alper* and S. Labrie, *Département des sciences des aliments et de nutrition, Centre de recherche en sciences et technologie du lait (STELA) – Institut des nutraceutiques et des aliments fonctionnels (INAF), Université Laval, Quebec, QC, Canada*.

Geotrichum candidum is a dimorphic yeast commonly inoculated on surface-ripened cheeses. The technological properties of *G. candidum* are strain-dependent, so analytical tools are vital for differentiating strains. The aim of the present study was to determine the genetic diversity of 16 *G. candidum* strains isolated from various environmental niches using ribotyping and random amplification of microsatellites by PCR (RAM-PCR). Ribotyping involves the sequencing of the operon coding for rDNA, especially the internal transcribed spacer regions, ITS1 and ITS2. We report, for the first time, the sequence of the rDNA operon of *G. candidum*. All the *G. candidum* strains were closely related phylogenetically and could be classified as members of de Hoog and Smith′s Group 1. While the strains could not be differentiated based solely on the sequence of the ITS1-5.8S-ITS2 region, seven could be differentiated by polymorphism analysis of the entire operon. Four RAM-PCR primers were tested, but only (GATA)4 resulted in PCR patterns that differentiated five strains. When combined, the two techniques made it possible to differentiate 10 of the 16 strains. These findings suggest that multilocus sequence typing, which is commonly used to differentiate strains of *Candida albicans*, a pathogenic yeast phylogenetically closer to *G. candidum*, may be an alternative method for studying the genetic diversity of *G. candidum* strains.

Key Words: *Geotrichum candidum*, rDNA operon, ribotyping

T57 Effect of somatic cell count on milk composition. R. Noorbakhsh*[1], A. Mortazavi[1], F. Shahidi[1], A. F. Mehdikhani[2], M. Ahoei[2], and A. Heravi Moussavi[2], [1]*Dept of Food Science and Technology, Ferdowsi University of Mashhad, Mashhad, Khorasan, Iran*, [2]*Dept of Animal Science, Ferdowsi University of Mashhad, Mashhad, Khorasan, Iran*.

The study was designed to evaluate the effect of somatic cell count (SCC) on milk composition. In total, 127 dairy farms bulk milk were used during 2007 and 2008. The farms located in east northern of Iran. Somatic cell count and milk composition were measured in the bulk milk. The SCC data was divided into five categories based on the California Mastitis Test (CMT) scores and these categories, rather than the continuous variable from which they were derived, were used for studying the effect of SCC on milk composition. The range of leukocyte levels in different CMT scores were: N, 0-200000; T, 200000-400000; 1, 400000-1200000; 2, 1200000-5000000; and 3, >5000000 per ml. Due to low number of records for the last score the data were excluded before further analysis. The model for analyzing the effect of CMT scores on milk composition also included year and season. The data were analyzed using General Linear Models. The SCC averaged 590730 ± 12353 leukocytes per ml. The median was 454000 cells and 25 and 75% quartiles were 322000 and 713000 leukocytes per ml, respectively. The distribution analysis showed that 44.3% of the data were between 250000 and 499000 leukocytes per ml. The SCC was numerically reduced in year 2008 compare with 2007 which shows an improvement in milk quality ($p=0.23$; 616614±60316 and 575043±54308 cells/ml, respectively for 2007 and 2008). The effect of season was significant and SCC was greatest in winter compare with summer and autumn ($p<0.01$). Milk fat ($p<0.01$; 3.46, 3.54, 3.56, and 3.63 ± 0.04%, respectively for N, T, 1, and 2) and protein ($p=0.04$; 3.08, 3.06, 3.05, and 3.07 ± 0.01%, respectively for N, T, 1, and 2) contents were affected by the CMT score groups. The effect of season was significant ($p<0.01$). Milk lactose and solids-not-fat contents were similar among the groups. The results demonstrated that milk fat and protein contents were affected by SCC. Results also presented a trend in milk quality improvement over the years.

Key Words: dairy cows, somatic cell count, milk composition

T58 Impact of *Lactobacillus acidophilus* NCFM surface protein expression on its binding properties toward the milk fat globule membrane. G. Brisson, H. F. Payken, E. Pettey, and R. Jimenez-Flores*, *California Polytechnic State University, San Luis Obispo*.

Dairy products are commonly used as a delivery system for the probiotic lactic acid bacteria (LAB). Recent genomics studies have revealed the importance of the milk environment in the expression of LAB probiotic functions. However, to date little is know on how the dairy products positively affect these probiotic bacteria function. The milk fat globule membrane (MFGM) contains components that are known to bind to LAB cell surface such as glycoproteins (mucins) and phospholipids. On the counterpart, proteins expressed at the surface of the lactic acid bacteria could also affect the bacterial adhesion to MFGM. This work aims to elucidate the impact *Lactobacillus acidophilus* NCFM cell surface protein on its ability to bind to the MFGM. Five mutant strains with single gene deletion on genes encoding for different surface proteins were obtained from Dr. T. Klaenhammer's laboratory (NC State University). The binding properties of these *L. acidophilus* NCFM mutant strains were tested toward the MFGM components present in buttermilk powder. The binding frequency of the different strains was determined by means of a sucrose density gradient procedure coupled to bacterial DNA quantification. The bacteria cell surface was characterized by determining their surface hydrophobicity and their surface protein profile after 5 M LiCl treatment. The results showed that the binding ability of the different strains was influenced by the bacterial surface hydrophobicity and their surface protein profile. The wild type NCFM and 4 of the mutants showed similar binding patterns, and under statistical scrutiny low significant difference. However, the deletion mutant to the S-layer protein slpA, showed a remarkable different binding pattern. This mutant bound tightly (average of 98% of cells in the assay) to buttermilk components. Verification of the differences in binding patterns were made by confocal fluorescent microscopy. Further work will focus on identifying the binding elements in the bacteria and the MFGM.

Key Words: lactobacillus, MFGM, probiotic

T59 Acid tolerance of *Lactobacillus acidophilus* LA-K as influenced by various pulsed electric field conditions. O. Cueva[1] and K. Aryana*[2,1], [1]*Louisiana State University, Baton Rouge*, [2]*Louisiana State University Agricultural Center, Baton Rouge*.

Pulsed electric field (PEF) processing involves the application of pulses of voltage for less than one second to fluid foods placed between two electrodes. *Lactobacillus acidophilus* is an important probiotic bacterium used for the production of fermented dairy products. Objective of this study was to elucidate the influence of certain PEF conditions on the acid tolerance of *Lactobacillus acidophilus* LA-K. Freshly thawed *Lactobacillus acidophilus* LA-K was suspended in sterile peptone 0.1% w/v distilled water and treated in a pilot plant PEF system. The treatments were pulse width (3, 6 and 9 µs), pulse period (10,000; 20,000 and 30,000 µs) and voltage (5, 15 and 25 kV/cm). Control was run through PEF system at 60 mL/min without receiving any pulsed electric field condition. Acid tolerance was determined at 0, 5, 10 and

15 minutes of incubation. Data were analyzed using the PROC GLM of the Statistical Analysis Systems (SAS). Differences of least square means were used to determine significant differences at $P < 0.05$. The control and the three different bipolar pulse widths studied were significantly different from each other. The acid tolerance of the control was significantly the highest, followed by the acid tolerance subjected to 3 μs and 6 μs. The acid tolerance subjected to 9 μs was the lowest. The control and the three different pulse periods studied were significantly different from each other. The acid tolerance of the control was significantly the highest, followed by the acid tolerances subjected to the pulse period of 30,000 and 20,000 us. The acid tolerance subjected to 10,000 μs was significantly the lowest. The control and the three different voltages studied were significantly different from each other. The acid tolerance of the control was significantly the highest followed by the acid tolerances subjected to 5 and 15 kV/cm. The acid tolerance subjected to 25 kV/cm was significantly the lowest. Acid tolerance of *Lactobacillus acidophilus* LA-K lowered by increasing pulse widths and voltages but lowering pulse periods.

Key Words: probiotic, PEF, lactobacillus acidophilus

T60 Growth of *Lactobacillus acidophilus* LA-K as influenced by certain pulsed electric field conditions. O. Cueva[1] and K. Aryana*[2,1], [1]*Louisiana State University, Baton Rouge*, [2]*Louisiana State University Agricultural Center, Baton Rouge*.

Pulsed electric field (PEF) processing involves the application of pulses of voltage for less than one second to fluid products placed between two electrodes. *Lactobacillus acidophilus* is an important probiotic bacterium used for the production of fermented dairy products. Objective of this study was to elucidate the influence of certain PEF conditions on the bile tolerance of *Lactobacillus acidophilus* LA-K. Freshly thawed *Lactobacillus acidophilus* LA-K was suspended in 0.1% w/v sterile peptone water and treated in a pilot plant PEF system. The treatments were pulse width (3, 6 and 9 μs), pulse period (10,000; 20,000 and 30,000 μs) and voltage (5, 15 and 25 kV/cm). Control was run through PEF system at 60 mL/min without receiving any pulsed electric field condition. Growth was determined hourly for 16 hours of anaerobic incubation at 37°C. Data were analyzed using the PROC GLM of the Statistical Analysis Systems (SAS). Differences of least square means were used to determine significant differences at $P < 0.05$. Bipolar pulse width effect had a significant ($p < 0.0001$) influence on the growth. Growth curve of the control was significantly higher than the growth of *Lactobacillus acidophilus* subjected at any of the bipolar pulse widths studied. There were no significant differences in growth among the three different bipolar pulse widths. Pulse period had a significant ($p = 0.0017$) influence on the growth. There were no significant differences among the control, 30,000 μs and 20,000 μs. The growth of *Lactobacillus acidophilus* subjected to the pulse period of 10,000 μs was significantly lower than the growth of the control and the growth when subjected to 30,000 μs. Voltage had a significant ($p < 0.0001$) influence on the growth. Growth subjected to 15 and 25 kV/cm were significantly lower than the control and 5 kV/cm. There were no significant differences between the control and 5 kV/cm. There were no significant differences between the growths when *Lactobacillus acidophilus* was subjected to 15 and 25 kV/cm.

Key Words: probiotic, growth, PEF

T61 Stability of *Bifidobacterium animalis* ssp. *lactis* BB12 in yogurt smoothie developed for use in clinical trials with children. E. Furumoto, L. Weir*, and R. Roberts, *Department of Food Science, The Pennsylvania State University, University Park*.

The objectives of this work were to develop a yogurt-based smoothie capable of delivering 10^{10} cfu of *Bifidobacterium animalis* ssp. *lactis* BB12/100 ml serving and to evaluate survival of BB12 during refrigerated storage at 5°C. Yogurt smoothie was manufactured using a two step process. In step one, a yogurt mix was pasteurized, homogenized, heat-treated for 30 minutes at 85°C, cooled to 42°C, inoculated with *Streptococcus thermophilus* and *Lactobacillus delbrueckii* ssp. *bulgaricus*, incubated quiescently to a final pH of 4.6 then cooled to 25°C. In step two, a "stabilizer slurry" containing pectin, sugar and 36DE CSS was prepared, heated to 85°C, held for 30 minutes then cooled to 40°C. Yogurt, stabilizer slurry and strawberry puree were blended, homogenized, packaged and cooled. To determine the population of BB12 in the product, samples were diluted in sterile peptone water and pour plated using modified MRS agar containing dicloxacillin, LiCl, and cysteine hydrochloride followed by anaerobic incubation at 37°C for 48 h. Representative colonies counted as BB12 were picked and evaluated by PCR using *B. animalis* ssp. *lactis* specific primers to verify the selectivity of the plating method. In preliminary experiments two procedures for addition of BB12 (10^9 cfu/ml) to the yogurt smoothie were evaluated. In one procedure BB12 was added at the same time as the lactic starter culture (i.e. prior to fermentation) and in the second procedure BB12 was added after fermentation and cooling to 25°C. When BB12 was added prior to fermentation a pronounced "acetic acid flavor", probably due to metabolic activity of the bifidobacteria, was observed in the product which was deemed undesirable. Therefore the second method was chosen for manufacture of the intervention for use in clinical trials. Stability data for intervention manufactured monthly for 12 months revealed the population of BB12 declined slowly (average D-value 47.4±12 days) over storage at 5°C but remained at acceptable levels i.e. above 10^8 cfu/ml (10^{10} cfu per serving) for at least 30 days with no appreciable changes in viscosity, pH or flavor.

Key Words: *Bifidobacterium*, yogurt, probiotic

T62 Bile tolerance of *Lactobacillus acidophilus* LA-K as influenced by certain pulsed electric field conditions. O. Cueva[1] and K. Aryana*[2,1], [1]*Louisiana State University, Baton Rouge*, [2]*Louisiana State University Agricultural Center, Baton Rouge*.

Pulsed electric field (PEF) processing involves the application of pulses of voltage for less than one second to fluid products placed between two electrodes. *Lactobacillus acidophilus* is an important probiotic bacterium used for the production of fermented dairy products. Objective of this study was to elucidate the influence of certain PEF conditions on the bile tolerance of *Lactobacillus acidophilus* LA-K. Freshly thawed *Lactobacillus acidophilus* LA-K was suspended in 0.1% w/v sterile peptone water and treated in a pilot plant PEF system. The treatments were pulse width (3, 6 and 9 μs), pulse period (10,000; 20,000 and 30,000 μs) and voltage (5, 15 and 25 kV/cm). Control was run through PEF system at 60 mL/min without receiving any pulsed electric field condition. Bile tolerance was determined hourly for 16 hours. Data were analyzed using the PROC GLM of the Statistical Analysis Systems (SAS). Differences of least square means were used to determine significant differences at $P < 0.05$. Bipolar pulse width effect had a significant ($p < 0.0001$) influence on the bile tolerance. Bile tolerance of the control was significantly higher than the bile tolerance subjected to any of the bipolar pulse widths studied. There were no significant differences among the three different bipolar pulse widths. Pulse period had a significant ($p < 0.0001$) influence on the bile tolerance. The control

and the three different pulse periods studied were significantly different from each other. The bile tolerance of the control was significantly the highest, followed by the bile tolerances subjected to 30,000 μs and 20,000 μs respectively. The bile tolerance subjected to 10,000 μs was significantly the lowest. Voltage had a significant ($p < 0.0001$) influence on the bile tolerance. Bile tolerance of the control and bile tolerance of *Lactobacillus acidophilus* LA-K subjected to 5 kV/cm were significantly the highest while the bile tolerance when subjected to 25 kV/cm was significantly the lowest.

Key Words: probiotic, bile, PEF

T63 European Union Decision 2073/2005: A comparison between 3M Petrifilm *Enterobacteriaceae* and ISO 21528:2 in a milk powder production chain. M. Ferraz*, M. Cerqueira, and M. Souza, *Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brasil*.

The experiment was carried out in a dairy industry located in Minas Gerais, Brazil. The objectives were to evaluate the presence of *Enterobacteriaceae* in the milk powder production chain (raw milk, pasteurized milk, milk powder, handler and equipments swabs) and also to verify the influence of the pre-enrichment of samples for microbiological recovery. The analyses were made in seven periods, during three months. The pre-enrichment of the samples yield in a significant variation in the initial population of *Enterobacteriaceae* only in raw milk ($p < 0.05$). It was concluded that there was an equivalence between methodologies International Organization for Standardization (ISO) 21528:2 and 3M Petrifilm *Enterobacteriaceae* for all the samples, with and without pre-enrichment ($p > 0.05$). There was a significant difference in the counting of *Enterobacteriaceae* in the raw milk compared to the other points ($p < 0.001$). When comparing the samples between them, except for raw milk, there was statistical equivalence in the counting of *Enterobacteriaceae* ($p > 0.01$). This indicates that raw milk is the main source of *Enterobacteriaceae* and also that the process of this company is efficient in its reduction. The average counting in raw milk was 5,68log and 5.83log and in the milk powder 0.45log and 0.97log, respectively to 3M Petrifilm *Enterobacteriaceae* and ISO 21528:2. The results obtained in this study indicate that the 3M Petrifilm may be an alternative method to the ISO 21528:2 for enumeration of *Enterobacteriaceae*. Another conclusion is that the industry used in this study can be considered a potential exporter of milk powder to the European Union in terms of *Enterobacteriaceae* counting.

Key Words: *Enterobacteriaceae*, milk powder, Petrifilm

T64 Environmental scanning of bacteria with the potential to produce ropy milk in a farm. A. Laubscher*[1], K. White[1], A. Cano[1], R. Cano[2], and R. Jimenez-Flores[1], [1]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo*, [2]*Biological Sciences Department, California Polytechnic State University, San Luis Obispo*.

Prevention of microbial contamination in raw milk is an important objective in farms where value added is tied with quality. Recent reports in some regions of ropy milk have made us aware again of the reoccurring problem. Ropy milk is characterized by its viscosity and tendency to form a slimy thread, which causes rejection. The viscous character of the milk is produced by a complex oligosaccharide present in the capsule of different microorganisms. Over 250 raw milk samples were received from plants throughout the southern states. Isolates from 160 positive "ropy tests" were found to belong to the enterobacteracea family. Using API biochemical identification tests, over 80% of the positives are in the *Klebsiella* species. This result gives us the belief that the presence of ropy milk can be correlated to coliform counts. The objectives were to identify high-risk areas for contamination of the responsible bacteria, the correlation with coliform and *Escherichia coli* (E/C) counts, and development of a subjective or quantitative method to evaluate the risk of finding ropy milk producing bacteria. Ten locations were examined on the Cal Poly Dairy Farm, with bedding having the highest E/C counts and the most probable source for ropy-causing bacteria contamination on the farm. The threshold for the enumeration of ropy-causing bacteria was determined to be only 2.5 CFU/10 ml in a sterile milk sample was enough to turn the milk ropy. The threshold of the ropy-causing bacteria is much higher in the presence of typical raw milk microorganisms, suggesting a poor competitive nature. Our results indicate that "ropyness" is a result of poor-competing bacteria and poor sanitary conditions, in particular those associated with biofilm formation.

Key Words: milk quality, food safety, exopolysaccharide

T65 Influence of growth medium composition on survival and storage stability and viability of lactobacilli during freeze-drying. M. I. Tudor, E. P. Cuesta-Alonso*, and S. E. Gilliland, *Oklahoma State University, Stillwater*.

Lactic acid bacteria (LAB) play important role as starter and probiotic cultures in the production of fermented foods. Preservation technologies, like freeze drying, are required to guarantee long-term viability and functional activity of the cultures. However undesirable effects are observed since some starter cultures are not resistant to freezing and are not stable during storage. The objectives of this study are to evaluate the effect of growth medium composition and pH of growth of probiotic strains of *Lactobacillus* on survival after freeze-drying and subsequent refrigerated storage. Four strains of *Lactobacillus acidophilus* (O-16, 381-IL-28, L-1, L-23), two strains of *L. casei* (E-5 and E-10) and *L. reuteri* X-18 were grown in MRS broth supplemented with different concentrations of Tween 80 (0, 0.1, 0.2, 0.3, 0.4, and 0.5). In the study of influence of growth pH, the cultures were grown in a fermentor with controlled pH (4.5, 5.0, 5.5, and 6.0). The cultures were harvested by centrifugation and resuspended in 10% milk. The cultures were freeze dried, sealed under vacuum, and stored at 4°C. The bacterial counts before and after freeze-drying and during storage of 1, 7, 14 and 21 days were determined. Strains of *Lactobacillus* varied in viability after freeze-drying and refrigerated storage up to 21 days with viable counts of up to 1010 CFU/mL. Tween 80 improved survival rate in some but not in all strains after freeze-drying. Survival rate of 99.2% was obtained from *L. acidophilus* O-16 grown in 0.2% Tween 80. Higher concentrations (0.4 and 0.5) of Tween 80 resulted in decreased survival of L. casei. In general, survival rates of cultures were lower when grown in pH 4.5. The results suggest that Tween 80 and pH influenced survival of some LAB during freeze-drying and that it is possible to grow LAB with a higher number of viable cells to be used for the development of stable probiotic freeze-dried cultures.

Key Words: lactic acid bacteria, *Lactobacillus*, freeze drying

T66 Development of a sequence-based molecular subtyping method for *Bacillus cereus* dairy isolates. D. Miller*, S. Doores, and R. Roberts, *Pennsylvania State University, University Park*.

Bacillus cereus is recognized as a foodborne pathogen and as a spoilage microorganism associated with development of quality defects limiting the shelf life of pasteurized milk. When trying to determine routes of contamination by *B. cereus* during manufacture of dairy products it is important to be able to subtype strains obtained at the farm, in raw milk silos and in the finished product. Multilocus sequence typing (MLST) is a DNA sequence-based approach to subtyping that produces unequivocal and highly portable data. However, the cost associated with sequencing seven housekeeping genes, as is done in many MLST schemes, may limit the utility of this subtyping method for large-scale tracking studies. To reduce the number of genes that must be examined to discriminate between strains, hypervariable genes, such as virulence genes may be employed in a MLST scheme. The objective of this work was to develop a two- or three-gene MLST scheme for subtyping *B. cereus* dairy isolates based on a combination of housekeeping genes and virulence genes. To select virulence genes for inclusion in the MLST scheme, the incidence of nine virulence genes (*entFM*, *hblA*, *hblB*, *hblC*, *hblD*, *nheA*, *nheB*, *nheC*, and *sph*) was evaluated in 13 *B. cereus* reference strains and milk isolates Two virulence genes, *entFM* and *nheC*, were detected in all strains evaluated The number of sequence types obtained using various combinations of housekeeping and virulence gene sequences was evaluated and was found to range from five (*ccpA* and *pyrE*, *adk* or *recF* and *sucC*) to eight (any housekeeping gene and *nheC*, or *entFM* and *nheC*) for the two-gene MLST schemes. The addition of a third gene to the MLST scheme did not increase the number of sequence types. The two-gene MLST schemes could be used in studies to identify sources of *B. cereus* contamination during milk production and processing.

Key Words: *Bacillus cereus*, multilocus sequence typing, subtyping

T67 Confirmation of *Bacillus cereus* milk isolates using traditional microbiological and a recently developed molecular method. D. Miller*, S. Doores, and R. Roberts, *Pennsylvania State University*, *University Park*.

Bacillus cereus, recognized as a foodborne pathogen and as a spoilage microorganism associated with development of quality defects limiting the shelf life of pasteurized milk, is a member of the *Bacillus cereus* group which is composed of a cluster of six closely related species. Mannitol-egg yolk-polymyxin (MYP) agar is the AOAC-approved medium for isolation of *B. cereus* from milk; however other members of the *Bacillus cereus* group exhibit similar reactions on MYP agar. Thus, *B. cereus* must be further differentiated from these closely related species. The objective of this study was to evaluate application of a recently developed PCR-based method for confirmation of *B. cereus* on a set of 58 presumptive-positive *B. cereus* group members and 315 presumptive-negative colonies isolated on MYP agar as part of a broader survey evaluating the microbiological quality of retail pasteurized milk. Samples were characterized using both traditional microbiological and PCR-based methods. Using PCR-based methods, 54 of 58 presumptive *B. cereus* isolates (93%) were confirmed as members of the *B. cereus* group but only 17 (32%) were further confirmed as *B. cereus* using the PCR-based confirmation method. All of these isolates were also confirmed as *B. cereus* with traditional microbiological methods. Isolates confirmed as *B. cereus* group members but not *B. cereus* exhibited growth at 7°C and may have been *B. weihenstephanensis*. Four known *B. weihenstephanensis* strains were evaluated with the PCR-based confirmation method, and none yielded a positive reaction. When the 315 non-presumptive *B. cereus* group isolates recovered on MYP agar were screened using the *B. cereus* group-specific PCR-based method, all yielded negative results, and none were confirmed as members of the *B. cereus* group. The findings of this study suggest the PCR-based method developed by Choo et al. (2007) can be used as a reliable means for confirmation of *B. cereus* dairy isolates.

Key Words: *Bacillus cereus*, *Bacillus cereus* group, polymerase chain reaction

T68 Influence of the sample pre-heating and time for reanalysis in the Total Bacteria Count of milk by flow cytometry. L. Clementino[1,2], F. A. Pinto[1,2], L. M. Fonseca[1,2], J. F. Castro[1], R. Rodrigues[1,2], M. M. O. P. Cerqueira*[1,2], M. O. Leite[1,2], C. S. P. Fonseca[1], C. F. A. M. Penna[1,2], and M. R. Souza[1,2], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis*, *Belo Horizonte, MG, Brazil*.

Flow cytometry is a technique that is becoming widely used to measure microbial counting for milk quality evaluation. In Brazil, legal requirements approved the use of these equipments for measurement of microbial contamination in raw milk. It is necessary to know the factors that can affect the efficiency of this technique. The objective of this research was to evaluate the effects of sample temperature and the viability of sample reanalysis when carry-over contamination from a previous sample demands a new analysis. The experiment was done in the Laboratory of Milk Quality Analysis (School of Veterinary Medicine, Federal University of Minas Gerais, Brazil). For Total Bacteria Count the equipment Bactocount IBC (Bentley®) was used. To verify the effect of sample pre-heating, 126 samples of raw milk were randomly obtained from bulk tank milk in farms close to Belo Horizonte-MG, collected in 250mL sterilized flasks containing Azidiol(conservante), and sent to the Laboratory under adequate conditions. The samples were analyzed in experimental groups of 20, with the 19th and 20th samples used as control of respectively, temperature, and bacteria counting. Each sample was divided in four aliquots, each pre-heated at temperatures of 5°C, 15°C, 20°C or 40°C for 15 minutes. The statistical analysis was done by general linear model, after logarithmic transformation of the colony forming units (CFU). Comparison between treatments was made by Fisher Test. The results showed that there was no statistical difference ($p \geq 0.05$) between the experimental groups. To evaluate the feasibility of sample reanalysis when high carry over contamination occurs, 440 samples of raw milk were obtained and processed as above indicated. Each sample was divided in 50 mL aliquots and analyzed after 20, 40, and 60 minutes of storage at 25°C, with a total of 1,760 samples. The statistical analysis (Tukey Test) showed that the time of storage for samples which demand reanalysis did not affect the bacteria counting up to 60 minutes after storage at 25°C, since preserved by azidiol. *Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq; CAPES.*

Key Words: Azidiol, flow cytometry, total bacteria count

T69 Methodology for differentiation of lactic acid bacteria in cheese made with probiotic adjunct cultures. C. J. Oberg*[1], L. Moyes[1], C. Brothersen[2], and D. J. McMahon[2], [1]*Microbiology Department, Weber State University*, *Ogden, UT*, [2]*Western Dairy Center, Utah State University*, *Logan*.

Many media have been developed to facilitate enumeration of lactic acid bacteria (LAB) with some media containing compounds or chemical adjustments. Defined strains of *Lactococcus*, *Lactobacillus*, and *Bifidobacterium* were screened on selective media designed to prevent growth

of competing LAB or to promote growth of certain LAB over others. Specific media were selected that gave the highest differential results, M17-Lactose for starter lactococci, MRS with added sorbitol for total LAB, either MRS or reinforced *Clostridium* agar (plus bromocresol green) with vancomycin for *Lb. casei* and *Lb. paracasei*, MRS with sorbitol as the sole sugar for *Lb. acidophilus*, and MRS supplemented with cysteine and an antibiotic cocktail (neomycin sulfate, nalidixic acid, lithium chloride, and paromomycin sulfate) for *Bifidobacterium*. Lactococci media was incubated aerobically at 30°C, *Lb. acidophilus* media was incubated at 45°C in a gaspak, with all other media incubated at 37°C in a gaspak. MRS plus sorbitol agar gave higher bacterial counts at all test periods even above *Lb. casei* specific media in aged cheese suggesting it could be used to obtain the total LAB count for cheese. Lactococci media must be analyzed at 24 h while all other media were analyzed at 48 h. Some strains of *Lb. casei* and *Lb. paracasei* appear able to grow on *Bifidobacterium* media making colony size exclusion an important consideration. Incubation time and temperature along with antibiotic concentrations are important when trying to suppress nonstarter (NS) LAB counts in aged cheese analysis. Even with these exact parameters, after 90 d, NSLABs appear in cheese flora on some selective media. It is important to test starter and adjunct cultures on selective media prior to cheese making trials as some lactobacilli can grow on other exclusionary media. Comparison of *Lb. casei* media to media for *Bifidobacterium* and *Lb. acidophilus* media during cheese aging can provide an indication of probiotic adjunct survival versus NSLAB growth. These media can provide an indication of probiotic adjunct survival in cheese but care must be taken in interpreting results particularly as cheese ages.

Key Words: probiotic, cheese, methodology

T70 Use of supercritical fluid extraction to remove non-polar lipids from whey buttermilk powder. M. R. Costa*[1,2], M. L. Gigante[2], and R. Jiménez-Flores[3], [1]*Universidade Norte do Paraná, Londrina, Paraná, Brazil*, [2]*Universidade Estadual de Campinas, Campinas, São Paulo, Brazil*, [3]*California Polytechnic State University, San Luis Obispo*.

The presence of glycoproteins and phospholipids in buttermilk makes this product unique in its function and reported health benefits. However, industrial production of ingredients containing high concentrations of milk fat globule membrane (MFGM) material is normally associated with high triglyceride concentration. Supercritical fluid extraction (SFE) has been utilized to extract lipids from foods, such as nuts and spices. More recently, our research group among others has used this technology on dairy products. The objective of this work was to evaluate the efficiency of the supercritical fluid extraction to remove the non-polar lipids from a whey buttermilk powder. A whey buttermilk powder was produced by ultrafiltration/diafiltration of whey buttermilk (membrane of 10 KDa molecular weight cutoff, at 25 °C) followed by spray-drying of the final retentate. The whey buttermilk powder was submitted to supercritical extraction (350 bar, 50 °C) using carbon dioxide. The powders, prior and after the supercritical extraction, had their gross composition, lipid profile by Thin Layer Chromatography (TLC), and phospholipids content by High Performance Liquid Chromatography (HPLC) evaluated. All the experiments were done in triplicate. The whey buttermilk powder prior the SFE had, in dry matter basis, 47.4, 47.3, 7.2, 3.0 and 2.3% of proteins, lipids, phospholipids, lactose and ash, respectively. The supercritical extraction removed approximately 34 g of lipids from each 100 g of sample, using 97 g of carbon dioxide to extract each gram of this fat. This extraction represented a reduction of 73% in the quantity of total lipids present originally in the powder sample. The process removed exclusively triglycerides from the powder matrix, as seen on the extracted lipids TLC profile. The proteins, lipids, phospholipids, lactose and ash contents in the final powder were 72.7, 20.6, 12.0, 3.5 and 3.2%, respectively.

Key Words: supercritical carbon dioxide, lipid profile, phospholipids

T71 Effect of pH and ionic strength on heat-induced deposition of whey proteins at the surface of fat droplets in oil-in-water emulsions. M. Britten* and S. Lamothe, *Food Research and Development Centre, Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada*.

The increasing demand for food products with improved nutritional qualities stimulates the food industry to develop new techniques to encapsulate and protect bioactive ingredients. Whey proteins are commonly used in food products as emulsifiers to form a protecting membrane around fat droplets during emulsification process. Controlling the amount of protein adsorbed at the droplets surface (protein load) could then modulate the properties of the emulsion, such as oxidative stability, kinetics of flavor release or texture of rennet and acid gels. The objective of this study was to increase whey protein load of emulsions using heat-induced protein deposition. The effect of pH and ionic strength during thermal treatment was studied. An emulsion was prepared by mixing 20% w/w sunflower oil with whey protein dispersion (2.75%) adjusted to 6.8. Homogenization was performed at 3000 psi (2 passes) and 500 psi (1 pass). These conditions were chosen to produce fine emulsion with droplet size of ~300 nm. Emulsion were diluted (1:1, w/w) in phosphate buffer 30 mM to the desired pH (6.8 to 6.0) and ionic strength (0 or 25mM NaCl) and thermal treatment (80°C, 60 min) was applied. Protein load and physical stability measurements were performed. Heat treatment had only a slight effect on protein load, which increased from 2.4 to 2.6 mg/m^2. However, protein loads higher than 4.0 mg/m^2 were obtained with appropriate adjustment of pH and ionic strength. This corresponds to the adsorption at the droplets surface of more than 90% of the proteins in the initial dispersion. Heat-induced protein deposition was irreversible since the increase of the pH to the initial pH of 6.8 did not cause a significant protein load decline. Protein deposition slightly increased the mean diameter of emulsions (from 300 to 345 nm) and polydispersity index remained lower than 0.3, indicating that the treatment did not induce flocculation. These results suggested that appropriate adjustement of pH and ionic strength during heat treatment can be used to control whey protein deposition at the surface of fat droplets.

Key Words: whey proteins, protein load, emulsion

T72 The impact of antioxidant addition on flavor stability of Cheddar whey and whey protein. I. W. Liaw*[1], H. Eshpari[2], P. S. Tong[2], and M. A. Drake[1], [1]*North Carolina State University, Raleigh*, [2]*CalPoly University, San Luis Obispo, CA*.

Whey protein ingredients are widely used in food formulations. Off-flavors in whey products can carry through into ingredient applications and negatively affect consumer acceptance. The objectives of this study were to evaluate the impact of antioxidant addition in prevention of flavor deterioration of fluid whey and flavor of whey protein concentrate (WPC). Cheddar cheeses were manufactured in triplicate. Fresh whey was collected and pasteurized followed by fat separation. Three treatments, 0.05% w/w ascorbic acid, 0.5% w/w whey protein hydrolysate (WPH), and nitrogen flushing, were administered to the pasteurized whey. A control with no antioxidant addition was also

evaluated. Wheys were stored at 4C and evaluated after 0, 2, 4, 6, and 8 days. Whey flavors were documented by descriptive sensory analysis. Volatile components were evaluated by solid phase micro-extraction with gas chromatography mass spectrometry. Selected treatments were subsequently incorporated into liquid whey and processed into spray dried WPC. Cardboard flavors increased in fluid wheys with storage. Liquid wheys with ascorbic acid, WPH, or nitrogen flushing had lower cardboard flavor across storage compared to control whey. Lipid oxidation products, such as hexanal, heptanal, and nonanal, increased in liquid whey during storage, but liquid whey with added ascorbic acid, WPH, or nitrogen flushing had lower concentrations of these products. WPC with added ascorbic acid or WPH had lower cardboard flavor and lower concentrations of hexanal, heptanal, and nonanal compared to control WPC. WPC with added WPH, however, had a distinct potato flavor by sensory analysis which was absent in control WPC or WPC with added ascorbic acid. These results suggest that addition of an antioxidant to liquid whey prior to further processing may be beneficial to flavor of spray dried whey protein ingredients.

Key Words: whey protein, flavor, antioxidant

T73 Comparison of composition, sensory and volatile components of 80% whey protein and serum protein concentrates. J. P. Evans*[1], J. Zulewska[2], M. Newbold[2], D. M. Barbano[2], and M. A. Drake[1], [1]*North Carolina State University*, *Raleigh*, [2]*Cornell University*, *Ithaca, NY*.

Serum or 'native' whey protein concentrates (SPC) are whey proteins that are removed from milk prior to cheese-making. Since SPC are not exposed to the cheese make-process, enzymatic and/or chemical reactions that can lead to off-flavors are reduced. The objectives of this study were to identify and compare the composition, flavor, and volatile components of 80% protein SPC and WPC (SPC80, WPC80). SPC80 and WPC80 were manufactured in triplicate with each pair of serum and traditional whey protein manufactured from the same lot of milk. At each replication, spray-dried (SD) product from each protein source was collected. Commercial WPC80 were also collected for sensory and volatile analyses. A trained sensory panel documented the sensory profiles of the rehydrated powders. Volatile components were extracted by solid phase micro-extraction (SPME) with gas chromatography-mass spectrometry. Consumer acceptance testing was conducted with 6% protein acidic beverages made with SPC80 and WPC80, as well as commercial WPC80. SPC80 was lower in fat and had a higher pH than pilot plant manufactured WPC80 and commercial WPC80 ($p<0.05$). Few sensory differences were documented between the directly rehydrated SPC80 and WPC80 manufactured in this study, but their flavor profiles were distinct from flavor of rehydrated commercial WPC80 ($p<0.05$). WPC80 manufactured in this study generally had higher concentrations of lipid oxidation products than SPC80, and concentrations of lipid oxidation products in commercial WPC80 were generally higher than those concentrations ($p<0.05$). Trained panelists documented protein-associated flavors in acidic beverages that were not detected in reconstituted neutral pH protein solutions. Protein beverages made with SPC80 were not liked as well as protein beverages made with WPC80 manufactured in this study or one commercial WPC80 ($p<0.05$). These results suggest that composition, physical properties and volatile compound composition of SPC80 are distinct from WPC80. These differences may contribute to differences in flavor in low pH ingredient applications.

Key Words: serum protein, whey protein, flavor

T74 Production efficiency of a 95% serum protein (SP) reduced micellar casein concentrate (MCC) produced with ceramic microfiltration (MF) membranes. E. E. Hurt*[1], J. Zulewska[2], M. W. Newbold[1], and D. M. Barbano[1], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Warmia and Mazury*, *Olsztyn, Poland*.

Four lots of pasteurized skim milk (72ºC, 15s) were microfiltered at 50°C [about 3X concentration] using a uniform-transmembrane-pressure bleed-and-feed process on a 0.1µm ceramic membrane. This was followed by 2 diafiltration steps, where the retentate was diluted 1:2 with reverse osmosis water. The MCC after the 3-stage process had a total solids of 10.8%, crude protein of 9.12% and fat of 0.37%. The L value (whiteness) of skim milk is typically about 74. Retentate whiteness increased by MF stage from 78.3 to 79.1 to 80.1. Whiteness of MCC from the 3rd stage was equivalent to milk containing 1.5% fat. The amount of SP removed from skim milk was determined by 2 methods. The 1st method used the mass of SP [(TN-NPN)*6.38] in permeate divided by the mass of SP [(NCN-NPN)*6.38] in skim milk where SP was determined using Kjeldahl. The 2nd method (SDS-PAGE) used SP (sum of the relative area of SP bands) in skim milk minus the same bands in retentate for each stage divided by the relative area of SP in skim milk. Theoretical (coefficient of rejection equals 0) SP removal is 68, 22 and 7% for the 1st, 2nd and 3rd stages, respectively with a total SP removal of 97% for a 3-stage 3X process. Based on the Kjeldahl method 67.15, 24.92, 12.24% of the SP was removed in the 1st, 2nd and 3rd stages, respectively for a total SP reduction of 104.31% in the present study. In a separate study, casein content of MF permeate was found to be as high as 0.03% and this would cause an overestimation of SP [(TN-NPN)*6.38] removal in the present study. If the amount of casein in the permeate was 0.01, 0.02 or 0.03%, then total SP reduction by the process described above would be 101.29, 98.26 and 95.21% respectively. According to SDS-PAGE analysis the SP removed was 68.5, 18.4 and 2.8% from the 1st, 2nd and 3rd stages, respectively with a total SP reduction of 89.7%. The 3-stage process using the conditions described above produced a 90 to 95% SP reduced MCC.

Key Words: microfiltration, micellar casein concentrate

T75 Functionality characterization of 65% and 95% serum protein (SP) reduced micellar casein concentrates (MCC): Concentration and drying effects. C. M. Beliciu*[1], J. Zulewska[2], M. Newbold[1], C. I. Moraru[1], and D. M. Barbano[1], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Warmia and Mazury*, *Olsztyn, Poland*.

This work evaluated the influence of SP removal and drying method on the functionality of 65% and 95% SP reduced MCC obtained by microfiltration. For powders, bulk density, solubility, wettability, emulsification and foaming properties were determined. For liquid preparations (fresh retentates and reconstituted powders), rheological and coagulation behavior were evaluated. Drying methods had no impact on bulk density of 65% SP reduced MCC powders, but affected wettability, solubility, emulsion and foaming. The degree of SP removal had no influence on wettability, emulsification and foaming, but did impact bulk density and solubility for both MCC types. The drying method and degree of SP removal had no significant influence on the rheological properties of reconstituted MCC. Viscosity and yield stress (at 20°C) of liquid MCC increased exponentially with casein (CN) concentration. Above 10% CN, the liquid MCC became shear thinning. The viscosity of liquid MCC increased exponentially as temperature decreased, with temperature effects being more pronounced at high CN concentration. To evaluate the coagulation behavior of liquid MCC, rennet was added at a constant rennet:CN ratio. Coagulation dynamics was monitored

by the change in elastic modulus (G′). Maximum G′ was used as a measure of coagulum firmness. Coagulation rate was evaluated using the time constant of the Scott-Blair model. For both fresh retentates and reconstituted MCC the degree of SP removal did not affect coagulum firmness. Fresh retentates had significantly higher G′max (1351±75Pa) than reconstituted MCC (1062±83Pa). Coagulation rate was higher for 95% SP reduced as compared to 65% SP reduced MCC. Reconstituted 95% SP reduced MCC formed weaker coagulum than 65% SP reduced MCC, possibly due to a lower calcium content of the 95% SP reduced caused by the use of diafiltration in the manufacturing process. This study provides processors with useful information for the processing, storage and use of MCC.

Key Words: casein concentrate, rheology, coagulation

Food Safety

T76 A modeling system to predict *S.aureus* growth and SEA production in milk. F. Zhao, X. Qu, X. Lv, L. Xiang, B. Yan, and Y. Jiang*, *Northeast Agricultural University*, *Harbin, China*.

Staphylococcus aureus food poisoning often breaks out among patients who ingest dairy products. The main cause of this food poisoning was staphylococcal enterotoxin A (SEA). So it is an importance to predict *S.aureus* growth and SEA production in contaminated milk. The objective of this study is to provide a modeling system to predict the growth and SEA production of *S.aureus* in milk. Growth and SEA production of *S.aureus* 13565 in milk were studied at constant temperatures of 10-30 centi-degree. At each temperature, pure culture of strain 13565 was added to bacteriologically negative and SEA-free sterilized liquid milk to obtain an initial inoculum of 10^2-10^3 cfu/ml. The inoculated milk was then dispensed to sterile tubes and placed in a controlled temperature incubator. The incubation time was determined by temperature. After each incubation period, duplicate sample tubes were removed from incubator. Viable cell counts of samples were determined with the spread plate method (three plates per dilution). Averages and standard deviations of the transformed values were then calculated. SEA in samples was measured by VIDAS Staph Enterotoxin Test. The SEA concentration was determined by a standard curve developed using purified SEA in milk. The averages of two measurements were calculated for each data point. Growth curves can be described with the modified logistic model and the modified Gompertz model at high temperatures, such as 20-30 centi-degree, but the former described more accurately than the latter model. The amount of toxin in milk increased linearly with time from the time the cell population reached about $10^{6.4}$ cfu/ml. And the rate of toxin production increased linearly at these temperatures. The modeling system for *S.aureus* growth and SEA production has been roughly established in the study. The predictions of the system can be used as an indication, and also as reminder. *This work was supported by the National Key Technology R&D Program of China (2006BAD04A08-13) and the Key Project of Chinese Ministry of Education (208036). Corresponding Author: Dr. Yujun Jiang.*

Key Words: *Staphylococcus aureus*, enterotoxin, modeling system

T77 *Salmonella* serotype shift during an endemic dairy infection. J. Van Kessel* and J. Karns, *USDA-ARS*, *Beltsville, MD*.

Dairy farms are known reservoirs for *Salmonella* spp. and control of this organism is challenging. Salmonellae have been shown to be endemic in herds in part because they are easily spread between animals and throughout the farm environment. The impact of the infection on the herd is variable and dependent, in part, on the serotype. More than 2500 serotypes are known and animal carriers can be difficult to identify because they are often asymptomatic. As part of a multi-herd study, a dairy herd with an endemic, asymptomatic *Salmonella* infection was monitored extensively for 4 years. Bulk milk and in-line milk filters were collected weekly, and individual fecal samples were collected from all adult animals every 6 to 8 weeks. *Salmonella* detection was based on traditional culture methods. Prevalence of fecal *Salmonella* shedding in the 105 cow herd averaged 56% (range 10-95%) during this time. Although several *Salmonella* serotypes were identified over the course of the study, the initial dominant (>99% of isolates) serotype was Cerro. After 1.5 years into the outbreak, the serotype Kentucky began to gradually increase in prevalence, and at 2 years 39% of the fecal isolates were Kentucky. Over the next six months Kentucky became the dominant serotype representing >85% of fecal isolates. The serotype conversion from Cerro to Kentucky was first detected via analysis of the weekly milk filters. However, while monitoring of the milk filters was useful for detecting major shifts in serotype dominance, serotype prevalence in the individual milk filters was not predictive of the concurrent fecal serotype prevalence. This is the first detailed description of an endemic *Salmonella* infection in a dairy herd that undergoes a gradual shift from one serotype to another.

Key Words: *Salmonella*, dairy, serotype

T78 Determination of the mechanism(s) by which direct-fed microbials control *Escherichia coli* O157:H7 in cattle. L. M. Guillen*, S. McCoy, M. R. Bible, L. O. Burciaga-Robles, M. M. James, C. R. Krehbiel, and S. E. Gilliland, *Oklahoma State University*, *Stillwater*.

The objective of this experiment was to determine if immune enhancement may be responsible for the success of the direct-fed microbials, *Lactobacillus acidophilus* and *Propionibacterium freudenreichii*, in reducing the carriage of *Escherichia coli* O157:H7 in live cattle. To examine this, 10 steers were fed a pelleted growing diet ad libitum. Five steers received the direct-fed microbials (1 x 10^9 cfu) while the control group received only lactose (carrier). Day 0 baseline weights, fecal samples, rectal swabs, and blood samples were taken prior to the initiation of treatments. Treatments were fed once daily for 14 days after which they were transported to a bovine BSL-2 barn for *E. coli* O157:H7 inoculation and for the rest of the trial. All 10 steers were rectally inoculated with *E. coli* O157:H7 ATCC 43894 (10 ml of 2×10^7 cfu/ml) and housed in separate pens. Feeding and treatments were continued as before. After inoculation the previously mentioned samples were taken every 12 hours for 48 hours, then daily until 7 days post-inoculation, and then weekly until day 42. After the day 14 samples were taken the animals were reinoculated with a higher dose of *E. coli* O157:H7 (10 ml of 1×10^9 cfu/ml). Performance, immunological, and microbial plating data were analyzed using Proc Mixed ANOVA, repeated measures ANOVA, and Fischers exact test respectively. The dry matter intake was higher in the control group at weeks 4 ($p=0.03$) and 6 ($p=0.0004$). The feed:gain was higher in the control group at weeks 4 ($p=0.03$) and 6 ($p=0.0002$). Average daily gain for the control group was higher at week 4 ($p=0.04$). The immunological results of the trial showed higher levels of serum IgA, granulocytes, and monocytes as a percentage of

white blood cells in the treatment group at 36 hours (p=0.04), 48 hours (p=0.006), and day 7 (p=0.04) post-challenge respectively. There were no significant differences between treatments for animals that were negative or positive for *E. coli* O157:H7 throughout the trial.

Key Words: direct-fed microbials, *E. coli* O157:H7, cattle

T79 PCR analysis of pathogenic *E. coli* on three dairy farms in the northeastern US. J. Karns* and J. Van Kessel, *USDA/ARS/BA/ANRI/EMFSL, Beltsville, MD*.

Cattle are considered a significant reservoir of pathogenic *Escherichia coli* that cause food borne illness in humans. The association of enterohemorrhagic *E. coli* O157:H7 with beef cattle is well known but less is known about the occurrence of this organism in dairy cattle. In this study real-time PCR assays were used to detect virulence genes associated with pathogenic forms of *E. coli* in feces and environmental samples collected bi-annually from 3 dairy farms in the northeast US over a three year period. The *eaeA* gene encoding intimin was detected in the feces of 79% (range 54-97%), 73% (54-89%), and 92% (75-100%) of the cows on Farms A, B, and C, respectively. The gamma allele of the translocated intimin receptor (*γ-tir*), that is associated with O157:H7 was detected in 28% (6-64%), 28% (2-58%), and 42% (3-90%) of the fecal samples from the respective farms. The *stx1* and *stx2* genes encoding shiga-like toxins were found less frequently in fecal samples from Farm A (*stx1* 47% [22-77%]; *stx2* 37% [25-57%]) than in those from Farm B (*stx1* 68% [53-84%]; *stx2* 69% [52-79%]) or Farm C (*stx1* 63% [39-88%]; *stx2* 62% [32-74%]). The combination of virulence factors suggestive of the presence of O157:H7 (*eaeA+, γ-tir+, stx2+, stx1+or -*) was found in numerous samples from farms B and C but O157:H7 was isolated from few fecal samples and only from environmental manure samples associated with young animals. O157:H7 did not seem to persist in individual animals as cows which yielded positive samples at one sample time tested negative for this organism in subsequent samplings. These results suggest that *E. coli* O157:H7 is somewhat rare on these dairy farms but that other types of shiga-toxin-producing *E. coli* are more frequent and may present risks to the public.

Key Words: EHEC, STEC, pathogenicity

T80 Effect of a mycotoxin deactivating feed additive on the transfer of aflatoxin from dairy feed into milk. U. Hofstetter*[1], I. Rodrigues[1], A. Pietri[2], and T. Bertuzzi[2], [1]*Biomin Holding GmbH, Herzogenburg, Austria*, [2]*Istituto di Scienze degli Alimenti e della Nutrizione - Facoltà di Agraria U.C.S.C., Piacenza, Italy*.

Aflatoxin B1 (AFB1) in animal feed and its metabolite aflatoxin M1 (AFM1) in milk for human consumption are regulated worldwide. Aflatoxins represent a worldwide problem in many agricultural commodities. The most common method to protect animals against aflatoxicosis and to avoid carry-over of aflatoxin into meat, milk and eggs is the use of adsorbents to reduce the bioavailability of the toxins. This study was carried out to test the carry-over of alfatoxin from naturally contaminated maize meal into milk. Eighteen disease-free animals were divided in 3 groups of 6 animals each and given the following treatments: 1) control diet without feed additive (CRT); 2) control diet with 20 g/cow/day of a mycotoxin deactivator (T1) and 3) control diet with 50 g/cow/day of the feed additve (T2). Each animal of the control group received one kg/day of the contaminated maize meal without product added to the total mixed ration (TMR); each animal of the T1 group received one kg/day of the contaminated maize meal with 20 g/cow/day of the feed additive and each animal of the T2 group received one kg/day of the contaminated maize meal with 50 g/cow/day of product added. The experimental design was a 3x3 Latin square with periods of 7 days each without washout periods. Morning and evening milk samples from each cow were collected on day 3 and 7 of the first week and on day 7 of the following weeks. Samples derived from individual cows were mixed in proportion to the morning and evening milk production and then again combined in proportion to the daily milk production of each cow to constitute a representative bulk milk sample of each group; these samples were analyzed for AFM1. The mean content of AFB1 in maize meal fed to the animals was 91.7 ± 4.4 µg/kg; this value was also the mean individual daily ingestion of AFB1. The addition of the mycotoxin deactivator reduced significantly ($P<0.01$) the milk AFM1 content from 120 ng/kg (CRT group) to 83 ng/kg (- 31%; T1 group) and to 72 ng/kg (- 41%; T2 group).

Key Words: aflatoxin B1, aflatoxin M1, carry over

T81 Food crisis consumer information needs. K. E. Olson*[1], D. Pelzer[2], and S. Stevens[2], [1]*KEO Consulting, Schaumburg, IL*, [2]*DMI, Rosemont, IL*.

Dairy Management, Inc. (DMI) conducted research designed to assess consumer emotions, reactions and questions during a hypothetical large scale outbreak of food-borne illness related to contaminated dairy products and to an outbreak of foot-and-mouth disease. The objective was to help prepare the dairy industry and its partners to communicate effectively with consumers during a fast moving crisis involving milk or dairy products. Qualitative and quantitative studies were conducted with consumers to determine the most effective responses to the types of outbreaks described. Focus groups, conducted in Chicago and Baltimore in April 2008, provided the qualitative results. The quantitative research consisted of an in-depth online survey conducted between late June and early July 2008. A total of 1,102 responses from adults 18 and over were included. A subgroup that was evaluated included 227 moms with children 17 years of age and younger. Data was weighted to reflect the demographic composition of the adult US population. Basic findings: – Consumers are confident in the safety of milk and dairy products with only 10% indicating they do not feel confident in the safety of the products. – Food contamination is a major concern with approximately 1/3 of the total population and 1/2 of the moms indicating concern – Consumers are most reassured when communication about food safety comes from government health or food safety agencies, medical professionals and academic experts in addition to industry – Consumption will be impacted in a crisis. Approximately 50% of the survey group would stop drinking milk in the case of a food-borne illness and 42% with an FMD outbreak. – Industry needs to be prepared to deliver straightforward, easily understood information to consumers Conclusions: – Industry must respond quickly with specific information to help consumers assess personal risk and how the situation is being handled – The industry must work actively with third party experts to ensure that consumers receive consistent, accurate, useful, easily understood information delivered in a timely manner during a crisis. – Consumers have a high degree of trust in dairy products that must be maintained.

Key Words: consumer, messaging

T82 Structure of Tanzania grass managed under different residual light area index at rotational stocking by goats. A. C. Ruggieri*[1,2], N. Lima Santos[1,2], I. A. M. Teixeira[1], V. C. e Silva[1], B. R. Vieira[1], and E. B. Malheiros[1], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*Fundação de Amparo a Pesquisa do Estado de São Paulo*, *São Paulo, São Paulo, Brazil*.

The effect of residual leaf area index (LAI) on the structure of Tanzania grass pasture under rotational stocking with goats was evaluated. It was studied 3 treatments, with 3 residual LAI (0.8-1.6-2.4) as a randomized blocks design with 6 replications. The rest period was adopted according to the criterion of 95% of light interception (LI). The paddocks were grazed by goats until residual LAI. There were made measurements of IAF and of IL with accupar® LAI meter. The spatial distribution of the plants components were done with the "inclined point quadrat" by considering the components leaf, stem and dead material. The values of total, leaf and stem herbage mass in the pre grazing were similar (P>0.05) between 1.6 and 2.4 residual LAI and larger (P<0.05) than 0.8 residual LAI. The lower residual LAI had a drastic effect to the recovered of the plants, consequently the paddocks subjected to this treatment presented lower herbage mass. The dead material mass were similar (P>0.05) among the tree different residual LAI. In the 0.8 residual LAI it was verified a great leaves concentration and an effective participation of stems in the sward layer of 17-24cm with 14.2% of leaves and 1.5% of stem. In the 1.6 residual LAI it was denoted a great concentration of leaves and a small participation of stems among the sward layer 25-32cm, corresponding at 14.8% of leaves and 0.9% of stem. Similar situation occurred at 2.4 residual LAI. However the largest concentration of leaves and short participation of stem occurred among the 33-40 cm, corresponding at 13.4% of leaves and 0.4% of stem. Thus, the adopted management was efficient in controlling stem growth, which is an structural trait that affects the ingestive behavior once that the herbage height post grazing were 25, 32 and 41cm for 0.8, 1.6 and 2.4 residual LAI respectively. The residual LAI measure is an effective tool to control and to define the grazing strategies. The spatial distributions of the morphologic components reflect the sward structure by grazing at different residual LAI.

Key Words: inclined point quadrat, spatial distribution, herbage mass

T83 Effects of stocking rate and supplementation on pasture quality, production, and utilization in pasture-based dairy systems in Eastern North Carolina. R. E. Vibart*[1], S. P. Washburn[2], G. A. Benson[2], and J. T. Green[2], [1]*AgResearch Limited*, *Palmerston North, New Zealand*, [2]*North Carolina State University*, *Raleigh*.

Pasture-based systems with appropriate stocking rates (SR) and grazing management can achieve efficient levels of milk production per cow while maintaining high levels of pasture quality and utilization. A seasonal, fall-calving, pasture-based system was established on a research farm to address the effects of SR on pasture quality, production, and utilization for three years. Groups of 40 cows (approximately 1/3 Holsteins, 1/3 Jerseys, and 1/3 crosses of those breeds) were assigned to either a low stocking (LSR; 2.2 cows per ha) or a high stocking rate group (HSR; 3.3 cows per ha). Relative proportions of a corn-based concentrate mix were kept at 1.0:1.5 for LSR vs. HSR, respectively. Pasture/forage crop rotations included annual ryegrass and sorghum-Sudan (50%), annual ryegrass overseeded on bermudagrass (20%), and an improved tall fescue (MaxQ) - white clover pasture (30%). Pre- and post-grazing herbage mass values did not differ among SR; means (± SE) were 3,342 ± 255.8 and 1,884 ± 160.6 kg DM/ha. Grazing area offered daily (m2/cow) was greatest (P = 0.001) for cows on LSR, whereas grazing intervals did not differ between SR (P > 0.30; 23.6 d). The nutritive value of fresh and conserved forages was similar among SR, except for freshly-grazed bermudagrass ADF (P = 0.006; 29.6 vs. 26.3% of DM for LSR and HSR, respectively). Cows on HSR spent more (P = 0.04) time on an extra feeding lot (85 vs. 61 days/year) as opposed to grazing (204 vs. 228 days/year), whereas the amount of conserved forage produced from the LSR area was 86% greater (1011 vs. 544 kg DM/cow) than that produced from the HSR. With the greater stocking rate, additional supplemental concentrate, forage, and time off of grazing paddocks were needed for supplemental feeding in times when pasture was limited.

Key Words: pasture-based dairy, stocking rate, grazing

T84 Predicting dry matter intake of grazing Brahman bulls selected for high and low feed efficiency. A. D. Aguiar*[1], L. O. Tedeschi[1], F. M. Rouquette, Jr.[2], T. D. A. Forbes[3], C. M. Hensarling[3], and R..D. Randel[2], [1]*Texas A&M University*, *College Station*, [2]*Texas AgriLife Research*, *Overton, TX*, [3]*Texas AgriLife Research*, *Uvalde, TX*.

Determining feed efficiency of beef cattle has become of increasing importance with the rising cost of feed and other inputs. Determination of feed efficiency on pasture might provide a more realistic methodology compared to conventional residual feed intake (RFI) tests; however, determination of intake under grazing conditions over extended periods has seldom been attempted. Our objectives were to determine if cattle previously phenotyped for feed efficiency maintained their rank on pasture, and to develop techniques that decreased the costs associated with intake determination. Purebred Brahman bulls, (438 ± 23 kg) previously phenotyped by conventional RFI procedures as either efficient (n = 8) or inefficient (n =8), were grazed on replicated (n = 4) Coastal bermudagrass pastures at Overton, TX in July 2008. Animals were individually fed 400g of corn gluten labeled with 200 mg C32 n-alkane twice a day (07.00 and 19.00 h) using Calan gates. Feeding the labeled supplement continued for 10 d. Fecal samples were collect twice per d. (07.00 and 19.00) for the first 5 d. and then 4 times per d. for the remaining 5 d. (07.00, 11.00, 15.00 and 19.00 h). Forage samples selected from the grazed horizon, were collected daily beginning 2 d. prior to the start of dosing. All forage and fecal samples were dried at 60 C., and ground using a cyclone mill fitted with a 1 mm screen, prior to extraction and subsequent alkane determination by gas chromatography. No difference (P > 0.1) in forage DM intake was detected between efficient and inefficient bulls. Dry matter intake averaged 10.2 ± 0.48 kg. A highly significant effect (P < 0.0001) of time of fecal sampling on intake estimation was observed, with intake estimates being 9.8, 9.9, 10.4, and 11.1 ± 0.35 kg DM for collections made at 07.00, 11.00, 15.00 and 19.00 h, respectively. These data suggest that animals previously phenotyped under confinement feeding may not provide the same ranking under grazing, and that fecal collections need to be widely separated in time to provide the most reliable intake estimates.

Key Words: feed efficiency, intake, n-alkanes

T85 Summer forage species alters animal performance, carcass characteristics and fatty acid composition of grazing beef steers. J. R. Schmidt, J. G. Andrae, S. K. Duckett*, and M. Miller, *Clemson University*, *Clemson, SC*.

The objective of this study was to evaluate various summer forages and their effects on live animal performance, carcass quality, and fatty acid composition of finishing beef cattle. Angus-cross steers (n=60) were finished on alfalfa (AL), bermudagrass (BG), chicory (CH), cowpea (CO), and pearl millet (PM) during this two year grazing study. Ten 2-ha paddocks were blocked and assigned to forage species (2 reps per species). Each year, three tester steers were randomly assigned to paddocks. Grazing began when adequate forage growth for individual species was present. Put and take grazing techniques were utilized throughout the trial. Animal gains and herbage mass were monitored at 28 d intervals. Steers were slaughtered when sufficient forage mass for individual species was inadequate for supporting animal gains or when average steer weight exceeded 568 kg. Carcass data were collected at 24 h postmortem. Data were analyzed using PROC MIXED of SAS. Average daily gains were greater (P = 0.02) for AL than BG, CO, and PM, while CH produced higher ADG than BG and PM. Dressing percentages were greater (P = 0.01) for AL and CO than BG and PM, while CH was higher than BG. Cowpea carcasses had the highest (P < 0.05) quality grades and marbling scores. Postmortem aging decreased (P < 0.01) LM shear force measures. Shear force scores were lower (P = 0.05) for AL and CO than BG and CH with PM being intermediate. CLA cis-9, trans-11 concentration was greater (P = 0.02) in BG and PM than other treatments. Chicory and CO treatments had higher (P < 0.01) concentrations of linolenic acid than other treatments, while AL was higher (P < 0.01 than PM. Stearic acid concentration was higher (P = 0.02) in CO than CH, PM, and AL, while BG was higher than PM and AL, and CH was higher than AL.

Key Words: beef, forages, fatty acid

T86 Performance by spring and fall-calving cows grazing with full access, limited access, or no access to endophyte -infected tall fescue 2 year summary. J. Caldwell*[1], K. Coffey[1], D. Philipp[1], J. Jennings[3], D. Hubbell III[1], T. Hess[1], D. Kreider[1], M. Looper[2], M. Popp[1], M. Savin[1], and C. Rosenkrans Jr.[1], [1]*University of Arkansas*, *Fayetteville*, [2]*USDA-ARS*, *Booneville, AR*, [3]*Cooperative Extension Service*, *Little Rock, AR*.

Replacing toxic *Neotyphodium coenophialum* -infected tall fescue (E+) with a non-toxic endophyte-infected fescue (NE+) has improved cow performance greatly, but producer acceptance of NE+ has been slow. Our objective was to compare performance by spring (S) and fall-calving (F) cows grazing either E+ or NE+ at different percentages of the total pasture area to determine to what extent having limited access to NE+ will enhance cow/calf performance. Gelbvieh Angus crossbred cows (n=178) were stratified by weight and age within calving season and allocated randomly to 1 of 14 groups representing 5 treatments: 1) F on 100% E+ (F100); 2) S on 100% E+ (S100); 3) F on 75% E+ and 25% NE+ (F75); 4) S on 75% E+ and 25% NE+ (S75); and 5) S on 100% NE+ (NE100; 2 replications). Cow BW at breeding, BW and BCS at the end of breeding, BW, BCS, and hair score at weaning, and calving rates were greater (P<0.05) for F compared with S. A calving season by NE+ % interaction tendency (P=0.07) was detected for cow BCS at weaning. Cow BCS at the end of breeding tended to be greater (P=0.08) for F100 and S100 compared with F75 and S75, but cow BW at weaning and calving rates were greater (P<0.05) for F75 and S75 compared with F100 and S100. Calf gain, actual weaning weight, ADG, and adjusted weaning weight were greater (P<0.05) for F compared with S. Therefore, a fall-calving season may be more desirable for cows grazing E+, resulting in greater calving rates, BW and BCS at critical times, and heavier calves at weaning. Limited access to NE+ may not improve calf BW through weaning, but may improve calving rates and cow BCS at certain stages of production. This project was supported by the National Research Initiative of the Cooperative State Research, Education and Extension Service, USDA, grant # 2006-55618-17114.

Key Words: calves, cows, novel endophyte fescue

T87 Characteristics of Tanzania (*Panicum maximum*) and Xaraés (*Brachiaria brizantha*) pastures under dairy cows grazing with two supplementation levels. C. A. M. Gomide*, D. S. C. Paciullo, D. Vilela, and J. H. Bruschi, *Embrapa Dairy Cattle Research Center*, *Juiz de Fora, MG, Brasil*.

In spite of the importance of comprehension of the plant-animal relationships to grazing management, there are few works that evaluate the influences of supplementation strategies under the pasture characteristics. This work aimed to evaluate the effect of two levels of supplementation on the characteristics of Tanzania grass and Xaraés grass pastures along the dry and rain seasons. The study was carried out with lactating dairy cows, under rotational grazing. The levels of supplementation were 3 and 6 kg of concentrate ration/cow/d. A 2 × 2 × 2 factorial blocks design with two replications was used. The total forage mass (TFM) did not vary with the studied factors, the average value was 6,894 kg/ha. Probably the high percentage of dead vegetation in the dry season (48.3%) caused the TFM to be overestimated in this period. A higher canopy was observed in the summer as well as higher values of leaf-stem ratio and percentage of leaf in the pre grazing forage. These two last attributes also were favorable regarding Tanzania grass, showing values of 2.03 and 43.2%, respectively. In Marandu grass pasture these values were 1.05 and 36.5%, respectively. The levels of supplementation influenced only the pasture height after grazing, when it was observed a residue of 58.1 cm with the 6 kg of concentrate supplementation against a residual height of 50.8 cm for the treatment of 3 kg of concentrate. Leaf-stem ratio and the percentage of leaves after grazing varied with the grass × season interaction. The percentage of residual leaves was higher in Tanzania grass during the dry season, while in the rainy season that percentages were 29.2 and 36.3%, respectively for Tanzania and Xaraés. The factor season was the more effective affecting the characteristics of the pasture, showing a bigger loss during the dry season. *Support by FAPEMIG/CNPq.*

Key Words: rotational stocking, sward structure, tropical pasture

T88 Characteristics of forages utilized by the Przewalski horse (*Equus ferus przewalskii*) in Hustai National Park, Mongolia. B. N. Petrukovich*, J. P. Stevens, and D. A. Christensen, *University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

Prezewalski horses were reintroduced to the Hustai National Park in Mongolia in 1990. Their reintroduction has been carefully monitored, but information on supply and quality of forage is limited. Therefore, the goal of this research was to collect representative samples of the forage available to three harems in the Park and to measure the composition, amount, digestibility and adequacy of pasture forages to meet horse nutrient requirements and for use in providing guidelines for other species. Within each three home ranges forage was clipped from seven

areas defined by dominant plant species in 1.0 m^2 quadrants. Collection occurred at the end of the rainy season in August and the forage collected was used to represent the amount of forage available to the horses until the next growing season. A natural mineral sample available to the horses was collected and four fecal samples were collected from each of the three harems to estimate digestibility using lignin as an internal marker. Nutrient analyses of the samples included DM, ash, crude protein, EE, ADF, NDF, ADICP, NDICP, lignin and macro and micro minerals. Digestible energy (DE) was estimated according to NRC Horse 2007. Estimated DE averaged 2.25 Mcal/kg for the three home ranges with no significant differences (P>0.05). Harem forage DM/ha averaged 1086 kg (SD 543), CP 10.4%, ADF 38.2%, and NDF 59.1%. Apparent digestibility of forage dry matter averaged 58.8%. Energy requirements were met from the available forage for 300 kg horses at maintenance from less than 2% of BW/day (4.45 kg DM/day) and for mares in late gestation (5.71 kg DM/day). Early lactating mares would need to consume 2.8% of BW per day (8.47 kg DM/day) to meet energy requirements. Results of this study suggest a marginal capacity of the available forage meeting all the requirements of Przewalski horses while lactating mares are at increased risk of losing condition and supporting foals.

Key Words: Przewalski horse, pasture forages, digestible energy

T89 Timing of herbage allocation in a strip grazing organic system: Effects on performance and milk composition of lactating dairy cows. L. Baldoceda*[1,2], G. Raggio[3], R. Bergeron[3], D. Pellerin[1], and R. Berthiaume[2], [1]*Université Laval, Québec, Québec Canada*, [2]*Dairy and Swine Research & Development Centre, Agriculture and Agri-Food Canada, Lennoxville, Québec, Canada,*, [3]*Campus Alfred Université de Guelph, Alfred, Ontario Canada*.

The aim of this study was to assess the effect of grazing management, more specifically timing of pasture allocation, on performance of dairy cows in an organic system. Thirty multiparous Holstein cows were blocked based on parity and milk yield, and then randomly assigned to one of 2 treatments that consisted in grazing fresh daily strips offered either after AM milking 6.00 (AM) or after PM milking 17.30 (PM). Plucked samples of herbage were collected in the morning, at noon, and in the afternoon to assess diurnal variation in the chemical composition of pasture (DM, NSC, NDF, ADF and CP). Milk yield was recorded daily and sampled weekly. Cow body weights were recorded every 2 weeks. Herbage availability for each group was measured by hand-clipping herbage at a stubble height of 3 cm from 9-30×30 cm quadrats before grazing, and herbage refused was determined by clipping 12-30× 30 cm quadrats after grazing. Data were analyzed as a randomized complete block design experiment using the MIXED procedure of SAS. Time of day (AM vs. PM) had an effect on herbage NSC concentration (11.01 vs. 13.76 ± 2.25%). Milk yield (27.7 vs. 27.4 ± 1.18 Kg/d; $P > 0.05$), concentration of milk fat (3.85 vs. 3.93 ± 0.10%; $P > 0.05$) and milk protein (2.93 vs. 2.97 ± 0.03%; $P > 0.05$), and body weight gain (+12 vs. +5 kg) did not differ comparing AM vs. PM treatment. Mean of herbage availabity was greater for the PM treatment (33.9 vs. 35.8 DM/d) as was the coefficient of herbage utilization (33 vs. 42%). These results suggest that a simple modification in the time of pasture allocation (PM vs. AM) can improve herbage utilization. This is likely associated to changes observed in the composition of pasture during the day. However, changes in herbage composition (i.e.:NSC) were smaller than anticipated and this may explain the lack of effect on milk yield and milk composition.

Key Words: strip grazing, dairy cow, organic

T90 Performance of stocker cattle fed hay and protein supplements during the winter and grazed on wheat pasture during the spring. W. A. Phillips*[1], C. A. Bandyk[2], and T. W. Geary[3], [1]*USDA-ARS, El Reno, OK*, [2]*Quality Liquid Feeds Inc., Dodgeville, WI*, [3]*USDA-ARS, Miles City, MT*.

In the southern Great Plains region, perennial warm- and annual cool-season grasses are used to grow stocker cattle. The objective of this experiment was to evaluate supplementation strategies used to winter stocker cattle on dormant warm-season grasses and the impact of these strategies on subsequent body weight gains during the graze-out period on spring wheat. Spring born calves (n = 152, BW = 219 kg) weaned in the fall were randomly assigned one of eight 3.2-ha pastures of dormant warm-season grasses in a completely random design. Steers had ad libitum access to hay (8.8% CP, 70% NDF, and 40% ADF) in addition to dormant warm-season grass. Four pastures were limit fed a dry supplement (20% CP plant protein based, 132 mg of lasalocid/kg) and four pastures had ad libitum access to a liquid supplement (24% CP, 17% CP equivalents from NPN, 63% DM, 165 mg of lassalocid/kg) in lick-wheel tanks. Pasture was the experimental unit and data were analyzed using GLM procedures with supplement type as the only source of variation. Average daily gains for the 98-d wintering period were not different (P = 0.96) between supplement groups (0.44 ± 0.04 kg). Daily supplement intake (as fed) was similar (P=0.21) between the dry and liquid supplements (mean = 1.45 kg/d), but steers fed dry supplement had 12% less (P = 0.7) CP intake (0.30 vs 0.34 kg/d) and 16% less (P = 0.07) lassalocid intake (200 vs 232 mg/d) than steers fed liquid supplement. During the subsequent 43-d graze-out period on winter wheat, ADG did not differ (P = 0.30) between the supplement groups, but were greater (P = 0.01) than for steers (n = 32) that had grazed winter wheat all winter (1.15 vs 1.02 kg). Feeding a dry or liquid supplement to calves during the winter resulted in similar performance and some compensatory gain during the spring as compared to calves winter on wheat. The cost of supplemental feed, labor, and the value of steers in the fall versus the spring would dictate the economic feasibility of purchasing calves in the fall and wintering them for use the following spring as opposed to purchasing animals as needed.

Key Words: stocker cattle, supplementation, compensatory gain

T91 Perennial forage kochia for increased production of winter grazed pastures. L. K. Greenhalgh[1], D. R. ZoBell*[1], B. L. Waldron[2], K. C. Olson[3], A. R. Moulton[1], and B. W. Davenport[4], [1]*Utah State University, Logan*, [2]*USDA-ARS, Logan, UT*, [3]*South Dakota State University, Rapid City*, [4]*USDA-NRCS, Tooele, UT*.

Grazing forage kochia (*Kochia prostrata*) during fall/winter has improved livestock health and reduced winter feeding costs. The objectives of this study were to compare forage production/quality and livestock performance of traditional winter pastures versus pastures with forage kochia. Two kochia pastures were established in Tooele County, Utah in January 2005. Mature, pregnant, crossbred cows at both locations were body condition scored (BCS) and randomly divided into groups, then placed in either forage kochia/crested wheatgrass (*Agropyron desertorum*) or crested wheatgrass/cheatgrass (*Bromus tectorum*) pastures. Grazing lasted for 60 days in 2007 and 84 days in 2008. Cows were combined and condition scored. Data were analyzed using the mixed procedure of SAS considering pasture treatments (improved with forage kochia vs. control) as fixed and each location by year combination as random blocks. Forage production data showed control and study pastures with 441 kg • ha^{-1} and 2586 kg • ha^{-1} of forage respectively. The nutritional quality of forage kochia plants was compared to that of

grass plants (primarily crested wheatgrass). *In vitro* true digestibility was similar (P > 0.50) for crested wheatgrass and forage kochia (63.0% and 64.0%, respectively), but crude protein was significantly greater (P < 0.001) for forage kochia than for crested wheatgrass (11.7% and 3.1% respectively). Cattle on improved ranges with forage kochia had a greater (P < 0.01) increase (+ 0.65) in BCS than cattle on unimproved rangelands (+ 0.39) comprised mostly of crested wheatgrass. Overall, this study found that both pastures had adequate forage to increase body condition; however, the most noteworthy result is the nearly six-fold increase in production (which translates to increased carrying capacity) in the forage kochia pastures.

Key Words: perennial forage kochia, body condition score, beef cattle

T92 Seasonal distribution of minerals in grazed and ungrazed cool-season tame grass pasture. C. L. Wright* and A. J. Smart, *South Dakota State University*, *Brookings*.

In each of 2 years, forage samples were collected from grazed and ungrazed cool-season tame grass pasture for analysis of mineral concentrations. In each year, 4 replicated 100 m^2 exclosures were randomly located within the pasture. Treatments were considered ungrazed (inside exclosure) and grazed (outside exclosure) forage. Forages contained in a single 0.25 m^2 quadrat was clipped near the soil surface within each treatment and replication. In year 2, the exclosures were placed in different locations so that the ungrazed treatment would not be confounded by the previous year's location. Samples were collected on 20 May, 3 Jun, 18 Jun, 22 Jul, 8 Aug, and 18 Aug in year 1, and 26 May, 8 Jun, 22 Jun, 4 Aug, and 17 Aug in year 2. Forage samples sorted into green and dead plant tissue. Green tissue from each treatment and replication was analyzed to determine Ca, Co, Cu, Fe, Mg, Mn, Mo, Na, P, K, S, and Zn concentrations. Concentrations of Co and Na were below detectable limits in nearly all samples. In year 1, concentrations of K, Mg, P, and S were affected (P < 0.03) and Mo tended (P = 0.06) to be affected by treatment × date interactions. Concentrations of each mineral were greater later into the grazing season in grazed forages than in ungrazed forages. The main effect of treatment influenced (P < 0.03) concentrations of P and S and tended to influence (P < 0.10) concentrations of Fe and K. Concentrations of each mineral were greater in grazed than in ungrazed forage. The main effect of sampling date influenced Ca, Cu, Mn, Mo, P, K, S (P < 0.01) and Zn (P < 0.05). Concentrations of Ca, Cu, P, K, S, and Zn decreased and concentrations of Mo and Mn increased over time. In year 2, concentrations of Mg and Mn were greater (P < 0.04) in grazed than in ungrazed forage. Concentrations of Ca, Co, Cu, Fe, Na, P, K, S, and Zn decreased (P < 0.01) and concentrations of Mg, Mo, and Mn increased (P < 0.01) over time. The concentration of various minerals in forages may be dependent upon whether or not it has been grazed and the sampling time within the growing season.

Key Words: forage, mineral, season

T93 Nutritive value of standing mature Buffel grass (*Cenchrus ciliaris*) for dry season feeding of cattle in Northeastern Mexico. H. Bernal-Barragan*[1,2], R. W. Blake[2], D. J. R. Cherney[2], and M. E. Van Amburgh[2], [1]*Facultad de Agronomía UANL, Escobedo, N.L., México*, [2]*Cornell University*, *Ithaca, NY*.

Extensive cow-calf systems in northeastern Mexico rely on stocks of senescent standing roughage during the dry season, about which there is little nutritional information. This study was conducted to evaluate the chemical composition and in vitro digestibility of NDF (IVNDFd) of Buffel grass from an ungrazed plot in semiarid Nuevo Leon, Mexico. Samples were hand-harvested at an above-ground cutting height of 40 cm and immediately dried at 65°C in a forced-air oven. Cuttings resulting from below average rainfall (September 2007 to July 2008) were analyzed in replicates for contents of ash, CP, soluble protein (SP), NPN, NDF, ADF, ADL, and 24-h IVNDFd. Crude protein exceeded 6% in only two months and the proportion of SP was 20% to 30% as a percent of CP. NPN averaged about 60% of SP from November to June; and ~85% in July/September. Monthly differences were not detected in NDF and ADF (76% and 44%). ADL increased from 4% to 9% of DM. Digestibility of NDF averaged ~34% from September to January; otherwise ~26%. Ash content declined from 11% in September to 5% in June. ADL increased from 4% to 9% of DM. Average in vitro DM digestibility also was greater (~48%) September to January than from February to July (~40%); however digestibilities may be overestimated due to added N and S for incubations. The feeding value of standing mature Buffel grass is comparable to that of maize or sorghum stover with 3% to 6% CP and 45% to 55% IVDMD. Taking an average value of the chemical composition at 1 × maintenance intake, the Cornell Net Carbohydrate and Protein System (CNCPS) predicted energy value for standing mature Buffel grass was 1.45 Mcal/kg ME. These results can be used to develop feed library values for programs like the CNCPS. Their application would allow users to develop dietary supplementation strategies for cattle grazing dormant Buffel grass during drought conditions.

Key Words: Buffel grass, nutritive value, CNCPS

T94 The effect of grazing and supplementing with corn byproducts on reproductive performance of Creole × Zebu cows: A simulation model. J. M. Tapia-Gonzalez*[1], A. Tewolde-Medhin[2], W. E. Grant[3], J. C. Martinez González[2], H. Diaz Solís[4], A. Moreno Valdéz[5], O. Z. Montañez Valdez[1], L. F. Galvan-Benavidez[1], and G. Rocha Chávez[1], [1]*CUSUR, Univ de Guadalajara, Cd Guzman Jalisco Mexico*, [2]*Univ Autonom de Tamaulipas, Cd Victoria Tamps. Mexico*, [3]*Texas A&M University, College Station*, [4]*UAAAN, Saltillo Coahuila Mexico*, [5]*Inst Tec de Cd Victoria, Cd Victoria Tamps. Mexico*.

The Software STELLA® II Version 5 was used for comparing a simulated scenario with a real beef cattle production system. Type of feeding (grazing only or grazing + supplement) was compared using the conceptual mathematical model to determine the effect of several types of corn by-products on fertility of cows. We used real data to feed the software and predicted production performance under four different scenarios: Grazing only, grazing+ corn silage, grazing + nutritional blocks and grazing + tree leaves. Nutritional blocks are made of crushed corn straw plus molasses and minerals pressed together whereas tree leaves is referred as branches of specific trees that are cut for cattle feeding. A total of 20 repetitions during 48 months were represented in the model and predicted performance of the cow since she is a month old up to her first calving and lactation. Special emphasis was put on dry season when zebu-crossed cows start to lose weight. Studied parameters as well as predicted results are depicted in table 1. We found this model useful since predicted parameters were similar to those reported by several authors (Hernandez, 2001, Martínez *et al*., 1999., Archondo, 1986., Manvielle y Hernandez 1962., Zaragoza y Castrellon, 1999). It was again confirmed that simulation models are useful tools to predict future scenarios that otherwise are expensive to develop.

Table 1. Type of feeding and its effects on severa production parameters of beef cattle.

Type of feeding	Age (months)	Body weight (Kg)	Daily Gain (grams)	*BCS	Fertility rate	Age at onset of puberty (months)
Grazing only	43	198.8	150	4	30%	39.5
grazing+ corn silage	45.8	279	203	6.6	50%	29.5
grazing + nutritional blocks	45.8	289	240	6.8	60%	24.9
grazing + tree leaves	36.3	301	276	7.1	70%	21.5

*BCS = Body condition score (from 1- 10)

Key Words: simulation, supplements, cows

T95 Evaluation of cultivated summer pastures for meat goats in Tennessee. M. Lema*, K. Suleyman, and R. Opio, *Tennessee State University, Nashville.*

A grazing trial was conducted to evaluate Puna forage chicory (*Cichorium intybus* L.), Hybrid Penleaf pearl millet (*Pennisetum glaucum*) and Sahara bermudagrass (*Cynodon dactylon*) as summer pasture for meat goats. Puna chicory was 28.3 and 67.7% higher ($P < 0.05$) in crude protein (CP), 28.1 and 35.4% lower ($P < 0.05$) in acid-detergent fiber (ADF) and 40.0 and 46.0% lower ($P < 0.05$) in neutral detergent fiber (NDF) than Penleaf pearl millet and Sahara bermudagrass, respectively. Penleaf pearl millet was 37.7% higher ($P < 0.05$) in CP, 10.2 and 10.0% lower ($P < 0.05$) in ADF and NDF than Sahara bermudagrass, respectively. Relative Feed Value (RFV), Ca, P, Mg and K contents were significantly higher ($P < 0.01$) for Puna chicory than for Peanleaf pearl millet and Sahara bermudagrass. Pennleaf pearl millet was higher ($P < 0.01$) than Sahara bermudagrass in P, K and Mg content. Puna chicory and Pearl millet produced 73 and 70% higher ($P < 0.05$) forage CP per ha, respectively than Sahara bermudagrass. Average daily gain (ADG) and live weight gain per ha of does grazing Puna chicory were significantly higher ($P < 0.05$) than those does grazing Sahara bermudagrass does and Penleaf pearl millet.

Key Words: chicory, pearl millet, summer pasture

T96 Dry matter yield and nutritional value of Kikuyu Grass grazed under phenological concepts in commercial dairy farms in Costa Rica. J. M. Sánchez*[1,2], K. Peters[1,3], and A. Martínez[1,2], [1]*Universidad de Costa Rica, San José, Costa Rica*, [2]*Centro de Investigación en Nutrición Animal, San José, Costa Rica*, [3]*Escuela de Zootecnia, San José, Costa Rica.*

Because of its high dry matter yield and good nutritional quality, Kikuyu Grass (*Kikuyuocloa clandestina*) is the most important grass species on dairy farms located between 1300 and 2700 m in altitude in Costa Rica. Thus, the aim of this study was to analyze dry matter yield, botanical composition and nutritional value of kikuyu-based pastures grazed under the leaf stage concept, on commercial dairy farms located in the Central Mountains in Costa Rica. Samples and measurements were taken every other month for 1 year on four randomly selected farms. The farms were located between 1900 and 2400 m in altitude, where annual average precipitation is 1800 mm and annual mean temperature is 18°C (minimum of 13°C; maximum of 23°C). Average DM yield was 29t/ha/year (with a range of 24 to 33 t/ha/year), which is similar to literature values when this grass is intensively managed. Lowest average DM yield per rotation cycle (31 to 37d) was during July and August (1.7t/ha), which coincides with the months of the lowest irradiation (14 Mj/m^2) and light hours (4 hours/d). Botanical composition analysis showed that 90.1% of the biomass was kikuyu grass, 1.9% other grasses, 1.6 clover, 1.6 weeds and 4% senescent material. On average, pasture dry matter contained 18.2% CP, 60.3% NDF, 32.1% ADF, 10.8% ash, 15.8 NFC, 3.2% lignin and 1.27 Mcal/ kg NE_L (3X). Cows grazed the kikuyu grass when it had an average number of 5.1 leaves, which is similar to the optimum value obtained by Australian researchers (4.5 leaves). Results showed that a grazing system based on the phenology of the plant is a good tool for managing kikuyu grass in the highlands of Costa Rica.

Table 1. Agronomic and nutritional data of kikuyu grass grazed under the leave stage concept in the highlands of Costa Rica[1]

Farm N°	Nº leaves at grazing	Regrowth period, d	DM yield kg/ ha/cut	CP DM%	NDF DM%	NE_L(3X) Mcal/kg DM
1	5.06[b]	35	2068[b]	18.6[a]	61.4[a]	1.31[a]
2	5.27[a]	37	3360[a]	19.3[a]	58.8[b]	1.28[b]
3	4.90[b]	31	2041[b]	17.3[b]	61.2[a]	1.22[c]
4	5.24[a]	33	3420[a]	17.6[b]	59.8[a]	1.25[c]
X	5.11	34	2722	18.2	60.3	1.27

[a,b,c] Means in a column with different superscripts are different ($P<0.05$). [1]Average of 6 samples or measurements

Key Words: Kikuyu grass, dry matter yield, nutritional value

T97 Nutritive value of the Tanzania grass managed under different residual LAI, at rotational stocking by goats. N. Lima Santos[1,2], A. C. Ruggieri*[1,2], I. A. M. Teixeira[1], V. C. e Silva[1], A. F. Campos[1], and E. B. Malheiros[1], [1]*São Paulo State University, Jaboticabal, São Paulo, Brazil*, [2]*Fundação de Amparo a Pesquisa do Estado de São Paulo, São Paulo, São Paulo, Brazil.*

The herbage nutritive value was evaluated during the grazing by goats in different residual leaf area index (residual LAI) by handing plucking samples. It was studied 3 treatments, with 3 levels of residual LAI (0.8-1.6-2.4) as randomized blocks design with 6 replications. The rest period was adopted according to the criterion of 95% of light interception (LI). There were made measurements of IAF and of IL with accupar® LAI meter. Hand-plucked samples were collected during three grazing cycles. It was collected approximately 300g of herbage by cutting with scissors. The samples were dried at at 55°C by 72h, and analyzed to ash, crude protein (PB), neutral detergent insoluble fiber (NDF) and acid detergent insoluble fiber (ADF). The NDF content in the first day of grazing was similar ($P>0.10$) between 1.6 and 2.4 residual LAI, and larger ($P>0.10$) than 0.8 residual LAI. In the third day of grazing the NDF content of the 2.4 residual LAI was similar ($P>0.10$) to the others, and the 0.8 residual LAI were smaller than 1.6 ($P<0.10$) with means approximately of 75%. The ADF content in the first day of grazing was different ($P<0.10$) between 0.8 and 1.6 residual LAI and similar to the 2.4 residual LAI. In the third day of grazing the ADF content were similar among the treatments. The values of ash in the 2.4 residual LAI, were smaller than the other residues, as the first as third day of grazing, with means varying from 34 to 39.9% in the first and third grazing respectively. The CP content was not influenced by residual LAI with means of 13,3%. However, it was observed that CP percentage was lower in the third day of grazing, mainly due to the higher amount of old

leaves in that day. The hand plucking technique is an excellent tool in the determination of the forage quality intake by the animal during the grazing. However, it is necessary a meticulous evaluation of the habit of grazing to the animal for sampling at a coherent way.

Key Words: light interception, hand-plucked, crude protein

Graduate Student Paper Competition-CSAS Poster Competition: CSAS Graduate Student Competition 2

T98 Effects of ruminally-degradable starch and ruminally-degradable protein levels on urea-nitrogen recycling, microbial protein synthesis, and nitrogen balance in beef heifers. K. Baker*[1], J. J. McKinnon[1], T. A. McAllister[2], and T. Mutsvangwa[1], [1]*University of Saskatchewan, Saskatoon, SK, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*.

The objective of this study was to determine the effects of dietary levels of ruminally-degradable starch (RDS) and ruminally-degradable protein (RDP) on urea-N recycling to the gastrointestinal tract (GIT), microbial protein synthesis and N balance of beef heifers. Four ruminally- and duodenally-cannulated beef heifers (723 ± 57 kg BW) were used in a 4 × 4 Latin square design with a factorial arrangement of dietary treatments and 23-d periods. Dietary treatments were 2 levels (DM basis) of RDS (30% vs. 70%) and 2 levels of RDP (36% vs. 52%). Levels of RDS were manipulated by feeding whole or steam-rolled corn. All diets contained 10% CP (DM basis). Jugular infusions of [$^{15}N^{15}N$]-urea (220 mg/d) were conducted for 4 d (d 18-22), with total collection of feces and urine to estimate urea-N kinetics. Both N intake and N balance were unaffected by diet ($P > 0.05$), however, ruminal NH_3-N concentrations were greater ($P = 0.01$) in heifers fed high RDP as compared to those fed low RDP (8.6 vs. 6.3 mg/dL). Endogenous production of urea-N (UER; 129.6 to 152.8 g/d) and urea-N transfer to the GIT (GER; 72.4 to 93.5 g/d) were similar across diets; however, there was a tendency for a RDS × RDP interaction for UER ($P = 0.11$) and UER ($P = 0.10$). The amount of urea-N returned to the ornithine cycle (ROC; 69.6 g/d vs. 61.9 g/d) tended (P = 0.08) to be greater in heifers fed high RDP compared to those fed low RDP. Feeding a high level of RDP increased ($P = 0.03$) microbial N supply to the duodenum compared to feeding low RDP. In summary, at a low dietary CP level (10%), feeding high RDP tended to increase the amount of urea-N returned to the ornithine cycle and increased microbial N supply to the doudenum compared to feeding low RDP.

Key Words: fermentable carbohydrate, ruminally-degradable protein, urea-N recycling

T99 Effect of ruminal protozoa on urea-nitrogen recycling in growing lambs fed diets varying in ruminally-fermentable carbohydrate. D. Kiran* and T. Mutsvangwa, *University of Saskatchewan, Saskatoon, SK, Canada*.

We examined how interactions between ruminal protozoa and ruminally-fermentable carbohydrate (RFC) alter urea-N recycling to the gastrointestinal tract (GIT), microbial protein synthesis and N balance in growing lambs. Four Suffolk ram lambs (61.5 ± 4.0 kg BW) were used in a 4 × 4 Latin square design with 28-d periods and a 2 × 2 factorial arrangement of treatments. Treatments were: 1) partial defaunation vs. faunation; and 2) dry-rolled vs. pelleted barley as the principal sources of RFC. Linoleic acid-rich sunflower oil was fed (6% of DM) as an anti-protozoal agent. Nitrogen balance was measured from d 22 to d 26, with concurrent measurements of urea-N kinetics using continuous intra-jugular infusions of [$^{15}N^{15}N$]-urea. Only minor ruminal protozoa × RFC interactions were detected. Feeding sunflower oil decreased ($P < 0.01$) total protozoa by 92%, thereby decreasing ($P < 0.01$) ruminal NH_3-N concentration. Intake of N was unaffected ($P \geq 0.12$) by diet; however, urinary N excretion was lower ($P < 0.01$) and retained N was higher ($P < 0.01$) in partially-defaunated compared to faunated lambs. Endogenous production of urea-N (UER) was similar across diets (22.6 to 24.6 g/d); however, urea-N transfer to the GIT (GER), when expressed in absolute amounts (16.4 vs. 13.1 g/d) or as a proportion of UER (0.69 vs. 0.57), and its anabolic use (9.0 vs. 6.0 g/d) were higher ($P < 0.01$) in partially-defaunated compared to faunated lambs. Partial defaunation increased ($P < 0.01$) microbial N supply. Source of RFC did not alter UER; however, urea-N loss in urine, when expressed in absolute amounts (9.5 vs. 7.5 g/d) or as a proportion of UER (0.40 vs. 0.34) were higher ($P < 0.01$), whereas GER as a proportion of UER was lower (0.60 vs. 0.66; $P < 0.01$) in lambs fed dry-rolled compared to those fed pelleted barley. Feeding pelleted barley tended ($P = 0.09$) to increase microbial N supply compared to feeding dry-rolled barley. In summary, partial defaunation or increasing RFC by feeding pelleted barley increased the proportion of UER that was recycled to the GIT, while also increasing microbial N supply.

Key Words: fermentable carbohydrate, ruminal protozoa, urea-N recycling

T100 Effect of feed borne *Fusarium* mycotoxins on the performance of grain fed veal calves. L. M. Martin*[1], K. M. Wood[1], P. L. McEwen[2,1], T. K. Smith[1], I. B. Mandell[1], A. Yiannikouris[3], and K. C. Swanson[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Ridgetown Campus, University of Guelph, Ridgetown, ON, Canada*, [3]*Alltech, Nicholasville, KY*.

Holstein bull calves (n=32; 177±6.7 kg body weight) were used in a randomized complete block design with a 2 × 2 factorial arrangement of treatments to determine the effects of corn naturally contaminated with *Fusarium* mycotoxins on grain fed veal production and to examine the efficacy of a polymeric glucomannan mycotoxin adsorbent (GMA). Calves were blocked according to room and fed in individual pens, one of four dietary treatments for at least 84 days: 1) control corn + pellet, 2) control corn + GMA pellet, 3) contaminated corn + pellet, and 4) contaminated corn + GMA pellet. Corn and GMA were fed at 75 and 1% of the diet respectively. Deoxynivalenol (DON) was the major mycotoxin contaminant present at 8.31 mg/kg of the total ration. Zearalenone (1.49 mg/kg) and 15-acetyl DON (1.01 mg/kg) were also present in the contaminated corn. Body weight, dry matter intake (DMI), acute phase proteins (haptoglobin, fibrinogen), immunoglobulin A (IgA), blood analytes [glucose (BG) and urea nitrogen (BUN)], organ weights and carcass traits (rib eye area, back fat (BF), marbling and colour value) were measured. Results were analyzed using Proc Mixed in SAS. There were no differences (P>0.05) in total weight gain, DMI, acute phase proteins, IgA, or organ weights between treatments. Calves fed the contaminated corn had a tendency for greater (P=0.07) average daily gain and decreased (P=0.003) feed:gain than calves fed control corn. BG and BUN decreased (P=0.004) and increased (P=0.001), respectively,

for calves fed contaminated corn compared to calves fed control corn. Calves fed contaminated corn had a tendency for less (P=0.06) marbling than calves fed control corn and those fed diets containing GMA had greater BF (P=0.02) than calves fed the control pellet. These results suggest that the levels and combination of *Fusarium* mycotoxins fed in this experiment can be largely tolerated by grain fed veal calves.

Key Words: veal calf, adsorbent, *Fusarium* mycotoxin

T101 Effect of replacing barley grain with triticale-based dry distillers grains with solubles on lamb performance and nutrient digestibility. L. E. McKeown*[1,2], A. V. Chaves[2], M. Oba[1], T. A. McAllister[2], and E. Okine[1], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada Research Centre, Lethbridge, AB, Canada*.

The objective of this research was to determine the effects of replacing increasing proportions of barley grain with triticale-based dried distillers′ grains with solubles (TDDGS) on growth, carcass traits and nutrient digestibility in lambs. In the growth study, sixty weaned lambs were blocked by live weight (26.6 ± 3.6 kg), and assigned to one of four diets. The control diet consisted of 72.5% barley grain, 10.0% beet pulp, 9.0% sunflower hulls, 3.0% alfalfa hay and a 5.5% mixture of molasses, calcium carbonate, vitamins and minerals. Treatment diets replaced barley grain with 20, 40 or 60% TDDGS (DM basis). The metabolism study used twelve ram lambs in a 4 × 4 replicated Latin square design with 16 d of adaptation followed by 5 d of total fecal and urine collection. Data were analyzed using the MIXED model of SAS and assessed for linear (L) and quadratic (Q) responses to amount of TDDGS. As TDDGS increased, DMI tended to increase (L, $P = 0.08$) whereas ADG tended to peak at 20% TDDGS (Q, $P = 0.08$) for growing lambs. At slaughter, both body weight and grade rule showed quadratic trends ($P < 0.08$) peaking at 20% TDDGS. Treatment did not affect other carcass traits ($P > 0.28$). As TDDGS increased in the diet, apparent total tract digestibility of DM, NDF and CP decreased (L, $P < 0.006$), and urine N excretion increased (L, $P < 0.006$). Increasing the amount of TDDGS in the diet resulted in excess protein supply. The energy used to convert excess protein to urea may explain why lambs fed 40 and 60% TDDGS did not have faster growth rates or higher carcass weights. In conclusion, 20% TDDGS inclusion may be optimal for maximizing lamb performance.

Key Words: triticale DDGS, carcass traits, apparent digestibility

T102 Effect of bioethanol co-product type and bioethanol plant on situ degradation kinetics, effective degradability and rumen bypass of nutrient components. W. G. Nuez Ortin* and P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*.

The objective was to investigate differences on rumen degradation characteristics among different types of dry distiller grains with solubles (DDGS) and between different bioethanol plants. Corn DDGS, wheat DDGS, blend DDGS (70% wheat:30% corn), wheat and corn feedstock samples were collected during 2007 in Canada. Degradation rate (Kd), lag time (T0), rapidly degradable (S), potentially degradable (D), and undegradable fraction (U), and effective degradability (% ED) for DM, OM, CP and NDF were determined by in situ technique and analyzed by the modified First Order Kinetic Model. Statistical analysis was performed using the Mixed procedure of SAS. In addition, the rumen undegraded fraction (% RU) of each component was determined according to NRC 2001. The results showed some significant differences ($P<0.05$) on rumen degradation kinetics among the three types of DDGS, between DDGS and original feedstock, and between plants. ED of DM was 79, 55, 58, 52 and 55% for wheat, corn, wheat DDGS, corn DDGS and blend DDGS respectively; for CP was 74, 40, 46, 34, and 36%; for NDF was 35, 42, 36, 37, and 32%, and for OM was 76, 49, 54, 46, and 49%. In comparison with original seed, S fraction of DM and OM as well as D fraction of NDF augmented ($P<0.05$) in DDGS. Thus, ED and RU fraction in DDGS were numerically lower and higher respectively for DM, CP and OM. Compared with corn DDGS, wheat DDGS and blend DDGS resulted numerically in higher U fraction of OM and NDF, and higher ($P<0.05$) D fraction of CP. Consequently, wheat DDGS showed the highest ($P<0.05$) ED of CP and DM, while corn DDGS showed the numerical highest RU fraction of DM, CP and OM (Kd numerically lower). In conclusion, rumen degradation characteristics of DDGS differ from original feedstock and among different types. While ED is numerically lower in DDGS than in original feedstock, it increases in DDGS samples as the proportion of wheat increases.

Key Words: dried distillers grains with solubles, effective degradability, rumen bypass

T103 Protein and carbohydrate fractions of new co-products of bioethanol production: Comparison among blend DDGS, wheat DDGS and corn DDGS, and between different bioethanol plants. W. G. Nuez Ortin* and P. Yu, *University of Saskatchewan, Saskatoon, SK, Canada*.

The objectives of this study were to compare different types of dry distiller grains with solubles (DDGS) and different bioethanol plants on protein (CP) and carbohydrate (CHO) fractions. The CP and CHO fractions were partitioned according to the Cornell Net Carbohydrate and Protein System (CNCPS). Protein fractions included rapidly non-protein degradable (PA), rapidly degradable (PB1), intermediately degradable (PB2), slowly degradable (PB3), and unavailable (PC), while carbohydrate fractions included highly degradable free sugars (CA), rapidly degradable (CB1), intermediately degradable (CB2), and unavailable (CC). Corn DDGS, wheat DDGS, blend DDGS (70% wheat: 30% corn) and wheat and corn feedstock samples from different batches were obtained during 2007 in Canada. Statistical analysis was performed using the Mixed procedure of SAS. The results showed that wheat and corn seeds had different ($P<0.05$) CP fractions but similar ($P>0.05$) CHO fractions. Comparing among DDGS, the three types of DDGS had zero PB1. Wheat DDGS was lower ($P<0.05$) in PB2 (27.7 vs. 54.2%CP) and higher ($P<0.05$) in PA (16.3 vs. 11.4%CP) and PB3 (51.2 vs. 27.9%CP) in comparison with corn DDGS, but similar ($P>0.05$) to blend DDGS. The content of NPN in wheat DDGS, corn DDGS and blend DDGS were 100% of SCP. In terms of CHO fractions, only wheat DDGS, corn DDGS, and blend DDGS showed significant differences. Wheat DDGS was higher ($P<0.05$) in the non-structural CHO fraction (48.3 vs. 18.4% CHO), higher ($P<0.05$) in CA (35.9 vs. 9.1%CHO), higher ($P<0.05$) in CC (20.4 vs. 14.2%CHO), similar ($P>0.05$) in CB (average 10.8%CHO), and lower ($P<0.05$) in CB2 (31.3 vs. 67.4%CHO) in comparison with corn DDGS. Moreover, there were significant bioethanol plant effects on CP and CHO fractions. The inclusion of wheat in DDGS improves the degradation of protein but reduces the degradation of carbohydrates in rumen.

Key Words: protein and carbohydrate fractions, bioethanol co–products, dried distillers grains with solubles

T104 Influence of feeding increasing levels of dry or modified wet corn distillers grains plus solubles in whole corn grain-based finishing diets on performance and carcass traits in feedlot cattle. H. Salim*[1], K. M. Wood[1], P. L. McEwen[2], I. B. Mandell[1], S. P. Miller[1], and K. C. Swanson[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Ridgetown Campus, University of Guelph, Ridgetown, ON, Canada*.

One hundred and fourteen cross-bred steer calves and seventeen heifers (BW = 357.2 ± 5.8 kg) were used in a completely randomized block design (2×3 factorial arrangement of treatments plus a control) to determine the effect of inclusion level and form of distillers grains plus solubles (DGS) on feedlot performance and carcass characteristics using whole corn grain-based finishing diets. The DGS were fed at 0 (control), 16.7, 33.3, and 50% of ration DM using dry (DDGS) or modified wet (50% DM; MWDGS) product. All diets contained 10% haylage as a forage source, and were formulated to meet or exceed the estimated requirements for MP. Steers were fed until ultrasound backfat thickness reached 10 mm. Data were analyzed using GLM of SAS; treatment means were compared using contrast statements (control vs. others, DDGS vs. MWDGS, inclusion levels of DGS (linear, quadratic), and interactions between form and linear and quadratic inclusion levels). There were no effects (P > 0.05) of dietary treatment on final BW, ADG, days on feed, rumen pH at slaughter, longissimus muscle area and marbling score. A form by quadratic effect of inclusion level interaction (P = 0.03) was observed for hot carcass weight (HCW) because HCW increased as DDGS increased from 16.7 to 33.3% of diet DM and then decreased as DDGS increased from 33.3 to 50%, while the opposite response occurred with increasing inclusion of MWDGS. These data indicate that feedlot performance and carcass characteristics were not affected by feeding DDGS or MWDGS up to 50% diet DM in whole corn grain-based finishing diets.

Key Words: distillers grains, beef cattle, growth performance

T105 Effects of supplementing beef cows grazing low quality roughages with wheat dried distillers grains with solubles. A. Van De Kerckhove*[1] and H. A. Lardner[1,2], [1]*University of Saskatchewan, Saskatoon, SK, Canada*, [2]*Western Beef Development Centre, Humboldt, SK, Canada*.

Two experiments were conducted to determine the effects of supplementing wheat dry distillers grains with solubles (DDGS) on cow performance and production costs. Dry, pregnant Black Angus cows (n=48, mean BW=598.2±4.2 kg) stratified by body weight and days pregnant were randomly allocated one of three replicated (n=2) treatments. Cows were managed on stockpiled crested wheatgrass pasture (TDN=43.0, CP=6.8 (% DM)) in experiment one (EXP 1) and barley straw-chaff residue (TDN=34.2, CP=8.5 (% DM)) in experiment two (EXP 2). EXP 1 treatments were (1) control (CONT) – no supplement; (2) 100% DDGS (DDGS); or (3) 100% commercial supplement (COMM). EXP 2 treatments were (1) 100% rolled barley grain (CONT); (2) 100% DDGS (DDGS); or (3) 50% DDGS + 50% rolled barley (50:50). Cow body weight (BW), body condition score, and rib and rump fat were measured at start and end of trial for both experiments. Cow BW was also measured every 14 d and results were analyzed using PROC MIXED repeated measures. Cow BW was corrected for conceptus gain based on calving data. Average cow BW in EXP 1 was greater (P=0.03) for DDGS supplemented cows than CONT cows over the course of the trial. Costs per cow per day were $0.75, $1.10, and $1.36 for CONT, DDGS, and COMM, respectively. In EXP 2, cow BW change was greater (P=0.003) for DDGS and 50:50 versus CONT treatments, with BW changes of -2, 12, and 8 kg for CONT, DDGS, and 50:50 treatments, respectively. Changes in rump fat were greater (P=0.04) for the DDGS treatment verses the CONT treatment. Costs per cow per day were $2.71, $2.63, and $2.66 for CONT, DDGS, and 50:50 treatments, respectively. Wheat DDGS showed no adverse effects on animal performance when used as a supplement for beef cows grazing low quality roughages.

Key Words: wheat dried distillers grains with solubles, low quality roughage, beef cows

T106 Effect of microalgal type and length of incubation on fatty acid composition *in vitro* cultures of rumen fluid. C. Whitney*[1], J. Ronquillo[1], C. Enright[1], J. Green-Johnson[2], L. MacLaren[1], A. Fredeen[1], and K. Glover[1], [1]*Nova Scotia Agricultural College, Truro, NS, Canada*, [2]*University of Ontario Institute of Technology, Oshawa, ON, Canada*.

Polyunsaturated fatty acids can be biohydrogenated in the rumen. The aim of this study was to determine the effect of microalgal type and length of incubation on the content of eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), saturated fatty acids (SFA), monounsaturated fatty acids (MUFA) and polyunsaturated fatty acids (PUFA) in *in vitro* batch cultures of rumen fluid. Three microalgal types: MA1 (diatom), MA2 (flagellate) and MA3 (heterotroph); and two controls: CS (cottonseed oil) and NL (no added lipid) were incubated at 39°C in a solution containing 10mL rumen fluid, 40mL buffer, 2mL reducing solution and 500mg dried TMR. Except for the NL control the cultures were isolipidic and contained 100mg supplemental lipid. The experiment was conducted as a completely randomized block with three replications incubated for 0, 6, 12, and 24h. The pH was measured at the beginning and end of each incubation when samples were taken for fatty acid analysis by gas chromotography. The pH consistently decreased for all treatments over time. Regression analysis was conducted on the natural logarithm of the data; the linear slope was used to calculate the rate of change (expressed as a percent) and differences were compared using LSD. The percent SFA present in the cultures remained relatively constant for all treatments over the 24 h incubation with the exception of the CS, where the SFA content dropped by 39% (P<0.05). The percent MUFA of all treatments increased over the 24 h incubation ranging from 11-44% for the MA (but this was not significantly different from NL) and 192% for CS (P<0.05). The percent PUFA decreased for all treatments (32-49%) except for MA3 which decreased by only 7% (P<0.05). With respect to percent EPA and DHA, MA3 showed no significant change over the incubation period whereas the percent EPA decreased for both MA1 and MA2 (~40%) but for percent DHA, MA2 had no change while MA1 decreased (~40%). Changes in fatty acid composition of *in vitro* ruminal cultures varied significantly with respect to microalgal type and should be considered in selection of a microalgal supplement for ruminants.

Key Words: microalgae, ruminal degradation, DHA

T107 Effects of alfalfa hay on chewing behavior, rumen pH, and milk production for lactating dairy cows fed dried distillers grains plus solubles in place of barley silage. S. Z. Zhang*, G. B. Penner, and M. Oba, *University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to determine the effects of alfalfa hay on chewing behavior, rumen fermentation and milk production when barley silage was partially replaced by wheat-based dried distillers grain plus solubles (DDGS). Thirty lactating Holstein cows (220 ± 51 days in milk), of which six were ruminally cannulated, were used in a 3×3 Latin square design with 21-d periods. Cows were fed the control

diet (CON: 50% barley silage, and 50% concentrate mix on DM basis), the diet partially replacing barley silage with DDGS (DG: 30% barley silage, 20% DDGS, and 50% concentrate mix on DM basis) or the diet partially replacing barley silage with DDGS and alfalfa hay (DG+AH: 20% barley silage, 20% DDGS, 10% alfalfa hay, and 50% concentrate mix on DM basis). All diets were formulated to contain 19.7% crude protein by replacing beet pulp in DG and DG+AH with corn gluten meal and urea in CON. Compared to CON, DG and DG+AH increased dry matter intake (23.2, 22.7 vs. 20.1 kg/d, $P < 0.0001$), milk yield (26.7, 27.5 vs. 23.9 kg/d, $P < 0.0001$), milk protein yield (0.97, 0.99 vs. 0.87 kg/d, $P < 0.0001$) and body weight gain (385, 408 vs. 84.7 g/d, $P < 0.0001$) but no differences were observed between DG and DG+AH. While milk fat concentration differed ($P < 0.0001$) among the three diets, (3.91%, 3.60% and 3.37% for CON, DG, and DG+AH, respectively), milk fat yield was not affected by treatment ($P = 0.52$) with an average of 0.92 kg/d. The DG and DG+AH decreased chewing time (703, 709 vs. 763 min/d, $P < 0.0001$) and mean ruminal pH (5.89, 5.85 vs. 6.11, $P = 0.005$) and increased the duration that ruminal pH was below 5.8 (667, 705 vs. 438 min/d, $P = 0.02$) with no differences between DG and DG+AH. These results indicate that partially replacing barley silage with DDGS can improve productivity of lactating dairy cows, but it may also decrease chewing time, rumen pH, and milk fat concentration. The dietary inclusion of alfalfa hay may not help alleviate such decreases.

Key Words: barley silage, DDGS, alfalfa hay

Growth and Development

T108 Genetic group and slaughter weight influence on carcass quantitative traits of feedlot cattle. R. Mello*[1], F. D. de Resende[2], A. C. de Queiroz[3], M. H. de Faria[2], P. V. R. Paulino[3], and G. R. Siqueira[2], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, São Paulo, Brazil*, [3]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*.

The purpose of this study was to investigate the genetic group and slaughter weight influence on carcass quantitative characteristics of the cattle. Thirty six young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) and 18 F1 Blonde D'Aquitaine × Nellore (1/2 BA 1/2 N) were used. The young bulls were finished in a feedlot and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW). A completely randomized experimental design of a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with six replicates was used. The animals were slaughtered in a commercial slaughter-house. Data were analyzed with SAS® software using initial SBW as a covariate. The table below shows the least-square means of cold carcass wt (CCW), carcass compactness index (CCI), daily carcass gain (DCG), kidney, pelvic and inguinal fat (KPI), backfat thickness (BFT), ribeye area (REA) and dressing percentage (DP). There was detected effect ($P<0.05$) of genetic group (GG) and slaughter weight (SW) on carcass quantitative characteristics. However, the interaction between GG and SW were not significant ($P>0.05$) for all measured traits. The 1/2 BA 1/2 N young bulls had a higher DCG, absolute (kg) and relative (kg/100kgCCW) KPI than 1/2 RA 1/2 N young bulls, or vice-versa. As the slaughter weight rised the CCW, CCI, absolute (kg) and relative (kg/100kgCCW) KPI, absolute (mm) and relative (mm/100kgCCW) BFT, absolute REA (cm^2) and DP increased; while the DCG decreased with increasing in SW. The relative REA was not affected by the different treatments (28.7 cm^2/100kgCCW). Thereby, finishing of crossbred F1 Blond D'Aquitaine × Nellore young bulls on feedlot until the animals achieve heavier slaughter weights allow the production of the better carcasses.

Table 1. Least square means

	Genetic Group (GG)		Slaughter Weight (SW)		
	½ RA ½ N	½ BA ½ N	480	520	560
CCW, kg	275.9	281.7	250.4^{c}	273.8^{b}	312.2^{a}
CCI, kg/cm	2.1	2.1	1.9^{c}	2.1^{b}	2.3^{a}
DCG, kg/d	1.2^{B}	1.4^{A}	1.5^{a}	1.1^{b}	1.2^{b}
KPI, kg	5.8^{B}	7.6^{A}	4.4^{c}	6.9^{b}	8.9^{a}
KPI, kg/100kgCCW	2.1^{B}	2.7^{A}	1.8^{b}	2.5^{a}	2.9^{a}
BFT, mm	2.9	3.2	2.1^{c}	2.7^{b}	4.4^{a}
BFT, mm/100kgCCW	1.0	1.1	0.8^{b}	1.0^{b}	1.4^{a}
REA, cm^2	80.2	78.0	72.9^{b}	79.2^{ab}	85.2^{a}
DP, %	53.0	53.7	52.3^{b}	52.7^{b}	55.1^{a}

Within a row, means followed by different capital and small letters differ (P<.05), respectively, among GG and SW by Tukey test.

Key Words: beef cattle, carcass dressing, subcutaneous fat thickness

T109 Physical carcass composition of crossbreed beef cattle slaughtered at different end points. R. Mello*[1], F. D. de Resende[2], A. C. de Queiroz[3], M. H. de Faria[2], G. F. Alleoni[2], and P. V. R. Paulino[3], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, São Paulo, Brazil*, [3]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*.

The objective in this trial was to assess the physical carcass composition of finished crossbred feedlot beef bulls and slaughtered at different body masses. Thirty six young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) and 18 F1 Blonde D'Aquitaine × Nellore (1/2 BA 1/2 N) were used. The young bulls were finished on feedlot and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW). A completely randomized experimental design in a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with six replicates was used. Physical composition was predicted for each carcass using separation (bone, lean, fat) of 9-10-11th rib sections from one side. Data were analyzed with SAS® software using initial SBW as a covariate. The table below shows the least-square means of physical carcass composition. There was significant effect ($P<0.05$) of genetic group (GG) and slaughter weight (SW) on physical composition of the carcasses. The interaction between GG and SW were not significant ($P>0.05$) for all measured traits. The 1/2 BA 1/2 N young bulls had a higher ($P<0.05$) lean proportion, lean to bone ratio, and lower ($P<0.05$) bone proportion than 1/2 RA 1/2 N young bulls. The lighter young bulls were associated ($P<0.05$) to a higher proportion of bone, leaner carcass, and lower lean

to bone and fat to bone ratios. The crossbred F1 Blonde D'Aquitaine × Nellore young bulls and heavier animals produced better carcasses in the finishing phase on feedlot than F1 Red Angus × Nellore and lighter animals.

Table 1. Least square means

	Genetic Group (GG)		Slaughter Weight (SW)		
	½ RA ½ N	½ BA ½ N	480	520	560
Bone, %	16.2^{A}	15.3^{B}	17.1^{a}	14.9^{b}	15.3^{b}
Lean, %	61.4^{B}	62.9^{A}	62.3^{ab}	63.2^{a}	61.0^{b}
Fat, %	22.4	21.8	20.6^{b}	21.9^{ab}	23.7^{a}
Lean:Bone ratio	3.8^{B}	4.1^{A}	3.7^{b}	4.3^{a}	4.0^{ab}
Fat:Bone ratio	1.4	1.4	1.2^{b}	1.5^{a}	1.6^{a}

Means followed by different capital and small letters within a row differ (P<0.05), respectively, among GG and SW by Tukey test.

Key Words: breeds, feedlot, 9-11th rib section

T110 Chemical composition of HH section from crossbred beef bulls slaughtered at different body masses. R. Mello*[1], A. C. de Queiroz[2], F. D. de Resende[3], M. H. de Faria[3], G. R. Siqueira[3], and G. F. Alleoni[3], [1]*Universidade Federal de Roraima, Boa Vista, Roraima, Brazil*, [2]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*, [3]*Agência Paulista de Tecnologia dos Agronegócios, Colina, São Paulo, Brazil*.

The aim of the present experiment was to study the effects of genetic groups and slaughter end points on chemical composition of the 9-10-11th rib section from one side to each carcass. Thirty six young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (½ RA ½ N) and 18 F1 Blonde D'Aquitaine × Nellore (½ BA ½ N) were used. The young bulls were feedlot finished and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW). A completely randomized experimental design of a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with six replicates was used. Data were analyzed with SAS® software using initial SBW as a covariate. The table below shows the least-square means of dependent variables. The genetic group (GG) and its interaction with slaughter weight (SW) were not significant (P>0.05) for all measured traits. There was significant effect (P<0.05) of slaughter weight on chemical composition of the HH sections. The heavier animals had been lower water content and fatter HH sections than lighter animals at slaughter. The protein and ash contents didn't differ (P>0.05) among the different treatments. Thus, young bulls with heavier slaughter weight have better chemical composition of the HH section than young bulls with heavier slaughter weight, independently of genetic group.

Table 1. Least square means

	Genetic Group (GG)		Slaughter Weight (SW)		
	½ RA ½ N	½ BA ½ N	480	520	560
Water, %	61.0	61.6	63.5^{a}	61.3^{b}	59.1^{c}
Ash, %	6.3	5.7	6.0	6.0	5.9
Protein, %	17.2	17.0	17.3	17.1	17.1
Lipid, %	15.5	15.7	13.2^{c}	15.6^{b}	17.9^{a}

Means followed by different capital and small letters within a row differ (P<0.05), respectively, among GG and SW by Tukey test.

Key Words: breeds, feedlot, 9-11th rib section

T111 Measurement of changes in body composition of piglets from birth to 4 kg using quantitative magnetic resonance (QMR). A. D. Mitchell*[1], G. Taicher[2], and I. Kovner[2], [1]*USDA, Agricultural Research Service, Beltsville, MD*, [2]*Echo Medical Systems, Houston, TX*.

During studies of the growth of neonatal piglets it is important to be able to accurately assess changes in body composition. Previous studies have demonstrated that QMR provides accurate measurements of total body fat, lean, and water in non-anesthetized piglets. The purpose of this study was to use QMR to measure changes in the body composition of piglets during growth from birth to 4 kg BW. Using a QMR instrument (EchoMRI), a total of 60 pigs were scanned an average of 5 times starting at 2.7±1.3 d of age (1.95±0.42 kg) and finally at 13.1±4.3 d (4.14±0.52 kg). Each scan consisted of triplicate measurements. The rates of total body growth and fat and lean deposition were analyzed by linear regression analysis. The mean (±SD) rate of total body growth was 236±76 g/d (R^2=0.98±0.04). The rate of fat deposition ranged from 10.6 to 64.9 g/d with a mean of 32±13 g/d (R^2=0.97±0.04). The rate of lean deposition ranged from 39.1 to 353.6 g/d with a mean of 188±60 g/d (R^2=0.95±0.10). The rates of both fat and lean deposition were highly correlated (P<0.001) with total body growth rate (r = 0.88 and 0.94, respectively). The correlation between the rates of fat and lean deposition was 0.74 (P<0.001). The results of this study demonstrate that QMR is a useful method for measuring changes in body composition in neonatal pigs. Furthermore, the results indicate that during the period of growth from birth to 4 kg, the rates of both fat and lean deposition are linear and highly correlated with total body growth.

Key Words: quantitative magnetic resonance, piglets, body composition

T112 An *in vivo* and *in vitro* comparison of muscle precursor cells originating from broiler and layer chick somites. P. E. Mozdziak*, D. Hodgson, and J. N. Petitte, *North Carolina State University, Raleigh*.

Unique avian genetic resources at NC State University were employed to test the hypothesis that the embryonic environment has a greater impact on muscle precursor cell contribution to growth than the genetically-determined growth potential of the muscle-precursor cells. The somites (#17-20; including a portion of the associated neural tube)that form the right *Pectoralis thoracicus* were removed from broiler chick embryos, which are genetically pre-disposed to form large muscles, and replaced with somites from transgenic, layer strain chick embryos (eGFP or lacZ), which are genetically pre-disposed to form small muscles. Embryos were cultured through hatching, and chicks were grown to 8 weeks of age. Muscle weights were lower ($P < 0.05$) in the transgenic layer-derived muscle (233 g) than the broiler-derived background muscle (244 g). Muscle precursor cell mitotic activity assessed using 5-Bromo-2' deoxyuridine (BrdU) labeling revealed a higher ($P < 0.05$)labeling index in the layer-derived muscle at 8 weeks of age (1.72±0.20) than in the broiler background muscle (0.40±0.01) suggesting that the muscle precursor cells in the layer derived muscle responded to the environmental cues provided by the broiler host, and it also suggests that the layer muscle may contain a smaller complement of muscle precursor cells to support growth. Furthermore, muscle precursor cells were fractionated from the layer-derived and the contra-lateral broiler-derived muscles and inoculated into culture. Muscle precursor cells originating from the layer-derived somites exhibited slower ($P < 0.05$) *in vitro* growth than muscle precursor cells originating from broiler-derived somites suggesting that the muscle precursor cells retained their genetically pre-determined responsiveness to cell culture conditions. The overall results of the study suggest that layer-derived muscle precursor cells

retain their genetic low responsiveness to cell culture conditions, but their proliferative activity *in vivo* reflects a response to environmental cues to support the growth potential reflective of the host animal.

Key Words: avian, embryo, development

T113 Glucose metabolism in preterm (PT) and term (T) born neonatal calves. H. M. Hammon*[1], J. Steinhoff[1], S. Görs[1], C. C. Metges[1], and R. M. Bruckmaier[2], [1]*Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*, [2]*University of Bern*, *Bern, Switzerland.*

In neonatal calves, the glucose status often is impaired, even more so in PT born calves. The objective of the present study was to investigate gluconeogenesis (GNG) *in vivo* and hepatic levels of key-enzymes involved in GNG in calves spontaneously born at term (T; n=7) and in calves delivered by sectio 9 d before term (PT; n=7). Calves were gavaged with Deuterium-labeled water (2 × 10 g D_2O /kg BW within 4 h) and received [$U^{13}C$]glucose i.v. (prime: 4.3 μmol/kg BW; infusion: 6.4 μmol/[kg BW × h] for 4 h) after birth. Calves were not fed on d 1 and received milk in amounts of 4% of BW on d 2. Blood samples were taken during tracer administration on d 1 and before and 2 h after milk intake on d 2 to measure total glucose production (GP) and GNG (on d 1) as well as plasma concentrations of glucose photometrically and insulin and glucagon by RIA. Thereafter, calves were slaughtered and liver samples were collected to measure glycogen content and mRNA levels and enzyme activities of pyruvate carboxylase (PC, EC 6.4.1.1), cytosolic phosphoenolpyruvate carboxykinase (PEPCK; EC 4.1.1.32) and glucose-6-phosphatase (G6-Pase; EC 3.1.3.9). Blood data were analyzed by Mixed Model of SAS and GP, GNG, and liver measurements by GLM. Plasma glucose concentrations decreased ($P < 0.05$) from d 1 to d 2 in PT. Plasma insulin concentrations decreased ($P < 0.05$) from d 1 to d 2 and increased ($P < 0.05$) after feed intake on d 2 in both groups. Plasma glucagon concentrations were higher ($P < 0.01$) in PT than T on d 1 and 2. GP and GNG ($P < 0.001$) on d 1 and hepatic glycogen content ($P < 0.05$) on d 2 were higher in T than PT. Enzyme activities of PEPCK ($P < 0.05$) and mRNA levels of PC ($P < 0.1$) were higher in T than PT, but activities of G6-Pase were higher ($P < 0.05$) in PT than T. In conclusion, PT calves showed lower endogenous GP and had difficulty maintaining glucose homeostasis. These data indicated function, but less maturation of hepatic glucose production in PT than T calves.

Key Words: neonatal calf, glucose metabolism, preterm

T114 Milk diet affects glucose status and postprandial hepatic glucose metabolism in neonatal calves. J. Steinhoff*[1], S. Görs[1], C. C. Metges[1], R. M. Bruckmaier[2], and H. M. Hammon[1], [1]*Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*, [2]*University of Bern*, *Bern, Switzerland.*

Calves show hypoglycemia at birth and lactose intake does not meet glucose demands. Therefore, we have investigated postnatal endogenous glucose production, especially gluconeogenesis (GNG), and hepatic glucose metabolism in neonatal calves depending on milk intake. Calves were fed twice daily either colostrum (C) or a milk-based formula (F; n=7 per group) with same nutrient density as colostrum, but no biologically active factors. Amounts (per meal) fed were 4% of BW on d 1 and 5% of BW on d 2-4. On d 3, calves went 15 h without food and were then gavaged with Deuterium-labeled water (2 × 10 g D_2O/kg BW within 4 h) and received [$U^{13}C$]glucose i.v. (prime: 4.3 μmol/kg BW; infusion: 6.4 μmol/[kg BW × h] for 4 h) to measure GNG. Blood samples were taken on d 1 before feeding, during tracer administration on d 3 and before and 2 h after feeding on d 4 to measure GNG (d 3) as well as plasma concentrations of glucose, insulin and glucagon. Calves were slaughtered 2 h after feed intake on d 4 and glycogen content as well as mRNA levels and enzyme activities of pyruvate carboxylase (PC, EC 6.4.1.1) and cytosolic phosphoenolpyruvate carboxykinase (PEPCK; EC 4.1.1.32) were measured in liver. Blood data were analyzed by Mixed Model of SAS and GNG and liver measurements by GLM. Plasma glucose and glucagon concentrations increased from d 1 to d 4 in both groups and plasma glucose was higher ($P < 0.05$), but plasma glucagon was lower ($P < 0.001$) in C than F. On d 4, plasma glucose and insulin concentrations increased ($P < 0.05$) after feed intake much more in C than F. GNG on d 3 was not affected by diet. Hepatic glycogen content was higher ($P < 0.001$) in C than F, whereas mRNA levels ($P = 0.1$) and activities ($P < 0.001$) of PC were lower in C than F. In conclusion, elevated plasma glucose concentrations and hepatic glycogen content in C-fed calves were associated with differences in postnatal endocrine changes and hepatic PC activities between C- and F-fed calves, but not with differences in GNG during feed restriction.

Key Words: neonatal calf, colostrum, glucose metabolism

T115 Metabolic maturity at birth and neonate lamb survival and growth. III. Association among pre-suckling plasma metabolic and endocrine factors and lamb growth to weaning. D. R. Miller*[1], R. B. Jackson[1], D. Blache[2], and J. R. Roche[1], [1]*Tasmanian Institute of Agricultural Research*, *Mt Pleasant, TAS, Australia*, [2]*University of Western Australia*, *Perth, WA, Australia*.

This study investigated the metabolic and hormonal characteristics of Dorset cross lambs at birth and their relationship to subsequent growth to weaning. Multiparous, fine-wool Merino ewes (60 ± 6.5 kg BW, n = 150) of equal numbers of single and twin-lamb bearing status were untreated, or treated with 1.5 or 3 mg dexamethasone (DEX) at either Day 130 or 141 of gestation (n = 30 ewes per treatment) and lambed over 20 d on ryegrass dominant pastures. A 4 to 5 ml blood sample was collected from lambs prior to suckling (30 min after birth) and plasma analyzed for glucose, BHBA, urea, NEFA, insulin, ghrelin and leptin. Ewes and lambs grazed perennial ryegrass-based pastures and lamb BW (22.2 ± 3.22 kg), crown to rump length, and heart girth were measured 75 d after the commencement of lambing, which was 3 d before weaning. Lambs (n= 130) grazed together for another 69 d on ryegrass pastures, and then for 4 d on a dual-purpose oat crop before final weighing and condition scoring. Data were analysed using stepwise multiple regression analysis where non-significant ($P > 0.05$) independent variables were removed, with final models including DEX treatment, rate and timing of DEX treatment, and their interaction term. After accounting for DEX effects, pre-suckling plasma leptin levels were negatively associated with rate of weight gain to ($P < 0.05$) and BW at ($P < 0.05$) weaning, and BCS at final weighing ($P < 0.01$). Lambs with greater heart girth at birth were heavier and larger at weaning ($P < 0.01$). Pre-suckling plasma glucose, BHBA, urea, NEFA, insulin, or ghrelin levels were not ($P > 0.05$) associated with growth to weaning or BW at trial completion. In conclusion, these results indicate that birth size and pre-sucking leptin concentrations are associated with subsequent growth rate in lambs.

Key Words: growth, leptin, sheep

T116 Glucagon-like peptide-2 increases splanchnic blood flow acutely in calves but loses effectiveness with chronic exposure. C. C. Taylor-Edwards*[1], D. G. Burrin[2], J. J. Holst[3], K. R. McLeod[1], and D. L. Harmon[1], [1]*University of Kentucky, Lexington*, [2]*USDA/ARS Children's Nutrition Research Center, Baylor College of Medicine, Houston, TX*, [3]*The Panum Institute, University of Copenhagen, Copenhagen, Denmark*.

Glucagon-like peptide-2 (GLP-2) is a 33-amino acid hormone secreted from the gastrointestinal tract that rapidly increases small intestinal blood flow. No experiments have been conducted evaluating the blood flow response to GLP-2 after extended administration, nor have investigations been performed in ruminants. Eight Holstein calves with an ultrasonic flow probe around the superior mesenteric artery (SMA) and catheters in the carotid artery, mesenteric vein, portal vein, and hepatic vein were paired by age and randomly assigned to treatment: Control (0.5% BSA in saline; n=4) or GLP-2 (50 μg/kg BW bovine GLP-2 in vehicle; n=4). Treatments were administered by subcutaneous injection every 12 h for 10 d. Calves were fed a 50:50 (DM basis) mixture of alfalfa cubes and calf starter at 2.75% of BW in 2 daily meals. A blood flow experiment was conducted on d 0 (Acute) and d 10 (Chronic) of administration and consisted of 3 periods: baseline saline infusion (30 min) to establish baseline blood flow, treatment infusion in which calves were infused with their assigned treatment, either BSA or GLP-2 (1000 pmol/kg/h) for 60 min, and saline infusion (60 min) to observe the recovery of blood flow after treatment infusion. Portal and hepatic plasma flows were measured by *p*-aminohippurate dilution. The statistical model included infusion, treatment, and their interaction as fixed effects and block as a random effect. Repeated measures were conducted on infusion with calf(trt) as the subject. Infusion of GLP-2 increased SMA blood flow to 175% of baseline on d 0 but to only 137% of baseline after Chronic treatment (interaction, P=0.0002). Similar trends were observed for portal and hepatic plasma flow. Our results show that GLP-2 increases splanchnic blood flow in ruminants but this response is attenuated after 10-d GLP-2 administration. These results suggest that GLP-2 could modulate nutrient absorption in ruminants through effects on splanchnic blood flow.

Key Words: glucagon-like peptide-2, gastrointestinal growth, hormone

T117 Glucagon-like peptide-2 increases small intestinal mass of calves. C. C. Taylor-Edwards*[1], D. G. Burrin[2], K. R. McLeod[1], and D. L. Harmon[1], [1]*University of Kentucky, Lexington*, [2]*USDA/ARS Children's Nutrition Research Center, Baylor College of Medicine, Houston, TX*.

Glucagon-like peptide-2 (GLP-2) is a 33-amino acid hormone secreted from the gastrointestinal tract in response to luminal nutrients that potently increases small intestinal mass in non-ruminants. However, the effects of GLP-2 on small intestinal mass and morphology of ruminants is unknown. Eight Holstein calves were paired by age and randomly assigned to treatment: Control (0.5% BSA in saline; n=4) or GLP-2 (50 μg/kg BW bovine GLP-2 in vehicle; n=4). Treatments were administered by subcutaneous injection every 12 h for 10 d. Calves were fed a 50:50 (DM basis) mixture of alfalfa cubes and calf starter at 2.75% of BW in 2 daily meals. On d 11, 2 h after an intravenous injection of 10 mg/kg BW 5-bromo-2′-deoxyuridine (BrdU), calves were killed, gastrointestinal tissues weighed, and epithelial samples obtained from the rumen, omasum, abomasum, duodenum, jejunum, ileum, and colon. Samples were analyzed for villus height, crypt depth, and BrdU staining. The statistical model included treatment as a fixed effect and block and block by treatment as random effects. Compared to Control, GLP-2 increased small intestinal mass by 24% (P=0.04). Intestinal length was unchanged but intestinal thickness was increased (P=0.02) by GLP-2, particularly because of increased epithelial mass in the jejunum (P=0.008) and ileum (P=0.04). Treatment with GLP-2 increased villus height in the duodenum (P=0.03), jejunum (P=0.06), and ileum (P=0.09). In addition, GLP-2 increased crypt depth in the duodenum (P=0.06) and jejunum (P=0.02). Treatment with GLP-2 increased crypt cell proliferation as indicated by increased BrdU-labeling in the duodenum (P=0.02), jejunum (P=0.01), and ileum (P=0.05). These results demonstrate that GLP-2 induces similar increases in ruminant intestinal growth as observed in non-ruminants and could be an important mediator of small intestinal growth in response to luminal nutrients in ruminants.

Key Words: glucagon-like peptide-2, gastrointestinal growth, hormone

T118 Maternal low and high protein diets during pregnancy affect body weight and stress reactivity in the offspring of pigs. M. Graebner*, E. Kanitz, M. Tuchscherer, B. Stabenow, C. C. Metges, C. Rehfeldt, and W. Otten, *Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*.

Objective: Nutritional imbalance during pregnancy can have long-term consequences on the development of the offspring. An inadequate nutrient supply and/or maternal hormones can cause fetal growth retardation, metabolic changes and alterations of stress-sensitive systems in the offspring. In this study, we determined the effects of low and high protein diets in pregnant sows on growth development and function of the HPA and SAM axis of their offspring. Methods: Forty-two German Landrace sows (first parity) were fed isocaloric diets with high (HP, 30%), low (LP, 6%) or control (CP, 12%) protein levels throughout gestation. The offspring was reared by foster sows until weaning on postnatal day (PND) 28. Salivary cortisol was measured in sows during gestation, and plasma cortisol and catecholamines were determined in the offspring on PND 1 and 27 (basal levels) as well as under challenging conditions (weaning, LPS-, ACTH- and insulin-challenge) later in life. Glucocorticoid receptor (GR) binding and neurotransmitter concentrations were measured in stress-related brain areas. Results: The LP diet caused a decreased growth performance of sows and reduced the birth weights of piglets. Salivary cortisol levels were increased in LP sows from mid gestation until parturition. HP piglets showed a decreased serotonergic activity in the locus coeruleus on PND 1. The GR binding in the hippocampus was increased in LP and HP offspring on PND 27. Basal stress hormone concentrations were not affected, however, there was a tendency for a higher cortisol response to weaning in female LP piglets. In addition, LP offspring showed an increased catecholamine response during an insulin challenge test. Conclusion: The present results indicate that dietary protein levels during pregnancy in sows can influence growth and the function of stress systems in the offspring. In particular, a dietary protein deficiency resulted in growth retardation in the offspring and an increased reactivity of their SAM system.

Key Words: fetal programming, stress reactivity, glucocorticoids

T119 Linoleic acid changes fatty acid profiles and alters gene expression in bovine adipocyte cultures. A. P. Burns*, S. K. Duckett, S. L. Pratt, and S. E. Ellis, *Clemson University, Clemson, SC*.

The objective of this study was to determine if differences in fatty acid profiles or gene expression exist when adipocytes are exposed to a linoleic acid (C18:2)-supplemented media post differentiation. With

limited information in the literature about the timing of lipid uptake in differentiated preadipocytes, a secondary objective of this study was to evaluate fatty acid composition and gene expression over time. Primary preadipocyte cultures were isolated from 18 mo old Angus crossbred steers. After plated cells reached confluence (d 0), differentiation media was applied for 2 d and cells were supplemented with 0 mM (C) or 0.3 mM (LA) C18:2 for 10 d. Cells were harvested on d 2, 6, and 12 for analysis using gas chromatography and RT-PCR. The percentages of palmitic (C16:0), stearic (C18:0), oleic (C18:1), and linolenic (C18:3) acids were decreased (P<0.001) in LA cells compared to C cells on d 6 and 12. LA cells had greater (P<0.001) C18:2 and total fatty acid content compared to C, in terms of percent composition and μg/well. Analysis of mRNA expression revealed that fatty acid synthase (FASN) and glucose transporter 4 (GLUT4) mRNAs were elevated (P<0.05) in LA cells compared to C. Regardless of C18:2 supplementation, FASN mRNA levels increased (P<0.001) and stearyl-CoA mRNA levels decreased (P<0.0001) over time. A significant interaction existed between time and treatment for sterol regulatory element binding protein, peroxisome proliferator-activated receptor gamma, and adipocyte protein 2 mRNA levels. C cells decreased (P<0.05) in their expression of all these mRNAs over time, whereas LA cells increased (P<0.05) slightly or stayed the same. In conclusion, supplementing culture media with C18:2 produced changes in fatty acid composition of bovine adipocytes by d 6 and influenced mRNA expression. Based on our data of fatty acid uptake and mRNA expression changes of differentiation-associated proteins, we propose to time future investigations of bovine adipocytes more closely with differentiation.

Key Words: adipocyte, linoleic acid, gene expression

T120 Docosahexaenoic acid enhances hepatic serum amyloid A expression via a protein kinase A-dependent mechanism. J. J. Dai, Y. C. Wang, P. H. Wang, H. J. Mersmann, and S. T. Ding*, *Institute of Biotechnology, National Taiwan University, Taipei, Taiwan*.

Serum amyloid A (SAA) can induce adipocyte lipolysis to reduce fat deposition in adipocytes and hepatocytes. Hepatic SAA1 mRNA is increased by docosahexaenoic acid (DHA) treatment in pigs. Understanding whether DHA can decrease fat deposition through SAA1 and what the mechanism is would help to develop strategies against the fatty liver symptom and obesity. In the current study, we demonstrated that DHA treatment simultaneously increased human SAA1 and C/EBP β mRNA expression in human hepatoma cells, SK-HEP-1. Utilizing a promoter deletion assay, we found that a C/EBPβ binding site in the SAA1 promoter region between -242 and -102 bp was crucial for DHA-mediated SAA1 expression. When we mutated the putative C/EBPβ binding site, the DHA-induced increment of SAA1 promoter activity was suppressed, suggesting that this binding sequence is very important for the DHA regulated function. The DHA also increased C/EBP β protein expression and the addition of a protein kinase A inhibitor, H89, abrogated the increase in C/EBPβ. In addition, the up-regulation of SAA1 expression by DHA was inhibited by H89. These data suggest that DHA up-regulates the expression of C/EBPβ by activating PKA. Indeed, DHA treatment increased both PKA activity and the expression of C/EBPβ in SK-HEP-1 cells. We have demonstrated that DHA activates PKA to increase the expression of SAA1. Because the increase of SAA1 will increase the lipolytic activity by increasing the expression of lipolytic genes, such as hormone sensitive lipase, DHA could reduce lipid accumulation in the liver and the body. These results may be useful to develop new approaches to reduce body fat deposition and fatty liver.

Key Words: DHA, SAA, C/EBPbeta

T121 Effects of arginine supplementation to gilts during early gestation on fetal myogenesis. C. Kalbe*[1], M. Porm[1], J. Bérard[2], G. Bee[2], and C. Rehfeldt[1], [1]*Research Institute for the Biology of Farm Animals, Dummerstorf, Germany*, [2]*Agroscope, Liebefeld Posieux, Switzerland*.

To study the impact of additional L-arginine intake during early gestation on cellular properties of skeletal muscle of the offspring, 20 Swiss Large White gilts were randomly allocated to either control (C) or arginine (A) group at the day of mating. Gilts were fed 3 kg daily of a standard diet and A-gilts received additionally 26 g/d L-arginine from d 14 to 28 of gestation. At d 75 of gestation the gilts were sacrificed with 3 C-gilts being excluded because of non-pregnancy. From each litter the lightest, heaviest, and one fetus with an average fetal weight from both genders were selected and the *longissimus* muscle (LM) was excised for analyses (n = 98 in total). Compared with the offspring from the C-gilts the protein/DNA ratio tended to be decreased (32.5 vs. 34.2; P = 0.08) in response to maternal arginine supplementation. This resulted from a numeric increase (1.80 vs. 1.74 mg/g tissue; P = 0.16) in DNA concentration and a concomitant numeric decrease in protein concentration (57.91 vs. 59.23 mg/g tissue; P = 0.36). Moreover, treatment × gender interactions revealed lower creatine kinase (CK) activity (P < 0.05) and protein concentration (P = 0.07) in female offspring of arginine-supplemented gilts. The mRNA expression of genes encoding for the muscle regulatory factors (MRF) was measured in the LM of light and heavy female fetuses (n = 28). In offspring of A-gilts the transcript expression of the Myf5 gene was increased (1.41 vs. 1.00; P < 0.05) compared with the offspring of C-gilts. The mRNA expression of the MyoD, myogenin and MRF4 genes remained unchanged by arginine intake. The results suggest that arginine supplementation during early gestation stimulates myogenic proliferation associated with a lower degree of muscular maturity at d 75 of gestation indicative of delayed differentiation. This effect is particularly pronounced in female offspring.

Key Words: pregnant gilts, arginine, myogenesis

T122 Identification and characterization of the bovine G protein-coupled receptor GPR41 and GPR43 genes. A. Wang, Z. Gu, B. Heid, R. M. Akers, and H. Jiang*, *Virginia Polytechnic Institute and State University, Blacksburg*.

Volatile fatty acids (VFA) regulate rumen development, insulin and glucagon secretion, and some other physiological processes in cattle. The underlying mechanisms are unknown. Recent "reverse pharmacology" studies identified human G protein-coupled receptors GPR41 and GPR43 as receptors for short-chain fatty acids. It is possible that proteins similar to human GPR41 and GPR43 mediate the regulatory effects of VFA in cattle. In this study, we determined first whether the bovine genome contains genes similar to the human GPR41 and GPR43 genes and secondly whether and where these genes are expressed in cattle, and if the proteins encoded by these genes can be activated by acetate, propionate, and butyrate. A search of GenBank revealed bovine genomic sequences and expressed sequence tags highly similar to the human GPR41 and GPR43 DNA and cDNA sequences. The protein-coding and 5′ untranslated regions of the bovine GPR41 and GPR43 mRNA were cloned and sequenced from the spleen tissue. Based on these sequences, the bovine GPR41 gene contains three exons and its transcription is initiated at two leader exons, generating two GPR41 mRNA variants differing in the 5′ untranslated region. The bovine GPR43 gene contains two exons, and transcription of this gene is initiated from a single start site. The amino acid sequences deduced from the bovine GPR41 and GPR43 mRNA sequences are more than 75% identical to those of the human GPR41 and GPR43 and are predicted to encode

seven transmembrane domains, typical of G protein-coupled receptors. By RT-PCR, both bovine GPR41 and GPR43 mRNA were detected in a variety to tissues, including rumen and pancreas. In a cell system, interaction of the overexpressed bovine GPR41 or GPR43 protein with acetate, propionate, or butyrate inhibited luciferase reporter expression from a cAMP-responsive promoter, suggesting that the bovine GPR41 and GPR43 proteins couple to Gαi/11. In total these results demonstrate that the bovine genome encodes functional GPR41 and GPR43 genes and suggest that GPR41 and GPR43 may play a role in the regulatory effects of VFA in cattle.

Key Words: G-protein-coupled receptors, cattle, sequence

T123 Potential role of low-density lipoprotein receptor-related protein (LRP)-1 and IGFBP-3 in the proliferation-suppressing actions of TGF-beta on cultured myogenic cells. E. Kamanga-Sollo, M. S. Pampusch, M. E. White*, M. R. Hathaway, and W. R. Dayton, *University of Minnesota*, *St. Paul*.

Myostatin and transforming growth factor (TGF)-beta suppress both proliferation and differentiation of cultured myogenic cells. Recent studies have shown that the IGF-independent actions of insulin-like growth factor binding protein (IGFBP)-3 facilitate the proliferation-suppressing actions of both myostatin and TGF-beta on cultured myogenic cells; however, the mechanism of this facilitation is not known. To assess this mechanism, we have transfected L6 myogenic cells, which do not produce detectable levels of IGFBP-3, with a construct containing the porcine IGFBP-3 cDNA behind a constitutively active promoter. These transfected cells (tL6) constitutively express porcine IGFBP-3. Consistent with our previous observation that IGFBP-3 facilitates the proliferation-suppressing actions of TGF-beta, dose response curves showed that proliferation of tL6 cells was inhibited at lower TGF-beta concentrations than was proliferation of mock-transfected or non-transfected L6 cells ($p < 0.05$). In non-muscle cells, IGFBP-3 suppresses proliferation by binding to LRP-1, suggesting that binding to this receptor may play a role in the ability of IGFBP-3 to facilitate the proliferation-suppressing actions of TGF-beta and myostatin on cultured myogenic cells. To assess the role of LRP-1 in this process, we have examined the effects of Receptor Associated Protein (RAP), a protein which inhibits ligand binding to LRP-1, on TGF-beta-induced suppression of proliferation of mock-transfected L6 and tL6 myogenic cells. RAP significantly ($p < 0.02$) increases proliferation of TGF-beta-treated tL6 cells, which produce IGFBP-3, while having no effect on proliferation of TGF-beta-treated mock transfected or control L6 cells, neither of which produces IGFBP-3. These data suggest that binding of IGFBP-3 to LRP-1 may play a role in the mechanism by which IGFBP-3 facilitates the proliferation-suppressing actions of TGF-beta on cultured myogenic cells.

Key Words: IGFBP-3, TGF-beta, muscle

T124 Clofibrate treatment up-regulates hepatic gene expression encoding fatty acid oxidation and ketogenesis enzymes in liver of pigs during early postnatal development. K. Shim, L. Xi*, S. Jacobi, and J. Odle, *North Carolina State University*, *Raleigh*.

The aim of this research was to investigate the effects of clofibrate on gene expression of hepatic fatty-acid-oxidation and ketogenesis enzymes in pigs during early neonatal development. Sixty colostrum-deprived newborn pigs were fed milk replacer and orally gavaged with either vehicle (2% Tween 80) or clofibrate (75 mg /kg body weight) ± etomoxir (5 mg/ kg body weight) once daily. The effect of treatment was evaluated on days 0, 1, 4 and 7. Clofibrate treatment did not significantly change liver weights. Messenger RNA abundances measured via qRT-PCR, were increased for carnitine palmitoyltransfersae I (CPT I; 2.8 fold), carnitine palmitoyltransfersae II (CPT II; 3.2 fold), and mitochondrial 3-methly-3-hydroxyglutaryl-CoA synthase (mHMG-CoA-S; 3.8 fold) in pigs fed clofibrate compared to vehicle. Addition of etomoxir did not affect mRNA abundances induced by clofibrate. Transcript levels increased as piglets aged, but the abundances remained relatively constant for CPT I and mHMG-CoA-S after four days and for CPT II after one day. There was no interaction between clofibrate treatment and age. Acyl-CoA oxidase, acetyl-CoA carboxylase and peroxisome proliferator-activated receptor α abundance were not altered by clofibrate, etomoxir or piglet age. In conclusion, clofibrate strongly up-regulates genes of fatty acid oxidation in the young, postnatal pig, but induction is not influenced by developmental age. *Supported by CSREES, USDA NRI program award 2007-35206-1 7897.*

Key Words: clofibrate, fatty acid oxidation, gene expression

T125 Use of gas chromatography to measure stearoyl-CoA desaturase activity and substrate preference. J. A. Stamey*, C. A. Umberger, M. D. Hanigan, and B. A. Corl, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Stearoyl-CoA desaturase (SCD) catalyzes the desaturation of saturated fatty acyl-CoA substrates, primarily synthesizing palmitoleoyl-CoA and oleoyl-CoA. SCD is a key enzyme controlling milk and body fat composition. Two known isoforms, SCD1 and SCD5, are present in the bovine genome, and found in adipose and brain tissue, respectively. Most SCD activity assays use radiolabeled substrates, and the variety of radiolabeled substrates available for assay can be limited. We developed a method permitting use of a variety of unlabeled fatty acid substrates to measure desaturase activity with gas chromatography based on procedure of Su and Brenna (Anal. Biochem. 261:43). Enzyme reactions (500 μL) were incubated at 37°C for 30 min, stopped with 12% ethanolic KOH, and saponified at 70°C for 30 min. Desaturase activity was assayed using myristate, palmitate, deuterium-labeled stearate, and arachidate complexed to bovine serum albumin as substrates. For myristate, palmitate, and arachidate, monounsaturated product fatty acids were undetectable at time 0, so labeled substrate was not required. Total lipids were extracted from enzyme reactions, methylated, and quantified by gas chromatography using nonadecanoic acid as the internal standard. Due to high levels of endogenous oleate in microsomes, stable-isotope-labeled stearate was used as a substrate and quantification of labeled oleate produced by SCD was performed using gas chromatography-electron ionization mass spectrometry. The assay was linear with microsomal protein up to 200 μg and time up to 45 min. Bovine adipose and brain microsomes were isolated from 14-20-mo old Angus and Angus-cross steers (n=3). Substrate-specific activities in adipose microsomes (100-200 μg protein) were 0.99±0.24, 1.02±0.76, 1.17±2.24, and 0.92±0.27 nmol/mg•min for myristate, palmitate, stearate, and arachidate, respectively. Brain microsome SCD activity was not detected. Application of this method will allow tissue-specific SCD isoform characterization, including substrate specificities and enzyme kinetics.

Key Words: desaturase, microsomes, gas chromatography

T126 Maternal weight and P8 fat amount affects *IGF2* expression in *semitendinosus* muscle tissue of the developing fetus. C. J. Fitzsimmons*[1,2], R. Feldmann[1], Z. A. Kruk[1,3], S. Truran[1], D. Lines[1], D. Rutley[1], and S. Hiendleder[1,4], [1]*JS Davies Epigenetics and Genetics Group, Discipline of Agricultural and Animal Science, The University of Adelaide, Roseworthy Campus, Roseworthy, South Australia, Australia*, [2]*Agriculture and Agri-Food Canada, Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [3]*Chungnam National University, Daejeon, South Korea*, [4]*Research Centre for Reproductive Health, The University of Adelaide, Adelaide, South Australia, Australia*.

Insulin-like growth factor 2 (*IGF2*) is an important promoter and regulator of fetal growth. We have measured *IGF2* exon 10 expression (present in almost all *IGF2* transcripts), in *semitendinosus* muscle of bovine fetuses obtained at Day 153 of pregnancy. Relative *IGF2* expression was examined using a univariate GLM including factors dam genetics, sire genetics, fetus sex, and covariate dam weight, and their 2, 3, and 4-way interactions, as explanatory variables in the model. There was a strong negative relationship between dam weight and expression of *IGF2* exon 10 in fetal muscle (P=0.015), and the average *IGF2* expression level of male fetuses was higher than that of females (P=0.025). To investigate the origin of the curious negative relationship between fetal *IGF2* expression and maternal weight, empty uterus weight of the dam was substituted into the model for dam weight. The results showed that uterus weight and fetal sex were both significant (P=0.049 and 0.025, respectively). Therefore, maternal size itself had a great influence on fetal gene expression, although there appeared to be some other, possibly nutritional, components involved. Several other measures of change in dam weight during pregnancy were tested in the model, but were not statistically significant. When P8 fat (fat depth as measured on top of the rump of the carcass) was used in the model instead of dam weight, it also was not significant. However, when both P8 fat and dam weight were included in the model, the R^2 value increased from 0.816 to 0.906. Now fetal sex*dam weight*P8 fat and dam genetics*P8 fat were significant (P=0.011 and 0.002, respectively). It also appeared that there was a particular dam weight where the relationship between an increase in maternal P8 fat and fetal *semintendinosus IGF2* expression changes.

Key Words: IGF2, gene expression, pre-natal

T127 Fetal growth is substantially modulated by at least two different genetic loci in the middle part of bovine chromosome 6. A. Eberlein[1], A. Takasuga[2], K. Setoguchi[3], R. Pfuhl[1], K. Flisikowski[4], R. Fries[4], N. Klopp[5], K. Suhre[5], R. Weikard[1], and Ch. Kühn*[1], [1]*Research Institute for the Biology of Farm Animals, Dummerstorf, Germany*, [2]*Shirikawa Institute of Animal Genetics, Fukushima, Japan*, [3]*Cattle Breeding Development Institute of Kagoshima Prefecture, Kagoshima, Japan*, [4]*Chair of Animal Breeding, Technische Universität München, Freising, Germany*, [5]*Helmholtz Zentrum, Munich, Germany*.

In cattle, fetal growth has raised attention for its impact on stillbirth and dystocia in conventional reproduction and also due to the still unknown fetal growth mechanisms impairing calves generated by somatic nuclear transfer techniques. For our analyses of the genetic background of fetal growth, birth weight data were available from a F_1 and F_2 resource population generated from purebred Charolais and German Holsteins by consistent application of embryo transfer. This approach enabled the specific analysis of the genetic background for divergent fetal growth dissected from maternal effects. After genotyping of 16 microsatellite markers, an initial line cross regression model assuming alternatively fixed QTL alleles in the founder breeds revealed a genome-wide significant QTL (F = 90.16, p<0.0001) in the middle part of BTA6. The QTL accounted for 16.3% of the genetic variance in the model and was located within a confidence interval of 12 cM. To further refine the QTL additional 36 targeted SNP were genotyped. Consecutive variance component QTL analyses fitting the QTL and an infinitesimal animal effect revealed that the QTL initially appearing as one, could be divided into two separate loci: one of the QTL, located at 49 cM (LRT 1 QTL vs. no QTL = 94.08), showed a fixed QTL effect. In contrast, the second QTL at 55 cM (LRT 2 QTL vs. 1 QTL = 70.45) evidently had a random effect without fixation of alleles in the founder breeds. While the QTL seem to have a major effect on intrauterine growth, no effect could be detected for the consecutive period from birth to day 121. Association analyses ($p<10^{-15}$) in line with concordance analyses of significantly segregating F_1 individuals identified a SNP at 49 cM, which is in very close linkage disequilibrium with a causal mutation affecting fetal growth or might be a causal mutation itself. The substantial effect size of the detected genetic locus will facilitate further functional investigations of its role in affecting growth during normal and aberrant fetal development in conventional reproduction or in assisted reproduction techniques.

Key Words: fetal growth, cattle, QTL

T128 Relationships between growth and metabolic parameters of replacement heifers on two nutrition programs. F. Abeni[1], L. Calamari[2], G. Pirlo*[1], and L. Stefanini[3], [1]*CRA-FLC, Cremona,Italy*, [2]*Istituto di Zootecnica, U.C.S.C., Piacenza, Italy*, [3]*Azienda Sperimentale V. Tadini, Gariga di Podenzano, Italy*.

In two experimental herds 141 replacement heifers were reared with the aim of investigating the relationships between growth from 5 to 18 mo of age and metabolic parameters. The heifers of both herds were fed on a moderate ADG (MADG: 0.7 kg/d) or on an accelerated ADG (AADG: 0.9 kg/d) diet. Heifers' BW, BCS, wither height (WH), hip height (HH), body length (BL), and hearth girth (HG) were recorded every 28 days. At 9 and 15 mo of age a blood sample was drawn for analysing metabolic profile. Data from body measurements were processed by analysis of variance and growth curve analysis, using Laird's form of Gompertz curve. Metabolic profiles were processed by Principal Components Analysis (PCA), followed by Pearson's correlation analysis between growth curve coefficients and PCs. The AADG heifers had greater actual ADG (0.83 vs 0.74 kg, P<0.001) and greater daily increase of HG (1.76 vs 1.65 mm, P<0.005) than MADG heifers. From 9 to 18 mo of age, BCS of AADG heifers diet was greater than BCS of MADG heifers (P<0.05). From the comparison of growth curve parameters between ADG groups, only the initial growth rate of HG was affected by diet, and no effect was found on maturation rate. The PCA showed a PC1 mainly composed of total protein and albumin (9 and 15 mo), Na and ceruplasmin (9 mo), glucose and Ca (15 mo). This component was positively correlated (P<0.05) with the maturation rate of the growth functions for BW, WH, HH, and HG.

Table 1. Coefficients of the growth curves

		MADG		AADG		
		Mean	SE	Mean	SE	P
BW	b_1_	2.874	0.0637	3.026	0.0849	0.15
	b_2_	0.0035	0.0001	0.0034	0.0002	ns
WH	b_1_	0.748	0.0199	0.761	0.0255	ns
	b_2_	0.0031	0.0001	0.0032	0.0002	ns
HH	b_1_	0.683	0.017	0.687	0.022	ns
	b_2_	0.0036	0.0002	0.0037	0.0001	ns
BL	b_1_	0.944	0.028	0.943	0.037	ns
	b_2_	0.0039	0.0002	0.0040	0.0002	ns
HG	b_1_	1.027	0.0235	1.113	0.0313	0.03
	b_2_	0.0035	0.0004	0.0042	0.0006	ns

Key Words: replacement heifers, ADG, metabolic profile

T129 Luminal energy supply (but not substrate) affects expression of mRNA for three proteins capable of amino acid transport by ileal epithelium (but not duodenal or jejunal) of forage-fed growing beef cattle. S. F. Liao*, J. A. Boling, and J. C. Matthews, *University of Kentucky*, *Lexington*.

To complete our *in vivo* study of whether basal expression of 20 amino acid (AA) transporter genes by duodenal (D), jejunal (J), and ileal (I) epithelia is affected by increased luminal supply of rumen-derived microbes (hence, AA substrates), starch-derived energy, or both, 18 ruminally and abomasally catheterized Angus steers (BW ~ 260 kg) were assigned (n = 6) to either water (basal) or ruminal or abomasal corn starch hydrolysate (SH, by α-amylase) infusion treatment (at 20% ME intake) and fed an alfalfa-cube based diet at 1.3× NE_m requirement. After a 14- or 16-d infusion, steers were killed, small intestinal epithelia harvested, and total RNA extracted. Real-time RT-PCR analysis of the effect of substrate and energy supply on expression of mRNA encoding AA transport systems x^-_c (xCT), T (TAT1), H^+-dependent AA (PAT1), and H^+-dependent peptide (PepT1) was conducted to quantify the relative expression of AA transporter mRNA:18S rRNA. Basal expression of mRNA differed ($0.01 \leq P \leq 0.09$) among the 3 epithelia. For xCT, TAT1, and PepT1, the expression pattern was D = J > I. For PAT1, however, the pattern was J > D = I. Increased luminal AA supply did not affect transporter mRNA content. Although, D and J expression were unaffected by increased luminal energy supply, I expression of xCT mRNA was increased by 41% ($P = 0.04$), PepT1 by 162% ($P = 0.03$), and TAT1 by 56% ($P = 0.08$). The findings that PAT1, TAT1, and xCT mRNA are expressed by cattle small intestinal epithelia are novel. Given the known localization and function of the proteins encoded by the evaluated mRNA, this study suggests that the potential for I apical uptake of luminal peptide-bound AA by PepT1, basolateral transfer of aromatic AA by TAT1 into blood, and cystine uptake from blood by xCT, is enhanced by increased luminal starch-derived energy supply to forage-fed growing cattle.

Key Words: bovine, nutrient-gene interaction, substrate reguation

T130 Early life management and long term productivity of dairy calves. F. Soberon*, E. Raffrenato, R. W. Everett, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

For many years, early life management of the calf has focused on survival rates and rumen development. However, recent studies suggest that colostrum status as well as nutritional status during the pre-weaning phase may have long term carry-over effects on milk yield potential. The objective of this study was to investigate this relationship in the Cornell Dairy Herd using a test day model (TDM) to evaluate the lactation response over eight years. The management objectives of the calf program have been to double the birth weight by weaning through increased milk replacer intake. The TDM was utilized to generate lactation residuals accounting for the effects of test day such as calving season, days carried calf, days in milk, and lactation number (Everett and Schmitz, 1994; Van Amburgh et al., 1997). Lactation residuals from the TDM were generated from 792 heifers with completed lactations and linear regressions were run on several measures of pre-weaning growth performance, management factors and TDM milk yield solutions. Significant correlations were found for pre-weaned average daily gain (ADG), weaning weight, year and month of birth. Pre-weaning ADG ranged from 0.13 kg to 1.23 kg and ADG had the greatest correlation with first lactation milk production. Using the TDM solutions, for every 1 kg of pre-weaning ADG, heifers produced 1,067 kg more milk during their first lactation ($P < 0.01$). Further, pre-weaning ADG accounted for 25 percent of the variation in first lactation milk yield. Other factors analyzed included age at first calving and birth weight but correlations with TDM lactation residuals were not significant. Data from other farms have yielded similar results and further work, incorporating multiple farms and data sets, is being conducted to better describe the correlation between early life nutritional status and long term productivity. These results demonstrate that increased growth rate, primarily through increased liquid feed intake, prior to weaning has positive effects on lactation milk yield.

Key Words: calves nutrition, milk production, test day model

T131 Metformin inhibits adipogenesis in fetal muscle of dam receiving high energy diet. J. F. Tong*, X. Yan, J. X. Zhao, and M. Du, *University of Wyoming*, *Laramie*.

At the later stage of fetal skeletal muscle development, adipogenesis within fetal muscle forms intramuscular adipocytes, which provide sites for intramuscular fat accumulation (marbling). High energy diet inhibits AMP-activated protein kinase (AMPK) and promotes adipogenesis in fetal muscle, but the cause and effect relationship between AMPK and adipogenesis in fetal muscle has not been established. The objective of current study is to evaluate the role of AMPK in adipogenesis in fetal skeletal muscle. Prior to pregnancy, female weanling C57BL/6J mice were randomized to receive either a control diet (Con, 10% energy by fat) or a high energy diet (Ob, 45% energy by fat) for 10 weeks. At three months of age, mice were mated. The Con mice continued to be fed with control diet, while the Ob mice were separated into 2 groups, with one group fed with high energy diet and the other group fed high energy diet plus metformin (2 mg/ml in drinking water, Met), a known activator of AMPK. Hindlimb and back muscles from newborn mice (Day 1, n = 6 per treatment) were collected for analyses. AMPK phosphorylation was lower in neonatal Ob skeletal muscle. β-Catenin and myogenic regulatory factors MyoD and myogenin were down-regulataed in Ob muscle, while the adipogenic marker, peroxisome proliferator-activated receptor γ (PPARγ), was up-regulated compared to Con muscle, indicating the down-regulation of myogenesis but up-regulation of adipogenesis in Ob neonatal muscle. Metformin administration stimulated AMPK activity, restored MyoD expression and decreased PPARγ expression. Hematoxylin and eosin staining showed more adipocytes were deposited in Ob neonatal skeletal muscle, but metformin reduced the deposition of intramuscular adipocytes. These data indicate that maternal high energy

diet enhances adipogenesis in fetal muscle via inhibition of AMPK. Therefore, AMPK is an attractive molecular target to enhance adipogenesis in fetal muscle and, thus, marbling in the muscle of offspring.

Key Words: adipogenesis, skeletal muscle, AMP-activated protein kinase

T132 Albumin induced cytokine expression in porcine adipose tissue explants. T. G. Ramsay*, M. Stoll, and T. J. Caperna, *USDA-ARS, Beltsville, MD*.

Albumin has historically been included in medium designed for use with adipose tissue when evaluating metabolism, gene expression or protein secretion. However, recent studies with mouse adipocytes (Ruan et al., J. Biol. Chem. 278:47585-47593, 2003) and human adipose tissue (Schlesinger et al., Amer. J. Physiol. 291:27-33, 2006) have demonstrated an acute cytokine response by cells derived from adipose tissue to albumin. The present study was designed to determine whether or not albumin can alter cytokine expression in porcine adipose tissue explants relative to explants not exposed to albumin. Subcutaneous adipose tissue explants (100 mg) were prepared from dorsal subcutaneous adipose tissue of 21 day old pigs using a Stadie-Riggs microtome. Slices were placed in Hanks′ balanced salt solution prior to albumin exposure. Triplicate slices were frozen in liquid nitrogen (controls). Additional slices were incubated in medium 199 supplemented with 100 mM HEPES and 0.5% bovine albumin (Sigma A7030) at 37°C. Triplicate tissue slices were removed from the medium at 1, 2 or 4 hours following exposure to the albumin containing medium and frozen in liquid nitrogen. Samples were extracted for RNA using Qiagen columns and RNA (1 ug) was reverse transcribed and used in real-time PCR analysis to assess the expression of the adipokines leptin, adiponectin, tumor necrosis factor alpha (TNF-alpha), interleukin (IL) 6 and IL15 relative to cyclophilin. Expression of leptin and adiponectin was not altered ($P > 0.05$) by exposure to 0.5% albumin. However TNF alpha mRNA abundance was elevated ($P < 0.001$) 1436 ± 134% within 1hr of exposure to albumin. Similarly, IL6 was elevated ($P < 0.001$) by greater than 1246 ± 286% within 1hr of incubation. In contrast, IL15 mRNA abundance was reduced ($P < 0.01$) by 62 ± 8% within 4hr. These data indicate that albumin alters the expression of specific adipocytokines. Secondly the data indicate that in vitro analysis of porcine adipocytokine expression may be confounded if albumin is utilized in the medium.

Key Words: adipose tissue, cytokine, swine

T133 Assisted reproductive technologies (ART) have a dramatic effect on cell proliferation in ovine fetal membranes (FM) during early pregnancy. P. P. Borowicz*[1], L. P. Reynolds[1], L. R. Coupe[1], G. Ptak[2], P. Loi[2], P. A. Scapolo[2], A. Cuomo[2], C. Palmieri[2], and A. T. Grazul-Bilska[1], [1]*North Dakota State University, Fargo*, [2]*Department of Comparative Biomedical Sciences, Faculty of Veterinary Medicine, University of Teramo, 64100 Teramo, Italy*.

Early pregnancy is a critical period for placentation and establishment of pregnancy. To determine the rates of cell proliferation in FM from pregnancies established after natural breeding (NAT) or after transfer of embryos created through ART, FM were collected on d 20 and 22 after breeding (n=4-6/day) from NAT pregnancies or after transfer of embryos created through natural breeding (ET), in vitro fertilization (IVF), or in vitro activation (IVA; parthenogenetic embryos). FM (n = 5-9/pregnancy type) were fixed in Carnoy's or formalin solution, embedded in paraffin and sectioned. Proliferating cells were identified using Ki67 immunohistochemstry, and nonproliferating cells were detected using nuclear fast red counterstaining. Micrographs of FM sections (n = 4-10/pregnancy type or day of pregnancy) were analyzed using image analysis (ImagePro Plus) to determine the labeling index (LI; proportion of proliferating cells out of the total cells per tissue area), which was similar for d 20 and 22 of NAT pregnancies. On d 20-22 of pregnancy, LI in FM was similar in NAT (21.5±3.9%) and ET (16.5±1.3%), which were greater ($P<0.01$) that IVF (9.9±1.7%) and IVA (8.5±1.4%) pregnancies. These data demonstrate that 1) the rate of cell proliferation is high in FM on d 20 and 22 of early pregnancy; 2) LI is similar for pregnancies from natural breeding or after ET from natural breeding on d 20 and 22; and 3) cellular proliferation in FM is decreased dramatically in embryos from ART such as IVF and IVA. Thus, application of ART may have profound effects on placentation and thus on pregnancy outcome. *Supported by USDA-NRI 2007-01215 to LPR and ATGB, and NIH P20 RR016741 (INBRE program of the National Center for Research Resource).*

Key Words: placenta, monoparental embryos, assisted reproduction

T134 SCD1 induction during early differentiation of bovine preadipocytes. L. Ma*, A. J. Lengi, and B. A. Corl, *Virginia Polytechnic Institute and State University, Blacksburg*.

Understanding the regulation of adipocytes and the role of stearoyl-CoA desaturase-1 (SCD1) in their differentiation is important for improving carcass quality. SCD1 catalyzes the synthesis of monounsaturated fatty acids. The first objective of this study was to determine the differentiation potential of primary bovine adipocytes in response to increasing passage number in culture. The second objective was to characterize SCD1 mRNA and protein induction during early differentiation of primary bovine adipocytes. Experiments were replicated at least 4 times using cells from different cattle. Preadipocytes were harvested from subcutaneous adipose tissue explants incubated in growth medium (DMEM with 10% FBS) for 12 d. After reaching confluence, differentiation medium was applied. To examine passage effects, cells were passed 1, 2, or 3 times before addition of differentiation media. Differentiation was assessed on d 8 using aP2 mRNA expression and glycerol-3 phosphate dehydrogenase (G3PDH) activity measured by microplate reader. With increasing pass number, mRNA abundance of aP2 decreased 50% (pass 2) and 90% (pass 3) compared to pass 1. G3PDH specific activity decreased about 30% (pass 2) and 70% (pass 3) compared to pass 1. To determine the induction of SCD1 expression during adipocyte differentiation, adipocytes were harvested 0, 1, 2, 3, and 8 d following induction of differentiation. mRNA expression of SCD1, aP2, and SREBP-1 were measured by real-time PCR, and SCD1 protein abundance was assayed by immunoblotting. The expression of aP2 mRNA increased 40-fold by d 1 and more than 400-fold by d 8 compared to d 0. SREBP-1 mRNA expression increased 4-fold on d 1 and was further increased almost 10-fold by d 8. For SCD1, mRNA abundance increased 4-fold at d 1 and was significantly increased more than 70-fold by d 8 compared to d 0. SCD1 protein increased more than 6-fold, 20-fold, and almost 900-fold by d 1, d 3, and d 8, respectively, compared to d 0. In conclusion, as passage number increases, the ability of preadipocytes to differentiate in culture decreases and during early differentiation of adipocytes, SCD1 is expressed and increases dramatically by d 8.

Key Words: adipocyte, differentiation

T135 Conjugated linoleic acid effects on adiposity are independent of spot 14 gene expression in mice. M. Hussein*, K. Harvatine, Y. Boisclair, and D. Bauman, *Cornell University*, *Ithaca, NY*.

Trans-10, cis-12 conjugated linoleic acid (CLA) decreases body fat accretion in several animal models when included as a dietary supplement. This CLA-mediated effect involves, but is not limited to, down-regulation of the expression and/or activity of transcription factors and key lipogenic enzymes regulating de novo lipid synthesis (DLS). Although its exact function is still unclear, thyroid hormone responsive spot 14 (S14) is expressed predominately in lipogenic tissues and is strongly correlated with DLS. Furthermore, S14 null mice exhibit impaired mammary DLS and CLA-induced reductions in synthesis of body fat (during growth) or milk fat (during lactation) correspond to a marked suppression of S14 expression. To test whether the effects on adiposity is mediated by S14, 9 wk old wild-type and S14-null mice (10/group) were orally dosed for 14 d with water (control) or 40 mg/d in two equal doses of CLA (50:50; t-10,c-12 and c-9,t-11 CLA isomers). Expression of selected transcription factors and lipogenic genes was assayed in white adipose tissue using quantitative RT-PCR. Epididymal and subcutaneous fat depots weighted slightly less for S14-null mice than wild type mice. In wild-type mice, the CLA supplement down regulated S14 expression in adipose tissue. CLA also reduced fat depot weights ($p<0.0001$), down regulated expression of fatty acid synthase, stearoyl-CoA desaturase, acetyl-CoA carboxylase, and sterol regulatory element binding protein-1c, and increased hepatic triglyceride content in wild- type mice; CLA had the exact same effects in S14-null mice. Taken together, the similarity of effects of CLA on adiposity and mRNA expression of selected lipogenic genes in S14-null and wild-type mice suggest that the effect of CLA on adipose tissue may be independent of the effects of CLA on S14 gene expression.

Key Words: CLA, Spot14, obesity

T136 The effect of KemTRACE® chromium propionate supplementation on global gene expression in adipocytes of finishing pigs. L. Wonderling*[1], J. Hahn[1], M. Spurlock[2], and A. Jourdan[1], [1]*Kemin Industries*, *Des Moines, IA*, [2]*Iowa State University*, *Ames*.

Supplementation with KemTRACE® Chromium Propionate (CrProp) has been demonstrated to benefit swine growth and health, but the molecular mechanism for these effects are largely unknown. To better understand KemTRACE® CrProp's molecular role, a global gene expression study was performed. KemTRACE® CrProp supplements were fed to 8 pigs over a 2 month period corresponding to the finishing stage of growth. A second set of 8 pigs were used as non-supplemented control animals. Adipose tissue was removed from the shoulders of all pigs prior to supplementation, and following 1 and 2 months of supplementation. RNA was isolated from the tissue samples and used in hybridization studies with the Affymetrix porcine microarray. Lists of differentially expressed genes for the control and treated groups were compiled ($\geq$ 1.5-fold, $p \leq 0.001$). The control gene list was subtracted from the treated group gene list to identify genes whose expression responded to KemTRACE® CrProp treatment over time. When comparing gene expression at the different study time points, CrProp affected the expression of 133 genes in the 1st month, 527 genes in the 2nd month, and 1328 genes if the pre-treatment to post-treatment gene expression is compared. The overlap of these gene lists was examined and the results suggest that 84 genes were specific to the 1st month of treatment, 232 genes were specific to the 2nd month of treatment, and 997 genes were only affected by CrProp when comparing the pre-treatment to the end of supplementation. Gene clustering was performed using NIH DAVID. Gene clusters affected by CrProp included those involved in central immune pathways, cell proliferation/apoptotic pathways, and in the development of muscle, extracellular matrix, bone and organs. Interestingly, the expression of several genes involved in key steps of insulin signaling was affected by CrProp supplementation including the PI3K, GLUT4, and AMPK genes. These results may indicate suppressed development of adipocytes in pigs supplemented with KemTRACE® CrProp.

Key Words: chromium, nutrition, adipocytes

T137 Expression of microRNA in bovine preadipocytes and adipocytes. S. L. Pratt, A. P. Burns, and S. K. Duckett*, *Clemson University*, *Clemson, SC*.

It has recently been demonstrated that adipogenesis involves microRNA (miRNA). miRNA are small non-coding inhibitory RNA that are present and expressed in the cells of all plants and animals examined to date, and regulate gene expression post-transcriptionally by either translational repression or RNA interference. To date, little information is available concerning either the identification or function of miRNA in bovine adipocyte differentiation. The objective of this study was to evaluate the expression profile of miRNA in pre- and differentiated adipocytes utilizing miRNA microarrays. Bovine preadipocyte cell lines 7-01 and 7-02, generated from subcutaneous adipose tissue obtained from 18 mo old steers were cultured to confluence and held 2 d in Dulbecco's modified eagles medium (DMEM) containing 10% fetal calf serum (FCS), and 2X antibiotiotic/antimycotic (AB/AM). Cells were differentiated using a two step process by culture for 2 d in DMEM containing 5% FCS, 2X AB/AM, Insulin at 2.5 µ/ml, 0.25 µM dexamethasone, 5 µM troglitasone and 0.5 µM isobutylmethylxanthine for followed by 4 d incubation in DMEM containing 5% FCS, 2X AB/AM, Insulin, and troglitasone. tcRNA was isolated for each cell line at 2 d confluence (Control), and after 2 d (D2) and 6 d (D6) of differentiation, and were then used in a 3 x 3 microarray using control, D2 and D6 samples. Data were subjected to t-test analysis and six miRNA were determined to be differentially regulated. For preadipocytes and adipocytes, 167 and 182 total miRNA were detected, respectively. The miRNA let-7a, let-7b, and let-7c were upregulated ($P<0.01$), while the miRNA, miR-21, miR-221, and the miR-222 were down regulated ($P<0.01$). All miRNA that were differentially expressed have been detected by RT-PCR except for let-7b. The let-7 miRNA have roles in differentiation of multiple cell and tissue types, while the miR-21, miR-221, and miR-222 all have been implicated in cell cycle regulation.

Key Words: microRNA, adipocyte, differentiation

T138 Characterization of ovine fetal heart gene expression during fetal growth restriction. K. A. Partyka*[1], J. S. Barry[2], R. V. Anthony[1,2], and H. Han[1], [1]*Colorado State University*, *Fort Collins*, [2]*University of Colorado Health Sciences Center*, *Aurora*.

Growth restricted fetuses (FGR) are hypoglycemic, hypoxemic and show increased systemic vascular resistance, all of which could impact heart development. Objective: To examine cardiac gene expression at two gestational ages in ovine FGR fetuses. Single bearing ewes were placed in a hyperthermic (HT) environment at 35 days gestation (dGA) (40°C 12 hrs/day and 35°C 12 hrs/day; n=11) to induce FGR. The ewes were maintained in the HT environment until studied at 90 dGA (n=6), or 120 dGA (n=5) then placed in control conditions until studied at 135 dGA. Pair-fed control (TN; 20°C ± 2°C 24 hrs/day; n=14) ewes

were also studied at 90 dGA (n=5) or 135 dGA (n=9). Fetal and heart weights were measured; the heart was sectioned into right ventricle (RV) and left ventricle plus septum (LV+S), snap frozen and stored at -80°C until analysis. Quantitative real-time PCR was used to determine mRNA concentrations for endothelial nitric oxide synthase (eNOS), type 1 (AT1) and 2 (AT2) angiotensin II receptor, angiopoietin 1 (Ang1) and 2 (Ang2), tunica interna endothelial cell kinase 2 (Tie2), vascular endothelial growth factor (VEGF), VEGF receptor 1 (VEGFR1) and 2 (VEGFR2), glucose transporter 1 (GLUT1) and 4 (GLUT4), insulin receptor β (IRβ), myosin heavy chain α (MHCα) and β (MHCβ). Data was analyzed by Students t-test. Neither fetal or heart weight was impacted by HT at 90 dGA, whereas both fetal (1529 g vs 3294 g; P≤0.01) and heart weight (13.6 g vs 29.1 g; P≤0.01) were reduced by HT at 135 dGA. HT 90 dGA showed an increased RV AT2 (P≤0.05) and AT2/AT1 ratio (P≤0.05), LV+S MHCβ (P≤0.05) and MHCβ/MHCα ratio (P≤0.01). HT 135 dGA, LV+S VEGF (P≤0.05) and RV VEGFR1 (P≤0.05) mRNA concentrations were greater. The fetal myocardium adapts during FGR by altering gene expression that may represent delayed maturation at 90 dGA and signal for increased myocardial angiogenesis near term, both changes that could be detrimental later in life. *Supported by NIH grant HD043089.*

Key Words: heart, sheep, fetal growth restriction

T139 Development of a protocol for staining BrdU-labeled cells within cryosections of bovine mammary tissue that is suitable for subsequent transcriptome analysis. R. K. Choudhary*[1], K. M. Daniels[2], C. Clover[2], and A. V. Capuco[2,1], [1]*University of Maryland, College Park*, [2]*Bovine Functional Genomics Laboratory, USDA-ARS, Beltsville, MD*.

Bromodeoxyuridine (BrdU) is a thymidine analog that is incorporated into the DNA of proliferating cells. Immunostaining of BrdU-labeled cells within a histological section requires heat or chemical-mediated antigen retrieval to open the dsDNA and expose the BrdU antigen. We found that in cryosections such treatments, while they do permit staining of the tissue, preclude its use in further gene expression experiments. With cryosections, long antibody incubations and several washing steps, lead to extensive RNA degradation and undesired RNA elution into wash buffers. We have developed a protocol for immunolocalization of BrdU-labeled cells in unfixed cryosections of bovine mammary tissue that does not require harsh DNA denaturation and minimizes RNA degradation and elution into wash buffers. This protocol uses an initial acetone treatment (2 min) followed staining with methyl green (0.5%, 2 min) to stabilize macromolecules, antigen retrieval with deionized formamide (70% in nuclease-free phosphate buffered saline, 5 min incubation), short (10 min) antibody incubations in the presence of RNase inhibitors, and minimal washing, to facilitate recovery of RNA from stained sections. Total RNA was obtained by column extraction (RNeasy Micro kit; Qiagen, Valencia, CA) of cell lysates from sections. Utility of the isolated RNA for gene expression analysis was confirmed using gene-specific primers and quantitative RT-PCR. Furthermore, RNA quality was evaluated by micro-fluidic electrophoresis (Agilent BioAnalyzer) and acceptable RNA integrity numbers (RIN 6.0) were obtained. Staining intensity obtained with this BrdU labeling protocol was similar to that obtained using conventional immunohistochemistry protocols. When coupled with laser microdissection and RNA amplification, this immunostaining protocol should provide a means for evaluating genes expressed by BrdU-labeled cells that are extracted from a complex tissue section.

Key Words: BrdU staining, gene expression, laser microdissection

T140 Analysis of protein oxidation in serum of fetal and newborn piglets and the influence of iron dextran on induction of protein carbonyls. T. J. Caperna*, A. E. Shannon, T. G. Ramsay, L. A. Blomberg, and W. M. Garrett, *USDA/ARS, Beltsville, MD*.

Oxidation of serum proteins leads to non-reversible carbonyl formation which alters their function and has long been associated with stress-related disease processes. The objective of this study was to identify serum protein biomarkers of metabolic stress in baby pigs. Protein carbonyls in serum, were converted to dinitrophenyl (DNP) derivatives with DNP-hydrazine, precipitated with TCA, extracted in ethyl acetate:ethanol (1:1) and quantified by spectrophotometry. DNP-labeled proteins were then separated by 2D PAGE, electro-blotted onto PVDF membranes and visualized by western immunoblot using polyclonal DNP antiserum. Proteins which reacted positively in western blots were extracted from duplicate 2D gels, digested with trypsin and identified by MALDI-TOF mass spectrometry (MS). At birth, significant amounts of oxidized proteins were readily determined in piglet serum (~1 nmole/mg protein). Fetuses at 50 and 110 d of gestation were also evaluated and found to have potentially higher levels of protein carbonyls, than newborns. We then determined that the standard iron dextran treatment used to prevent anemia in pigs (100 mg iron given intramuscularly), was associated with a two-fold increase (P<.05) in oxidized proteins by 48 hrs, if given on postnatal day 1 (n = 7 pigs/group). Oxidized proteins identified by MS included; albumin, transferrin, alpha fetoprotein, haptoglobin, immunoglobulins and fetuin. Postponement of iron treatment until day 3 also resulted in an increase in protein carbonyls, but at attenuated levels (P<.05) compared to piglets treated on day 1. Therefore, adjusting the timing of treatment should reduce the impact of iron dextran as a source of oxidative stress in newborn pigs. These results indicate that the sensitivity and simplicity of the analysis to evaluate protein carbonyls, which was routinely performed using one mg of serum protein, may be a relatively non-invasive, rapid and useful tool to monitor oxidative stress associated with neonatal mortality in the pig.

Key Words: protein carbonyl, oxidative stress, mass spectrometry

T141 AMP-activated protein kinase γ3 subunit mutation in transgenic mice corresponding to RN- allele in pigs inhibits adipogenesis. J. X. Zhao*, X. Yan, J. F. Tong, M. J. Zhu, and M. Du, *University of Wyoming, Laramie*.

Due to genetic selection for lean growth, Rendement Napole (RN-) allele has increased in frequency in Hampshire pigs. Recently, the RN- allele was identified as a R225Q mutation in AMP-activated protein kinase (AMPK) γ3 subunit. The mechanisms linking AMPK and leanness in RN- pigs remain largely undefined. Since AMPK is a kinase controlling energy metabolism, we hypothesized that AMPK mutation in RN- pigs inhibits adipogenesis, especially when fed a high-energy diet, and diverts this excessive energy for lean growth. The objective of this study was to study the role of AMPK in adipogenesis and myogenesis of RN- pig using a transgenic mouse model. Wild-type (WT) and transgenic mice carrying the R225Q mutation (RN) were assigned to four groups according to the genotype and diet: control group with normal energy diet (WTnormal, n=6), control group with high energy diet (WTfat, n=6), mutated group with normal energy diet (RNnormal, n=6) and mutated group with high energy diet (RNfat, n=6). One month-old mice were fed the treatment diets for one month. Then, mice were euthanized, and carcass, muscle samples, gonad and skin fat were collected and weighed. In WTnormal, the gonad fat weight was 0.91±0.14 g and skin fat weight was 0.68±0.08 g, versus 0.80±0.10 g and 0.58±0.05 g in RNnormal, without significant difference. However, difference was

observed between WTfat and RNfat mice. In WTfat, the gonad fat and skin fat weights were 1.16±0.13 g and 0.74±0.07 g versus 0.77±0.08 g and 0.56±0.04 g respectively ($P < 0.05$) for RNfat mice. Intriguingly, RN mutation enhanced feed consumption ($P < 0.05$) of mice both in normal- and high-energy diets. The high feed intake but increased leanness indicates that RN- allele enhances energy expenditure which warrants further studies.

Key Words: AMPK, skeletal muscle, adipogenesis

T142 Growth hormone does not stimulate IGF-I mRNA expression in bovine skeletal muscle, myoblasts, or myotubes. X. Ge and H. Jiang*, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Growth hormone (GH) is a major regulator of muscle growth in animals, including cattle. The growth-stimulating effect of GH had long been thought to be mediated by circulating IGF-I produced from the liver. However, recent knockout mouse studies support the concept that IGF-I produced in the skeletal muscle and IGF-I-independent mechanisms mediate the effect of GH on growth. To clarify the mechanism by which GH stimulates skeletal muscle growth in cattle, we determined whether GH increased IGF-I mRNA expression in bovine skeletal muscle in vivo and bovine myoblasts and myotubes in vitro. Five nonlactating, nonpregnant beef cows were administrated subcutaneously with 500 mg of recombinant bovine GH formulated for slow release, and longissimus muscle biopsies and blood samples were taken seven days before and seven days after GH administration. Serum IGF-I concentrations, measured by an ELISA, were four times higher after GH injection than before GH injection ($P < 0.01$). Skeletal muscle IGF-I mRNA abundance, measured by real-time RT-PCR, was not different between before and after GH injection ($P > 0.1$). Western blotting analyses showed that GH administration increased the levels of phosphorylated JAK2 and STAT5, known protein components of GH signaling, in the skeletal muscle ($P < 0.05$). In the in vitro experiments, myoblasts were isolated from bovine skeletal muscle and were allowed to proliferate or induced to form myotubes in culture. Growth hormone at the concentrations of 10 ng/ml and 100 ng/ml did not affect IGF-I mRNA expression in either the myoblasts or myotubes ($P > 0.1$). These in vitro data echoed the earlier in vivo observation that GH did not increase IGF-I mRNA expression in the skeletal muscle. Taken together, the data of this study demonstrate that GH does not increase skeletal muscle IGF-I mRNA expression in cattle and suggest that GH stimulation of muscle growth in cattle is not mediated by the locally produced IGF-I.

Key Words: growth hormone, skeletal muscle, IGF-I

T143 Early-weaning down-regulates the expression of aminopeptidase N gene in the jejunum of the piglet. D. Lackeyram*, T. Archbold, K. C. Swanson, and M. Z. Fan, *University of Guelph*, *Guelph, Ontario, Canada*.

Aminopeptidase N (APN) cleaves neutral AA from oligopeptides during digestion in the small intestine. The objectives of this study were to examine the responses of APN activity and protein abundances in the partitioned mucosal homogenate (H), intracellular soluble and the apical membrane (M) fractions as well as APN mRNA abundance during early-weaning in comparison with suckling pigs. A total of 20 Yorkshire piglets, 10 suckling (SU) and 10 early-weaning (WN) with an average BW of 3 kg at the age of 10 d, were used in this study. Weanling piglets were fed a corn and SBM-based diet for 12 d. Proximal jejunal samples from both SU and WN groups were collected. L-alanine-P-nitroanilide hydrochloride (0-16 mM) was used in the enzymatic kinetic experiments. Abundances of APN protein and mRNA were analyzed by Western blot and the real time RT-PCR using β-actin as the housekeeping gene. The jejunal APN maximal specific activity (μmol/mg protein.min) was decreased ($P<0.05$) in weaning piglets (H: WN, 0.122±0.01 vs. SU, 0.172±0.01; and M: WN, 0.5479±0.02 vs. SU, 0.721±0.01). There were decreases ($P<0.05$) in the APN protein abundance (arbitrary units) for the WN group in the jejunal fractions (H: WN, 0.655±0.03 vs. SU, 0.992±0.05; and M: WN, 0.232±0.02 vs. SU, 0.515±0.01). There were correlations ($P<0.05$) between the APN maximal specific activity and its protein abundance (H, $r = 0.87$; M, $r = 0.91$, $n=20$). Furthermore, early-weaning decreased ($P<0.05$) the relative abundance of APN mRNA by 39% (WN, 0.304±0.02 vs. SU, 0.498±0.02). The APN mRNA abundance was also correlated ($P<0.05$, $n=20$) with its protein abundances in both homogenate (H, $r = 0.82$) and membrane (M, $r = 0.86$) fractions. We conclude that the reduced activity of APN during early-weaning can be attributed to a down-regulation of the APN gene at the transcriptional and translational levels.

Key Words: aminopeptidase N, gene expression, weanling pigs

Horse Species

T144 Influence of extension on the stock-type western pleasure jog. M. Nicodemus* and J. Williams, *Mississippi State University*, *Mississippi State*.

One of the most popular performance classes for the stock-type breed is the western pleasure class. Previous research of the stock-type western pleasure gaits found the jog and lope were performed as 4-beat stepping gaits with periods of quadrupedal support. To encourage breeds to perform with more forward motion, stock-type breed associations added to the class requirements extension of the jog. Study objectives were to determine the influence of extension on the temporal variables of the stock-type jog. 5 registered stock-type horses showing in a western pleasure class were filmed at 60 Hz. Strides of both the jog and extended jog that were judged as desirable by carded judges were evaluated using frame-by-frame analysis. Means (SD) were determined for 5 strides for each horse for both gaits with variables given as % of stride. Effect of extension for each variable was tested using a one-way analysis of variance ($p<0.05$). Velocity (Jog: 1.5±0.1 m/s, Extended: 2.2±0.2 m/s) and stride length (Jog: 1.6±0.1 m, Extended: 2.5±0.2 m) and duration (Jog: 917±67 ms, Extended: 873±42 ms) were not significantly influenced by extension ($p>0.05$). Majority of stride for both the jog (Right: Fore=67±2%, Hind=63±6%; Left: Fore=66±3%, Hind=64±4%) and extended jog (Right: Fore=66±4%, Hind=60±3%; Left: Fore=64±2%, Hind=61±3%) was spent in stance with hind stance shortening with extension ($p<0.05$). Rhythm changed from 4 to 2 beats as extension created diagonal limb pairing during the extended jog (Jog: Right Hind-Left Fore Advanced Placement=4±1%, Left Hind-Right fore=4±1%; Extended: Right Hind-Left Fore Advanced Placement=0±0%, Left Hind-Right Fore Advanced Placement=0±0%). While both gaits were performed as stepping gaits with the greatest % of stride spent in diagonal bipedal support (Jog: 63±7%, Extended: 70±5%), extension shortened limb support during tripedal support with 2 hind limbs (Jog: 5±3%,

Extended: 0±0%) and quadrupedal support (Jog: 23±7%, Extended: 20±4%) ($p<0.05$). Although extension did not create a gait that follows current breed standards, extension did improve upon the timing and limb support of the jogging gait.

Key Words: western pleasure, stock-type horse breeds, jog

T145 Manure management practices on equine farms. M. L. Westendorf*[1], T. Joshua[2], S. J. Komar[1], C. Williams[1], and R. Govindasamy[1], [1]*Rutgers, The State University of New Jersey, New Brunswick*, [2]*USDA National Agricultural Statistics Service, Trenton, NJ.*

According to the 2007 USDA Census of Agriculture there are over 65,000 equine farms with 465,000 horses, ponies, mules, etc. in Northeastern and Mid-Atlantic states. These farms may influence environmental and water quality due to equine manure collection, storage, spreading, and disposal practices. A manure management survey was mailed to 2000 New Jersey equine farms during the winter of 2006-2007. The study tested the hypotheses that equine producers who store or spread manure will also implement certain best management practices. Four hundred and seventy-two surveys were returned; 18.5% were training or performance farms, the remainder (81.5%) were breeding, boarding or pleasure farms. Fifty-four percent of all farms indicated that they spread manure on farm. Of those who spread, only 27% indicated having more than 8.09 hectares (20 acres) available for spreading. Seventy-four percent had a designated area for manure storage. Eighty-three percent said their manure storage was greater than 200 feet from water or wetlands; 86% percent said storage was greater than 200 feet from neighbors. Data were modeled to determine the relationship of manure storage or manure spreading with other management practices. The storage model showed that farms with 6-10 horses were more likely to have manure storages than farms not included in the model. This model had a predictive accuracy of 83.3%, and R^2 of 0.35 ($P<0.01$). The manure spreading model showed that those who spread manure were also likely to credit manure for its fertilizer value. The spreading model had an overall predictive accuracy of 95.5%, and R^2 of 0.795 ($P<0.01$). These results indicate that while most equine farms did not pose a direct risk to water quality or to a neighbor, some do not currently utilize best management practices in managing, spreading, or storing manure.

Key Words: manure storage, manure spreading, equine manure management

T146 Temporal variables of the Marsh Tacky intermediate gait. M. Nicodemus*[1] and J. Beranger[2], [1]*Mississippi State University, Mississippi State*, [2]*American Livestock Breeds Conservancy, Pittsboro, NC.*

Marsh Tacky is listed as a critical horse breed according to the American Livestock Breeds Conservancy (ALBC) due to its scarce population. Originating from Colonial Spanish horses the breed can be found in the coastal marshlands of South Carolina and Georgia. Due to the breed′s heritage it is thought to be gaited, but research concerning the gaits is lacking. Study objectives were to define the Marsh Tacky intermediate gait using temporal variable measurements. 10 Marsh Tacky horses selected by the ALBC as representatives of the breed were filmed performing their intermediate gait. 10 strides that were consistent with visible hoof contact and lift-off were evaluated using frame-by-frame analysis. Descriptive statistics comprising mean and standard deviation were computed for each stride variable with variables given as % of stride. Coefficient of variation (CV) expressed as a % of mean was calculated as an indicator of variability. Velocity of the Marsh Tacky intermediate gait was 3.9±0.2 m/s (CV 5.1%) with a stride length of 2.9±0.3 m (CV 10.3%) and duration of 727±46 ms (CV 6.3%). The majority of stride was spent in stance (Right Fore: 52±3%, CV 5.8%; Left Fore: 53±5%, CV 9.4%; Right Hind: 54±2%, CV 3.7%; Left Hind: 52±4%, CV 7.7%). The gait demonstrated disassociation of the diagonal limb pairs so that the forelimb made impact before the diagonal hind (Diagonal Advanced Placements: Right Hind-Left Fore-3±1%, CV 17.6%; Left Hind-Right Fore-3±1%, CV 18.9%) and the hind limb lifted off before the diagonal fore (Diagonal Advanced Lift-Offs: Right Hind-Left Fore-5±2%, CV 26.7%; Left Hind-Right Fore-4±1%, CV 15.0%). The gait was a stepping gait alternating between periods of diagonal bipedal (85±11%, CV 12.9%), quadrupedal (7±2%, CV 28.5%), and tripedal (8±1%, CV 12.5%) support. Due to the 4-beat rhythm and the lack of suspension of the intermediate gait, the Marsh Tacky can be considered gaited. The durations, timing, and limb support are similar to the marcha batida of the Mangalarga Marchador in which both breeds share similar Spanish bloodlines. These gait variables will assist in identifying characteristics that are unique to the breed in comparison to other gaited horse breeds.

Key Words: Marsh Tacky, locomotion

T147 The use of Doppler ultrasonography to measure vasoconstriction in horses consuming endophyte-infected tall fescue. K. C. Gradert*[1], J. M. Bormann[1], S. F. DeWitt[2], L. W. Lomas[3], J. M. Kouba[1], and T. L. Slough[1], [1]*Kansas State University, Manhattan*, [2]*Woodside Equine Clinic, Ashland, VA*, [3]*Southeast Agricultural Research Center, Parsons, KS.*

While fescue foot has not been described in horses, endophyte-produced toxins have been reported to induce vasoconstriction in equine tissue *in vitro*. This study was designed to evaluate whether the consumption of endophyte-infected tall fescue in horses would alter digital circulation *in vivo*. Twelve clinically sound, three-year-old Quarter horses with a mean BW of 459 + 31 kg were blocked by weight, sex, and HYPP status and divided into two groups: control horses (n = 6) received an endophyte-free diet (E-) and treatment horses (n = 6) received an endophyte-infected diet (E+). Fescue seed was integrated into the concentrate at a rate sufficient to bring daily ergovaline consumption in the E+ diet to a minimum of 0.20 ppm. The E- concentrate contained an equal amount of endophyte-free fescue seed. Horses were also allowed *ad libitum* access to native prairie hay, which was replaced by fescue hay from d 30 to d 60. Control horses received a low-endophyte fescue variety and treatment horses received a high-endophyte fescue variety. Based on assumed daily DM consumption of 2.0% BW, total daily ergovaline consumption was calculated to be 0.19 ppm (E-) and 1.04 ppm (E+) with the inclusion of fescue hay. Doppler ultrasonography was utilized to record velocity of flow and diameter of the medial palmar artery on d 0, d 30, d 60, and d 90. Five serial readings were taken from the left forelimb on each horse following the morning feeding. Regardless of treatment on d 30 and d 90, the regression coefficient for weight was positive ($P < 0.05$), indicating heavier horses had an increased rate of flow compared to lighter weight horses. When changes from d 0 to d 90 were compared, E+ horses had increased ($P = 0.04$) velocity and reduced ($P = 0.04$) cross-sectional diameter of the medial palmar artery. Horses consuming endophyte-infected tall fescue demonstrated vasoconstriction of the medial palmar artery as measured by Doppler ultrasonography.

Key Words: fescue, Doppler ultrasonography, horse

T148 Genistein does not work through estrogen receptors to reduce lipopolysaccharide stimulated tumor necrosis factor α release from equine peripheral blood mononuclear cells (PBMC). A. Taylor*, C. Paulson, and J. Clapper, *South Dakota State University, Brookings*.

Previously we have demonstrated that genistein, a non-steroidal tyrosine kinase inhibitor, decreased the release of tumor necrosis factor (TNF) from circulating PBMC in response to lipopolysaccharide (LPS) in the horse. Genistein also has estrogenic properties and estrogens have been shown to reduce LPS stimulated TNF production in other species. To further examine if the estrogenic properties of genistein are involved in reducing LPS stimulated TNF release in the horse the following experiment was performed. Blood (180 mLs) was collected by jugular venipuncture from a mature healthy gelding and PBMC were isolated. PBMC were then added to polystyrene tubes (4×10^6 cells/tube) and incubated at 37°C in 5% CO_2 for 2 h to allow PBMC to adhere. Non-adherent cells were decanted and PBMC were covered with cell culture media containing 1% fetal bovine serum and various concentrations of estradiol (E2), genistein, and an estrogen receptor antagonist (ICI) with and without 100 pg/mL LPS (E. coli O55:B5) and incubated for 6 h at 37°C in 5% CO_2 after which the supernatants were collected by centrifugation and frozen at -80°C until assayed for TNF by ELISA. Triplicate tubes were prepared for each treatment combination. Differences in supernatant concentrations of TNF were determined using the Proc Mixed procedure of SAS. Supernatant concentrations of TNF were not different (P>.05) in tubes containing 0.1 pM to 10 nM E2+LPS vs LPS. Supernatant concentrations of TNF were increased (P<.05) in tubes containing 1 nM to 10 μM ICI+LPS vs LPS. Supernatant concentrations of TNF were increased (P<.05) in tubes containing ICI+E2+LPS vs LPS. Supernatant concentrations of TNF were decreased (P<.05) in tubes containing ICI+genistein+LPS vs LPS. These preliminary data suggest that estradiol does not inhibit LPS stimulated TNF in the horse. However, genistein does not appear to work through estrogen receptors to decrease LPS stimulated TNF production in horse.

Key Words: equine, genistein, LPS

T149 The evaluation of the miniature horse as a nutritional model for full size horses fed various levels of dietary fat. J. S. Pendergraft*[1], B. Gutierrez[1], and M. J. Arns[2], [1]*Sul Ross State University, Alpine, TX*, [2]*University of Arizona, Tucson*.

Eight mature male horses, 4 Quarter horses (F) and 4 Miniature horses (M) were used in a split-plot design with repeated measures to evaluate the miniature horse as a nutrition model for full size horses fed various concentrations of supplemented fat. Horse size was the main-plot treatment, and 3 fat treatments were the sub-plot. Horses were considered replicates. Horse types were paired and then randomly assigned to fat treatments over time. The dietary treatments were: 0% fat supplementation (NF); 3% fat supplementation (LF); and 7% fat supplementation (HF). Soybean oil was used to supplement the treatment diets. All horses were housed individually and received a basal diet of coastal bermudagrass hay (1.37 kg/100kg BW) and a textured concentrate (.4kg/100kg BW) over three equal feedings a day and had ad libitum access to water. The supplemental fat was evenly top-dressed on the concentrate during the 0700 and 1800 feeding. The experiment periods lasted 14 d in length consisting of a 9 d adaptation period, followed by a 5 d total fecal and urine collection period. Concentrate, forage, ort, and feces samples were analyzed for DM, CP, GE, NDF, and ADF. Urinary subsamples were analyzed for GE. Data were expressed on a body weight basis. Blood samples were obtained prior to feeding at 0600 h on d 1, 7, and 14 during each experimental period. Blood samples were analyzed for serum glucose (GLU), cholesterol (CHOL), lipase (LIPA), and triglycerides (TRIG). All data were analyzed by the PROC GLM procedure using SAS statistical software. Apparent digestibilities were not different between horse sizes when diets were supplemented with 3% and 7% fat. However, M horses had higher (P<.02) apparent digestibilities for DM, DE, CP ADF, NDF for diets not supplemented with fat, and higher (P<.04) NDF digestibilities for high fat diets compared to F. There were no differences between size for ME, serum GLU, TRIG, CHOL, or LIPA. Results suggest that miniature horses consuming diets supplemented with 3-7% fat could be used to measure nutrient utilization for full size horses.

Key Words: miniature, fat, model

T150 The effect of forage nonstructural carbohydrate on glucose, insulin and lipid response in Morgan horses. L. A. Perry*[1,2], B. A. Younge[2], K. W. Cotanch[1], K. N. Lassell[1], and C. S. Ballard[1], [1]*William H. Miner Agricultural Research Institute, Chazy, NY*, [2]*University of Limerick, Castletroy, Limerick, Ireland*.

Research evaluating dietary nonstructural carbohydrates (NSC) has focused on effects of varying NSC levels of concentrate meals fed horses. The objective of this study was to evaluate the metabolic response of horses fed a forage-only diet differing in NSC content (water soluble carbohydrate + starch). Six Morgan horses were assigned randomly to one of two treatments; (1) Low NSC hay (<100 g/kg) or (2) High NSC hay (~200 g/kg). Multiple hay sources were core sampled and analyzed prior to study to identify low NSC and high NSC hay. Study was conducted using a crossover design consisting of two 21-d treatment periods with 7-d washout between periods when all horses were fed Low NSC hay. Horses consumed hay (1.75% BW) twice daily (0800 and 1700). Blood and forage samples were taken prefeeding (0730) on days 1, 7, 14, and 21. On days 1 and 21 blood was sampled at 0, 1, 2, 4 and 8 h post feeding. Plasma was analyzed for glucose, insulin, and triglycerides. Neck and girth circumference, BW, and BCS, were measured on days 1 and 21. Forage composites were analyzed for starch, water soluble carbohydrate (WSC) and ether soluble carbohydrate (ESC). Data were analyzed using MIXED procedure of SAS. Forage NSC varied greatly (low NSC: 94-152 g/kg; high NSC: 137-196 g/kg). On day 1, horses fed high NSC had higher plasma glucose and insulin 2 h post-feeding (glucose 104.8 vs. 94.1±2.1 mg/dl, $P<0.01$; insulin 25.0 vs. 17.5 ±2.2 mIU, $P<0.01$). On day 21, plasma glucose was similar for both diets, however insulin levels were lower 2 h postfeeding for horses fed high NSC hay (glucose 96.8 vs. 96.7 ±2.6 mg/dl, $P=0.96$; insulin 21.6 vs. 31.4 ±2.7 mIU, $P<0.01$). High forage NSC significantly increased plasma triglycerides from 1 to 21 days while low NSC diet had no effect ($P=0.01$). There was no effect of diet on physical measurements. This study demonstrated the variability that exists in forage NSC levels. Initially horses responded to high NSC forages with elevated glucose and insulin levels. However, by 21 d there was no difference in glucose response to diet. Forage with high NSC, particularly fructans, may increase plasma triglyceride concentrations.

Key Words: carbohydrate, forage, horse

T151 Retail and sensory quality of Longissimus thoracis from steers fed corn- or wheat-based dry distillers grains plus solubles (DDGS). N. Aldai*[1], J. L. Aalhus[1], M. E. R. Dugan[1], T. A. McAllister[2], L. J. Walter[3], and J. J. McKinnon[3], [1]*Agriculture & Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada*, [2]*Agriculture & Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*, [3]*Department of Animal & Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*.

Wheat is the cereal of choice for ethanol production in western Canada. However, in the USA corn is the principal source of DDGS and considerable volumes of this byproduct have been imported and used in western Canadian feedlots. While more is known about the feeding value and effects of corn DDGS on meat quality, there is limited data on wheat DDGS, and no direct comparison has been conducted. Hence, the objectives of the current study were to examine the objective and subjective retail display and sensory quality traits of 20 d aged steaks from cattle fed finishing diets containing corn (20 or 40%) or wheat (20 or 40%) DDGS (DM basis) compared to the barley control (n=20 per diet). After 4 d of display, DDGS samples had higher hue values (brownish-red) than control which coincided with a higher content of metmyoglobin (P<0.05). However, at the same time, 20% corn DDGS had a higher % of discolouration than 40% corn DDGS (P<0.05). Initial and overall tenderness were highest, perceived connective tissue was lowest, and the texture was the least rubbery in steaks from steers fed corn DDGS (P<0.05). In general, DDGS samples were rated higher for flavour desirability than the controls (P<0.05), and 20% corn DDGS had higher beef flavour intensity than 40% corn DDGS and were rated higher for overall palatability than any other sample (P<0.05). Some slight differences were observed in flavour descriptors, however there was no difference in liver-like off-flavour (P>0.10) which has been suggested as a possible consequence of feeding high levels of corn DDGS. According to these results, feeding wheat DDGS had no negative effects and any effect of the corn DDGS may ultimately be related to the fat content and/or composition of the carcasses.

Key Words: dried distillers' grains, retail measurements, sensory analysis

T152 Effects of feeding cattle increasing levels of dried distillers grains with solubles (DDGS) from wheat on muscle fatty acid composition. M. E. R. Dugan*[1], N. Aldai[1], D. J. Gibb[3], T. A. McAllister[3], and J. K. G. Kramer[2], [1]*Lacombe Reseach Centre, Lacombe, AB, Canada*, [2]*Guelph Food Research Centre, Guelph, ON, Canada*, [3]*Lethbridge Research Centre, Lethbridge, AB, Canada*.

Government incentives in North America have increased biofuel production and the most economical grain in western Canada for ethanol production is wheat. As demand for wheat increases so do grain prices which in turn creates incentives for feeding lower cost distillers′ byproducts. Substitution of barley for wheat DDGS may also create opportunities for enhancing beef fatty acid profiles as reducing starch concomitantly increases dietary oil and may shift biohydrogenation towards healthier fatty acids. To study this potential, heifers were fed diets containing either 0, 20, 40 or 60% wheat DDGS (DM basis) substituted for rolled barley (n = 24; 133d finishing period). Adding DDGS increased dietary oil (from 1.9 to 3.7%) but dietary fatty acid compositions remained consistent. Feeding DDGS linearly decreased total diaphragm fatty acids on a mg/100g basis (P=0.03). On a percentage basis, feeding 20% DDGS yielded more 16:0 (22.3%) than feeding 40% or 60% (21.2% and 22.0% respectively; P<0.05) but was not different from control (22.4%). Greater 16:0 is consistent with both a higher level of neutral lipid and total fatty acids. Increasing dietary DDGS linearly increased diaphragm 18:2n-6 (P<0.01) and total n-6 fatty acids (P<0.01) and this was accompanied by a linear decrease in 10t-18:1 (1.2 to 0.69%; P < 0.01), a linear increase in 11t-18:1 (1.07 to 1.37%; P < 0.01) but no change in total trans-18:1. Feeding DDGS also linearly increased 9c11t-conjugated linoleic acid (CLA) (0.34 to 0.41%; P=0.02) and linearly increased total CLA (0.48% to 0.55%; P=0.04). Feeding DDGS had no effect on diaphragm 18:3n-3 or total n-3 fatty acids. Overall, feeding DDGS enhanced the fatty acid composition of diaphragm muscle by decreasing the atherogenic 10t-18:1 while increasing 9c11t-CLA and its precursor 11t-18:1 that have potential roles in prevention and treatment of several diseases including cancer.

Key Words: beef, DDGS, fatty acid

T153 Effects of wet distillers grains feeding supplemented with vitamin E on fatty acid composition and sensory attributes of beef steaks. L. S. Senaratne*, C. R. Calkins, A. S. de Mello Jr., T. P. Carr, and G. A. Sullivan, *University of Nebraska, Lincoln*.

Effects of feeding wet distillers grains (WDG), distillers solubles (DS), and vitamin E (E) supplementation on fatty acid composition and sensory attributes of beef strip steaks (*M. longissimus lumborum*) were investigated. Crossbred yearlings (n = 90) were randomly assigned to one of ten diets contained 0, 20, or 40% (DM basis) WDG with or without E (500 IU of α–tocopherol/steer daily for 100 d) and DS (0 or 30% by wt of WDG). Strip loins were aged for 7 and 28 d at 2 °C and displayed for 7 d under simulated retail display conditions. Fatty acids profiles of steaks were analyzed using gas chromatography. Aged (7 and 28 d), pre– and post–displayed steaks were grilled (71°C) and presented to a trained sensory panel (8 panelists) to evaluate tenderness, juiciness, connective tissue content and off–flavor intensity based on 8–point hedonic scales. Diets having WDG increased ($P \leq 0.05$) the amount of polyunsaturated fatty acids containing 18 or more carbons, omega–6, omega–3 and trans fatty acids of 18:1 isomers. No significant differences were found for total saturated, unsaturated and monounsaturated fatty acids. Tenderness, connective tissue contents and juiciness of pre– and post–displayed, 7 d aged steaks were not ($P \geq 0.05$) influenced by E, WDG, DS, or their combination. Pre–displayed 7 d aged steaks from animals fed WDG+DS had higher off–flavor contents over steaks from cattle fed non-WDG+DS diets ($P \leq 0.05$). However, WDG, DS, E, or their combination diets did not ($P \geq 0.05$) influence tenderness, connective tissue contents, or off–flavor intensity of steaks from pre– and post–displayed 28 d aged steaks. The incidence of livery flavor was significantly higher in post-displayed, 7 d aged steaks from animals fed WDG+DS. Steaks from pre–displayed, 7 d aged from other diets did not have off–flavors ($P \leq 0.05$). Feeding supplemented E resulted in lower levels of livery flavor for 28 d aged, post displayed steaks compared to steaks from non–E diets ($P \leq 0.05$). Diets containing WDG+DS+E alter the fatty acid composition of beef and thereby increase off–flavors in strip steaks after retail display.

Key Words: beef, wet distillers grains, vitamin E

T154 Wet distillers grains with or without solubles and vitamin E supplementation alter proximate and mineral composition of beef. L. S. Senaratne, C. R. Calkins*, and A. S. de Mello Jr., *University of Nebraska, Lincoln*.

Increasing levels of certain minerals (S, and Fe) may contribute to subsequent off-flavor production in beef during cooler aging. Therefore, this study was conducted to evaluate the effect of wet distiller grains (WDG), with or without distillers solubles (DS), and/or vitamin E (E) supplementation on proximate and mineral composition of beef. Crossbred steers (n = 90) were fed 0, 20, and 40% WDG with or without DS and with or without E supplementation (500 IU of α–tocopherol acetate/head daily for 100 d) as a finishing ration for a period of 140 d. After slaughter, short loins (5 USDA Choice and 5 USDA Select carcasses from each dietary treatment) were aged for 7 d at 0 to 2 °C. Strip loins (*M. longissimus lumborum*) and tenderloins (*M. psoas major*) were analyzed for moisture, fat, ash, and mineral (Ca, P, K, Mg, Zn, Fe, Mn, Cu, S, and Na) levels. Fat, moisture, and ash percentages of strip loins and tenderloins from animals fed no DS diets containing 0, 20, or 40% WDG with or without E supplementation did not differ significantly. However, diets having DS or 40% WDG increased the fat levels of strip loins compared to no DS or 20% WDG diets ($P < 0.05$). Feeding DS to cattle increased the levels of Ca ($P < .0001$), P ($P = 0.0002$), Fe ($P < 0.0001$), Mn ($P = 0.01$), and S ($P = 0.01$) in strip loins. Strip loins from cattle fed WDG, DS, E or their combinations had similar levels of Zn, Na, and K ($P > 0.05$). In contrast, tenderloins from cattle fed WDG diets with E, DS or their combinations showed similar levels of Ca, K, Fe, Zn, S, and Cu ($P > 0.05$). However, Na and Mg levels in tenderloins significantly decreased when cattle were fed DS diets compared no DS diets. Feeding WDG, DS, and E supplementation significantly changes the mineral composition of beef strip loins and tenderloin muscles.

Key Words: beef, wet distillers grains, mineral

T155 Alternative muscles for traditional Japanese and Korean beef recipes. C. R. Calkins, A. S. de Mello Jr.*, L. S. Senaratne, and K. Watanabe, *University of Nebraska, Lincoln*.

The objective of this study was to verify the performance of different muscles in important Asian dishes. Typical dishes were tested twice (6 panels per country) using the traditional and three different beef muscles. Dishes were compared regarding appearance, aroma, juiciness, tenderness, flavor, and overall acceptability using a linear scale. Japanese dishes were sukiyaki (sauté), shabu-shabu (hot pot), and yakiniku (grill), whereas Korean dishes were jang jo rim (boiled), miyeok-guk (soup), and kalbi (grill). Native Japanese (n = 30 per session) and Korean (n = 20 per session) panelists and cooks (1 per country) were used. For sukiyaki, the alternative muscles *Biceps femoris* (BF), *Rectus femoris* (RF), and *Semimembranosus* (SM), were compared to *Longissimus dorsi* (LD) and no differences were observed in any attribute ($P \leq 0.05$). *Tensor fascia latae* (TFL), RF, and SM muscles were compared to *Triceps brachii* (TB) in shabu-shabu. The *Semimembranosus* was least desirable of all muscles ($P \leq 0.05$). *Tensor fascia latae*, RF, and TB were similar in all attributes except tenderness, where RF was least desirable ($P \leq 0.05$). For yakiniku, *Biceps femoris* - top sirloin cap (BFc), and *Infraspinatus* (IF), TF, were compared to *Serratus ventralis* (SV). The SV had highest juiciness ratings ($P \leq 0.05$), but BFc and IF were similar to SV in tenderness, flavor and overall acceptability. No differences were observed among muscles in appearance and aroma. For jang jo rim, BF, *Trapezius* (TP), and *Pectoralis* (PE) were compared to *Semitendinosus* (ST). No differences were observed except in tenderness where BF was significantly more tender ($P \leq 0.05$). *Digital extensor* (DE), TFL, and SM were compared to SV in miyeok-guk. No differences in appearance were observed among all four muscles ($P > 0.05$). However, DG, TFL, and SV had higher values for all attributes when compared to SM ($P \leq 0.05$). For Kalbi, TFL, BFc, and IF were similar to SV in all traits ($P > 0.05$). Results indicate that other muscles may be used to replace traditional beef cuts from Japanese and Korean dishes, suggesting nontraditional U.S. beef cuts for the Asian market.

Key Words: beef, exports, Asia

T156 Fatty acid composition of western Canadian beef: Hamburger. N. Aldai*[1], M. E. R. Dugan[1], D. C. Rolland[1], and J. K. G. Kramer[2], [1]*Lacombe Research Centre, Lacombe, AB, Canada*, [2]*Guelph Food Research Centre, Guelph, ON, Canada*.

Canadian regulations concerning trans fat levels in foods are being considered due to their atherogenic nature. However, not all fatty acids containing trans double bonds are unhealthy and some may actually be beneficial (i.e., c9,t11-conjugated linoleic acid (CLA) and its precursor vaccenic acid (t11-18:1)). A retail survey of lean beef, hamburger and backfat fatty acid composition in western Canada and a complementary study in eastern Canada have been conducted. Results for lean hamburger (15% fat) collected in western Canada are reported here. Hamburger samples were collected in February and July, 2007, from 30 supermarkets in Calgary (AB). Ground meat samples were freeze-dried and lipids were extracted using a mixture of chloroform â€“ methanol (1:1, v/v). Lipid aliquots from each sample were methylated separately using acidic (methanolic HCl) and basic (sodium methoxide) reagents. Fatty acid methyl esters were analyzed using Ag+-HPLC and GC with a 100m column (CP-Sil 88). Summer samples (July) had significantly higher fat content than winter samples (February) (14.4% vs 12.4%; P<0.01). Consequently, summer samples had significantly more saturated (6.6g vs 5.7g/100g; P<0.01), branched-chain (320mg vs 256mg/100g; P<0.001), monounsaturated (7.15g vs 6.11g/100g; P<0.01) and polyunsaturated fatty acids (378mg vs 328mg/100g; P<0.01). In percentages, however, the differences found between collections were less evident, which means differences found on a mg/100g basis were mostly due to the difference in fat content. Across collection periods, total CLA averaged 84.9mg/100g and total trans-18:1 averaged 424mg/100g. The major CLA isomer was c9,t11-CLA followed by t7,c9-CLA while the major trans isomer was t11-18:1 followed by t10-18:1. The CLA and trans 18:1 isomer profiles of hamburger were healthier than the profile we previously reported for backfat and striploin steaks which had higher levels of t10-18:1 and lower levels of c9,t11-CLA.

Key Words: beef, survey, trans

T157 Effect of slaughter end point on pH of beef carcasses from British or Continental versus Nellore crossbred cattle. R. Mello*[1], F. D. de Resende[2], A. C. de Queiroz[3], M. H. de Faria[2], F. Maldonado[2], and P. V. R. Paulino[3], [1]*Universidade Federal de Roraima, Boa Vista, Roraima, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios, Colina, São Paulo, Brazil*, [3]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*.

The large variation in post-mortem muscle pH profiles may result in differences in meat quality traits. In the present study the aim was to investigate post-mortem variations in pH of *Longissimus dorsi* (LM) and *Semimembranosus* (SM) muscles from crossbred bulls carcasses at different body masses. Thirty six young (20 mo) bulls, 18 crossbred

F1 Red Angus × Nellore (½ RA ½ N) and 18 F1 Blonde D'Aquitaine × Nellore (1/2 BA 1/2 N) were used. The young bulls were feedlot finished and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW was measured before slaughter as the BW after 18 h without feed and water). A completely randomized experimental design in a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with six replicates was used. pH measurements were carried out at 0, 2, 4, 6, 10, 14, 18 and 24 h after slaughter in the LM and SM muscles. Data were analyzed using polynomial regression. Parameters were estimated through the REG procedure of SAS®. F test was applied with the purpose of verifying the equality of the regression parameters and identity of models fitted for the genetic group, slaughter weight and combination of both. The table below shows estimated parameters for the curves. There was no effect (P>0.05) of genetic group (GG) to curve parameters and identity of models for both muscles. However, there were effect (P<0.05) of slaughter weight (SW) and combination of both to all curve parameters and identity of models for the LM, and to initial pH (intercept) and identity of models for the SM. Therefore, muscle pH during carcasses chilling should be represented by different equations for the LM, but with common rates on pH change (L, Q, C) for the SM, respectively, according to the equations: $Y_{LM} = I+LX+QX^2+CX^3$ and $Y_{SM} = I+0.2625X-0.0288X^2+0.0008X^3$.

Table 1. Parameter estimates of the muscle pH curves

	½ RA ½ N			½ BA ½ N		
Coefficients	480	520	560	480	520	560
LM						
I	5.6263	6.2726	5.4311	5.6766	5.8742	5.5242
L	0.3182	0.1458	0.2913	0.3277	0.3011	0.2924
Q	-0.0330	-0.0190	-0.0344	-0.0348	-0.0321	-0.0346
C	0.0008	0.0005	0.0010	0.0009	0.0008	0.0010
SM						
I	5.7281	6.2275	5.4655	5.6764	5.9436	5.6332
L	0.2887	0.1737	0.2949	0.2747	0.2876	0.2554
Q	-0.0302	-0.0199	-0.0336	-0.0285	-0.0300	-0.0307
C	0.0008	0.0005	0.0009	0.0007	0.0007	0.0009

I = intercept; L = linear term; Q = quadratic term; C = cubic term

Key Words: young bulls, *Longissimus dorsi*, *Semimembranosus*

T158 Post-mortem variation in temperature of beef carcasses in relation to breed and slaughter end point. R. Mello*[1], A. C. de Queiroz[2], F. D. de Resende[3], M. H. de Faria[3], G. R. Siqueira[3], and J. S. de Oliveira[2], [1]*Universidade Federal de Roraima, Boa Vista, Roraima, Brazil*, [2]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*, [3]*Agência Paulista de Tecnologia dos Agronegócios, Colina, São Paulo, Brazil*.

The large variation in post-mortem muscle temperature profiles may result in differences in meat quality traits. In the present study the aim was to investigate post-mortem variations in temperature of *Longissimus muscle* (LM) and *Semimembranosus* (SM) muscles from crossbred bulls carcasses at different body masses. Thirty six young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (½ RA ½ N) and 18 F1 Blonde D'Aquitaine × Nellore (½ BA ½ N) were used. The young bulls were feedlot finished and slaughtered at 480, 520 and 560 kg of shrunk body weight. A completely randomized experimental design in a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with six replicates was used. Temperature measurements were carried out at 0, 2, 4, 6, 10, 14, 18 and 24 h after slaughter in the LM and SM muscles. Data were analyzed using nonlinear exponential model. Parameters of the model in question were estimated through the modified Gauss-Newton algorithm inserted in the NLIN procedure of SAS®. The likelihood ratio test with rapprochement through F statistical was applied to verify the equality of nonlinear regression parameters and identity of models fitted for the genetic group, slaughter weight and combination of both. The table below shows estimated parameters for the curves. There was no effect (P>0.05) of genetic group (GG) to curve parameters and identity of models for both muscles. However, there were effect (P<0.05) of slaughter weight (SW) and combination of both to all curve parameters and identity of models for both muscles, except to initial temperature (A) from SM. Therefore, muscle temperature during carcasses chilling should be represented by different curves for the LM, but with a common initial temperature for the SM, respectively, according to the equations: $Y_{LM} = B+(A-B)\exp(-Ch)$ and $Y_{SM} = B+(41.2-B)\exp(-Ch)$.

Table 1. Parameter estimates of the muscle temperature curves

	½ RA ½ N			½ BA ½ N		
	480	520	560	480	520	560
LM muscle						
A, °C	32.7	35.6	36.9	32.8	36.1	34.8
B, °C	1.5	1.9	3.5	1.8	2.0	3.6
C, h^{-1}	0.25	0.23	0.21	0.27	0.24	0.20
SM muscle						
A, °C	41.3	41.6	40.5	42.6	40.8	40.1
B, °C	1..3	3.3	-6.7	-4.6	4.1	-21.6
C, h^{-1}	0.09	0.08	0.04	0.06	0.09	0.03

A = initial temperature; B = asymptotic temperature; C = rate of temperature decline

Key Words: crossbreed bulls, *Longissimus dorsi*, *Semimembranosus*

T159 Effect of breed and production system on the content of *cis*-9, *trans*-11 CLA in m. *longissimus lumborum* and m. *semimembranosus* of lambs. G. Davila El Rassi*[1], V. Banskalieva[1], and M. Brown[2], [1]*R. M. Kerr Food and Agricultural Products Center, Oklahoma State University, Stillwater*, [2]*USDA-ARS, Grazinglands Research Laboratory, El Reno, OK*.

Katahdin (KK), Katahdin × Suffolk KS), Suffolk × Katahdin (SK), and Suffolk (SS) wether lambs (n=24) born spring of 2007 were used to evaluate levels of CLA ($C18:2_{c9t11}$) from *longissimus lumborum* (LL) and *semimembranosus* (SM) muscle in concentrate and forage-fed lambs. Lambs were weaned and grazed on bermudagrass pasture until the end of August. Concentrate lambs were moved to drylot and 3 lambs of each breed group were fed on a mixed grain ration (12% CP, 76%TDN) for 88 d while a contemporary group of forage-fed lambs remained on bermudagrass until late September and then was moved to drylot and fed wheat silage for 69 days. Lambs were harvested at the Food and Agricultural Products Center, Oklahoma State University and muscle tissues sampled for fatty acid analyses. Data were analyzed by least squares procedures with linear models including fixed effects of treatment (concentrate *vs* forage-fed), sire breed, and dam breed, and all possible 2- and 3-factor interactions. There was little evidence of any interactions among fixed effects in these data. There was evidence (P< 0.05) of treatment differences in CLA proportion in LL with forage-fed lambs greater than concentrate-fed lambs. There was also evidence of

direct breed effects in favor of Katahdin for CLA production in LL and SM lipids (P < 0.01) but little evidence of heterosis or maternal breed effects. Proportions of CLA in LL were greater in KK compared to KS (P < 0.10), SK (P <0.05), and SS (P <0.01). Proportions of CLA in SM were greater in KK compared to KS (P = 0.05), SK (P < 0.01), and SS (P < 0.01) and CLA in SM of KS and SK were greater than that of SS (P <0.01 and P < 0.10, respectively). These results suggest that meat from Katahdin lambs is greater in CLA than meat from either crosses with Suffolk or purebred Suffolk and that meat from forage-fed lambs is greater in CLA concentration compared to meat from concentrate-fed lambs.

Key Words: breed, Diet, CLA

T160 Free amino acids profile in *Biceps femoris* of Iberian gilts fed betaine, CLA or both. I. Fernandez-Figares*, M. Lachica, J. M. Rodriguez-Lopez, L. Gonzalez-Valero, and J. F. Aguilera, *Spanish Research Council, CSIC, Granada, Spain*.

Betaine (BET) and CLA have the potential to alter growth and body composition in swine. Previous results in Iberian pigs have shown that BET and CLA have a synergistic effect on growth and carcass composition (Fernandez-Figares et al., 2008). The association BET+CLA elicited changes of the serum free AA profile in growing pigs consistent with an increased use of essential AA by peripheral tissues. Muscle is the tissue that has the largest need for essential AA, and that contains the largest free AA pool. The aim of the present work was to gain further insight by evaluating changes in Biceps femoris free AA profile of growing Iberian pigs fed BET, CLA or BET+CLA supplemented diets. Twenty Iberian gilts (20 kg BW) were individually penned and fed at 95% ad libitum barley-soybean meal based diets (12% CP, 0.81% lysine and 14.8 MJ ME/ kg DM) containing either no added BET or CLA, 0.5% BET, 1% CLA, or 0.5% BET + 1% CLA. At 50 kg, pigs were slaughtered after an overnight fast and muscle samples were dissected and immediately frozen at -80ºC until analysis. Free AA were determined by HPLC using the PicoTag method as described elsewhere (Fernández-Fígares et al., 2003). AA concentrations are presented as µmol/g of wet tissue. Data were analyzed as an ANOVA-I in a completely randomized design with treatment as the fixed effect. Significance was set at P<0.05 and differences among means were determined using a Duncan's t-test. Tau, Ala and Gln were the most abundant non essential free AA. Val, Arg and Lys were the most abundant essential free AA. Overall, no significant differences were found between treatments for essential or non essential AA in the free AA pool. Increased carcass protein deposition in pigs fed BET+CLA supplemented diets was not reflected as changes in free AA at the Biceps femoris. It is possible that other muscles could have been more sensitive to the differences encountered at the whole animal level. Fernandez-Figares, Cuadros Rodríguez, González-Casado. (2003). J. Chromat. B 799: 73-79. Fernandez-Figares, Conde-Aguilera, Nieto, Lachica, Aguilera. (2008). J. Anim. Sci. 86: 102-111.

Key Words: free amino acids, betaine and cla, Iberian pig

T161 Feeding flaxseed to beef cows increases plasma omega-3 linolenic acid levels. M. L. He*[1,2], Y.-H. Chung[1], K. A. Beauchemin[1], P. S. Mir[1], J. L. Aalhus[3], M. E. R. Dugan[3], and T. A. McAllister[1], [1]*Agriculture & Agri-Food Canada Research Centre, Lethbridge, Alberta, Canada*, [2]*Dept. of Animal and Poultry Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada*, [3]*Agriculture & Agri-Food Canada Research Centre, Lacombe, Alberta, Canada*.

Flax is an oilseed rich in omega-3 linolenic acid (LNA), which can be a precursor for other functional fatty acids such as conjugated linoleic acid (CLA) or elongate to eicosapentaenoic acid (EPA) and docosahexanoic acid (DHA). Supplementing diets for beef cows with flaxseed may increase the LNA accumulation in muscle and fat tissues, but it has been speculated that omega-3 fatty acid enrichment is impeded when diets include silage. This study investigated the effect of supplementation of flax on plasma fatty acid profiles of beef cows fed diets containing different forage sources. Twelve Holstein cull cows were used in an experiment designed as a replicated 4 × 4 Latin Square with four 21-d periods. Diets were formulated to a 50:50 forage:concentrate ratio (dry matter (DM) basis), with forage comprising hay or silage, and with flaxseed supplemented at 0 or 15% of diet DM, replacing barley grain in the concentrate. The four diets, i.e., hay control (HC), hay plus flax (HF), silage control (SC), and silage plus flax (SF), were offered at 1300 h daily for ad libitum consumption. Blood samples were collected at 1500 h on d 14 and d 21. The lipids were extracted and methylated for fatty acid determination using gas chromatography. On d 21, mean LNA concentrations in plasma and weight % in total fatty acids were 244 mg/L and 17.9%, respectively, in the HF group, and 248 mg/L and 16.4% in SF. These values were much higher ($P < 0.01$) than were observed in the HC (66 mg/L and 6.6%) and SC (48 mg/L and 4.8%) groups. No differences in plasma LNA levels were observed between cows fed HF and those fed SF. Plasma EPA and CLA c9, t11 concentration, but not their weight % in total fatty acids, were also significantly increased in cows fed flaxseed. These findings suggest that relatively high levels of dietary LNA from flax will be delivered to muscle and fat tissues. Short-term flax supplementation of diets can be used to increase the healthy properties of beef.

Key Words: flaxseed, omega-3 fatty acids, conjugated linoleic acid

T162 Grazing or concentrate feeding for 11 months prior to slaughter: Influence on colour and sensory characteristics of beef. A. P. Moloney*[1,2], A. Black[1], P. G. Dunne[2], and F. J. Monahan[3], [1]*Teagasc, Grange Beef Research Centre, Dunsany, County Meath, Ireland*, [2]*Teagasc, Ashtown Food Research Centre, Ashtown, Dublin, Ireland*, [3]*University College Dublin, Belfield, Dublin, Ireland*.

The effect of long-term pre-slaughter grazing or concentrate feeding on beef quality was determined. Fifty Charolais heifers (BW = 275 + 27.0 kg, age = 252 + 28 days) were assigned to either a pasture (P) or concentrate (C) ration on December 1. The P animals grazed a predominantly *Lolium perenne* pasture while C animals were housed in a slatted floor shed and offered a rolled barley (430 g/kg)/molassed beet pulp (430 g/kg) ration and 20% barley straw. The strategy was for P cattle to achieve their growth potential and to restrict the allowance of concentrates/straw such that both groups had a similar carcass weight. Rations were offered for 332 days prior to slaughter. Post mortem (48h), the colour of subcutaneous adipose tissue and longissimus muscle (LM) was measured using a Hunter Lab Ultra Scan colorimeter. Sensory characteristics of 14-day aged LM were assessed by a trained taste panel. Data were analysed accordingly to a randomized block (BW) design with assessor included as appropriate. Adipose tissue from P heifers was more yellow (P<0.05) (′b′ value 25.0 vs 17.7), more red (P<0.05) (′a′ value 11.1 vs 8.6) and darker (P<0.05) (′L′ value 67.6 vs 71.4), than that from C cattle. There was no effect of pre-slaughter diet on ultimate muscle pH (5.54). Muscle from P heifers was darker (P<0.05) (34.3 vs 35.60), less red (P<0.05) (15.2 vs 17.2), less tender (P<0.05) (4.23 vs 4.48, 8 point scale) and less preferred (P<0.05) (39.0 vs 42.3, 100 line scale) than muscle from C heifers. There was no difference between

rations in juiciness, beef flavour intensity, abnormal flavour intensity or in the flavour attributes of greasy, bloody livery, metallic, bitter, sweet, rancid, fishy, acidic, cardboard or vegetable/grassy. It is concluded that while statistically significant, the absolute differences in colour and tenderness were small and may not be detected by consumers.

Key Words: beef colour, sensory

T163 The influence of forage diets and aging on beef palatability. T. Jiang*[1], J. R. Busboom[1], M. L. Nelson[1], J. O'Fallon[1], T. P. Ringkob[2], D. Joos[2], K. R. Rogers-Klette[2], and K. Piper[2], [1]*Washington State University*, *Pullman*, [2]*University of Nevada*, *Reno*.

To investigate the influence of diet and aging on beef palatability (beef steak and ground beef), lipid oxidative stability, and fatty acid composition, crossbred steers were assigned in a Completely Randomized Design to dietary treatments of Feedlot S (finished on alfalfa and grain), Forage 1 (triticale and annual rye grass), Forage 2 (triticale and kale), or Combination (grazing rye, fescue and orchard, finished on alfalfa and grain). Heifers were finished on alfalfa and grain (Feedlot H). Two longissimus muscle steaks from five animals per dietary treatment and three trimmed triceps brachii muscle samples from four animals per dietary treatment were collected. Steaks were either dry- or wet-aged for 14d. Ground beef samples were dry-aged, or wet-aged for 14d, or not aged. Nine-member trained sensory panels were conducted to evaluate palatability attributes of beef steaks (beef flavor, off-flavor, initial tenderness, sustained tenderness, and juiciness) and ground beef (beef aroma, off-aroma, beef flavor, off-flavor, tenderness, and juiciness). There was no ($P > 0.05$) effect of diet or aging on cooking weight loss. Diet and aging treatment did not ($P > 0.05$) influence the palatability of beef steaks. Similarly, diet did not ($P > 0.05$) influence the palatability of ground beef. However, aging impacted ($P < 0.05$) ground beef sensory attributes and the influence depended on dietary treatment or possibly animal sex. In general, aging negatively affected ground beef palatability. Furthermore, dry-aging had more negative effects on palatability than wet-aging. Dietary and aging treatments had no ($P > 0.05$) impact on lipid oxidative stability of raw ground beef but affected the fatty acid composition. Therefore, to maintain ground beef palatability aging should not be practiced.

Key Words: beef palatability, beef aging, cattle diet

T164 Influence of management systems on meat quality of heifers fed with different lipid supplements in the finishing phase. M. C. A. Santana*[1], T. T. Berchielli[1], R. A. Reis[1], A. V. Pires[2], G. Fiorentini[1], and M. A. A. Balsalobre[3], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*São Paulo University*, *Piracicaba, São Paulo, Brazil*, [3]*Bellman*, *Mirassol, São Paulo, Brazil*.

The feeding strategy is the management tool most widely used as a quality control method in the production conditions of meat. The areas of focus in this experiment are colors a, b, L and shear force (WBSF), water-holding capacity (WHC), pH and cooking loss percentage (CLoss) in meat from heifers fed with different lipid supplements in the finishing phase system. The experiment was completely random design, using a 3 × 2 factorial arrangement (3 supplements and 2 systems). The supplements came from 3 different sources; soybean grains, soybean oil and protected fat (MEGALAC- E), the two finishing phase systems came from pasture (0.75% of BW) or feedlot (60:40 concentrate: corn silage) .The treatments were compared by analyzing variables using the GLM procedure (SAS 9.1, SAS Institute, Inc., Cary, NC). Mean values were compared using the Tukey test at a significance level of 0, 05. Using a colorimeter, the color of the longissimus muscle (LM) at the 12th and 13th rib interface in the L*a*b* color space (CIE system) was determined. A time span of 30 minutes was awaited before color analysis. The WBSF was obtained from steaks previously thawed and roasted using an insert thermometer until 70°C was obtained. Later, the samples were cut into cubes; the data collected was achieved using a Warner-Bratzler shear machine. The muscle pH (pHu) measurements were taken from the interior of the LM at 24 h postmortem using a portable pH meter. The water holding capacity was obtained by determining the difference of the sample weights under 10 kg of pressure for 5 minutes. The cooking loss value was determined according to the reduced percentage rate before and after the meat was cooked. The meat attributes were not influenced by the supplements, however, the meat from the pasture systems showed a significantly higher grade in muscle pH as well as in colors a and L. The results of this experiment confirm that the feeding strategy used can in fact influence the quality of meat by altering the pH and color (a,L).

Table 1. Means for the colours a, b and L, meat pHu, water-holding capacity (WHC), pH and percentage cooking loss (CLoss) and shear force (WBSF) of heifer's meat from finishing phase systems, pasture and feedlot.

Systems	Color a	Color b	Color L	pHu	WHC	CLoss	WBSF
Feedlot	16,58 b	3,59 a	34,62 b	5,64 b	72,30 a	33,74 a	7,54 a
Pasture	18,17 a	3,77 a	36,96 a	5,72 a	73,23 a	33,19 a	7,99 a

Means followed by different letters in the same column are different ($P<0.05$).

Key Words: pasture, feedlot, lipids

Nonruminant Nutrition: Feed Additives I

T165 Hypocholestromic effect of turmeric powder and sodium selenite in Ross broilers reared under heat stress conditions. A. Zeinali*[1], A. Riasi[1], H. Farhangfar[1], and H. Ziaei[2], [1]*Birjand University*, *Birjand, Iran*, [2]*Agricultural Research Center*, *Birjand, Iran*.

An experiment was conducted using 180 Ross broiler chickens to evaluate the effect of different levels of sodium selenite (SS) and turmeric powder (TP) on lipid concentrations of broilers. One-day old chicks were randomly allocated to 6 treatments (T1= control, T2= control + 5 g TP /kg, T3= control + 10 g TP /kg, T4= control + 0.3 mg Se/kg, T5= control + 0.3 mg Se + 5 g TP/kg, and T6= control + 0.3 mg Se + 10 g TP /kg) with 3 replicates and 10 birds per each replicate. The air temperature was increased (32-35°C) from day 28 to day 42. At 28 and 42 d of age, two birds (one male and one female) of each replicate were randomly selected and blood samples were taken from the wing vein with heparinized syringes. Statistical analysis of data was undertaken using the GLM procedure of SAS. Results showed that the interaction between selenium and turmeric powder resulted in a decrease in plasma cholesterol concentration at 28 days of age ($P<0.05$). Birds fed the

control diet and T3 had the highest and lowest concentration of cholesterol respectively (120.0 mg/ml versus 99.5 mg/ml) and no difference was found between T3 and T6. At 42 days of age, T6 had the lowest cholesterol concentration. Repeated measurement analysis showed that the effect of sampling time on the difference between treatments was significant ($P<0.05$). At 28 days of age, supplementation of diets with sodium selenite and turmeric powder significantly decreased triglyceride concentration ($P<0.05$), but this difference was not significant at 42 days of age. In conclusion, using turmeric powder (10 g/kg diet) and sodium selenite (0.3 mg/kg diet) could reduce the cholesterol level of serum of broilers under heat stress conditions.

Key Words: broiler, serum lipid, heat stress

T166 Cloning and expression of porcine carboxypeptidase A1 for feed application. Y. Zhao[1], H. Zhao[1], J. C. Zhou[1], X. J. Xia[1], and X. G. Lei*[1,2], [1]*Int. Ctr of Future Agriculture for Human Health, Sichuan Agri. Univ., Ya'an 625014, China*, [2]*Cornell University*, *Ithaca, NY*.

Carboxypeptidase A (CPA1, EC 3.4.16) is a digestive enzyme that hydrolyzes peptide bonds nearest to the terminal carbonyl group in polypeptide chains. The enzyme can be used to improve feed protein digestion by young animals. To produce recombinant porcine pancreatic proCPA1, the full-length cDNA of porcine carboxypeptidase A gene was isolated from porcine pancreas by RACE and cloned into the pPICZαA vector (Invitrogen, Shanghai, China). The DNA construct was transformed into *Pichia pastoris* X33 cells. Transformants with high-level expression were selected by Syber-green quantitative real-time RT-PCR Analysis (ABI 7900HT, Applied Biosystems, Foster City, CA). The extracellular recombinant proCPA1 contained a histidine tag in the C terminus and was purified using Ni-Sepharose affinity chromatography (GE Healthcare, Piscataway, NJ). The purified protein exhibited a molecular mass of approximately 47 kDa as determined by SDS-PAGE analysis. Western blot analysis using an anti-porcine carboxypeptidase A antibody and peptide mass fingerprint analysis confirmed the purified 47 kDa protein as the target enzyme. In conclusion, the successful production of the recombinant proCPA1 in *P. pastoris* enabled further functional study of the enzyme in animal feeding. This project was supported by the 863 Program of the State High-Tech Development Plan funded and administered by the government of the People's Republic of China (2007AA100601-6).

Key Words: porcine, *Pichia pastoris*, enzyme

T167 Determination of optimal conditions for hydrolysis of conjugated deoxynivalenol in corn and wheat with trifluoromethanesulfonic acid. S.-T. Tran* and T. K. Smith, *University of Guelph*, *Guelph, Ontario, Canada*.

Deoxynivalenol (DON, vomitoxin), is a common type B trichothecene mycotoxin produced by many *Fusarium* species and is found as a contaminant of crops worldwide. DON can reduce production efficiency and cause serious economic losses to livestock and poultry producers. Recent studies have suggested that common analytical methods for DON analysis in feedstuffs do not detect conjugated (masked) mycotoxins. The aim of the current study, therefore, was to determine the optimal conditions in which non-extractable (conjugated) DON in corn and wheat can be hydrolyzed by trifluoromethanesulfonic acid (TFMSA) which has been reported to deglycosylate glycoproteins regardless of linkage and composition. The optimal hydrolysis procedure was determined based on reaction time, reaction temperature and TFMSA concentration. Total DON concentrations were determined using ELISA kits (AgraQuant® DON kit). The optimal hydrolysis conditions for determination of conjugated DON in corn were found to be 0.5N TFMSA incubated for 20 min at 22°C. Optimal conditions for wheat samples were 0.5N TFMSA incubated for 40 min at 40°C. Using these optimal hydrolysis conditions, 6 naturally contaminated corn samples and 5 naturally contaminated wheat samples were analyzed to determine the presence of conjugated DON. All samples contained conjugated DON in significant amounts with an increase of 17-69% of DON in corn following hydrolysis and an increase of 21-72% of DON in wheat following hydrolysis. It can be concluded that the optimal conditions for TFMSA hydrolysis of conjugated DON in corn and wheat have been determined and that this will be useful in acurately determining total DON content of grains and detection of conjugated DON in feeds and foodstuffs.

Key Words: *Fusarium* spp., conjugated deoxynivalenol, trifluoromethanesulfonic acid

T168 Efficacy of a commercial purified phylosilicate in preventing fumonisin toxicity in finishing pigs. C. A. Mallmann[1], P. Dilkin[1], L. Giacomini[1], R. H. Rauber[1], and J. Garcia-Sirera*[2], [1]*Universidade Federal de Santa Maria, Laboratorio de Analises Micotoxicologicas (LAMIC)*, *Santa Maria, RS, Brasil*, [2]*Special Nutrients*, *Miami, FL*.

Two experiments of different lengths of time (28 and 56 days) were conducted to study the efficacy of a commercial purified phylosilicate (Myco-Ad A-Z) in preventing the deleterious effects of fumonisin (FUM) in finishing pigs. Twelve male pigs averaging 58.5 kg initial body weight were used in each experiment. Pigs were individually housed and randomly distributed into 3 dietary treatments with 4 replications and fed corn-SBM diets meeting or exceeding NRC recommendations. All ingredients used tested free of mycotoxin contamination. Treatments were: (1) control diet; (2) control + 25 ppm FUM; and (3) control + 25 ppm FUM + 4.0 kg/mt Myco-Ad A-Z. FUM was obtained from a culture material containing 72% FUM B1 and 28% FUM B2 produced in LAMIC. Performance and organs (lungs, heart and liver) relative weights (g/kg body weight) were evaluated in experiment 1 (EX1). Performance, relative weight of lungs and serum sphinganine / sphingosine ratio (SA:SO) were determined in experiment 2 (EX2). Results from both experiments showed that pigs fed 25 ppm FUM had significantly ($P\leq0.05$) poorer performance; increased relative weights of lungs, heart and liverl, and increased serum SA:SO than pigs fed the control diet. The addition of Myco-Ad A-Z to the contaminated diet significantly ($P\leq0.05$) improved performance parameters and relative organ weights, feed intake (2615 vs 2315 g EX1) (2948 vs 2810 g EX2), daily gain (861 vs 722 g EX1) (1084 vs 996 g EX2), feed efficiency (2.70 vs 3.08 EX1) (3.21 vs 3.46 EX2), lungs (6.68 vs 9.69 EX1) (5.94 vs 6.34 EX2), heart (3.75 vs 4.87 EX1), and liver (18.65 vs 20.89 EX1). Serum SA:SO, a key marker of FUM toxicity, was significantly ($P\leq0.05$) increased in pigs fed FUM compared to control and Myco-Ad A-Z fed pigs (0.78 vs 0.38 and 0.49). These results indicate that Myco-Ad A-Z was very effective in preventing the toxic effects of FUM in finishing pigs.

Key Words: Myco-Ad A-Z, fumonisin, pigs

T169 Development and validation of an analysis method for carvacrol encapsulated in different matrixes and set in pelleted feed. S. Oguey*, A. Vienne, C. Ionescu, and D. Bravo, *Pancosma*, *Geneva, Switzerland*.

Carvacrol, the active compound of oregano, was encapsulated into different matrixes and technologies in order to determine the most efficient way to protect it during the feed manufacturing process and storage. It was necessary to develop and validate a new analytical method for the carvacrol formulations in feed. Most of the encapsulation matrixes tested were polar, while carvacrol had a much lower polarity. The challenge was to dissolve the encapsulation and carvacrol at the same time. The initial carvacrol concentration in the feed was around 1 g/kg. A single method was developed for all carvacrol formulations. Accelerated solvent extraction (ASE) was used for the extraction. The separation and quantification was done by gas chromatography with a flame ionisation detector (GC-FID). Twenty grams of sample were weighed in a 33 mL extraction cell and extracted with methanol at 110°C and 100 bar. The Flush was set at 10%, the static time was 19 minutes with 2 cycles. The heat time was set to 6 minutes. Each extraction cell was extracted 3 times and the extracts were transferred in a 200 mL flask. The solution was filtered and analysed by GC-FID with a capillary column ZB-5ms 20 m × 0.18 mm × 0.36 mm. The split ratio was 1:10 and 1 mL was injected. The injector and detector temperature were respectively set at 250°C and 300°C. The carrier gas was helium and the flow rate was 0.8 mL/min. The temperature program started at 100°C for 1 min, then a 15°C/min gradient was applied up to 180°C and a second one to 300 at 50°C/min and kept at 300°C for 30 s. The method proved to be valid for all tested formulations in feed, the carvacrol solutions were stable for 36 days (R^2 of the calibration curve > 0.999). The application range was far over the quantification limit and was in the linear range, the repeatability had a RSD < 10%, the method was true with a normalised deviation < 1 and the extraction yield was > 98.5%. This method allowed a precise comparison of the carvacrol stability depending on the encapsulation.

Key Words: essential oil, encapsulation, traceability

T170 Heterologous expression of recombinant porcine elastase 2 as a feed enzyme. Y. J. Zhang[1], H. Zhao[1], J. C. Zhou[1], X. J. Xia[1], and X. G. Lei*[1,2], [1]*Int. Ctr of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Ya'an 625014, China*, [2]*Cornell University*, *Ithaca, NY*.

Porcine pancreatic elastase is a protease that specifically degrades insoluble elastin. A recombinant elastase can be used to improve feed protein utilization by swine and poultry. The objective of this study was to develop an efficient expression system to produce porcine elastase 2. A cDNA fragment encoding the proELA2 was isolated from porcine pancreas by RT-PCR and cloned into the pPICZαA (Invitrogen, Shanghai, China) expressing vector. The pPICZαA- proELA2 construct was transformed into *Pichia pastoris* KM71 cells. The transformants were screened by Syber-green quantitative real-time RT-PCR (ABI 7900HT, Applied Biosystems, Foster City, CA). After 72-h of 0.5% methanol induction, the extracellular proELA2 protein containing a histidine tag appended to the C terminus was purified using Ni Sepharose High Performance affinity column (GE Healthcare, Piscataway, NJ). The purified protein had a molecular mass of approximately 31 kDa as determined by SDS-PAGE analysis, and was verified by both Western blot and peptide mass fingerprint analyses. After optimizing the medium temperature and methanol induction procedure, a yield of 45 mg of recombinant proELA2 per liter was obtained. In summary, the recombinant porcine pancreatic proelastase2 was expressed extracellularly at a relative high level under the control of AOX1 promoter in *Pichia pastoris*. *This project was supported by the 863 Program of the State High-Tech Development Plan funded and administered by the government of the People's Republic of China (2007AA100601-6).*

Key Words: Porcine, feed enzyme, *Pichia pastoris*

T171 Expression and purification of porcine pancreatic carboxypeptidase B in a yeast system. Y. Liu[1], H. Zhao[1], J. C. Zhou[1], X. J. Xia[1], and X. G. Lei*[1,2], [1]*Int. Ctr of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Ya'an, China*, [2]*Cornell University*, *Ithaca, NY*.

Pancreatic carboxypeptidase B (CPB) is a key enzyme highly specific for excising C-terminal lysine and arginine from peptides and proteins, and can be used as a feed additive to improve protein digestion by animals. To express the recombinant proCPB at high level in *Pichia pastoris*, a cDNA fragment encoding the porcine pancreatic proCPB along with its own secretion signal peptide was cloned into the pPICZαA vector (Invitrogen, Shanghai, China) under the control of AOX1 promoter. The recombinant proCPB protein contained a histidine sequence appended to the C terminus and was purified from the supernatant by the immobilized metal ion affinity chromatography (Ni-NTA Sepharose (GE Healthcare, Piscataway, NJ). The extracellular enzyme showed a molecular mass of approximately 47 kDa as determined by SDS-PAGE analysis. The identity of the enzyme was verified by both Western blot and peptide mass fingerprint analyses. In conclusion, the recombinant proCPB was successfully expressed in *P. pastoris* as an extracellular enzyme. *This project was supported by the 863 Program of the State High-Tech Development Plan funded and administered by the government of the People's Republic of China (2007AA100601-6).*

Key Words: porcine, pancreatic carboxypeptidase B, *Pichia pastoris*

T172 Effects of antioxidants on growth performance and antioxidant status of broiler chickens. Y. Zou, Z .B. Yang*, W. R. Yang, S. Z. Jiang, and G. G. Zhang, *Shandong Agricultural University*, *Tai-an, Shandong, P. R. China*.

The experiment was designed to assess the effects of two kinds of antioxidants provided by Novus International, Inc., SQ M6 (Santoquin M6) and SQ Max (Santoquin Max), on growth performance and antioxidant status in broiler chickens. A total of 96 day-old AA broilers were randomly allocated to three treatments: 1) the control group: a basal diet without supplementation of any antioxidants; 2) SQ M6 (48 mg/kg) supplemented group; 3) SQMax (80 mg/kg) supplemented group. There were 4 replicate pens per treatment and 8 birds each. The birds were housed in 12 wire pens in an environmentally controlled room with artificial lighting (24hrs), and fed ab libitum with a starter diet from 1 to 28 days of age. Body weight and feed intake of chicks of each pen were measured weekly for determination of average daily gain (ADG), average daily feed intake (ADFI), and feed conversion rate (FCR). Blood samples were taken from 16 birds (4 birds each replicate) at the end of the experiment to determine the antioxidant status of the birds, including activities of total Cu-Zn superoxide dismutase (Cu-Zn SOD) and total anti-oxidation capability (T-AOC), and serum malondialdehyde (MDA) concentration. The results showed that there was no significant difference in performance (ADG, DMI or FCR) between different treatment groups (Table 1). SQ M6 improved ADG and FCR numerically in broilers as compared with both control and SQ Max supplemented group. However, supplementation of antioxidants significantly increased ($P<0.05$) activities of Cu-Zn SOD and T-AOC, and reduced ($P<0.05$)

serum MDA concentrations in broilers. Compared with the control group, dietary addition of SQ M6 and SQ Max significantly improved the Cu-Zn SOD (29.63% and 33.33% respectively), T-AOC (6.39% and 31.72% respectively), and decreased serum MDA levels (15.49% and 11.10%, respectively). Supplementation of SQ M6 and SQ Max, had no significant effects on growth performance of broiler chickens. However, of the three treatment groups, SQ M6 supplemented birds showed better growth rate and lower FCR. Both SQ M6 and SQ Max significantly improved antioxidant status of broilers.

Table 1. Effects of antioxidants on performance and antioxidant status in broiler chickens

Results	Control	SQ M6	SQ Max
ADG , g/d	36.92	38.15	36.74
ADFI , g/d	72.32	68.62	69.18
FCR	1.58	1.45	1.52
SOD, U/mg	61.63^{a}	79.89^{b}	82.17^{b}
T-AOC, U/ml	7.00^{a}	7.45^{a}	9.22^{b}
MDA, nmol/ml	4.66^{a}	3.94^{b}	4.14^{ab}

^{abc}different superscript letters within the same row represent a significant difference between treatments (P<0.05).

Key Words: antioxidant, broilers growth, antioxidant status

T173 Comparative effects of *Escherichia coli* AppA2 and *Aspergillus niger* PhyA phytases on bone property of weanling pigs fed a high phosphorus diet. C. E. Mills, C. A. Faber, K. R. Roneker, and X. G. Lei*, *Cornell University*, *Ithaca, NY*.

Enhancing peak bone mass in early life may reduce bone degenerative diseases such as osteoporosis in later life. Previous research in our laboratory has demonstrated potential benefits of supplementing high levels of *Escherichia coli* AppA2 phytase to bone metabolism in young pigs fed phosphorus-adequate diets. The objective of this study was to compare effects of AppA2 with those of *Aspergillus niger* PhyA on bone characteristics of weanling pigs. A total of 30 crossbreds (3-week old, Yorkshire-Landrace-Hampshire crossbred) were allotted to three groups (n = 10) and fed a corn-soybean-mean basal diet (BD, supplemented with 0.35% inorganic phosphorus), the BD plus 3,500 units of AppA2/kg (Optiphos, JBS United, Sheridan, IN), or the BD plus 3,500 units of PhyA/kg (Natuphos, BASF, Florham Park, NJ) for six weeks. All pigs were bled biweekly for assays of plasma inorganic phosphorus concentration and alkaline phosphatase activity. Eight pigs of each treatment group were killed at the end of the study to collect the right femur and humerus for biomechanics analyses. Compared with those fed BD, Pigs fed AppA2 showed 25% higher plasma alkaline phosphatase activity at week 4 (P < 0.05) and week 6 (P = 0.08). Pigs fed PhyA displayed a 13% increase (P = 0.06) in the maximal load of humerus and a 14% increase (P < 0.01) in femoral cortical thickness than pigs fed BD. In conclusion, AppA2 and PhyA seemed to exert different impacts on bone biochemical and biomechanics measures of young pigs fed the high phosphorus diet.

Key Words: alkaline phosphatase, biomechanics, phytase

T174 Effects of dietary marine microbe accumulating ω-3 fatty acid supplementation on growth performance and carcass characteristics in finishing pigs. H. J. Kim*[1], T. X. Zhou[1], J. H. Jung[1], M. S. Ryu[2], H. J. Kim[2], and I. H. Kim[1], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*JINIS Inc*, *Wanju, Jeonbuk, Korea*.

This study was conducted to investigate the effects of dietary marine microbe accumulating ω-3 fatty acid supplementation on growth performance and carcass traits in finishing pigs. A total of 96 pigs (73.01 kg, average initial body weight) were used during 42 days. Dietary treatments included: 1) CON (basal diet), 2) M2 [basal diet + 0.2% marine microbe (Ostreococcus tauri) accumulating ω-3 fatty acid] and 3) M4 [basal diet + 0.4% marine microbe (Ostreococcus tauri) accumulating ω-3 fatty acid]. Each treatment had 8 replicates of 4 pigs per pen in a randomized complete block design. In growth performance, ADFI was higher (P<0.05) in M2 treatment than CON and M4 treatments. In meat color, redness (a*) was significantly higher in M4 treatment than CON treatment and yellowness (b*) was significantly lower in marine microbe groups than CON treatment. In sensory evaluation, color score of M4 treatment was improved compared with CON and M2 treatments. Drip loss was significantly higher in M4 treatment than CON treatment at 1 day and was significantly higher in CON and M4 treatments than M2 treatment. Meat pH was significantly higher in M4 treatment than CON and M2 treatments. Total mono-unsaturated fatty acid content was significantly higher in marine microbe groups than CON treatment. Total ω-6 fatty acid content was significantly lower in marine microbe groups than CON treatment (P <0.05). Total ω-3 fatty acid content was significantly highest in M4 treatment among treatments and was significantly lowest in CON treatment. Total ω-6/ω-3 ratio was significantly higher in M2 treatment than M4 treatment. In conclusion, dietary marine microbe accumulating ω-3 fatty acid supplementation improved meat color and fatty acid content.

Key Words: marine microbe, carcass trait, ω-3 fatty acid

T175 Comparative effects of phytase derived from *Escherichia coli* and *Aspergillus niger* in laying hens. L. Yan*[1], H. D. Jang[1], S. M. Hong[1], H. S. Kim[2], Y. Hyun[2], and I. H. Kim[1], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*Seoul Feed, Co. LTD*, *Seoul, Korea*.

A total of two hundred and sixteen 68-week-old Hy-Line brown laying hens were used in a 6-week feeding trial to compare the efficacy of phytase Optiphos (OPT) and Natuphos (NAT), which were isolated from the strain of *Escherichia coli*and *Aspergillus niger*, respectively. Hens were randomly allotted into six treatments with six replications (six layers in adjacent three cages) per treatment according to the initial BW. Dietary treatments including: 1) PC (basal diet + available phosphorus (AP) 0.4%); 2) NC (basal diet + AP 0.2%); 3) NP1 (NC + 250 FTU/kg NAT); 4) NP2 (NC + 500 FTU/kg NAT); 5) OP1 (NC + 250 FTU/kg OPT); 6) OP2 (NC + 500 FTU/kg OPT). Feed intake, egg production, egg quality, nutrients apparent digestibility, and serum P and Ca concentration were investigated to compare the effect of the two phytases. In the current study, feed intake and eggshell thickness were not affected by the treatments. Superior effects (P<0.05) of OPT were only observed in egg production and egg weight compared with NAT in this experiment. Both phytases were equally effective in increasing (P<0.05) eggshell breaking strength, apparent digestibility of N, Ca, P and serum P concentration, whereas no significant difference was observed in the contrast between PC and phytase supplementation at 500 FTU/kg to the NC diet. Equally effective improvements were also observed in egg production and DM digestibility (P<0.05), but those were not as high as that in PC treatment with the phytase supplementation at 500 FTU/kg. Both phytases equally increased serum Ca compared to the PC. However, a linear effect was only observed for the OPT treatment. Data from the study suggest that NAT and OPT are equally effective in liberating phytate-bound complex

when included in P-deficient diets for 68-week-old laying hens. Either source can be fed to commercial laying hens to improve phytate-bound nutrients utilization.

Key Words: phytase, laying hens, comparative

T176 Effects of cysteamine to replace antibiotics on growth performance and nutrient digestibility in weaning pigs. J. H. Jung*, T. X. Zhou, L. Yan, S. M. Hong, and I. H. Kim, *Dankook University, Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of cysteamine to replace antibiotics on growth performance and nutrient digestibility in weaning pigs. A total of eighty pigs [(Landrace×Yorkshire)×Duroc] (initial body weight 6.95 ± 0.48kg) were used for the 42 day feeding trial. Dietary treatments included 1) CON (basal diet), 2) ANT (phase 1 : basal diet with 40ppm of avilamycin and 100ppm of OTC; phase 2, phase 3 : basal diet + 100ppm of avilamycin and 40ppm of chlortetracy), 3) CYS0.05 (basal diet + cysteamine 0.05%) and 4) CYS0.1 (basal diet + cysteamine 0.1%). There were four dietary treatments with four replicate pens per treatment and five pigs per pen. ADG in phase 2, 3 and overall periods, for ANT, CYS0.05 and CYS0.1 treatments were higher than Con treatment ($p<0.05$). During the whole experimental period, no significant differences were observed in ADFI, while G:F ratio was lower in the CON treatment than other treatments ($p<0.05$) during phase 2. ANT and CYS0.1 treatments had higher dry matter and nitrogen digestibilities compared to CON and CYS0.05 treatments at 3 and 6 weeks ($p<0.05$). No significant differences were observed in blood characteristic values among treatments. The results of this experiment indicated that dietary supplementation of cysteamine 0.1%, improved ADG and nutrient digestibility in weanling pigs.

Key Words: cysteamine, digestibility, weaning pigs

T177 Effects of different dietary combinations of antibiotics, benzoic acid and probiotic for weaning pigs. G. F. Lopes[1], L. Alebrante[1], D. L. Santos[1], G. G. Garcia[2], A. A. Passos*[3], R. Balestrin[3], and G. J. M. M. Lima[4], [1]*Vitamix Animal Nutrition*, [2]*Santa Maria Federal University*, [3]*DSM*, [4]*Embrapa*.

This study was conducted to evaluate different combinations of growth promoters. Four classes of antibiotics (AT) were used (colistin sulphate-CS, bacitracin methylene disalicylate-BD, neomycin sulfate-NS, tetracycline-TC) in association with benzoic acid (BA) and probiotic (*Enterococcus faecium*-EF). Seventy-two piglets (21 day old, 6.7 kg live wt) were sorted across three treatments and 12 replicates (2 piglets per pen) according to a randomized block design. Diets were divided in three phases: 1 - weeks 1 and 2; 2 - weeks 3 and 4; 3 - weeks 5 and 6 of experiment. Treatments were defined as: A - phase 1 diet with CS (160 ppm) + BD (55 ppm), phase 2 diet with CS (100 ppm) + TC (250 ppm) and phase 3 diet with NS (108 ppm) + BD (55 ppm); B - all phase diets with CS (40 ppm) + BA (5 kg/ton); C - all phase diets with CS (40 ppm) + BA (5 kg /ton) + EF (1.4×10^9 CFU/g). Average daily gain (ADG), feed intake (ADFI) and feed conversion ratio (FC) were measured every week considering accumulated data. Piglets fed C had greater ADG ($P<0.1$) compared to A during the first week. ADG did not differ ($P>0.1$) among treatments after that. There were no differences ($P>0.1$) in ADFI and FC among treatments at any week. A combination of AT, BA and EF was most effective during the early weaning period. However, there were no differences between treatments for the entire nursery period.

Table 1. Effects of combining different growth promoters on post weaning pigs

		Week					
	Treatment	1	2	3	4	5	6
ADG g/d	A	153[a]	269	352	413	467	511
	B	198[ab]	295	348	413	471	521
	C	209[b]	271	330	401	456	504
	sd	0.07	0.06	0.06	0.06	0.06	0.06
ADFI g/d	A	236	378	517	624	743	842
	B	297	408	529	657	780	886
	C	285	390	516	635	750	859
	sd	0.08	0.06	0.07	0.08	0.08	0.09
FC	A	1.94	1.47	1.50	1.52	1.60	1.65
	B	1.60	1.40	1.53	1.60	1.67	1.71
	C	1.47	1.46	1.57	1.59	1.65	1.71
	sd	0.63	0.18	0.14	0.14	0.13	0.10

[ab]Means within column followed by different letters are different – Tukey ($P<0.1$) sd – Standard Deviation

Key Words: piglet, acidifier, probiotic

T178 Effect of phytase supplementation on the calcium and phosphorus balance in adult cannulated ganders. J. Tossenberger[1], L. Babinszky*[1], and D. Feuerstein[2,3], [1]*Kaposvár University, Kaposvár, Hungary*, [2]*BASF SE, Ludwigshafen, Germany*.

The objective of this study was to determine the effect of dietary phytase supplementation on P and Ca digestibility and urinary excretion in adult ganders. The trials used 4 hybrid ganders per treatment (Trt) in 2 replicates (8 birds/Trt, initial LW:4.4±0.5kg). Prior to the trial a simple T-cannula was implanted in the terminal colon for separate quantitative collection of feces and urine. Basal diets were formulated on a corn-soybean basis. Diets in Trts 1,2,3,4 contained no P_i (P:3.4, Ca 4.4 g/kg) and were supplemented with phytase (3-phytase, from *Aspergillus niger*) at the rate of 0 (negative control=NC), 150, 300 and 450 FTU/kg. No phytase was added to the Trt 5 diet (positive control=PC); its P and Ca content met the NRC (1994) recommendations. Measured phytase activity of the diets was <70, 210, 270, 510 and <70 FTU/kg. Data were analyzed by ANOVA and regression analysis (SAS, 2004). Phytase supplementation of 150 FTU/kg improve P digestibility from 42.1 to 50.2% ($P<.05$). The supplementation with 300 and 450 FTU/kg phytase improved P digestibility by 10.4 and 13.5%, compared to the NC (42.1% vs. 52.5% & 55.6%) ($P<.05$). P digestibility in the PC group was 54.6%. Trt did not affect Ca digestibility ($P>.05$). Urinary P excretion was lowest in NC birds (13 mg/kg$^{0.75}$/d). A 150 FTU/kg phytase supplementation increased P excretion by 57% ($P<.05$). A phytase supplementation of 300 and 450 FTU/kg increased urinary P excretion by 47.3% and 64.1%, compared to NC ($P<.05$). Urinary P excretion of PC birds was 32 mg/kg$^{0.75}$/d. In contrast to P retention of NC birds (33.6%), phytase supplementation improved it up to 36.9%, 39.9% and 41.7% ($P<.05$). Higher phytase dosages resulted higher P retention (except in Trt 4) ($P<.05$). Ca retention was the same in all Trts ($P>.05$). The data show that supplementing 3-phytase from *Aspergillus niger* to corn-soybean based geese diets at levels between 150 and 450 FTU/kg increased their digestible P content ($P<.05$).

Key Words: digestibility, goose, phosphorous

T179 Genetic engineering of an *Escherichia coli* mutant phytase for thermostability does not affect the enzymatic efficacy in a diet for young pigs. L. E. Denmark, J. D. Weaver, K. R. Roneker, and X. G. Lei*, *Cornell University*, *Ithaca, NY*.

Previous protein engineering research in this laboratory has yielded an *Escherichia coli* AppA2 mutant phytase with improved thermostability and an *Aspergillus niger* PhyA mutant phytase with improved thermostability and pH profile. The objective of this study was to determine the effectiveness of these phytase variants in improving phytate phosphorus utilization by weanling pigs. A total of 40 pigs (5-week old, Yorkshire-Landrace-Hampshire crossbred) were fed a corn-soybean meal based basal diet (BD, without supplemental inorganic phosphorus) or the BD supplemented with the wild-type of AppA2, the AppA2 mutant, or the PhyA mutant at 300 U/kg of diet for four weeks. The phytase activity was assayed using the molybdenum blue method in 0.2 M citrate buffer, pH 5.5 with 5.4 mM sodium-phytate as substrate. Pigs (n = 10/treatment) were housed individually and had *ad libitum* access to feed and water. Daily feed intake and weekly body weight change of individual pigs were recorded, and blood samples of individual pigs were taken weekly to measure plasma inorganic phosphorus concentrations and alkaline phosphatase activity. Pigs fed the wild-type and the AppA2 mutant phytases had higher ($P < 0.01$) plasma inorganic phosphorus concentrations from week 2 through week 4 and lower ($P < 0.05$) plasma alkaline phosphatase activity in week 4 than did pigs fed the BD or the PhyA mutant. The latter two groups showed similar values in these measures. The overall growth performance of pigs was not affected by the dietary treatments. In conclusion, the AppA2 mutant phytase engineered for improved thermostability was as effective as the wild-type in releasing phytate-phosphorus from the diet for weanling pigs. The feeding performance of the PhyA mutant reinforces the difficulty in predicting nutritional value of recombinant enzymes.

Key Words: phytase, thermostability, pH

T180 The effects of lactose inclusion and seaweed sugars on performance, nutrient digestibility and microbial populations in newly weaned piglets. J. V. O'Doherty*, S. Dillon, J. J. Callan, and T. Sweeney, *University College Dublin*, *Belfield, Dublin 4, Ireland*.

A 2 x 2 factorial experiment was conducted to investigate the interactions between 2 different lactose levels (150 g/kg vs. 250 g/kg) and seaweed extract (containing laminarin and fucoidan) derived from Laminaria spp on growth performance, nutrient digestibility and fecal microbial population in the weanling pig. Two hundred and forty piglets were selected after weaning (24 days of age, 7.6 kg (s.d 0.9 kg) live weight) and blocked on the basis of live weight and within each block assigned to one of four dietary treatments. The piglets were offered the following diets ad-libitum for 25 days: 1) 150 g/kg lactose 2) 150 g/kg lactose plus seaweed extract; 3) 250 g/kg lactose; 4) 250 g/kg lactose plus seaweed extract. Piglets offered diets supplemented with seaweed extract had a higher average daily gain (ADG) (0.322 vs. 0.281 kg, s.e. ± 0.009) ($P<0.01$) and gain to feed ratio (0.669 vs. 0.611 kg/kg, s.e. ± 0.019) ($P<0.05$) between days 0-25 compared with piglets offered unsupplemented seaweed extract diets. Piglets offered high lactose diets had a higher ADG (0.319 vs. 0.283 kg, s.e. ± 0.009) ($P<0.05$) and average daily feed intake between days 0-25 (0.480 vs. 0.447 kg, s.e. ± 0.011) ($P<0.05$) compared with piglets offered the low lactose diets. The inclusion of seaweed extract increased ($P<0.001$) the apparent digestibility of nitrogen (N Dig) and gross energy (GE Dig) and decreased fecal E. coli populations compared with unsupplemented seaweed extract diets. Piglets offered the high lactose diets had increased GE dig ($P<0.001$) N dig ($P<0.05$) and decreased fecal E. coli populations compared with piglets offered low lactose diets. In conclusion, the inclusion of either a high dietary concentration of lactose or a laminarin-fucoidan extract increased daily gain and gain to feed ratio of post weaned piglets through an increase in nutrient digestibility and decreased E.coli populations in the gut.

Key Words: laminarin, fucoidan, piglet

T181 Screening based on antibacterial and phytase activities of lactic acid bacteria towards their use as a chicken probiotic supplement. H. R. Taheri*[1], H. Moravej[1], F. Tabandeh[2], M. Zaghari[1], and M. Shivazad[1], [1]*University of Tehran*, *Karaj, Tehran, Iran*, [2]*National Institute of Genetic Engineering and Biotechnology*, *Tehran, Iran*.

The objective of this research was to screen the lactic acid bacteria of the chicken digestive tract to identify a strain as a source of probiotic. This selection was carried out to find a strain with high antibacterial and phytase activities. A total of 62 strains of lactic acid bacteria of broiler origin were investigated for their use as a probiotic feed supplement. In vitro studies included antibacterial and phytase activities. Antibacterial activities were examined against *Salmonella enteritidis*, *Salmonella typhimurium* and *Escherichia col* O78:K80 by well diffusion assay, and the medium culture that contained calcium phytate was used for measuring the halo zone of phytase activity. Additionally, aggregation, co-aggregation, amylase, lipase and protease activities, cell surface hydrophobicity, growth with bile salts (ox gall) and tolerance to acidic pH of this strain were tested. Among all the isolates, strain LT171 was selected for high antibacterial and phytase activities. Also this strain had aggregation (90 min), amylase and protease activities, cell surface hydrophobicity (85%), and resistance to pH 3 and bile salts (0.075% in medium culture). This strain didn't show any co-aggregation, and lipase activity. This research showed that there is a strain with high antibacterial and phytase activities as a source of a chicken probiotic. Previous studies have not selected the final strain based on these characteristics. This strain could potentially be used as a feed additive.

Key Words: phytase activity, antibacterial activity, probiotic

T182 Effects of different pen types and dietary antibiotics on growth performance, immune response and diarrhea occurrence of weanling pigs. Y. S. Noh*, K. W. Kang, Y. H. Choi, S. K. Jang, Y. D. Jang, H. K. Oh, and Y. Y. Kim, *Seoul National University*, *Seoul, Korea*.

The objective of this experiment was to evaluate the effect of different pen types and dietary antibiotics on the growth performance, immune response and diarrhea occurrence of weanling pigs. The treatments were assigned according to a 2×2 factorial arrangement. The first factor was 2 levels of added dietary antibiotics (0 and 0.10%) and the second factor was different pen types (elevated pen and floor-slotted pens). Avilamycin was supplemented in antibiotic treatment diets. For the feeding trial, a total of 192 piglets, 24±2 d of age with initial body weight 7.90±0.25kg, were allotted to treatments by body weight and gender in a RCB design with 6 replicates and 8 pigs per pen. Until 3 weeks, floor-slotted pen treatments showed higher body weight ($P<0.05$, 10.32 vs. 11.18kg) and ADFI ($P<0.01$, 288 vs. 350g) than the elevated pen treatments. However, after 3 weeks, the elevated pen treatments showed significantly higher body weight, ADG ($P<0.01$, 610 vs. 510g) and ADFI ($P<0.01$, 938 vs. 807g) than the floor-slotted treatments. During the whole experimental period (0 to 5 weeks), ADFI was higher

in the elevated pen treatment compared to the floor-slotted pen treatment (P<0.01, 696 vs. 643g in ADFI). However, no differences were found in ADG and G:F ratio among all treatments. At 3 weeks the elevated pen treatments showed a lower diarrhea occurrence score (P<0.05, 3.2 vs. 3.7) compared to the floor-slotted pen treatment. The dietary antibiotics did not influence diarrhea score. Floor-slotted pen treatments at Wk 2 were significantly higher in serum IgG concentration (P<0.01, 0.9 vs. 2.0mg/ml). These results demonstrated that elevated pens were better than floor-slotted pens for improving growth performance and immune responses in weanling pigs.

Key Words: pen type, weaning pig, growth performance

T183 Evaluation of antimicrobial activity of organic acids against *Salmonella typhimurium* isolated from swine. M. R. Messina*[1], E. Grilli[1], S. Albonetti[2], and A. Piva[1], [1]*DIMORFIPA, University of Bologna, Italy*, [2]*DSPVPA, University of Bologna, Italy*.

Aim of the study was to investigate the antibacterial activity of organic acids against the serovar *typhimurium* of *Salmonella enterica* subsp *enterica* isolated from pig slurry. Organic acids (OA) tested were: citric, sorbic, malic, fumaric, benzoic, lactic, heptanoic and octanoic. A broth dilution assay was performed as follows: 96-wells microtiter plates were filled with 10^4 CFU of *Salmonella*/well and with each OA solutions at concentrations from 0.49 mM to 500 mM. The positive control wells were inoculated in the same way without the addition of any substance. Medium was buffered at pH 6.5 and plates were incubated at 37 °C. The turbidity of cultures after 24 hours was used as indicator of bacterial growth and evaluated by absorbance measurement at 630 nm. Optical density (OD) data were analyzed by ANOVA followed by a Dunnett post-test; Pearson correlation, and linear regression between the OD data and OA concentrations were also exploited. Compared to control, benzoic acid at 125 mM completely inhibited *Salmonella* growth ($P<0.01$), while other acids were effective at much lower concentrations in reducing the OD of *Salmonella* by -85% heptanoic acid and by -83% octanoic acid at 1.82 mM, by -92% sorbic acid at 50 mM ($P<0.01$); citric and malic acids reduced OD by -51% and -85% at 250 mM and 500 mM, respectively($P<0.01$). Fumaric and lactic acids did not significantly inhibit *Salmonella*. Linear regression analysis showed an interesting dose-effect for citric, malic, heptanoic and octanoic acid (R^2=0.99; R^2=0.98; R^2=0.94; R^2=0.91, respectively, $P<0.01$). The interaction and possible synergistic effect of these acids should be tested to improve their efficacy. Heptanoic, octanoic, sorbic, citric, malic, and benzoic acids showed strong antibacterial properties, and therefore could be regarded as useful instruments both as food preservatives as well as feed additives in animal nutrition against *Salmonella*.

Key Words: swine, *Salmonella*, organic acids

T184 Effect of Natuzyme supplementation on broiler performance in deficient standardized ileal threonine diets. S. Khalaji, M. Zaghari*, and M. Shivazad, *University of Tehran, Karaj, Iran*.

The objective of this study was to determine the effects of Natuzyme supplemention on broiler performance in a threonine deficient diet. Day-old male broiler chicks were randomly assigned to 20 battery cage pens in a completely randomized block design and grown to 6 wk of age. Birds were fed dietary treatments from 1 to 42 d of age. The 6 treatments were basal diets containing 0.56 and 0.46% standardized ileal threonine (SID Thr) in starter and grower periods, respectively. Treatments 2 to 6 were the basal diets supplemented with 0.1, 0.2, 0.3, 0.4 and 0.5 g/kg Natuzyme. Body weight and feed intake of birds were recorded at 28 and 42 d of age. In vivo lymphoproliferation of birds against Phytohemagglutinin-P (PHA-P) was measured at 36 d of age. Data was analyzed using the GLM procedure of SAS. Means were compared by Duncan`s multiple range test. Supplementing diets with Natuzyme significantly (P<0.001) improved feed conversion ratio (FCR) at 28 and 42 d of age. The effect of Natuzyme on body weight was significant (P<0.05) at 28 d of age but it had no effect on body weight at 42 d of age. In vivo lymphoproliferation against the Phytohemagglutinin-P (PHA-P) at 36 d of age significantly (P<0.05) increased with supplementation of Natuzyme. There were no significant differences in breast, thigh and abdominal fat at 42 d of age. These results showed that Natuzyme improved the efficiency of broilers fed a low threonine diet during the starter period.

Key Words: Natuzyme, threonine, broiler performance

Nonruminant Nutrition: Nutrients

T185 Effects of protein and sulfur AA concentration in diets fed to weanling pigs on growth performance and diarrhea incidence. T. C. S. Reis*[1], G. Mariscal-Landin[2], P. E. Urriola[3], and H. H. Stein[3], [1]*Universidad Autonoma de Queretaro, Queretaro, Mexico*, [2]*INIFAB CENID Fisiologica, Queretaro, Mexico*, [3]*University of Illinois, Urbana*.

A 3-wk experiment was conducted to measure the effect of dietary CP, Met, and Cys levels on pig growth performance, and incidence (ID) and severity of diarrhea (SD) during the post-weaning period. Sixty pigs were weaned at 23.9±3.6 d of age (initial BW: 7.48±0.50 kg) and allotted to 4 treatment groups based on sex, litter of origin, and BW. There were 3 pigs per pen and 5 pens per treatment. Four antibiotic-free diets were formulated. The HCP diet contained 23.58% CP, 0.34% Met, and 0.33% Cys. The LCP diet contained 17.64% CP, 0.25% Met, and 0.26% Cys. The HMet diet contained 16.95% CP, 0.32% Met, and 0.24% Cys. The HCys diet contained 17.68% CP, 0.26% Met, and 0.49% Cys. The ID was the number of days where diarrhea was observed within a pen. The SD was based on a daily visual fecal consistency score on a scale of 0 to 3. Results showed that for the entire 21-d period, no differences in ADG or ADFI were observed among treatments. However, G:F were greater ($P < 0.01$) for pigs fed the HCP diet (0.656 kg/kg) than for pigs fed the LCP (0.501 kg/kg), the HMet diet (0.495 kg/kg), or the HCys diet (0.479 kg/kg). The ID in wk 1 was greater ($P < 0.01$) in pigs fed the HCP diet (4.6 d) than in pigs fed the other diets (2.0, 2.0 and 2.0 d, for LCP, HMet, and HCys diets, respectively). In week 2 and 3, no differences among diets were observed for ID. Pigs fed the HCys diet had lower ($P < 0.05$) ID (6.4 d) over the entire period than pigs fed the HCP diet (15.2d). The SD was greater ($P < 0.01$) in pigs fed the HCP diet during wk 1 than for pigs fed LCP, HMet, and HCys diets (0.94, vs. 0.34, 0.37, and 0.32, respectively). In wk 2, no differences in SD among treatments were observed, but pigs fed the HCys diet had the lowest ($P < 0.05$) SD in wk 3 (0.31) and over the entire period (0.33) compared with pigs fed the HCP, the LCP, and the HMet diets (1.17, 0.57, 0.66, and 1.04, 0.53, 0.55, respectively). In conclusion, pigs fed a HCP diet gained weight more efficiently, but had also greater incidence and severity of post-weaning diarrhea than pigs fed LCP, HMet, or HFCys diets. High levels of Cys in the diet reduce post-weaning ID and SD.

Key Words: pigs, diarrhea, dietary CP

T186 Effect of the degree and duration of early dietary amino acid restrictions on subsequent and overall pig performance and physical and sensory characteristics of pork. R. B. Kamalakar*, L. I. Chiba, K. C. Divakala, S. P. Rodning, E. G. Welles, W. G. Bergen, C. R. Kerth, D. L. Kuhlers, and N. K. Nadarajah, *Auburn University*, *Auburn, AL*.

The objective of this study was to investigate the effect of the degree and duration of early dietary AA restrictions on subsequent and overall pig performance and physical and sensory traits of pork. For the grower (G) and finisher-1 (F1) phases, 3 corn-soybean meal diets were formulated to contain 100, 80, or 60% of the 1998 NRC total Lys recommendations (100G, 80G, or 60G, and 100F1, 80F1, or 60F1, for the G and F1 phases, respectively). A common finisher-2 (F2) diet was used. Thirty gilts and 30 barrows (22.7 kg; 2 gilts or 2 barrows/pen) were randomly assigned to 5 diet combinations (100G-100F1, 80G-100F1, 80G-80F1, 60G-100F1, and 60G-60F1), and pigs were switched to F1 and F2 diets at 50.7 and 79.9 kg, respectively. The LM samples were collected at 110.7 kg. Pigs fed the 60G diet had lower ($P \leq 0.05$) ADG during the G phase and greater ($P \leq 0.05$) ultrasound backfat (UBF) at the end of the G phase than those fed the 100G diet. Although serum total protein (TP) and albumin concentrations in pigs fed the 60G-100F1 diets were lower ($P \leq 0.05$) than those fed the 100G-100F1 diets at the end of the G phase, TP and UBF at the end of the F1 phase and ADG during the F1 phase were similar between the 2 groups. Feeding the 80G diet resulted in decreased ADG during the G phase but no differences in ADG during the F1 and F2 phases and UBF between pigs fed the 80G and 100G diets. Overall, pigs fed the 80G-80F1 diets had similar ADG but less ($P \leq 0.05$) fat-free lean gain (LG) and TP and albumin throughout the study than those fed the 100G-100F1 diets. Pigs fed the 60G-60F1 diets had lower ($P \leq 0.05$) overall ADG and G:F and less ($P \leq 0.05$) LM area and LG but a higher ($P \leq 0.05$) marbling score than those fed the 100G-100F1 diets. In summary, pigs fed the 80G-80F1diets may have exhibited compensatory growth in ADG but not in terms of LG. The ADG and carcass traits of pigs fed the 60G-60F1 diets were depressed, indicating that the restriction may have been too severe or too long or both. Early dietary AA restrictions had no clear effect on physical and sensory traits of pork.

Key Words: amino acid restrictions, pork, pig

T187 Apparent ileal digestibility of CP and amino acids in pigs fed sorghum-soybean meal diets supplemented with phytase. M. Cervantes*[1], E. Sánchez[1], A. Morales[1], A. Araiza[1], W. Sauer[1], M. Barrera[1], and J. Yáñez[2], [1]*ICA, Universidad Autónoma de Baja California, Mexicali, BC, México*, [2]*Universidad Autónoma de Tlaxcala*, *Tlaxcala, México*.

An experiment was conducted to evaluate the effect of supplementing phytase to sorghum-based diets on the apparent ileal digestibility (AID) of CP and amino acids (AA). Twelve pigs (average initial BW 18.6 kg) fitted with a simple T-cannula at the distal ileum were fed six diets in a repeated 6×6 Latin square design. Diet 1 was the positive control (PC), sorghum-soybean meal diet, with supplemental inorganic P. Diet 2 was the negative control (NC), sorghum-soybean meal diet, with no supplemental inorganic P. Diets 3, 4, and 5 were the NC diets supplemented with phytase A at 250, 500, and 1000 units of phytase activity (FTU/kg diet), respectively. Diet 6 was the NC diet supplemented with 500 FTU of phytase B per kg. All diets were added with vitamins and trace minerals, as well as chromic oxide as a digestibility marker. Five contrasts were constructed as follows: C1, NC vs. PC diet; C2, NC vs. diets added with phytase A, C3, Linear effect; C4, Quadratic effect; C5, Phytase A vs. B, at 500 FTU/kg. The AID values (%) for CP and AA in Diets 1 to 6 were: CP, 64.5, 69.8, 69.7, 68.3, 67.2, 69.2; Arg, 85.8, 86.2, 88.0, 86.5, 86.3, 86.6; His, 78.1, 79.5, 80.0, 78.7, 77.6, 78.0; Ile, 74.1, 76.9, 77.7, 76.4, 75.9, 78.0; Leu, 76.3, 78.4, 79.1, 77.9, 77.2, 79.5; Lys, 83.1, 85.0, 86.2, 85.1, 85.0, 86.1, Met, 75.6, 79.0, 79.4, 79.1, 78.0, 80.2; Phe, 76.7, 78.8, 80.0, 78.5, 78.1, 80.0, Thr, 69.0, 72.3, 74.1, 72.8, 70.9, 73.5; Val, 68,5, 70.3, 72.4, 71.1, 69.5, 71.9. The AID of CP in the PC was higher ($P < 0.01$) than in the NC, but there was no difference in the AID of AA. There was no effect of phytase supplementation, at any level, on the AID of CP and AA ($P>0.10$). There was no difference between phytase A and B. These data indicate that phytase supplementation to sorghum-based diets had no effect on the digestibility of protein and amino acids in growing pigs. These also indicate that the supplementation of inorganic P reduces the AID of CP and some AA

Key Words: pigs, phytase, amino acids

T188 Effects of low-CP feeding on growth, nutrient utilization and manure odor in weanling pigs. M. Z. Fan*, T. Archbold, Z. R. Wang, and C. Yang, *University of Guelph*, *Guelph, Ontario, Canada*.

The objectives of this study were to examine effects of low-protein feeding on growth performance, efficiency of dietary N and P utilization, carcass fat content and fecal total volatile sulfides in weanling pigs fed corn and SBM-based diets. The study was conducted with 36 Yorkshire weanling barrows of average initial and final BW of 9.6 and 12.9 kg and the pigs were fed six diets according to a completely randomized block design. The six diets were corn and SBM-based, including diets 1-4 with graded declining levels of total CP (diet 1, control, 18.5; diet 2, 17.5; diet 3, 16.5; and diet 4, 15.5 CP%) plus diet 5 (15.1% CP+5% cellulose), and diet 6 (15.1% CP+extra crystalline L-Leu). Chromic oxide (0.30%) was included as a digestibility marker. Each experimental period consisted of 15 d with 10-d adaptation and 5-d collection of representative fecal and urinary samples. Reduction in CP content from 18.5 to 15.5% did not have effects ($P>0.05$) on performance endpoints. A reduction in net energy content of the low-CP diet with 5% cellulose (diet 5) did not affect ($P>0.05$) the growth performance endpoints. While 5% cellulose supplementation (diet 5) reduced total fecal sulfide excretion, it also decreased ($P<0.05$) dry matter digestibility. Fortification of the low-CP diet with L-Leu (diet 6) did not affect ($P>0.05$) the growth performance endpoints. The reduction of dietary CP content in 3% did not affect ($P>0.05$) carcass fat content. Decreases in dietary CP levels had a linear positive effect ($P<0.05$) on efficiency of apparent CP retention with optimal responses observed in diets 3 and 4. Both cellulose supplementation and L-Leu fortification reduced ($P<0.05$) efficiency of apparent P retention. In summary, a reduction of dietary CP content at 3% of the NRC (1998) recommended level through use of crystalline limiting essential AA can significantly improve efficiency of N utilization and reduce manure N excretion by up to 20% of the conventional diet without negatively affecting performance, carcass fat content, as well as manure sulfide and P excretions in weanling pigs fed corn and SBM-based diets.

Key Words: dietary protein, nutrient utilization, weanling pigs

T189 Effects of NCG or Arginine on immune function of intestinal mucosa in weaning period of piglets. X. Wu, Y. Gao, Y. Yin*, X. Zhou, R. Huang, Z. Tang, M. Geng, and T. Li, *Laboratory of Animal Nutritional Physiology and Metabolic Process, Institute of Subtropical Agriculture, the Chinese Academy of Sciences*, *Changsha, China*.

The aim of this study was to assess the effects of N-Carbamylglutamate (NCG) and L-Arginine (Arg) on immune function of the intestinal mucosa in early-weaned piglets. Eighty-nine healthy Landrace×Yorkshine piglets weaned at 21 d (average pen weight 5.56±0.51 kg) were randomly divided into 3 treatments, supplying with one of the following diets for 7 days: a standard diet (SD), SD+NCG (0.08%), or SD+Arg (0.6%), respectively. Six piglets were selected from each treatment randomly for serum samples. Then the selected piglets were slaughtered for intestinal and mucosa samples. Results showed that Serum IgM concentration in the NCG group was lower than that of the Arg group (P<0.05). Both arginine and NCG increased IEL counts along the villous mucosal epithelium of the ileum significantly (P<0.05), compared with control piglets. However, IEL counts were similar between the three groups in the duodenum and jejunum. Western blotting further confirmed that CD4 expression was higher in the ileum mucosa (P<0.05), and had a high trend in jejunum (P>0.05) in the Arg and NCG group. Also, the results showed that NCG increased TNF-α in jejunum and ileum mucosa (P>0.05). The results indicated that dietary supplementation with 0.08% NCG or 0.6% Arg could improve immune function of intestinal mucosa in weaning period of piglets. *Supported by NSFC, CAS.*

Key Words: N-Carbamylglutamate, L-Arginine, intestinal mucosa

T190 Effect of varying levels of metabolizable energy and crude protein in phytase-supplemented diets on nitrogen retention and growth performance in young pigs. M. J. M. Almeida, E. T. Fialho*, J. A. F Lima, P. B. Rodrigues, V. S. Cantarelli, and H. O. Silva, *University Federal of Lavras*, *Lavras-MG-BRAZIL-Financed By FAPEMIG*.

A study was conducted to evaluate the effects of different levels of metabolizable energy (ME) and crude protein (CP) in diets formulated according to the ideal protein concept and supplemented with phytase (Natuphos®) on growth performance in piglets. A total of 84 barrows and gilts with initial BW 15.3 ± 1.2kg were blocked by weight and sex and randomly allotted to one of seven treatments. There were two pigs (one barrow and one gilt) per pen and six pens per treatment. Pigs were fed corn and soybean meal based diets formulated according to ideal protein concept. The treatments were in a 3x2+1 factorial arrangement with three ME levels (3080, 3230 and 3380 kcal ME/kg) and two CP levels (14% and 16% ; diets were supplemented with synthetic amino acids and phytase (750 U/Kg) and with calcium levels decreased by 25% and phosphorus decreased by 30%. The additional treatment was formulated on the basis of CP and no phytase to meet the nutrient requirements of piglets according to NRC (1998). Diets and water were available ad libitum for 25 d. Throughout the experiment, there were no energy or CP treatment effects (P > 0.05) on body weight as well as ADG, F:G, daily ME intake, or on weight of organs (heart, kidney, liver, muscle, and spleen) for the piglets. Feed intake was lower (P<0.05) and fat deposition rate in the carcass was higher (P< 0.05) for the levels of 3380 kcal ME/kg. The control diet without phytase supplementation yielded a higher blood urea content and an increased (P<0.05) nitrogen, calcium and phosphorus excretion in pigs as compared to the phytase-supplemented diets with 14% CP. In conclusion, the levels of ME, CP and lower P and Ca content on diets can be reduced to 3080 Kcal/kg, 14% , 0.54% and 0.28%, respectively for piglets in diets based on ideal protein concept with supplementation of phytase, since better growth performance and lower nitrogen, calcium and phosphorus excretion is shown in piglets from 15 to 30 kg.

Key Words: amino acids, enzyme, ideal protein

T191 The effects of reduction in protein and phosphorus in finishing broiler chicken diets supplemented with phytase. Y. L. Silva, P. B. Rodrigues, E. T. Fialho*, R. T. F. Freitas, and A. G. Bertechini, *University Federal of Lavras*, *Lavras, MG, Brazil*.

A study was conducted to evaluate the growth performance, carcass characteristics and nutrient levels in litter of broiler chickens from 22 to 42 days old fed low-Crude Protein (CP) and low available Phosphorus (AP) diets supplemented with synthetic amino acids (AA) and phytase. A total of 1200 male broiler chickens (Cobb, 21 days of age,initial weight of 646+ 8 g) were fed diets based on corn-soybean meal . Chicks were fed in a randomized block design with six replicates (20 birds per pen). Treatments were arranged as a 3 × 3 +1 factorial with main effects of CP (14, 16 and 18%) and levels of AP (0.20, 0.30, and 0.40%) and a control diet with nutritional requirements according to (NRC, 1994). In the diets with 0.20 and 0.30% AP, were added 500 FTU of phytase (Natuphos® 5000) and the Ca requirement level was lowered 20% when phytase was added. The broilers fed diets with 14% CP and 0.20% AP + phytase had lower weight gain (P<0.05) and better feed conversion (P<0.05) in relation to those fed the control diet. The performance of the broilers fed diets with 14% CP and 0.30% AP + phytase were similar (P>0.05) in relation to those fed the control diet. The P content in litter was lower for the broilers fed low-CP and low AP diets supplemented with synthetic amino acids and phytase. The Ca content in litter was lower for broilers fed diets with 16% CP at all levels of AP than those fed the control diet. There were no differences (P>0.05) among diets for N, Zn and Cu in the litter. No differences (P>0.05) in carcass yield were observed for broilers fed diets with low-CP and low AP supplemented with synthetic AA and phytase compared to those fed the control diet. In conclusion, dietary CP, AP and Ca can be reduced 27.8, 25.0 and 19.5%, respectively when synthetic amino acids and phytase are added to the diet while performance and carcass characteristics are maintained.

Key Words: additive, environmental, enzyme

T192 Intestinal absorption of vitamin B_{12} in growing pigs. D. Prévéraud[2,1], C. L. Girard[1], F. Guay[2], N. LeFloc'h[3], and J. J. Matte*[1], [1]*Dairy & Swine R & D Centre. Agriculture & Agri-Food Canada*, *STN-Lennoxville, Sherbrooke, QC, Canada*, [2]*Laval University*, *Quebec City, QC, Canada*, [3]*UMR 1079 SENAH, INRA*, *St-Gilles, France*.

There are few data on the bioavailability of dietary vitamin B_{12} for pigs. The aim of the present project was to estimate intestinal absorption of this vitamin using the measurement of portal flux after ingestion of dietary supplements. Eleven pigs (35.1 ± 4.0 kg BW), fed a B_{12} free diet from weaning at 21 d of age, were surgically equipped at 75.4 ± 5.9 d of age with catheters in the portal vein and carotid artery; an ultrasonic flow probe was also installed around the portal vein. According to a cross-over design, pigs received 3 doses of dietary vitamin B_{12}: 0, 25 and 250 µg in 1.2 kg of a vitamin-free semi-purified diet (<1.4 µg of vitamin B_{12}). Blood samples were collected simultaneously from the 2 catheters before meal, every 45 min for the first 3 h post-feeding, and every hour for the following 21 h. Portal blood flow was recorded continuously for 24 h. The total amount of vitamin B_{12} reaching the portal circulation during the 24 h post-feeding was the cumulation of portal net flux of vitamin B_{12}

at each sampling time multiplied by the time interval between samples. Portal concentrations of vitamin B_{12} were stable at 130.1 ± 1.0 pg/mL during the whole post-meal period with 250 µg while post-meal values for 25 and 0 µg were 7.2 and 27.0% lower than pre-meal concentration (treatment × time, P<0.01). Changes in portal net flux during the 24 h post-meal showed that most of the absorption occurred between 5 and 14 h post-feeding with 25 and 250 µg of vitamin B_{12} but another period of absorption was observed from 15 to 18 hours with 250 µg. The total amount of vitamin B_{12} reaching the portal circulation during the 24 h post-feeding differed among treatments (P=0.02); the value was higher (P≤0.03) for 250 µg (6.0 ± 1.2 µg) than for 25 (2.1 ± 1.2 µg) and 0 µg, the latter was not different from zero (P=0.32). Therefore, although the absolute amount of vitamin B_{12} reaching portal blood increased with the dose ingested, the proportion of oral intake followed an opposite trend, from 8.5 to 2.4% for 25 and 250 µg, respectively. The peculiar kinetic of vitamin B_{12} absorption as compared to other nutrients deserves further investigations

Key Words: vitamin B_{12}, absorption, pig

T193 Multivariate nonlinear mixed effect models for protein and lipid deposition in growing pigs. A. B. Strathe*[1] and E. Kebreab[2], [1]*University of Copenhagen, Copenhagen, Denmark*, [2]*University of Manitoba, Winnipeg, Manitoba, Canada*.

Dealing with animal to animal variation in utilization of dietary energy is a key determinant in predicting efficiency of whole pig production units. Recently, stochastic simulation models for pig growth have been constructed to address this issue. Parameterization of these models required determination of both mean values and the variation around the mean in key metabolic parameters. In this study a novel multivariate energy deposition model (protein (PD) and lipid deposition (LD) as dependent variables) was developed. It was assumed that PD was a quadratic function of the metabolic size of the pig. The parameters in the simple function could be expressed in terms of the inflexion point i.e. the maximum rate of PD (PDmax) and corresponding BW (BWPDmax) at that point. The LD was equated as the difference between ME intake and the sum of ME used for maintenance and ME for PD which was used with efficiency kf. NLMIXED procedure in SAS was used for parameter estimation, where the general option in the model statement was implemented to specify a conditional multivariate normal distribution for the PD and LD data given the random effects. The approach was applied to energy balance data collected from 48 barrows, where each balance was determined 8 times for each pig. Variance components ($\sigma PDmax^2$ and $\sigma kf2$) for the traits PDmax and kf and their correlation (ρ) were estimated and are reported as standard deviations because their units match the parameter dimension. The values were 11.4 (g/d), 0.06 and -0.02 σPDmax σkf and ρ, respectively. The correlation was not significantly different from zero (P = 0.73). For purposes of stochastic simulation modeling, these traits may be assumed independent which simplifies construction and execution of the model.

Key Words: nonlinear mixed model, protein deposition, pigs

T194 Impacts of zinc and arginine in the piglets diets at weaning on inflammatory reaction and antioxidant potential. N. Bergeron*, A. Hudon-Thibault, M. Roy, and F. Guay, *Université Laval, Québec, QC, Canada*.

The objective of this experiment was to evaluate the effects of dietary zinc (ZN) and arginine (ARG) supplementation on oxidative and inflammatory status of weaning piglets. Thirty-two weaned piglets were allotted in a completely randomized block design with dietary ZN (0 vs 2500 mg/kg) and ARG (0 vs 1%) supplementation as main factors. The 4 diets were the following: control (standard post-weaning diet), ZN2500, ARG1 and ZN2500ARG1. The piglets were assigned to 1 of the 4 diets, maintained individually in pen and fed 3 times per day for a period of 12 days. At the end of the feeding period, blood samples were taken before (T0) and 3 hours following (T1) an intraperitoneal injection of LPS (10 mg/kg BW) in order to assess the inflammatory reaction (Tumour Necrosis Factor (TNF), Prostaglandin E2 (PGE) and Nitric Oxide (NO)) and antioxidant response (Malondialdehyde (MDA), Ferric Reducing Ability of Plasma (FRAP) and Superoxide Dismutase (SOD)). The piglets fed ZN supplemented diets had lower MDA at T0 (P<0.001) but not at T1. At T1, FRAP increased in piglets fed ARG supplemented diets (P<0.05) especially if ZN was added (ZN*ARG, P<0.07). ZN supplementation reduced SOD activity at T1 (P<0.05), especially when the ARG was added (ZN*ARG, P<0.07). No difference was noted at T0 for FRAP and SOD activity. PGE tended to be increased in piglets fed ARG diets (P<0.07) at T1. The piglets fed ZN supplemented diets had higher TNF at T1. At T0, no difference was noted for PGE and TNF. For NO, no difference was noted at T0 and T1. However, ratio T1/T0 for NO tended to be increased in piglets fed ARG supplemented diets (P<.06). In summary, the present results showed that ZN and ARG did not reduce inflammatory reaction in peripheral blood circulation at T0 and T1. In fact, ZN increased TNF and ARG increased NO and PGE at T1. However, ZN and ARG had a synergistic effect on improvement of antioxidant status in inflammatory conditions.

Key Words: antioxidant, inflammatory reaction, zinc arginine

T195 Meta-analytic study of phosphorus excretion in pigs. R. S. Dias*[1], J. Chen[1], J. Ellis[1], E. Kebreab[2], S. Lopes[3], D. M. S. S. Vitti[4], M. Fan[1], and J. France[1], [1]*University of Guelph, Guelph, Ontario, Canada*, [2]*University of Manitoba, Winnipeg, Manitoba, Canada*, [3]*Universidad de Leon, Leon, Leon, Spain*, [4]*Centro de Energia Nuclear na Agricultura, Piracicaba, Sao Paulo, Brazil*.

Many studies have been carried out to better understand the factors affecting P excretion in pigs in an attempt to search for more efficient ways of minimizing its detrimental effects on the environment. The large amount of data available allows researchers to use meta-analysis as a tool to synthesize results from several studies. In the present work, initially 69 studies were assembled and used in a meta-analysis to generate different information related to phosphorus excretion in pigs. The database contained information on diet, feed intake, P intake, P excretion and weight of pig. First all data were assessed to determine which are the most important dietary features affecting P excretion in pigs. The meta-analysis was performed using 190 data points resulting in the following model: P feces (g/kg of BW $^{0.75}$.d) = 0.00002 phytase × phytate + 0.33 P – 0.05 Ca/P + 0.14, with all parameters significant. For a second analysis, a subset of the data (total 27 studies and 71 data points) containing only values of P excreted in feces of animals that were not fed phytase was selected and the following linear model was elicited: P feces (g/kg of BW $^{0.75}$.d) = 0.4 P intake + 0.07. Further, the model was validated using data from another 27 studies. The predicted values were strongly related to measured values as shown by MSPE (mean square prediction error) analysis. The bulk of MSPE was due to random variation in the data set. According to the linear model when P intake is zero endogenous P in feces is 70 mg/kg of BW $^{0.75}$.d, a value that agrees with the literature. The first model indicates that P, Ca/P and the interaction between phytate and phytase present in the diet affect

P excretion in feces of pigs. The linear model presented may be used to predict P excretion in pigs when P ingested is given and no phytase is added to diet.

Key Words: phosphorus excretion, pigs, meta-analysis

T196 Effects of dietary lactose levels during different starter phases on the performance of weanling pigs. J. S. Kim, Y. X. Yang, K. Yun, J. Y. Choi, P. L. Shinde, and B. J. Chae*, *College of Animal Life Sciences, Kangwon National University*, *Chuncheon, Republic of Korea*.

Two experiments were conducted to evaluate dietary lactose levels during different starter phases on growth performance, nutrient digestibility and fecal microbial populations. In Exp. 1, 192 weanling pigs (Landrace × Yorkshire; 21 ± 2 d of age; 6.94 ± 0.97 kg) were used and allotted by a 2 × 2 factorial arrangement to test the effects of dietary lactose levels and different starter feeding programs (FP). Phase I diets containing two levels of lactose (low, 15 and high, 25%) were prepared, then the same phase II and phase III diets were used containing 10% and 0% lactose, respectively. Phase I, II, III diets were provided for wk 1, wk 2 to 3, and wk 4 to 5 for FP 1 and for wk 1 to 2, wk 3, and wk 4 to 5 for FP 2, respectively. Pigs fed high lactose diets had improved ADG, ADFI and better nutrient digestibility at the end of wk 1 and 2 of the experiment. Also, increased fecal *Lactobacillus* spp. (d 7 and 14, P < 0.05) and reduced coliforms (d 7, P = 0.049) were noticed in pigs fed high lactose diets. Experiment 2, involved 192 weanling pigs (Landrace × Yorkshire; 28 ± 3 d of age; 9.57 ± 0.79 kg) in a 2 × 2 factorial design similar to Exp. 1 and the same phase I, II and III diets were used. For FP 1, phase I, II, III diets were provided for wk 1, wk 2, and wk 3 to 5 and for FP 2, phase I, II, III diets were provided for wk 1, wk 2 to 3, and wk 4 to 5, respectively. Improved ADG (P = 0.001), ADFI (P = 0.003), and nutrient digestibility (P < 0.001) at the end of 1 wk were noticed in pigs fed high lactose diets. In addition, pigs fed high lactose diets had higher fecal *Lactobacillus* spp. on d 7 (P = 0.007) and d 14 (P = 0.054) than pigs fed low lactose diets. In both the experiments, the FP had no effect on the performance, nutrient digestibility and fecal microflora except for increased fecal *Lactobacillus* spp. on d 14 (P = 0.013) in pigs of FP 2 in Exp. 1.These results demonstrated that improved performance could be obtained by including 25% lactose during the initial two weeks post-weaning in pigs weaned at 21 d of age and during the first week post-weaning in pigs weaned at 28 d of age, respectively.

Key Words: starter feeding program, lactose, weanling pigs

T197 Effect of lysine levels in gestating and lactating diets on reproductive performance of sows and their progeny. J. S. Chang*[1], H. F. Long[2], L. G. Piao[2], W. S. Ju[2], Y. D. Jang[2], and Y. Y. Kim[2], [1]*CJ Cheiljedang Corporation*, *Seoul, Korea*, [2]*Seoul National University*, *Seoul, Korea*.

The objective of this experiment was to investigate the effect of dietary lysine levels in gestation and lactation diets on the reproductive performance of sows and their progeny. Two experiments were conducted using 4 different levels of lysine in each diet for the gestation and lactation periods, respectively. Exp. 1 was conducted during gestation and treatments were: 1) GA - diet contained 0.49% lysine, 2) GB - diet contained 0.62% lysine, 3) GC - diet contained 0.74% lysine, and 4) GD - diet contained 0.86% lysine. Exp. 2 was conducted during lactation and treatments were: 1) LA - diet contained 0.76% lysine, 2) LB - diet contained 0.90% lysine, 3) LC - diet contained 1.03% lysine, and 4) LD - diet contained 1.16% lysine. All other nutrients met or exceeded NRC (1998) requirements. A total of 43 F1(Yorkshire × Landrace) sows, with initial body weight 210.9 ± 7.7kg, were allotted in 4 treatments with replicates by body weight, backfat thickness and parity in a completely randomized design. After Exp. 1, sows were reallotted to treatments for Exp. 2. In Exp. 1, no significant differences were observed in body weight and backfat thickness due to dietary lysine levels. At farrowing, no statistical difference was found in litter size among dietary treatments. For the first week of Exp. 2, the body weight of sows tended to decrease linearly with increasing dietary lysine levels (P=0.092, 13.59, 12.18, 9.61 and 10.15 kg for LA, LB, LC and LD, respectively). For the third week of Exp. 2, ADFI of sows was decreased quadratically by increasing lysine levels (P<0.05, 8.21, 7.36, 7.27 and 7.93 kg for LA, LB, LC and LD, respectively). However, there were no significant differences in litter weight and litter weight gain among all treatments during lactation. Consequently, these results demonstrated that dietary lysine levels in lactation influenced ADFI, body weight and backfat thickness of sows but gestating sows were not affected by different lysine levels.

Key Words: lysine level, sow, reproductive performance

T198 Effect of betaine partially replacing dietary methionine on nutrient digestibility and on serum metabolites and enzymes of broiler chickens. H. Sun[1], W. R. Yang[1], Y. Wang[2], Z. B. Yang*[1], S. Z. Jiang[1], and G. G. Zhang[1], [1]*Shandong Agricultural University*, *Tai-an, Shandong, P.R. China*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, P.O. Box 3000*, *Lethbridge, AB, Canada*.

Studies showed inconsistent animal production response to partial replacement of dietary methionine (Met) by betaine (BET). Effect of BET supplementation on nutrient digestibility and metabolism is rarely determined. A total of 900 day-old AA broiler chicks were fed three corn-soybean meal-based starters (d 1-21) and growers (d 22-42). Dietary treatments were: Diet 1, Met content at the recommended level (4.8 (starter) and 4.0 (grower) g/kg DM); Diet 2, Met level at 85% of the Diet 1 with BET supplementing at the rate of 400 (starter) or 300 (grower) mg/ kg DM; Diet 3, Met level at 75% of the Diet 1 with BET supplementing at 600 (starter) or 500 (grower) mg/kg DM. The broilers were raised in nine pens (100 birds/pen, 3 pens/treatment) in a temperature controlled house with continuous lighting. Chicks were fed for *ad libitum* intake, had free access to water and weighed weekly. Nutrient digestibility was determined (6 birds per diet in individual metabolic cages) by excreta collection for three days at the end of the feeding experiment. Concentrations of metabolites and enzyme activity in the serum were measured on d 21 and 42. All broilers had similar ADG, ADFI or G:F in each period or during entire feeding experiment. Broilers consuming Diet 3 had higher (P < 0.05) apparent digestibility of CP and ether extract than broilers consuming Diets 1 and 2, whereas all broilers had a similar digestibility for DM or GE. Compared to Diet 1, broilers fed Diet 3 had lower (P < 0.05) concentrations of low density lipoprotein-cholesterol at d 21 and 42, uric acids and triglyeride, but higher (P < 0.05) high density lipoprotein-cholesterol at d 42 but not d 21. Broilers fed Diet 3 also had higher (P < 0.05) activity of serum alkaline phoaphatase and lactate dehydrogenase, but lower (P < 0.05) activity of creatine kinase than that fed Diet 1, whereas activity of spartate aminotransferase and alanine aminotransferase were similar among treatments. The results demonstrated that BET can replace up to 25% of total Met in the diet that was formulated to meet the requirement based on the Feeding Standard of China.

Key Words: broilers, betaine, digestibility

T199 Effects of decreased levels of crude protein in nursery diets on growth performance and diarrhea occurrence of pigs weaned at 21 days. C. J. Girotto Jr.*, F. F. Barbosa, P. F. Campos, P. C. Brustolini, and J. V. Moutinho, *Federal University of Viçosa*, *Viçosa, Minas Gerais, Brazil*.

A 21-d experiment with 126 pigs was conducted to evaluate growth performance and diarrhea occurrence of nursery pigs fed different levels of crude protein. Pigs (6.05 ± 0.35 kg of initial weight) were allotted in pens with three pigs each on day 21 after weaning, with six treatments, and seven blocks on a randomized blocks experimental design. The treatments were six corn-soybean meal based diets with decreased levels of crude protein (24%; 23%; 22%; 21%; 20%; and 19%). Increased levels of synthetic amino acid were added to the diets in order to keep the ratio between lysine and each one of the following amino acids constant (methionine + cystine, threonine, tryptophan, valine, and isoleucine). The performance results are presented in the Table 1. Decreasing levels of crude protein from 24% to 19% did not influence average daily feed intake (P>0.05), feed:gain (P>0.05) or carcass weight (P>0.05) but increased linearly (P<0.05) weight at 42 days of age of the pigs. Decreasing levels of crude protein also did not influence (P>0.05) the diarrhea occurrence. In summary, decreasing levels of crude protein in nursery diets from 24% to 19% did not affect ADFI, F:G, carcass weight, and diarrhea occurrence but improved weight at 42 days of pigs weaned at 21 days.

Table 1 – Performance of pigs weaned at 21 days of age fed decreased levels of crude protein.

	Treatments							
Parameters	24	23	22	21	20	19	Mean	CV%
Weight, lb (21d)	13.73	13.75	13.68	13.70	13.62	13.59	13.68	4.05
Weight, lb (42d)1	30.27	30.12	30.34	31.68	31.68	31.28	30.89	12.69
ADG (g/d)	375	354	358	386	385	361	370	13.56
ADFI (g/d)	450	490	460	480	510	510	483	12.43
F:G	1.23	1.40	1.24	1.26	1.31	1.39	1.31	10.85
Carcass weight, lb	20.67	20.33	20.89	21.33	22.25	21.48	21.15	21.08

[1] Linear effect (P<0.05)

Key Words: crude protein, diarrhea, weaning

T200 Effects of decreasing nutrient density of diet on Cu and nutrient absorption in ileal tissue of broilers. B. E. Aldridge* and J. S. Radcliffe, *Purdue University*, *West Lafayette, IN*.

Ileal tissue was harvested from 15 male broiler chickens and mounted in modified Ussing chambers to investigate the effect of a reduced plane of nutrition on active Cu absorption from a Cu proteinate and $CuSO_4$, as well as from Glucose, Phosphorus, Carbachol and Gly-Sar. Seven birds were fed a corn-SBM based, 20% CP diet, and 8 birds were fed a reduced nutrient density diet by diluting the 20% CP diet with 50% cellulose for three days prior to euthanasia. Ileal tissue was removed and used in duplicates on days 16-23 in modified Ussing Chambers. All tissue were challenged with Glucose, Phosphorus or Carbachol, but only one piece of tissue (plus duplicate) was challenged with either $CuSO_4$ or Cu proteinate or Gly-Sar (indicative of dipeptide uptake).Active uptake was based on the change in short circuit current resulting from the addition of 10 mM Glucose, Phosphorus, Carbachol and (2 mM) Cu proteinate, $CuSO_4$ or 10 mM Gly-Sar to the brush border membrane buffer solution. Cu concentrations in the mucosal and serosal buffer were determined using ICP-MS. The 50% nutrient reduced diet not only increased ($P < 0.001$) basal Isc (5.08 $\mu A/cm^2$ vs. 0.37 $\mu A/cm^2$) compared to the control diet, but also increased ($P < 0.001$) glucose, copper and gly-sar active transport compared to the control diet, which suggests up regulation of membrane transport proteins during times of low nutrient intake.Carbachol tended ($P = 0.07$) to increase chloride ion secretion for the 50% reduced nutrient diet compared to the control.Phosphorus active transport was not affected by dietary treatment ($P = 0.59$). Active copper transport for the 50% cellulose diet increased ($P < 0.04$) for both copper sources (4.3 $\mu A/cm^2$ vs. 0.47 $\mu A/cm^2$), but differences between sources were not observed.Copper concentration in the mucosal and serosal buffer did not differ between diets (P=0.15) or between $CuSO_4$ and Cu proteinate (mucosal side: $P = 0.1$; serosal side: P=0.99). Overall, a reduced plane of nutrition in broilers increased active transport for a variety of core nutrients, presumably due to more active versus passive activated transport systems in the intestine.

Key Words: nutrient uptake, intestine, chicken

T201 The effect of period and duration of feeding restriction on nitrogen balance in pigs. M. Richer-Lanciault[1], M. Roy*[1], J. F. Bernier[1], R. Fillion[3], M. Lessard[2], and F. Guay[1], [1]*Universite Laval*, *Quebec, Quebec, Canada*, [2]*Agriculture and Agrifood Canada*, *Sherbrooke, Quebec, Canada*, [3]*CDPQ*, *Quebec, Quebec, Canada*.

The objective of this experiment was to evaluate the effect of period and duration of qualitative feed restriction or compensatory feeding on N balance in pigs. For N balance trial, 24 castrated pigs (18 kg) were maintained in individual pens and fed ad libitum, except during collection period, according to four different feeding strategies. The first group of pigs (CON) fed with a conventional feeding sequence (starter (1.02% digestible Lys, 0.54% P, 0.76% Ca), grower (0.95% Lys, 0.47% P, 0.69% Ca), finisher1 (0.75% Lys, 0.43% P, 0.52% Ca) and finisher2 (0.63% Lys, 0.35% P, 0.49% Ca). The other feeding sequences were: RES0-21: finisher1, grower, finisher1 and finisher2; RES21-49: starter, finisher2, finisher1 and finisher2; RES0-49: finisher1, finisher2, finisher1 and finisher2; when the restriction was applied, Lys, P and total Ca were reduced by 30%. Pigs were placed in metabolic crates for a 7-d period during each of the starter (0-21d), grower (21-49d), finisher1 (49-70d) and finisher2 (70-slaughter) phases on days 14 (28 kg), 35 (48 kg), 63 (79 kg), 84 (100 kg), respectively, to determine N balance (N intake, retention, digestibility, utilization (retention/intake), fecal and urinary). Data was analyzed with SAS Mixed procedure and restricted groups were compared to CON. During starter phase (0 to 21d), RES0-21 and RES0-49 pigs had lower N intake (38, 37 vs 44 g/d) digestibility (81, 81, vs 84%) utilization (57, 57 vs 62%) and retention (22, 21 vs 27 g/d) than CON pigs. During grower phase, RES21-49 and RES0-49 pigs had lower N intake (43, 41 vs 59 g/d), urinary (12, 11 vs 19 g/d) and retention (25, 23 vs 32 g/d). During grower phase, corresponding to a compensatory feeding period for RES0-21 pigs, their N balance was not different from CON pigs. However, during finisher1 phase, RES0-21 had higher N retention (39 vs 29 g/d), digestibility (89 vs 86%, P<0.07) and utilization (61 vs 48%, P<0.09) than CON pigs. Finally, during finisher2 phase, N balance was not affected by previous feeding restriction. These results show that pigs subjected to early feeding restriction can improve N utilization and retention during compensatory phases.

Key Words: growing pigs, compensatory growth, N balance

T202 Effects of feeding sodium selenite vs. selenium yeast as the selenium source for sows during late gestation and lactation. T. E. Shipp*, D. W. Funderburke, and C. L. Funderburke, *Cape Fear Consulting, LLC, Warsaw, NC.*

Litter and sow performance were compared when sows were fed 0.3 ppm added Se as sodium selenite (Control, C) or Se yeast (SY, SelPlex, Alltech Inc.). Sows were balanced by parity group and season and allotted to one of the two treatments. SY treatment began 3 wk pre-farrowing and continued through lactation. Respectively, C and SY gestation and lactation diets were equal in nutrients, except for Se source. Each farrowing group had 20 to 24 sows; litters were weaned at 23 to 24 d. Lactation feed intake was measured on a subset of sows (C, n = 51; SY, n = 54). All other parameters were measured on the entire data set of C (n = 309) and SY (n = 310) sow observations. All data were analyzed by the GLM procedure of SAS with fixed effects of treatment, parity group (group 1 = parity 1; group 2 = parity 2; group 3 = parities 3 to 5; group 4 = parities 6 and above), and season (season 1 = Oct through Mar; season 2 = Apr through Sept). Experimental unit was individual sow observation. There were no differences by treatment for sow mortality, re-breeding rate, cull rate, average parity, or beginning or ending body condition score. There were also no differences by treatment for sow lactation feed intake as measured on the subset of sows. Pigs born alive, total pigs born, stillborns, mummies, pigs weaned, and individual and litter birth weight did not differ with treatment. SY sows produced heavier weaned litters (75.82 kg vs. 72.04 kg; $P < 0.007$) and heavier pigs at weaning (7.56 kg vs. 7.09 kg; $P < 0.001$) than C sows. Selenium yeast can replace added Se from sodium selenite for sows, with resulting improvements in weaning pig weights.

Key Words: litter performance, lactation, selenium yeast

T203 Efficacy of Cr (III) supplementation on growth, carcass composition, blood metabolites, and endocrine parameters in finishing pigs. M. Q. Wang*[1,2], Y. D. He[1,2], and Z. R. Xu[1,2], [1]*Animal Science College of Zhejiang University, Hangzhou, Zhejiang, P. R. China*, [2]*The Key Laboratory of Molecular Animal Nutrition, Ministry of Education, Hangzhou, Zhejiang, P. R. China*.

The objective of this study was to evaluate the effects of trivalent chromium from different sources on growth, carcass composition, and serum parameters in finishing pigs. Ninety-six crossbred pigs with an initial average body weight 65.57 ± 1.05 kg were blocked by body weight and randomly assigned to four treatments with three replicates. Pigs were offered one of four diets including a control diet or the control diet supplemented with 200 μg/kg chromium from either chromium chloride (CrCl3), chromium picolinate (CrPic) or Chromium nanocomposite (CrNano) for 40 days. After completion of the feeding trial, eight pigs from each treatment were selected to collect blood samples, and slaughtered to measure carcass composition. The results showed that supplemental CrNano had no effects on average daily gain and feed conversion rate, while it increased carcass lean proportion and loin longissimus muscle area ($P<0.05$), and decreased carcass fat proportion and 10th rib backfat depth ($P<0.05$). CrPic supplementation also resulted in lower fat proportion and larger longissimus muscle area ($P<0.05$). The addition of Cr from CrNano or CrPic decreased serum glucose ($P<0.05$), increased concentrations of total protein and free fat acid in serum ($P<0.05$). Serum urea nitrogen, triglyceride and cholesterol were decreased ($P<0.05$), and serum high density lipoprotein and lipase activity were increased ($P<0.05$) with the supplementation of CrNano. Serum insulin was decreased ($P<0.05$) by supplemental Cr from CrNano or CrPic, and serum insulin like growth factor I was increased in the CrNano treated group. These results suggest that chromium nanocomposite has higher efficacy on carcass composition in pigs compared to the traditional chromium sources.

Key Words: chromium, pigs, nanocomposite

T204 Biochemical profile of broiler chicken supplemented with organic selenium (SelPlex®) in total replacement of inorganic selenium (sodium selenite). F. M. Gonçalves, M. N. Corrêa*, M. A. Anciuti, F. Rutz, and F. A. B. Del Pino, *Federal University of Pelotas, Pelotas, RS, Brazil.*

The aim of this study was to evaluate the biochemical profile of broiler chickens supplemented with selenium yeast in total replacement of sodium selenite in the diets. A total of 704 day-old Cobb male chicks were used until 42 days of age. The experimental design was a completely randomized design with two treatments which consisted of two different sources of selenium in the diets (sodium selenite and selenium yeast), in a total of 16 replicates per treatment. The basal diet was prepared using corn and soybean meal in agreement with the nutritional values established by the breeder manual. Calcium (Ca), phosphorus (P), aspartate aminotransfer (AST), gamma glutamil-transfer (GGT), albumin (Alb.), total proteins (TPs), cholesterol (Chol), uric acid (UA) and creatine kinase (CK) were evaluated by specific kits. The highest level of creatine kinase was observed at 35 days of age in the chicks supplemented with sodium selenite. Selenium yeast-fed birds showed higher level of total serum proteins in the same period. Se from sodium selenite can be replaced by Se from selenium yeast in broilers diets slightly altering blood biochemistry.

Table 1. Biochemical profile of broilers supplemented with two differents sources of selenium in the diets

Age, days	28		35		42	
Se Source	SeO	SeI	SeO	SeI	SeO	SeI
Ca (mg/dL)	8.22	8.26	9.52	9.58	10.65	10.70
P (mg/dL)	6.60	6.78	6.75	6.21	5.58	5.62
AST (UI/l)	92.55	96.72	76.69	80.60	73.84	95.03
GGT (UI/l)	50.78	39.47	63.99	61.65	-	-
Alb (g/dL)	1.87	1.80	1.68	1.61	1.58	1.54
TPs (g/dL)	2.86	3.00	2.84a	2.64b	3.29	3.02
Chol (mg/dL)	136.18	148.68	132.46	140.37	106.97	111.77
UA (g/dL)	5.63	4.17	3.67	3.07	4.30	3.88
CK (U/l)	1335.26	1437.34	2207.26b	3349.50a	4081.23	4015.12

Key Words: selenium-yeast, bioavailability, metabolites

T205 Effects of level of soybean oil in diets on true and ileal digestibility and endogenous losses of amino acids in growing pigs. E. C. Almeida, E. T. Fialho*, V. S. Cantarelli, M. G. Zangeronimo, R. A. N Pereira, and P. B. Rodrigues, *University Federal of Lavras, Lavras, MG, Brazil*.

A total of 16 barrows with an initial BW of 42.3± 2.3 kg were surgically equipped with a T-cannula in the distal ileum and used to evaluate the effect of different levels of soybean oil on endogenous amino acid losses, as well as the apparent and true ileal digestibility of amino acids in growing pigs. The pigs were randomly allotted to four dietary treatments for a 4-wk experiment. Dietary treatments were increased

levels of soybean oil (0.0, 1.5, 3.0, and 4.5%) added to corn and soybean meal based diets formulated to meet the requirements for apparent ileal digestible lysine (0.61%) for growing pigs according to NRC (1998). Chromic oxide (0.25%) was used as an indigestible marker. During wk 1, pigs were fed only a basal diet; during wk 2 to 4, treatment diets were provided, and ileal samples were collected on days 6 and 7 of each week. The digesta samples were pooled. There was no effect of the supplementation of soybean oil levels on the apparent ileal digestibility of Glu, Gly, Arg, Ala, Pro, Tyr, His and Lys. However, a linear increase in the true and apparent ileal digestibility of Thr and Ser was observed with increasing soybean oil concentrations. A quadratic effect of soybean oil concentration was observed for the true and apparent ileal digestibility of Val, Phe, total non-essential and total of essential amino acids. True ileal digestibility coefficients of Arg and Tyr, also responded quadratically to soybean oil supplementation. In conclusion, the present results indicate that diets with soybean oil supplementation at the 2.5 to 3.0% level improves ileal digestibility of most indispensable AA, and that this effect is not further enhanced by providing more than 3.0% of soybean oil to diets for growing pigs.

Key Words: energy, metabolism assay, cannulated pigs

T206 Antagonistic strains isolated from the porcine gastrointestinal tract. V. Klose*[1], K. Bayer[1], R. Bruckbeck[1], A. P. Loibner[1], and G. Schatzmayr[2], [1]*BOKU-University, Vienna, A-3430 Tulln, Austria*, [2]*BIOMIN Research Center, A-3430 Tulln, Austria*.

The supplementation of feed with beneficial strains originating from the porcine gastrointestinal tract (GIT) appears to be a promising alternative to the use of antibiotics, in order to maintain the health of weaner piglets by suppressing pathogens in a competition-like manner. A successful alternative must protect piglets from a myriad of enteric pathogens. Therefore, the combination of multiple strains may offer a competitive advantage to single-strain probiotics. The present work was part of the selection process of probiotic strains for their combined use as feed additives in pig production. Eleven strains, phylogenetically affiliated to *Bacillus subtilis* (n = 1), *Lactobacillus salivarius* (n = 2), *L. reuteri* (n = 2), *L. amylovorus* (n = 2), *L. mucosae* (n = 2) and *B. thermophilum* (n = 2), were isolated from the porcine gastrointestinal tract and examined for their antagonistic effect against a broad panel of pathogens. Using an agar spot test, the most effective strains were shown to inhibit various pathogens such as enterotoxigenic and enterohemorrhagic *E.coli* serotypes O8 K88, O138, O139, O147, O157, O6, as well as *S.enterica* serovar Enteritidis, Choleraesuis and Typhimurium and/or *Clostridium perfringens* type A. Six strains were able to suppress the growth of *Brachyspira hyodysenteriae*, the main causing agent of Swine Dysentery. These results encouraged us to explore the potential of four porcine strains belonging to *E. faecium*, *L. salivarius*, *L. reuteri* and *B. thermophilum* for their combined use as feed additives. Their effect will be examined in future feeding trials.

Key Words: pig, enteric pathogens, antagonistic activity

T207 The effect of period and duration of feeding restriction on compensatory growth and global growth performances in pigs. M. Richer-Lanciault*[1], J. F. Bernier[1], R. Fillion[3], M. Lessard[2], and F. Guay[1], [1]*Universite Laval, Quebec, Quebec, Canada*, [2]*Agriculture and AgriFood Canada, Sherbrooke, Quebec, Canada*, [3]*CDPQ, Quebec, Quebec, Canada*.

The objective of this experiment was to evaluate the effect of period and duration of qualitative feed restriction on compensatory growth in pigs. For the growth trial, 96 castrated piglets (18.7 kg) were maintained two per pen and fed ad libitum according to four different feeding sequences. The first group of pigs (CON) fed with a conventional feeding sequence (starter (1.02% digestible Lys, 0.54% P, 0.76% Ca), grower (0.95% digestible Lys, 0.47% P, 0.69% Ca), finisher1 (0.75% digestible Lys, 0.43% P, 0.52% Ca) and finisher2 (0.63% digestible Lys, 0.35% P, 0.49% Ca)). The other feeding sequences were: RES0-21: finisher1, grower, finisher1 and finisher2; RES21-49: starter, finisher2, finisher1 and finisher2; RES0-49: finisher1, finisher2, finisher1 and finisher2; when the restriction was applied Lys, P and Ca were reduced by 30%. Pigs were weighed at the initiation of the experiment, at each diet change (21d, 49d and 70d) and the day before slaughter (120 kg). Feed disappearance was measured on each weigh day. All pigs had 10th rib backfat and muscle thickness taken by ultrasonic scan at d45, d66 and d87. Data was analyzed with Mixed procedure and restricted groups were compared to CON. In the starter phase, RES0-21 and RES0-49 has lower G/F and ADG than CON pigs (0.51, 0.47 vs 0.59 and 0.68, 0.63 vs 0.82 kg/d, $P<0.05$). In the grower phase, RES21-49 and RES0-49 had lower G/F and ADG than CON pigs (0.42, 0.41 vs 0.45 and 0.89, 0.91 vs 1.07 kg/d, $P<0.05$). In the grower phase, corresponding to a compensatory feeding period for RES0-21 pigs, their G/F was higher than CON (0.48 vs 0.44, $P<0.05$). In finisher1 and 2 phases (their compensatory growth period), RES21-49 and RES0-49 groups also had higher G/F than CON (0.43, 0.42 vs 0.38 and 0.36, 0.37 vs 0.32, $P<0.05$). Finally, overall G/F and ADG, as well as backfat thickness in restricted groups were not different from CON. Muscle depth was lower in RES0-49 than in CON, but only on d45 and d66 (Time x Diet, $P<0.05$). These results show that growing pigs subjected to an early feed restriction compensated completely and can maintain global growth performances.

Key Words: growing pig, compensatory growth, growing performances

T208 Citrulline as a parameter for villus atrophy in weaned piglets. L. der Kinderen*[1], H. Zwolschen[2], D. Bravo[3], A. Mul[1], and E. Bruininx[1,4], [1]*CCL Research, Veghel, the Netherlands*, [2]*Cehave Landbouwbelang Voeders Nederland, Veghel, the Netherlands*, [3]*Pancosma, Geneva, Switzerland*, [4]*Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands*.

In order to test plasma citrulline concentration (PCC) as a longitudinal marker for small intestinal morphology, 2 groups of twelve 23-day-old crossbred piglets (initial BW 7.75 kg ± 1.28) were used during a 5 day experiment. Group 1 (control) consisted of unweaned piglets remaining with the sow during the total experimental period. Group 2 (weaned) consisted of weaned piglets at 23 days of age and housed individually. The weaned piglets were fasted for 72 hrs after weaning and were fed 0.5 of their NEm (≈ 500 kJ ME/kg$^{0.75}$/d) including Phaseolus Vulgaris lectins. Blood samples of all piglets in both groups were collected daily and analyzed on PCC. At day 5, piglets were euthanized via intracardial injection with sodiumpentobarbital and samples of intestinal tissues were taken at 0.5 m distal from the Treitz ligamentum. Daily PCC values were analysed using a split plot model using group treatment (Control vs. Weaned) as a whole plot factor and time as a split plot factor. Overall treatment effects were tested with differences between days within a group as the error term. Additionally, overall linear relationships between PCC and morphological parameters were assessed using regression analysis. Averaged over all sampling days, PCC for the control group was higher ($P < 0.001$) than for the weaned piglets (111 vs. 60 μmol/L).

Moreover, time related changes in PCC were affected by experimental treatments as well ($P < 0.001$). Overall linear regression analysis showed a significant relation ($P < 0.0001$) between citrulline plasma levels measured on day 4 and villus/crypt ratio and villus height ($\alpha = 0.027$ μmol/L, SE = 0.003 and $\alpha = 3.679$ μmol/L, SE = 0.410 respectively). This study suggests that PCC can be used as a longitudinal marker for small intestinal morphology in weaned piglets. As such, PCC could be a useful parameter in monitoring the effects of different feeding strategies on small intestinal morphology in weaned piglets.

Key Words: citrulline, Intestinal marker, Intestinal morphology

Physiology and Endocrinology: Estrous Synchronization

T209 Effect of progesterone insert during presynchronization program on reproductive responses of dairy cows. R .G. S. Bruno*[1], A. C. Denicol[1], D. F. Resende[1], G. Lopes Jr.[1], L. G. D. Mendonça[1], F. A. Rivera[1], J. E. P. Santos[2], and R.C. Chebel[1], [1]*University of California - Davis*, *Tulare*, [2]*University of Florida*, *Gainesville*.

Lactating Holstein cows from two commercial dairies, 552 (392 multiparous and 160 primiparous) were blocked by parity and body condition at 44±3 d in milk (DIM) and randomly assigned to one of two presynchronization programs, a control (CON, n=282) or a controlled internal drug-releasing (CIDR, n=272) containing 1.38 g of progesterone were inserted at 44±3 DIM and removed on day 51±3 DIM, 11 d before the initiation of the timed AI protocol (GnRH, 7 d PGF2a, and 3 d GnRH + timed AI). All cows were time inseminated at 72±3 DIM. Ovaries were scanned at 62±3 and 69±3 DIM in order to identify ovarian structures and blood was sampled at 62±3, 72±3, and 80±3 DIM for progesterone analyses. Pregnancy was diagnosed at 38 and 66 d after timed AI by palpation per rectum. Data were analyzes by the LOGISTIC procedure of SAS. Pregnancy per AI (P/AI) at 38 and 66 d after insemination was not affected (P=0.45) by type of presynchronization program (35.9 vs 34.6% for CIDR and CON respectively). However cows in the CIDR group had increased (P=0.04) ovulation synchronization following the timed AI program than CON cows (84.8 vs 77.6%, respectively) and synchronized cows had greater (P<0.001) P/AI at 38 and 66 d after AI (40.3 vs. 13.2% at 38 d; 38.2 vs. 12.1% at 66 d). Presynchronization with CIDR did not affect (P=0.72) the number of CL at the time of the initiation of the timed AI protocol, but increased (P=0.05) the proportion of cows with multiple CL at the time of the PGF (62.7 vs. 55.5% for CIDR and CON respectively) and increased (P<0.01) ovulation to the first GnRH of the timed AI (79.7 vs 68.9% for CIDR and CON respectively). Presynchronization with CIDR increased the proportion of cows responding to the synchronization program but did not improve P/AI.

Key Words: dairy cows, presynchronization, progesterone

T210 Effect of duration of CIDR treatment on reproductive performance of dairy heifers using a timed-AI protocol. G. Lopes Jr.*[1], L. G. D. Mendonça[1], R. C. Chebel[1], J. C. Dalton[2], and A. Ahmadzadeh[3], [1]*Veterinary Medicine Cooperative Extension, University of California-Davis*, *Tulare*, [2]*Caldwell Research and Extension Center, University of Idaho*, *Caldwell*, [3]*University of Idaho*, *Moscow*.

The objective of this experiment was to determine the effect of reducing the duration of CIDR insert exposure in a timed-AI (TAI) protocol (CIDR-$PGF_{2\alpha}$-GnRH and AI)on pregnancy per AI (P/AI) in dairy heifers. Holstein heifers (n=415) were assigned randomly to one of three treatments: 1) Control heifers (CONT, n=141) received two $PGF_{2\alpha}$ (25mg) injections every 11 d until inseminated on detected estrus or 22 d after enrollment; 2) CIDR7 heifers (n=135) received a CIDR insert for 7 d; and 3) CIDR5 heifers (n=139) received a CIDR insert for 5 d. Heifers in CIDR7 and CIDR5 were given (i.m.) $PGF_{2\alpha}$upon CIDR removal followed by GnRH (i.m., 100μg) and concomitant with AI approximately 50 h after CIDR removal. All heifers were re-inseminated following 1st AI if detected in estrus. Pregnancy status was diagnosed 36±1 d after AI. Data were analyzed by logistic regression, ANOVA, and Cox proportional hazard regression. Interval from enrollment to 1st AI tended to (P=0.07) and was (P=0.02) shorter for CIDR5 (7.0±0.6) than CONT (8.6±0.6) and CIDR7 (9.0±0.6), respectively, but there was no difference between CONT and CIDR7. Treatment affected ($P < 0.01$) P/AI as CONT (60%) had greater (P<0.05) P/AI compared with CIDR5 (45.3%) and CIDR7 (28.1%). Moreover, CIDR5 had greater (P<0.05) P/AI than CIDR7. Heifers in CONT become pregnant faster (P<0.01) than CIDR5 and CIDR7, and CIDR5 tended to (P=0.06) become pregnant faster than CIDR7. Interval from enrollment to pregnancy was (P<0.01) shortest for CONT (CONT=29.5 ±2.9, CIDR5=43.4±4.3, and CIDR7=49.3 ±3.9 d). Proportion of heifers pregnant at the end of 180 d after enrollment tended to (P=0.11) and was (P<0.01) greater for CONT (97.2%) than CIDR5 (92.8%) and CIDR7 (88.2%). Reducing the duration of CIDR treatment from 7 to 5 d in a CIDR-based TAI protocol increased P/AI; however, heifers inseminated on detected estrus following $PGF_{2\alpha}$ synchronization had greater P/AI compared with either the CIDR5 or CIDR7 TAI protocols.

Key Words: synchronization, CIDR, dairy heifers

T211 Effect of reusing CIDRs on the pregnancy rate of beef cattle. W. A. Greene* and M. L. Borger, *The Ohio State University*, *Wooster*.

The objective of this study was to determine the effect of reusing intravaginal progesterone inserts (CIDRs), as a part of a synchronization program, on pregnancy rates (PR) in beef cattle. One hundred and twenty-four animals were allotted to two similar groups, new CIDR (N) and used CIDR (U), based upon breed, age, postpartum interval, and postpartum cyclicity (as determined by estrus detection and ultrasonography). On d 0, all cattle received 100 μg GnRH i.m., N group cattle received a new CIDR, containing 1.38 g progesterone, and U group cattle received a CIDR previously used for 7d. Used CIDRs had been thoroughly rinsed with a mild disinfectant solution, air-dried, and stored in a dry, enclosed container after first use. Blood samples were collected for plasma progesterone (P4) analyses on d 2. On d 7, CIDRs were removed and animals received 25 mg $PGF_{2\alpha}$ i.m. Each CIDR was evaluated for signs of vaginal infection and scored from 1 (clear) to 5 (heavy pus). Animals were observed for estrus 0700 and 1900 and were artificially inseminated (AI) 11 - 13 h after estrus was observed. If estrus was not observed, animals were timed AI and received 100 μg GnRH i.m. 70 - 72 h after $PGF_{2\alpha}$. Following the synchronization period, repeat breedings were done until d 75. Cattle were pregnancy diagnosed by ultrasonography on d 111. N and U groups had similar ($P > 0.05$) estrus detection rates [EDR] (57.8 and 53.3%). The N group had higher ($P < 0.05$) PR to synchronization (50.0 vs. 28.3%) and higher ($P = .09$) overall PR (93.8 vs. 83.3%) than the U group. The rates of high vaginal

scores (4 & 5) were similar (P > 0.05) for the N and U groups (78.1 and 71.7%). EDR were higher (P < 0.05) for cycling (n=79) animals (63.3%) than anestrus animals (42.2%) while PR to synchronization (41.8 vs. 35.6%) and overall PR (86.1 vs. 93.3%) were similar (P > 0.05) for these two groups. Mean P4 levels (ng/ml) were similar (P > 0.05) for N (1.4 ± 1.5) and U (1.2 ± 1.3) cattle. Reusing CIDRs in a beef cattle synchronization program resulted in lower pregnancy rates than the use of new CIDRs.

Key Words: synchronization, CIDR reuse, progesterone

T212 Reproductive outcomes of beef heifers treated with various duration of CIDR exposure in a modified timed-AI protocol. A. Ahmadzadeh*[1], D. Falk[1], D. Gunn[2], J. B. Hall[3], and B. Glaze[4], [1]*University of Idaho*, *Moscow*, [2]*University of Idaho, R & E Center*, *Fort Hall*, [3]*University of Idaho, R & E Center*, *Salmon*, [4]*University of Idaho, R & E Center*, *Twin Falls*.

The objective of this experiment was to determine the effect of reducing the duration of exposure to an intravaginal progesterone insert (CIDR), in a modified CIDR-synch timed-AI protocol (CIDR-$PGF_{2\alpha}$-GnRH and AI), on pregnancy per AI (P/AI,) and pregnancy rates in beef heifers. The experiment was conducted in three consecutive years. British cross-bred heifers (yr 1, n=88; yr 2, n=70; yr 3, n=86) were stratified by (BW and age; and were assigned randomly to one of two treatments: 1) CIDR7 heifers (n = 120) received CIDR for 7 days, $PGF_{2\alpha}$ (i.m., 25 mg) at CIDR removal, GnRH (i.m., 75 ug) 56 h after CIDR removal and immediate AI and 2) CIDR5 heifers (n=118) received CIDR (d -5) for 5 days, $PGF_{2\alpha}$ (25 mg) at CIDR removal (d 0), GnRH (75 μg) 56 h after CIDR removal and immediate AI. Estrual behavior was monitored for three days following CIDR removal. Heifers were inseminated by a single technician and were exposed to bulls 14 days after AI. Blood samples were collected on the day of CIDR insertion and day of AI. Pregnancy status was determined by ultrasonography at d 32 to 35 and d 67 to 82 after AI. Data were analyzed by logistic regression. Percentage of heifers detected in estrus was different (P<0.05) between years (69%, 44%, 51% for yr 1, 2, and 3, respectively) but not different between treatments. Based on progesterone (P_4) results, the synchronization rates were similar between treatments and across the years. There was a treatment by year interaction effect on P/AI (P<0.05). For CIDR7 and CIDR5, in yr 1 P/AI was 39% and 65.8% (P<0.05); in yr 2, P/AI was 64.7% and 41% (P<0.05), and yr 3 P/AI was 59% and 73.8% (P=0.09). At experiment initiation, greater proportions (P<0.05) of CIDR7 heifers had serum P_4 greater than 1 ng/mL compared with CIDR5 (60% vs 43%). Final pregnancy rates were unaffected by the treatment protocols or year (92% and 95.5% for CIDR7 and CIDR5, respectively). The yearly P/AI results from this study are inconsistent regarding the effect of reducing the duration of CIDR treatment (5-d vs. 7-d) and thus further research is warranted.

Key Words: synchronization, CIDR, beef heifers

T213 Increasing circulating P4 in lactating dairy cattle by treatment with hCG and/or CIDR. A. B. Nascimento*, A. H. Souza, J. N. Guenther, F. P. Dalla Costa, and M. C. Wiltbank, *University of Wisconsin*, *Madison*.

Adequate circulating P4 after AI is important for pregnancy success. Lactating dairy cattle have lower P4 and this problem may be compounded by ovulation of smaller follicles using timed AI protocols, such as Double-Ovsynch (~14mm ovulatory follicle). Our objective was to determine the supplementation strategy, after Double-Ovsynch, which resulted in P4 that approached the concentrations in heifers. Lactating Holstein cows (n=41) were synchronized with Double-Ovsynch (Ovsynch-7d-Ovsynch-timed AI). After AI (Day 5) cows were assigned randomly to receive no treatment (control), 1 CIDR, 2 CIDRs (1st Day 5, 2nd Day 8), 3,300 IU hCG, hCG+CIDR, or hCG+2 CIDRs. A group of heifers after normal estrus were followed as controls (heifers; n=10). Ultrasound and blood samples were used to determine luteal size and circulating P4. Circulating P4 profiles for each treatment were compared to heifers using repeated measures (Proc Mixed, SAS; Treat effect=T; TreatXtime interaction=TXt). Heifers had greater P4 than cows at all times after Day 5 (T and TXt P<.0001). Cows receiving 1 CIDR still had lower P4 than heifers (T P=.0037; TXt NS) with lower P4 at all times from Day 8 to 16. Supplementation with 2 CIDRs produced similar P4 to heifers on all days (T and TXt NS). All cows ovulated after hCG treatment. Treatment of cows with hCG produced P4 similar to heifers (T P=.59); although, there was an interaction (TXt P=.01) with some times tending to be lower in cows treated with hCG. Supplementation with a CIDR+hCG produced a profile similar to heifers (T, TXt NS). Treatment with 2 CIDRs+hCG produced P4 that tended to be greater than heifers (T P=.06; TXt P=.007) with higher P4 from Days 9 to 16. After Day 17, non-pregnant heifers (n=6) and cows (n=13) had CL regression with fewer hCG-treated cows showing luteolysis by Day 19 (P<0.05). Thus, use of CIDRs and production of an accessory CL with hCG can elevate P4 to concentrations found in heifers. This information will be useful for designing future trials that supplement P4 after AI to improve fertility in lactating cows.

Key Words: hCG, CIDR

T214 Effect of increasing GnRH and $PGF_{2\alpha}$ dose during double–Ovsynch on fertility of lactating dairy cows at first postpartum timed artificial insemination. J. O. Giordano*[1], P. M. Fricke[1], S. Bas[1], A. P. Cunha[1], R. A. Pawlisch[2], J. N. Guenther[1], and M. C. Wiltbank[1], [1]*Department of Dairy Science, University of Wisconsin*, *Madison*, [2]*Brodhead Veterinary Clinic*, *Brodhead, WI*.

Our objective was to determine the effect on pregnancies per AI (P/AI) of increasing the dose of the 1st GnRH and $PGF_{2\alpha}$ injections during the Breeding–Ovsynch of Double–Ovsynch (DO; Pre–Ovsynch, GnRH–7d–$PGF_{2\alpha}$–3d–GnRH; 7d later Breeding–Ovsynch, GnRH–7d–$PGF_{2\alpha}$–56h–GnRH–16h–TAI) for 1st post–partum TAI. In Exp.1, cows were blocked by parity and randomly assigned to a 2x2 factorial design to receive either low (L) or high (H) dose of GnRH (100 vs. 200 μg) and either L or high H dose of cloprostenol (500 vs. 750 μg) resulting in the following treatments: LL (*n*=263), HL (*n*=277), LH (*n*=270), and HH (*n*=274). Ovarian ultrasound and serum progesterone (P4) were used to assess ovulation to 1st GnRH and luteal regression after $PGF_{2\alpha}$ (P4 ≤0.5 ng/ml at 2nd GnRH) of Breeding-Ovsynch in a subgroup of cows. Pregnancy status was assessed 29 and 74 d after TAI. In Exp. 2, cows were blocked by parity and randomly assigned to LL (*n*=222) or HH (*n*=226) treatments described for Exp. 1. For Exp.1, P/AI was 47.0% (509/1084) at 29 d and 39.7% (430/1084) at 74 d after TAI, did not differ (*P*=0.31) among treatments at 74 d (LL, 34.6%; HL, 40.8%; LH, 42.2%; HH, 40.9%), and was greater (*P*<0.0001) for primiparous than multiparous cows (46.1 vs. 33.8%). Pregnancy loss from 29 to 74 d did not differ (*P*=0.47) among treatments [LL, 20.0%; HL, 14.6%; LH, 14.4%; HH, 14.8%] and was not affected (*P*=0.37) by parity. Ovulation to the 1st GnRH injection of Breeding–Ovsynch was greater (*P*=0.03) for cows receiving H vs. L GnRH [66.8% (241/361) vs. 58.9% (211/358)];

however, luteal regression after $PGF_{2\alpha}$ did not differ for cows receiving H vs. L dose of $PGF_{2\alpha}$ (93.8% vs. 91.5%). For Exp. 2, P/AI at 29 d did not differ (*P*=0.49) between H vs. L treatments [44.3% (100/226) vs. 41.0% (91/222)], and was not affected by parity (*P*=0.48). Thus, despite an increase in ovulation to the 1st GnRH injection of Breeding–Ovsynch, there was no detectable effect of increasing the dose of GnRH or $PGF_{2\alpha}$ on fertility to 1st post–partum TAI after Double–Ovsynch. *Supported by Hatch project WIS01171*

Key Words: Double–Ovsynch, fertility

T215 Use of eCG, hCG, or estradiol cypionate (ECP) after CIDR removal in Creole Rodeo multiparous cows. J. A. Ramirez-Godinez*, L. V. Beltran-Prieto, E. Santellano-Estrada, and A. Flores-Mariñelareña, *Universidad Autonoma de Chihuahua*, *Chihuahua, Chihuahua, Mexico*.

The aim of the present study was to compare the estrus response (ER), conception rate (CR), and serum progesterone concentrations (P_4) in Creole (C) Rodeo cows treated with ECP, eCG or hCG, in addition to a CIDR + Estradiol Benzoate (EB) and $PGF_{2\infty}$ protocol of estrus synchronization. Thirty-one multiparous C cows received a CIDR with 1.9 g of P_4, and an IM injection of 1 mg of EB. On day 7, the CIDR was removed and 30 mg of $PGF_{2\infty}$ were administered IM and the cows were randomly assigned to one of three treatments: T1 (n=11) received 1mg ECP IM and T2 (n=10) 500 IU eCG IM 24h after CIDR removal, and T3 (n=10) 2000 IU hCG IM 56h after CIDR removal. Estrual behavior was monitored for three days following CIDR removal. Cows in T1 and T2 were AI 12 to 18 h after detected in estrus, and in T3 were fixed-time AI 56h after CIDR removal. Blood samples were collected at CIDR insertion, removal and 24 h after, at breeding, on days 8 (day 0 = AI) and 17 to estrus (repeats), and to day 23 (non repeats). Estrous and conception rates were analyzed with a Fisher exact test using PROC FREQ of SAS. A mixed model with treatment (T), day (D) and their interaction (T*D) as fixed effects and cow within treatment as random effect was adjusted for P_4 using PROC MIXED of SAS. All cows treated with ECP were detected in estrus compared to 80% receiving eCG and 30% hCG ($P < 0.01$), suggesting that the use of ECP promoted the ER. Conception rate was similar between treatments ($P = 0.2421$); however, the numeric difference favored T2 (60%) over T1 (27.27%) and T3 (30%), suggesting that the use of the eCG might have promoted follicular development and ovulation as it has been reported in beef cattle. Serum P_4 did not differ between treatments ($P = 0.4396$) and there was not T*D interaction ($P = 0.9474$). These results suggest that the use of eCG after CIDR removal might improve the conception rate in Creole Rodeo cows.

Key Words: Creole Rodeo cows, eCG, hCG

T216 Effect of body condition score on estrus expression, and AI and breeding season pregnancy rates in beef cows synchronized with progesterone supplemented protocols. R. Kasimanickam* and W. D. Whittier, *Virginia-Maryland Regional College of Veterinary Medicine*, *Blacksburg*.

The objective of the study was to determine the effect of body condition score (BCS) at initiation of synchronization on estrus expression, and AI and breeding season pregnancy rates. Data collected between 2004 and 2007 AI breedings that occurred on eleven beef farms were evaluated retrospectively. Cows (N=4885) were synchronized with progesterone supplemented protocols. The BCS (1-emaciated; 9-obese) of all cows were recorded on Day 0 of synchronization. On Day 7, all cows received a Kamar heatmount device. Cows in estrus were observed for 30 min in the morning, noon and later afternoon on Day 9 and at the time of AI on Day 10. A cows was determined to be in estrus if it was visually observed to stand for mounting or based on if it had an activated, lost (with mount marks) or partially activated Kamar device. Natural service bulls (approximately 1:40 bull:cow ratio) were introduced 14 days after AI and maintained for a 45 to 50 d breeding period. Cows were examined for pregnancy at 57 days and at 120 days after AI by palpation per rectum and/or transrectal ultrasonography to distinguish AI pregnancy from sire pregnancy. Glimmix procedure was employed to analyse the effect of BCS on estrus expression, and AI and breeding season pregnancy rates. The BCS ranged from 3 to 8. The estrus expression, and AI and breeding season pregnancy rates were influenced by BCS ($P<0.01$). The estrus expression for corresponding BCS was 3-41.2%, 4-37.9%, 5-58.0%, 6-57.9%, 7-57.9% and 8-39.3%. The AI pregnancy rates were 35.3, 47.7, 52.1, 55.0, 53.8 and 44.3 for the BCS from 3 to 8 respectively. The overall pregnancy rates 76.4, 84.7, 88.0, 90.2, 89.2, and 87.0 for the BCS from 3 to 8 respectively. The BCS of beef cows at the time of initiation of synchronization protocol influenced the estrus expression, AI and overall pregnancy rates. In conclusion, a minimum BCS of 5 should be maintained during breeding season to ensure acceptable reproductive performance.

Key Words: beef cows, body condition score, pregnancy

T217 Comparison of the CIDR Select and 5 day CO-Synch + CIDR protocols for synchronizing estrus in beef heifers. P. J. Gunn*[1], K. C. Culp[1], R. P. Arias[1], R. P. Lemenager[1], K. Heaton[2], S. L. Lake[3], and G. A. Bridges[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*Utah State University*, *Logan*, [3]*University of Wyoming*, *Laramie*.

The objective of this study was to compare artificial insemination (AI) pregnancy rates between the 5 d CO-Synch + CIDR (5D) and CIDR Select (CS) programs in replacement beef heifers. Crossbred beef heifers (n = 318) were equally and randomly assigned to either the 5D or CS treatment. The CS treatment consisted of insertion of an EAZI-BREED™ CIDR® insert (CIDR) for 14 d, an injection of GnRH (100 µg; Cystorelin®) 9 d after CIDR removal, and administration of $PGF_{2\alpha}$ (25 mg; Lutalyse®; PG) 7 d following GnRH. The 5D treatment consisted of GnRH and CIDR insertion, followed 5 d later by CIDR removal and administration of two 25 mg doses of PG given approximately 12 h apart. To facilitate animal handling, treatments were offset by 24 h, as the 5D treatment received the initial PG 24 h following the CS treatment. In both treatments, heifers were detected for estrus for 56 h following PG and those exhibiting estrus were AI based on the AM/PM rule. Heifers not observed in estrus were timed-AI (TAI) 72 h after PG, concurrent with GnRH administration. Ten d following TAI, bulls were placed with the heifers for approximately 45 d. Determination of AI and breeding season pregnancy rates were achieved by ultrasonography approximately 35 d after TAI and 30 d after the breeding season, respectively. Estrous response tended ($P = 0.07$) to be greater in the CS (63.5%) than in the 5D (53.5%) treatment. However, conception rate of heifers exhibiting estrus (CS; 75.2%, 5D; 76.5%), TAI conception rate (CS; 62.1%, 5D; 63.5%), AI pregnancy rate (CS; 70.4% 5D; 70.4%), and breeding season pregnancy rate (CS; 92.2%, 5D; 88.0%) did not differ between treatments. In conclusion, both the CIDR Select and the 5 day CO-Synch + CIDR were effective programs for synchronizing estrus in replacement beef heifers.

Key Words: 5 day CO-Synch + CIDR, CIDR Select, beef heifer

T218 Effect of double prostaglandin injections in the Ovsynch® protocol on serum progesterone in cycling dairy cows. J. L. Fain*, E. R. Waggoner, and J. R. Gibbons, *Clemson University*, *Clemson, SC*.

Pregnancy rates in dairy cows are low in part because corpora luteal regression following prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) is inefficient. The experimental objective was to compare serum progesterone values (P4), CL regression, and pregnancy rates following administration of the Ovsynch® (d0 GnRH, d7 $PGF_{2\alpha}$, d9 GnRH, and d10 Timed AI) protocol with a single (1PG) $PGF_{2\alpha}$ or 2 (2PG) $PGF_{2\alpha}$ injections 12 hr apart in lactating dairy cows. Holstein (n=26) and Jersey (n=7) cows, were randomly assigned to one of the two groups. Controls (n=15;1PG) or treatment animals (n=18;2PG) were evaluated ultrasonically to map ovarian dynamics daily from the first GnRH injection to d 10 (day of Timed AI) and blood was sampled in 12 h intervals beginning 12 h prior to the first $PGF_{2\alpha}$ until 12 h post Timed AI. Cows detected in estrus early were removed from the study. Both the PG1 and PG2 groups consisted of primi and multi-parous cows averaging 80 lbs of milk. Daily ovarian ultrasound indicated 40% of 1PG animals and 55.6% of 2PG animals ovulated following the initial GnRH and in all of these animals two CLs were present at the time of first $PGF_{2\alpha}$ with there being a tendency (P=0.08) for a sharper decline in P4 values in the PG2 group versus the PG1. Overall, 60% of PG1 animals and 61% of PG2 animals had a functional CL at the time of first $PGF_{2\alpha}$ as indicated by P4 values > 1.0 ng/ml and regardless of treatment luteolsysis was complete in these animals 24 h following initial $PGF_{2\alpha}$ as indicated by P4 levels <1.0 ng/ml. Initial indications show no differences (P>0.05) in pregnancy rates between 1PG and 2PG groups. In both groups, there was a higher tendency (P=0.08) for animals with P4 levels < 0.10 ng/ml, 48 h following $PGF_{2\alpha}$ to be diagnosed pregnant at d 35 ultrasound versus those animals with P4 levels > 0.10 ng/ml at the same time point. An important note is the tendency (P= 0.07) for animals in the PG2 group to have P4 levels <0.10 ng/ml during the sampling time. Though not significant, 72% of the PG2 group showed secondary signs of estrus compared to 60% in the PG1 group. Further research is needed to fully investigate these dynamics.

Key Words: Ovsynch, P4, dairy

T219 In vitro assessment of corpus luteum function in cows induced to ovulate with porcine LH, GnRH or estradiol benzoate. D. J. Ambrose*[1,3], M. G. Colazo[1], J. P. Kastelic[2], T. O. Ree[3,4], M. K. Dyck[3], P. Ponce Barajas[1,3], and A. G. A. Lamont[1,3], [1]*Alberta Agriculture and Rural Development*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [3]*University of Alberta*, *Edmonton, AB, Canada*, [4]*Lakeland College*, *Vermilion, AB, Canada*.

Objectives were to compare CL structure and function in nonlactating Holstein cows ovulating spontaneously or following treatment (during proestrus) with porcine LH (pLH), GnRH, or estradiol benzoate (EB). Cows (n=28) were given a 1.9 g progesterone (P4) intravaginal device (CIDR) for 5 d and 500 µg cloprostenol (PG) at CIDR removal. On d 6 (estrus = d 0), all cows received PG twice, 12 h apart, and were allocated to receive: no treatment (Control); 1 mg EB 20 h after first PG; 12.5 or 25 mg pLH or 100 µg GnRH 36 h after PG. Cows (n=4/group) were ovariectomized on d 12. The CL weight (g) was greater (P<0.05) in Control (6.1±0.5) than in GnRH-treated cows (4.5±0.5) but not different from other groups (mean, 5.5±0.5). Preovulatory follicle diameter was correlated to CL weight (P<0.03, r=0.47). The no. of small luteal cells / unit area (235.6±18.2) did not differ (P>0.05) among groups. However, CL of cows given GnRH had fewer (P<0.05) large luteal cells per unit area (25.5±4.4) than that of EB (41.8±4.4) or Control (40.0±4.4); also, 12.5 mg pLH (27.8±4.4) differed from EB (P<0.05). GnRH-induced CL had more (P<0.02) capillary cells (57.0±8.3) than Control (26.0±8.3). The number of fibroblasts in the CL was greatest (P<0.05) in cows treated with 12.5 mg pLH (96.8±7.6) than in all other treatments (mean, 60.4±7.6). Portions of CL (250 mg, as 3-4 mm cubes) were cultured for 2 h in vitro in modified Eagle′s medium (DMEM) with 0, 20 or 40 ng/mL bovine LH. Although mean plasma P4 concentration (ng/mL) on d 12 was lower (P<0.05) in cows induced to ovulate with 12.5 mg pLH (4.8±0.6) than in GnRH-treated cows (6.7±0.6), in vitro P4 production (ng/mL) was not affected by either in vivo treatment (13.2±0.7) or LH dose in vitro (13.3±0.7).

Key Words: corpus luteum, progesterone, in vitro

T220 Reproductive performance of grazing dairy cows following presynchronization and resynchronization protocols. E. S. Ribeiro*, R. L. A. Cerri, R. S. Bisinotto, F. S. Lima, F. T. Silvestre, W. W. Thatcher, and J. E. P. Santos, *University of Florida*, *Gainesville*.

Objectives were to evaluate reproductive performance of grazing dairy cows subjected to different presynchronization and resynchronization protocols. Lactating cows (n=1268) in two dairies were blocked by parity, breed (Holstein, H=538; Jersey, J=235; and Holstein/Jersey Cross, C=494), and d postpartum, and then randomly assigned to 1 of 4 treatments in a 2x2 factorial: 1) Presynch: 2 injections of PGF given 14 d apart and starting the timed AI (TAI) protocol 11 d later; 2) G6G: injection of PGF followed 3 d later by GnRH and starting the TAI protocol 6 d later. The TAI protocol consisted of GnRH on d 0, PGF on d 5 and 6, and GnRH+TAI on d 8. On d 12 after the TAI, half of the cows in each presynchronization received one of the two resynchronizations: 1) RCON, cows were observed daily for estrus and inseminated starting on d 19 after TAI; 2) RCIDR, cows received a CIDR from d 12 to 19 after the TAI and were observed for estrus starting on d 19. Cows in estrus were inseminated. Blood was sampled and analyzed for progesterone on the first GnRH of the TAI. Pregnancy per AI (P/AI) was determined 30 and 60 d after the first TAI. The proportion of cows in estrus at timed AI did not differ (P=0.61) between Presynch and G6G (41.0 vs. 41.7%), but it was less (P=0.003) for H than J and C (29.6 vs. 47.7 vs. 46.4%). P/AI following the first TAI were 48.6 and 51.9% for G6G and Presynch (P=0.60), respectively. Method of resynchronization did not (P=0.65) influence P/AI; however, H had less (P=0.03) P/AI than J and C (42.2 vs. 54.2 vs. 54.0%). Cows in estrus at TAI had greater (P=0.004) P/AI than those not in estrus (57.9 vs. 44.9%). Although resynchronization influenced the pattern of return to estrus, it did not influence (P=0.96) the proportion of nonpregnant cows re-inseminated before d 30 (RCIDR=72.1 vs. RCON=71.5%). Breed influenced (P=0.05) the proportion of nonpregnant cows that was re-inseminated, and it lowest for H (66.0%) followed by C (72.0%) and then J (83.1%). Breed but not reproductive program influenced reproductive performance of grazing dairy cows.

Key Words: dairy cow, grazing, reproduction

T221 Follicular wave of the ovulatory follicle and not cyclic status influences fertility of dairy cows. R. S. Bisinotto*[1], R. C. Chebel[2], and J. E. P. Santos[1], [1]*University of Florida*, *Gainesville*, [2]*University of California Davis*, *Tulare*.

Two studies evaluated the influence of follicular wave at AI on fertility of dairy cows. In EXP1, data from 5,630 lactating cows enrolled in a

presynchronized timed AI protocol were analyzed. Cows had blood analyzed for progesterone (P4) 12 to 14 d apart, on the days of second PGF of the presynchronization and the first GnRH (GnRH1) of the timed AI protocol (Ovsynch or Cosynch72). Cows were classified as cyclic if P4>1 ng/mL and anovular if both samples had P4<1 ng/mL. Cyclic cows were categorized as low (CLow: <1 ng/mL) or high (CHigh: ≥1 ng/mL) P4 on the day of GnRH1, which would result in ovulation of the dominant follicle of the first (FW) and second (SW) follicular waves, respectively, at AI. Pregnancy per AI (P/AI) was determined 31 and 66 d after AI. In EXP2, 220 Holstein received 2 PGF given 14 d apart. The Ovsynch protocol (GnRH, 7 d PGF, 48 h GnRH, 12 h timed AI) initiated either 3 or 10 d after the second PGF to result in insemination to the FW or SW dominant follicles. Blood was analyzed for P4 and ovaries were scanned on the days of the second PGF of the presynchronization, GnRH1 and PGF of the Ovsynch. Only cyclic cows were enrolled. Pregnancy was determined on days 32 and 66 after AI. In EXP1, P/AI on d 31 was greater (P<0.001) for CHigh than anovular and CLow cows (43.0 vs. 29.7 vs. 31.3%, respectively). Short-cycling differed (P<0.001) among groups and were 7.1, 11.9, and 15.7% for CHigh, anovular and CLow, respectively. Pregnancy loss differed (P<0.05) only between anovular and CLow (10.0 vs. 15.0%), and it was intermediate for CHigh (13.5%). In EXP2, 9.8 and 97.2% of the FW and SW cows, respectively, had P4>1ng/mL at the GnRH1. Concentrations of P4 at GnRH1 (0.4±0.1 vs. 2.6±0.1 ng/mL) and PGF (2.1±0.2 vs. 2.9±0.2 ng/mL) were greater (P<0.002) for SW than FW cows. P/AI was greater (P=0.04) for SW than FW cows (41.7 vs. 30.4%), despite less (P=0.05) ovulation to GnRH1 in SW than FW cows (78.7 vs. 88.3%). These data indicate that follicular wave of the ovulatory follicle and not cyclic status influences fertility of dairy cows. Synchronization programs that induce ovulation of the FW follicle reduced P/AI of cows.

Key Words: anovular, dairy cow, follicular wave

T222 Resynchronization strategies to improve fertility in lactating dairy cows utilizing a presynchronization injection of GnRH or supplemental progesterone: II. Economic evaluation. L. G. D. Mendonça*[1], S. T. Dewey[2], G. Lopes Jr.[1], F. A. Rivera[1], F. Guagnini[1], J. Fetrow[4], T. R. Bilby[2,3], and R. C. Chebel[1], [1]*Veterinary Medicine Cooperative Extension, University of California Davis, Tulare*, [2]*Department of Animal Sciences, University of Arizona, Tucson*, [3]*Texas A&M AgriLife Research and Extension, Texas A&M System, Stephenville*, [4]*Veterinary Population Medicine, University of Minnesota, St. Paul*.

Objectives were to evaluate economics of resynchronization protocols for lactating dairy cows in 2 farms in CA and AZ. One week before pregnancy diagnosis (32±3 d post-AI) cows were enrolled in the study and assigned to 1 of 3 resynchronization protocols after balancing for parity, DIM, and number of AI. Treatments were control (CON), GGPG, and CIDR. GGPG cows received an injection of GnRH at enrollment (32±3 d post AI). At non-pregnancy diagnosis all cows were submitted to a timed AI (TAI) protocol (GnRH, 7 d later PGF, and 72 h later GnRH and TAI). CIDR cows received a CIDR insert at first GnRH until PGF injection. Cows were examined for pregnancy 39±3 d post-AI. For economic evaluation, parameters used were pregnancy value=$275, and cost of PGF=$1.5, GnRH=$1.5, CIDR=$10, and labor=$10/h. Number of cows submitted to resynchronization were CON=386, GGPG=357, and CIDR=316. Costs of resynchronization protocols for non-pregnant cows were (P<0.01) different (CON=$5.1±0.1, GGPG=$10.1±0.1, CIDR=$14.9±0.1). Pregnancy at 60 d after resynchronized AI was greater (P<0.02) for GGPG (30.9%) and CIDR (29.9%) cows than CON (22.2%). Average value of cows was greater (P=0.01) for GGPG ($85.86±7.07) than CON cows ($60.92±6.98), with CIDR cows ($75.99±7.53) not differing (P>0.10) from CON or GGPG cows. Average return per cow submitted to the resynchronization protocol tended to be affected by treatment, being GGPG treatment ($71.25±6.67) greater return than CON ($53.02±6.51), but CIDR ($63.88±7.07) was not different from CON or GGPG. By altering assumptions for pregnancy value from $100 to $500 ($50 increments), CIDR insert cost from $5 to $15 ($2.5 increments), and GnRH injection cost from $1 to $5 ($0.5 increments), 81 scenarios were generated and used to evaluate resynchronization protocols when proportion of cows not pregnant to pre-enrollment AI ranges from 20 to 70% (5% increments). The GGPG ($32.71±2.25) and CIDR ($32.59±2.25) treatments had (P<0.05) a greater average return than CON ($26.05±2.25), but no difference between GGPG and CIDR treatment was observed.

Key Words: resynchronization, dairy cow, economics

T223 Low progesterone concentration during superstimulation of the first follicular wave impairs embryo quality of lactating dairy cows. F. A. Rivera*[1], L. G. D. Mendonça[1], G. Lopes Jr.[1], R. V. Perez[1], F. Guagnini[1], M. Amstalden[2], R. G. S. Bruno[1], J. E. P. Santos[3], and R. C. Chebel[1], [1]*Veterinary Medicine Cooperative Extension, University of California Davis, Tulare*, [2]*Animal Reproduction Laboratory, Texas A&M University Agricultural Research Station, Beeville*, [3]*Department of Animal Science, University of Florida, Gainesville*.

Objectives were to determine the influence of progesterone (P4) concentration during superstimulation of the first follicular wave on embryo quality of lactating dairy cows. Holstein cows (n = 102) were enrolled in 1 of 3 treatments (first follicular wave, FW; first follicular wave with CIDR, FWC; and second follicular wave, SW). All cows received GnRH+CIDR, followed 7 d later by PGF2∝ and CIDR removal, and 2 d later cows received a second GnRH (study d 0). FW and FWC cows started the superstimulation on d 1, and SW cows received GnRH on d 6 and started the superstimulation on d 7. Cows were received 400 mg of FSH given twice daily for 5 d, and PGF2∝ concurrent with the ninth and tenth FSH injections. FWC cows received 2 CIDR inserts during superstimulation. All cows received GnRH 48 h after the first PGF2∝ and were inseminated 12 and 24 h later. Embryos were recovered 7 d after AI and embryos were classified according to IETS (grade 1, excellent/good; grade 2, fair; grade 3, poor; and grade 4, degenerated). Blood was sampled at each injection of the presynchronization, daily during the superstimulation, and at AI and embryo recovery. Concentration of P4 during the superstimulation protocol was smallest (P<0.01) for FW cows (FW=0.61 ± 0.16, FWC=1.85 ± 0.14, SW=3.34 ± 0.16 ng/mL), but there was no (P=0.84) difference in P4 concentration on the day of embryo recovery. Number of embryo/oocytes recovered was not (P=0.21) affected by treatments, but treatment affected (P=0.04) and tended (P=0.09) to affect number of embryos grades 1-3 (FW = 4.0 ± 0.7, FWC = 8.1 ± 1.7, SW = 5.2 ± 1.2) and oocytes (FW=2.4 ± 0.6, FWC=1.1 ± 0.4, SW=1.1 ± 0.4) recovered, respectively. Proportion of embryo/oocytes classified as embryos grades 1-2 was smallest (P<0.01) for FW cows (FW=41.6 ± 5.6, FWC=62.9 ± 6.3, SW=71.5 ± 6.7%) and proportion classified as oocyte tended (P=0.11) to be larger for FW cows (FW=27.8 ± 5.0, FWC=14.0 ± 5.6, SW=14.4 ± 6.0). Progesterone concentration during the superstimulation of the first follicular wave affects embryo quality and fertilization rate of lactating dairy cows.

Key Words: follicular wave, progesterone, superstimulation

T224 Resynchronization strategies to improve fertility in lactating dairy cows utilizing a presynchronization injection of GnRH or supplemental progesterone: I. Pregnancy rates and ovarian responses. S. T. Dewey*[1], L. G. D. Mendonca[2], G. Lopes Jr.[2], F. A. Rivera[2], F. Guagnini[2], R. C. Chebel[2], and T. R. Bilby[1,3], [1]*University of Arizona, Department of Animal Sciences, Tucson*, [2]*Veterinary Medicine Cooperative Extension, University of California-Davis, Tulare*, [3]*Texas A&M AgriLife Research and Extension, Texas A&M System, Stephenville*.

Objectives were to evaluate three resynchronization protocols for lactating dairy cows in two farms in CA and AZ. One week before pregnancy diagnosis (32±3 d after pre-enrollment AI) cows were enrolled and assigned to 1 of 3 resynchronization protocols after balancing for parity, DIM, and number of AI. Treatments were control (CON), GGPG, and CIDR. The GGPG cows received an injection of GnRH at enrollment (32±3 d post AI). At non-pregnancy diagnosis (39±3 d) all cows were submitted to a timed AI (TAI) protocol (GnRH, 7 d later PGF, and 72 h later GnRH and TAI). The CIDR cows received a CIDR insert at first GnRH until PGF injection of the TAI protocol. In total, 1,059 cows were submitted to resynchronization protocols (CON=386, GGPG=357, and CIDR=316). In a subgroup of cows, ovaries were scanned and blood for progesterone (P4) was sampled on day of first GnRH and PGF injections. All cows were diagnosed for pregnancy at 39±3 d (PR1), and reconfirmed at either 60 or 120 d (PR2). The GGPG cows had more CL than CIDR and CON cows on day of first GnRH (1.19 vs. 0.93 vs. 0.91±0.05, respectively) and PGF (1.25 vs. 0.82 vs. 0.81±0.05) injections, but CIDR and CON cows did not differ. Greater proportion of GGPG cows had P4≥1 ng/mL on day of first GnRH than CIDR and CON cows (79.14% vs. 64.53% vs. 71.81%, respectively), but CIDR and CON did not differ. There were no differences between treatments in proportion of cows with P4≥1 ng/mL on day of PGF injection or mean P4 concentrations on day of GnRH and PGF injections. The PR1 was and tended to be greater for GGPG (33.6%) and CIDR (31.3%) cows, respectively, than CON (24.6%) cows, and GGPG (31.2%) and CIDR (29.5%) cows had greater PR2 than CON cows (22.1%). The PR1 and PR2 were not different between GGPG and CIDR cows. The interaction between treatment and BCS affected PR1 and PR2, because GGPG treatment increased PR1 and PR2 of cows with BCS>2.75, and CIDR treatment increased PR1 and PR2 of cows with BCS≤2.75. Presynchronizing cows with an injection of GnRH or use of supplemental progesterone can increase pregnancy rates.

T225 Effect of follicular replacement prior to ovsynch and use of somatotropin at insemination on pregnancy rate at first service of Holstein cows exposed to warm climate. D. R. Lozano*[1] and C. F. Aréchiga[2], [1]*Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Aguascalientes, Aguascalientes, México*, [2]*Universidad Autónoma de Zacatecas, Zacatecas, Zacatecas, México*.

Objective was to evaluate the effect of follicular replacement prior to Ovsynch protocol (d 0, GnRH; d 7, PG; d 9, GnRH; d 10, timed artificial insemination) as well as the use of bovine somatotropin (bST) at the time of insemination on pregnancy rates at first service. Lactating Holstein cows were assigned at random to the following treatments: 1) PG (n=80), cows were induced to estrus synchronization with 500 mg of synthetic prostaglandin; 2) PG+ bST (n=70), cows were induced to estrus with synthetic prostaglandin and received 500 mg of bovine somatotropin at the time of artificial insemination; 3) Ovsynch protocol (n=83); 4) Ovsynch + bST at the time of insemination (n=78); 5) GnRH + Ovsynch (n=72), cows received 100 µg of a GnRH analogue to induce follicular replacement 5 days before the beginning of Ovsynch protocol (d -5 GnRH-a; d 0-9, Ovsynch); 6) GnRH + Ovsynch + bST (n=73), (d -5, GnRH-a; d 0-9, Ovsynch; d 10, bST). Days in milk (DIM) and body condition score (BCS) at the beginning of treatment, and days to conception were analyzed by lineal models. Pregnancy rate to first service and postpartum distribution of pregnant cows were analyzed by Xi-square. DIM (56.4 ± 3.6) and BCS (3.0 ± 0.4) were similar among treatments (P>0.05). Follicular replacement before Ovsynch did not increase pregnancy rates to first service (35.2%) nor reduced the days to conception (122.8 ± 6.9) (P>0.05). Administration of bST did not improve pregnancy rates to first service (P>0.05). Ovsynch improved pregnancy rate to first service (36.6%) and reduced days to conception (111.1 ± 6.7 d) compared to prostaglandin program (26.6% and 136.5 ± 5.3 d, respectively) (P<0.05). 60.0% of the cows assigned to Ovsynch were pregnant in the first 93 days postpartum, such percentage was superior to ones observed in prostaglandin program (31.1%, P<0.05). Neither follicular replacement before Ovsynch nor bST at the time of insemination improved fertility at first service in lactating Holstein cows exposed to warm climate in central Mexico.

Key Words: warm season, somatotropin, fertility

T226 Dynamics of luteolysis using two $PGF_{2\alpha}$ analogs and subsequent differences in fertility. J. P. N. Martins*, R. Policelli, and J. R. Pursley, *Michigan State University, East Lansing*.

Probability of pregnancy decreases substantially in lactating dairy cows treated with Ovsynch if CL regression is delayed or incomplete. This is observed in ~10% of cows treated with Ovsynch utilizing dinoprost tromethamine (DINO). DINO has a shorter half-life (t½) of 7 to 18 minutes compared to cloprostenol sodium (CLO), which is more resistant to endogenous metabolism and maintains a higher circulating concentration for a longer time (t½ ~ 3 hours). We hypothesized that CLO could reduce the time to complete luteolysis (defined as P4 decreasing to and maintaining concentrations less than 0.5 ng/ml) and increase conception rates. In Study 1, lactating dairy cows (n=36) received the same synchronization strategy (25mg of $PGF_{2\alpha}$ – 2d later 100 µg GnRH – 6 d later GnRH – 7 d later $PGF_{2\alpha}$). At time of final $PGF_{2\alpha}$, cows were assigned randomly to receive either 500 µg CLO or 25 mg DINO. Blood samples were collected prior to (daily) and after (hourly) $PGF_{2\alpha}$ treatment to analyze circulating concentrations of P4. Utilizing ultrasound, only cows that responded to injections prior to $PGF_{2\alpha}$ treatment were included. The decline in P4 was accelerated for CLO at time points between 2 and 10 h post-injection, but not at 12, 24, 36 and 48 h in cows with complete luteolysis. Percent of cows that did not have complete CL regression did not differ between treatments. Cows that did not have complete CL regression did not ovulate (0/5). Time to complete luteolysis was 29.7 ± 1.2 vs. 29.4 ± 1.7 h, P = 0.89, and ovulation was 101 vs. 103 h, P = 0.56, in CLO vs. DINO. There was a rapid drop in P4 one hour after $PGF_{2\alpha}$ then complete rebound 1 h later followed by a steady decline. In Study 2, lactating dairy cows were treated with a pre-synch/Ovsynch program comparing DINO vs. CLO (n=652) to determine differences in fertility of the two products. There was a tendency for greater conception rates in CLO vs. DINO (41 vs. 36%; P=0.11) with similar differences within each parity. In summary, there was a difference in the dynamics of luteolysis early but not late following CLO or DINO and a trend for greater conception rates following CLO.

Key Words: cloprostenol sodium, dinoprost tromethamine, luteolysis

T227 Effects of presynchronization with hCG 7 d prior to estrous synchronization and fixed-time AI (TAI) on fertility and concentrations of progesterone in suckled beef cows. G. Marquezini*[1], C. R. Dahlen[2], S. L. Bird[3], B. J. Funnell[3], and G. C. Lamb[1], [1]*North Florida Research and Education Center, University of Florida, Marianna*, [2]*Northwest Research and Outreach Center, University of Minnesota, Crookston*, [3]*North Central Research and Outreach Center, University of Minnesota, Grand Rapids*.

We determined whether hCG administered 7 d prior initiation of estrous synchronization would affect concentrations of progesterone and increase pregnancy rates. Suckled beef cows at three separate locations were stratified by days postpartum and parity and randomly assigned to two treatments: 1) cows received 100 μg of GnRH at CIDR insertion (d -7) and 25 mg of $PGF_{2\alpha}$ at CIDR removal (d 0), followed in 67 h by GnRH and TAI (d 3; control; n = 130). 2) same as control, plus cows received 1,000 IU of hCG 7 d (day -14) prior to CIDR insertion (hCG; n=129). Transrectal ultrasonography was used to determine pregnancy status on d 30. Blood samples were collected on d -25, -14, -7, 0 and 3 to determine concentrations of progesterone. Pregnancy rates were similar between control (53.4%) and hCG (54.2%). Pregnancy rates for estrous cycling cows (62.5%) tended ($P = 0.11$) to be greater than noncycling cows (47.6%); however, treatment with hCG failed to increase pregnancy rates in noncycling cows. Of noncycling cows on d -14, hCG (37.9%) induced a greater ($P < 0.05$) percentage of cows to have elevated progesterone (>1 ng/mL) than controls (17.0%) on d -7. Percentage of cycling cows was greater ($P < 0.05$) at location 3 than locations 1 and 2. In addition, location 3 had greater ($P < 0.01$) concentrations of progesterone on d -25, -14, -7, and 0 than locations 1 and 2. Concentrations of progesterone were greater ($P < 0.01$) on d -7 for hCG than control cows (1.84 ± 0.19 vs 1.22 ± 0.19, respectively), but were similar between treatments on d 0 and 3. Although pretreatment with hCG increased concentrations of progesterone and percentage of cycling cows at initiation of estrous synchronization, pregnancy rates were not enhanced.

Key Words: human chorionic gonadotropin, beef cows, estrous synchronization

T228 Comparison of two protocols to achieve pregnancy to fixed-time artificial insemination (TAI) in suckled beef cows. S. E. Echternkamp*, W. G. Hays, S. A. Jones, and R. A. Cushman, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

Application of AI in extensive beef cattle production is limited by the necessity to monitor estrus and handle animals twice daily for several weeks. Protocols that effectively synchronize ovarian follicular development and ovulation to enable TAI would facilitate use of AI. Objective was to determine whether adding a controlled internal drug-release device (CIDR) to a GnRH-based protocol would increase blood progesterone (P4) concentrations, ovarian synchrony, and pregnancy rate to TAI. Cyclic suckled beef cows (n=1238) in 6 herds on Center received 1 of 2 treatments: 1) an injection of GnRH (100 μg i.m.) followed by 25 mg $PGF_{2\alpha}$ (PGF) i.m. 7 d later, followed by GnRH (100 μg i.m.) 60 h after PGF (CO-Synch), or 2) Co-Synch plus a CIDR during the 7-d interval between GnRH and PGF injections (Co-Synch + CIDR). All cows were bred by TAI 60 h after PGF. Cows were fitted with an Estrotect heat detector. Estrus was monitored 3 wk before and during treatment and at TAI. Blood samples were collected at GnRH (first) and PGF injections; P4 was assayed in plasma by RIA. Pregnancy was diagnosed 70 to 90 d after AI. Results did not differ among herds. Progesterone did not differ between protocols at first GnRH (4.0±0.1 ng/mL) but was greater ($P < 0.01$) at PGF injection in Co-Synch + CIDR- vs. Co-Synch-treated cows (4.6 vs. 3.5±0.1 ng/mL, respectively), and fewer CIDR-treated cows had P4 ≤1 ng/mL at PGF (10.7 vs. 28.4±1.0%, respectively). A greater ($P < 0.01$) percentage of Co-Synch + CIDR vs. Co-Synch cows expressed estrus after PGF (63.4 vs. 54.4±2.0%) and were pregnant to TAI (53.5 vs. 43.2±2.0%, respectively). For cows with P4 ≤1 ng/mL at PGF, CIDR increased pregnancy rate (59.1 vs. 27.6±2.0% with vs. without CIDR), whereas pregnancy rates did not differ between protocols when P4 was >1 ng/mL. Inclusion of a CIDR in the synchronization protocol increased plasma P4 concentrations, estrus detection, and pregnancy rates, primarily in cows with low endogenous P4 secretion.

Key Words: beef cows, progesterone, timed insemination

T229 Relationship between follicular profiles and the superovulatory responses in cattle. H. Kohram* and H. Kermani Moakhar, *Department of Animal Science, Faculty of Agriculture, Karaj, Tehran, Iran*.

The objective of this experiment was to determine the influence of follicular profiles over 4 days prior to superovulation on superovulatory responses in terms of the number of large follicles (F; ≥ 7mm) at estrus and corpus luteum (CL) 7 days later. Ultrasonography was performed once daily prior to gonadotropin treatment, on the day of estrus during superovulation and 7 days later. Animals conventionally superovulatd (400 mg Folltropin-V) between days 8 to 12 of the estrous cycles and 88 superovulation cycles were considered in the present experiment. Data were analyzed by means of the GLM procedure of the SAS. In these cases, the diameter of largest follicle (F1) and the difference between the diameter of F1 and the second largest (F2) follicle (F1-F2) responses were indicative of a morphologically dominant follicle in the growing and regressing phases in animals. Each type of superovulatory responses was divided in the three classes as low (≤4), medium (5-9) and high (≥10) numbers of F and CL, respectively. The number of superovulatory cycles with low, medium and high responses showed in Table 1. The diameters of F1 (11.8±.31 vs 10.9±1.55 and 10.9±.2) and F1-F2 (6.73±.57 vs 3.78±.59 and 4.8±.47) during 4 days before superovulation were not different (p>0.1) between the three groups of animals. In conclusion, the profile of F1 and F1-F2 before a conventional superovulatory treatment did not affect the number of large follicles at estrus and corpus luteum 7 days later.

Table 1. The number of superovulatory cycles with low, medium and high responses.

	Nb. of superovulatory cycles		
Type of responses	Low (≤4)	Medium (5-6)	High (≥10)
Follicular at estrus	9	18	61
CL 7 days after superovulation	20	21	47

Key Words: cattle, follicle, superovulation

T230 Ovarian follicular dynamics during the estrous cycle in water buffalo. H. Kohram*[1], G. Mohammadi[2], and E. Dirandeh[1], [1]*University of Tehran, Iran*, [2]*Shahid Chamran University, Ahvaz, Khoozestan, Iran*.

There are few studies done to clarify the pattern of ovarian follicular growth and manipulation of these phenomena in female buffaloes. The purpose of the present study was to characterize follicular dynamics during the estrous cycle in water buffalo. Buffaloes (n=5) were synchro-

nized with 2 intramuscular injections of prostaglandin F2Î± given 11 days apart (estrus = d 0). Ovarian follicular development was monitored daily from estrus d 0 to the next estrus by real-time ultrasonography, B-mode instrument with a 7 MHz linear-array transducer. Data were analyzed using the GLM procedure of SAS. Result showed that follicular growth during the estrous cycle occurs in a wave like pattern. The buffalo showed two wave (n=2) or three wave (n=3) of follicular growth. The first follicular wave begin at d 1.0 in buffaloes with two and three follicular waves (ovulation=d 0). The second wave appeared at d 9.5±0.5 and 8.0±0.0 d (P<0.05) for the 2 and 3 wave cycle animals, respectively. The third wave started at 14.6±0.7 d. During the two and three follicular waves the maximum diameters of the dominant follicles (±SEM) were 15.0±1.0 and 10.0±1.0, respectively. The mean length interval between ovulation in 2 and 3 wave cycles was (18.5±0.5 vs 20.3±0.5 d, P<0.05). Our results suggest that follicular growth in water buffaloes is a dynamic process, and occurs in waves.

Key Words: ultrasonography, buffalo, follicle

T231 The response to a progestin-based ovulation induction in anoestrous goats is enhanced by bovine somatotropin applied 5 days before the end of progestin treatment. A. M. Martinez, C. G. Gutierrez, Y. Dominguez, and J. Hernandez-Ceron*, *Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México*, *México*.

Fertility and prolificacy are lower in anoestrous goats induced to ovulate than in cycling goats. Treatment with bST during synchronization increases fertility and prolificacy in sheep during the reproductive season. Here, we tested whether a single dose of long acting bST 5 days before the end of progestin treatment increases kidding rate and prolificacy in anoestrous goats induced to ovulate. One hundred nine cross breed goats (Boer and Alpina) varying in parity received an intravaginal sponge containing 45 mg of fluorogestone acetate, which remained in place for 12 days. On day twelve of treatment, does received 300 UI of eCG. Five days before sponge withdrawal goats were randomly assigned to two groups: bST group (n =53) received a depot injection of 125 mg sc of bST. The control group (n = 56) received equal amount of saline solution. After withdrawal of progestin treatment, goats were observed for signs of estrous, by means of a male goat fitted with an apron. Goats in estrus were mated with males of proved fertility. Treatment with bST increased (P=0.018) the proportion of goats in estrus (bST, 73% vs. control, 52%). Conception rate did not differ (P=0.12) (bST, 82% vs. control, 65%). The kidding rate was higher (P=0.005) in bST (60%) than in the control group (34%). Treatment with bST did not increase (P=0.9) the proportion of goats delivering twins (bST, 59% vs. control, 63%). IGF-I and insulin concentrations were higher (P=0.001) in goats treated with bST than in control goats. It is concluded that a single dose of bovine somatotropin 5 days before the end of progestin-based ovulation induction in anoestrous goats increases kidding rate.

Key Words: fertility, goats, bST

T232 Ovarian response to different doses of eCG after synchronization of estrous and ovulation with CIDR during 14 days in the breeding season in goats. L. F. Uribe-Velásquez*[1], M. I. Lenz Souza[2], and J. H. Osorio[1], [1]*University of Caldas*, *Manizales, Caldas, Colombia*, [2]*Federal University of Mato Grosso do Sul*, *Campo Grande, MS, Brazil*.

The objective was compare the effect of equine chorionic gonadotrophin (eCG) on the follicular dynamics and hormonal concentrations in Alpine goats, which were subjected to estrous synchronization protocols with controlled internal drug released (CIDR) devices containing progesterone for 14 days during breeding season. Female goats (n=24) were divided at random into four groups of 6 animals each. On the day of dispositive removal, the animals received 0 (T1-Control), 200 (T2), 300 (T3) and 400 UI of eCG (T4). Echographic inspection of the ovaries was conducted with a real-time scanner (ALOKA SSD 500) equipped with a transrectal 7.5 MHz linear-array transducer. During examination, the animals were fixed in a standing position. Ultrasound examination was started 1d day prior to administration of eCG until next ovulation. All ovarian follicles ≥2mm were measured, and their relative locations were recorded on an ovarian map in order to follow the sequential development. Daily plasma estradiol and progesterone concentrations were determined using RIA. The continuous variables were evaluated with the variance analyses under GLM procedures of SAS. Size of the largest follicle was smaller (P<0.01) in control animals of wave 3 (5.5± 0.50 mm) when compared with the Treatment 3 at the same wave (7.17 ± 0.35 mm). The effects of eCG on follicular growth showed higher mean number of small follicles (P<0.05) in wave 1 (T3: 11.2± 0.62) and 2 (T4: 9.6±0.22) compared with control group (4.2±0.13 and 6.2±0.14 small follicles in wave 1 and 2, respectively). There were significant differences in P4 (P<000.01) and E2 (P<0.001) concentrations. Progesterone were higher in the eCG group treated with 300 UI (4.34±0.21 ng/mL) as compared with the others groups on day 4. The animals in T3 and T4 had significantly higher concentrations of estradiol with values of 15.05±0.86 vs 17.72±0.34 pg/mL and 17.27±0.32 vs 14.64±0.85 pg/mL on days 10 and 17, respectively. The use of CIDR+eCG increased the recruitment of small follicles and accelerated the mechanism of follicular growth.

Key Words: goats, follicular dynamics, eCG

T233 Origin and fate of preovulatory follicles after induced luteolisis at different stages of the luteal phase of the estrous cycle in ewes. L. F. Uribe Velásquez*[1], M. I. Lenz Souza[2], and M. Vélez Marín[1], [1]*University of Caldas*, *Manizales, Caldas, Colombia*, [2]*Federal University of Mato Grosso do Sul*, *Campo Grande, MS, Brazil*.

The purpose of this study was to evaluate ovarian response, using transrectal ovarian ultrasonography, to 2 injections of Prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) given at differents intervals. Fourteen Bergamasca ewes were examined during the breeding season. All ewes were injected with an i.m. dose of $PGF_{2\alpha}$ analogue. Ewes were randomly allocated to two groups (n = 7) which received $PGF_{2\alpha}$ 7d (G7) or 9d (G9) after ovulation (when the dominant follicle of wave 2 was expected to be in the growing and plateau phase, respectively). Ovaries were examined daily with transrectal ultrasonography Aloka 500 with 7.5 MHz linear array transducer. Jugular vein blood samples were collected daily for progesterone (P_4) assay. Serum P_4concentration were lower in G7 that in G9 immediately before $PGF_{2\alpha}$ treatment (4.10±0.17 vs. 4.91±0.29 ng/ml., respectively; P<0.05). Mean maximum diameter size attained by the dominant follicle of wave 2 tended to be larger in the group treated in G7 when compared with G9 (5.5±0.19 vs. 4.29±0.26 mm; P<0.05). There was effect of day with total follicles (P<0.001). Number of small follicles (2-2.5 mm) was greater (4.57±0.78 vs. 8.42±1.36) at day 6, for G7 and G9, respectively, whereas no changes were observed in medium follicles (3-3.5 mm) between groups treated. The proportion of large follicles (4 mm) increased after luteolysis. Values were lower for ewes treated on G7, whereas values were more stable over time for

ewes treated on G9. In conclusion, ewes with rapid and complete luteal regression, ovulation occurred from the dominant follicle of wave 2 when the animals are treated on days 7 and 9.

Key Words: follicles, prostaglandin, ultrasonography

T234 Endocrine function and follicular growth in sheep treated with exogen progesterone. L. F. Uribe Velásquez*[1], M. I. Lenz Souza[2], and A. Correa Orozco[1], [1]*University of Caldas*, *Manizales, Caldas, Colombia*, [2]*Federal University of Mato Grosso do Sul*, *Campo Grande, MS, Brazil*.

The effects of progesterone (P_4) on ovarian follicular growth and reproductive endocrinology were studied. Fourteen ewes, synchronized using prostaglandin ($PGF_{2\alpha}$), were randomly divided in two groups (n=7/group); control group and progesterone-treated group (CIDR) after ovulation (day zero). From one day before PG injection until day 10, ultrasonic scanning was carried out transrectally while the animals were fixed in a standing position using an Aloka SSD-500 with a 7.5 MHz for to establish follicular growth. Blood samples were collected from one day before PG until day 10 post-ovulation and serum concentrations of P_4 were determined by radioinmmunoassay. For profile of luteinizing hormone (LH) pulses, blood samples were collected at 30-min intervals for a period of 8h on days one and six. LH were determined by previously validated radioinmmunoassay. The growth rate was different between groups (P<0.001), being 0.91±0.15 and 0.70±0.16mm/d for control and treated group, respectively. Mean concentrations of P_4 (P<0.001) were different between treatments, with values on the day of maximum follicular growth of 3.82±0.17 ng/ml (control) and 5.56±0.56 ng/ml (treated). Mean plasma LH concentration and LH pulse amplitude there were no significant differences between groups (P<0.05). Differences in LH pulse frequency on day one (P<0.01) and day six (P<0.05) were observed (Table1). These data suggest that the inhibitory effects of exogen P_4 on the diameter of dominant follicle was mediated by reduced LH pulse.

Table 1. Mean LH concentrations (µg/L) and LH pulse frequency (pulse/8h) and amplitude (µg/L) on day one and day six of the estrous cycle (Mean ± SD).

Day	Group	Concentration	Pulse amplitude	Pulse frequency
1	Control	0.66±0.11 a	0.33±0.30 a	2.55±0.09 a
1	Treated	0.56±0.27 a	0.42±0.21 a	1.49±0.11 b
6	Control	0.68±0.11 A	0.87±0.30 A	2.20±0.09 A
6	Treated	0.58±0.27 A	0.70±0.21 A	1.22±0.11 B

Mean with different letters within columns differ: a vs b (P<0.01) y A vs B (P<0.05)

Key Words: follicular dynamic, LH, progesterone

T235 Real time PCR quantification of mRNA expression in the corpus luteum of cows induced to ovulate following different hormonal treatments. P. Ponce Barajas*[1,2], M. G. Colazo[1], J. P. Kastelic[3], M. K. Dyck[2], and D. J. Ambrose[1,2], [1]*Alberta Agriculture and Rural Development*, *Edmonton, AB, Canada*, [2]*University of Alberta, Dept of Agricultural Food and Nutritional Science*, *Edmonton, AB, Canada*, [3]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

The objective was to determine if the expression of genes involved in steroidogenesis (StAR, P450scc) or otherwise relevant to CL function (NR3C1, VEGFA, FAS, EP2, PGHS2, SREBP1, OCT4, OXTR, and PGFR) differed among CL formed spontaneously or after ovulation induced with GnRH, porcine LH, or estradiol benzoate (EB). Twenty-four cows were induced to ovulate naturally without any treatment (Control; n=4) or with 1 of 4 treatments [12.5 mg pLH (n=4), 25 mg pLH (n=6), 100µg GnRH (n=5) or 1 mg EB (n=5)]. On Day 12 post ovulation, ovaries were surgically removed for the total RNA (1µg) purification from CL tissue sections using TRIzol®Plus kit for a two-step real-time Q RT-PCR analysis with Power SYBR® Green PCR Mix in a 7900HT Fast Real-Time PCR System. Data obtained as cycle threshold (C_T) value, were normalized in the comparative C_T method using a normalization factor of the geometric mean of three selected house keeping genes (H2AFZ, G3PDH and SDHA). Data were transformed with control group mean as calibrator (Vandesompele et al. 2002; Genome Biol. 3/7/research/0034). GLM procedure was used to analyze the data and comparison of means performed using the pdiff option in SAS. No statistical differences were evident in the expression of most genes analyzed. The expression of StAR in CL of cows induced to ovulate with 12.5 mg pLH tended (P<0.07) to be greater than in Control (1.94 vs. 1.00), whereas the expression of OXTR gene was lower in CL induced after EB and GnRH treatments, relative to Control (0.33 and 0.29 vs. 1.00; P<0.05).

Key Words: corpus luteum, gene expression

Production, Management and the Environment: Dairy

T236 A stochastic decision support system tool for dairy expansion. J. Janowski* and V. E. Cabrera, *University of Wisconsin*, *Madison*.

Study objectives included addressing specific producer needs during periods of herd growth and developing a stochastic decision support system tool employed for risk management in dairy production and expansion. Three million lactations from the past five years have been compiled in a database which includes monthly recordings of milk and component production, pregnancy status, and culling decisions. Simulation based on those records will guide the development of best management practices using identified performance measures as benchmarks. Markov chain simulation assigns probabilities to predicted performance levels of individuals or groups of cattle within specific time periods. Creation of a decision support system tool with functions designed for modeling herd structure and production over time will allow users to run "what-if" analyses adapted to a wide variety of herd management and economic conditions. Four bred heifer purchasing strategies were evaluated over a 54-month period and income over variable cost calculations were conducted to identify optimal herd growth strategies for a herd that grew from 150 to 300 cows. A strategy which involved purchasing 98 bred heifers within the first three months of the expansion phase

produced a 14% higher income over variable cost compared to mean values of all scenarios evaluated. Sensitivity analysis was conducted to further validate these results using price levels 10% above and below past five year averages for milk, culling, and bred heifer prices. Mean total income over variable costs for the optimal purchasing strategy during the 54-month term was $1,743,282 (SD = 457,117) or $5,267 (SD = $1,380) per cow. Although initial results indicate strong positive gains in income over variable costs for all growth strategies, facility and other capital investments were not considered in this study. Inclusion of these costs is subject to further development.

Key Words: decision support system, simulation, dairy expansion

T237 Airborne endotoxin concentrations at a large open lot dairy in Southern Idaho. R. S. Dungan and A. B. Leytem*, *USDA-ARS, Kimberly, ID*.

Endotoxins are derived from Gram-negative bacteria and are a potential respiratory health risk for animals and humans. To determine the potential for endotoxin transport from a large open lot dairy, total airborne endotoxin concentrations were determined at an upwind location (background) and five downwind locations on three separate days. The downwind locations consisted of the edge of the lot, 200 and 1,390 m downwind from the lot, and downwind from a manure composting area and wastewater holding pond. When the wind was predominantly from the west, the average endotoxin concentration at the upwind location was 24 (SE = 11) endotoxin units (EU) m^{-3}, while at the edge of the lot on the downwind side it was 259 (SE = 68) EU m^{-3}. At 200 and 1,390 m downwind from the edge of the lot, the average endotoxin concentrations were 168 (SE = 27) and 49 (SE = 9) EU m^{-3}, respectively. Airborne endotoxin concentrations downwind from the composting site and wastewater holding pond, and 1,390 m from the edge of the lot, were not significantly different than the upwind location. In addition, there were no significant correlations between ambient weather data collected and endotoxin concentrations over the experimental period. The downwind data show that the airborne endotoxin concentrations decreased exponentially with distance from the lot edge. Decreasing an individual's proximity to the dairy should lower their risk of airborne endotoxin exposure and associated health effects.

Key Words: endotoxin, dairy, lipopolysaccharide

T238 Iodine levels in Canadian bulk-tank milk. S. I. Borucki-Castro*[1], R. Berthiaume[1], S. Turcotte[2], A. Robichaud[2], and P. Lacasse[1], [1]*Dairy and Swine R&D Centre, Sherbrooke, QC, Canada*, [2]*Health Canada, Food Directorate, Health Products and Food Branch, Longueil, QC, Canada*.

A study was conducted, to determine concentration of iodine in bulk-tank milk and its relationship with milking and feeding management practices. Milk samples were collected from the bulk-tank of 501 farms across all provinces of Canada. In order to obtain further information about the farm's management, a questionnaire was completed by each of the selected farms. Total iodine concentration (organic and inorganic) of milk was determined using inductively coupled plasma mass spectrometry. Descriptive statistics and the analysis of the relationship between management practices and iodine levels were done using Student- t and ANOVA statistic tests. The mean iodine level in Canadian bulk-tank milk was 304 ± 8.4 μg/kg. There was a wide range of iodine concentrations (54 to 1,902 μg/kg), with a high coefficient of variation (61.7%). Analysis of the questionnaire′s data suggests that farms using total mixed rations instead of component feeding produced higher milk iodine (340 vs. 269 μg/kg; $P < 0.001$). Interestingly, neither usage of mineral supplementation nor the form of the supplementation affected iodine levels in milk. Washing the teats before milking was associated with lower concentrations of iodine (314 vs. 286 μg/kg; $P = 0.09$). Teat dipping before milking resulted in higher levels of iodine in bulk-tank milk (328 vs. 274 μg/kg; $P < 0.001$), but the form of application of the teat sanitizers appears important as spray applications (in line or hand spray) were associated with higher levels compared with the dip cup procedure (408 vs. 312 μg/kg; $P < 0.05$). As the vast majority of farms used teat dipping after milking, no significant association was found. However, its form of application appears important ($P<0.01$) averaging 296, 447 and 328 μg/kg for dip cup, in line spray and hand spray respectively. In conclusion, Canadian bulk-tank milk iodine concentration varies considerably and appears to be influenced by feeding and milking practices. *This research was supported by the Dairy Farmers of Canada.*

T239 Sicilian dairy herd demographics with a focus on culling. D. Galligan*[1], G. Azzaro[2], A. Pozzebon[2], S. Ventura[2], and G. Licitra[2,3], [1]*University of Pennsylvania, School of Veterinary Medicine, Kennett Square*, [2]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [3]*D.A.C.P.A., University of Catania, Italy*.

Measuring culling is an important metric in managing a dairy herd. Basic, herd demographic data (number of cows, age, reproductive status, etc) and culling information (date of culling, reason for culling) was collected from 1999-2008, on the CoRFiLaC computer record system for dairy farms in the Hyblean region, Province of Ragusa, Sicily. Over the study period, a total of 403 dairy farms participated with 388 herds starting in 1999. Complete culling records (27,714) from 32,819 culled cows were examined and comparisons made to similar records from the US dairy NAHMS (2007) report. The top ranking reasons for culling (% of culled cows), reproductive inefficiency (28.8%), and mastitis (13.1%) matched in ranking the findings of the NAHMS for US dairy herds. Other reasons for culling included traumatic reticulitis 10.9%, low production 6.2%, and lameness 2.4%. Eight percent of culls occurred before 42 days in lactation. Four methods were used to estimate the annual culling rate/herd: A) culled/calving per year, B) number culled/ (average of starting and ending population), C) number culled/(average of starting and ending + culls), and D) based on the average age of cows and heifers calving. These methods were compared to an epidemiological rate based on the (number annually culled/(sum of total cow days in the herd/365)). Equation B was symmetrical to the epidemiological rate, reflecting the limitations of estimating the average annual population on a beginning and ending point. Equation A over-estimated the culling rate, reflecting the fact that many cows have calving intervals greater then 12 months thus reducing their measured presence in the denominator. At very low culling levels, equation C was symmetrical around the epidemiological calculation but then underestimated the rate at higher levels.

Key Words: culling rate, management, dairy cattle

T240 The effect of pregnancy on milk fat percent. C. D. Dechow*[1], J. E. Vallimont[1], J. S. Clay[2], and C. G. Sattler[3], [1]*The Pennsylvania State University, University Park*, [2]*Dairy Records Management Systems, Raleigh, NC*, [3]*Select Sires, Inc., Plain City, OH*.

The objective of this study was to estimate the effect of pregnancy on test day milk fat percent (TDFAT). Dairy Records Management Systems, Raleigh, NC, provided lactation records for 12,726 Holstein cows with

a successful first service that could be confirmed by a subsequent calving date. Lactations commenced between September 2005 and March 2007. Days to first service were limited to 41 to 216 d and first through ninth lactations were represented. Data analysis included 64,041 test days after confirmed conception. Three seasons of calving were used and duration of pregnancy was defined as months carried calf (MCC). Values for MCC were one to eight, as month nine had few observations (n=23) and was combined with month eight (n=2339). Initially, a two trait model in ASREML was used for data analysis of TDFAT and test day milk yield (TDMILK), and variables were MCC, week of lactation, herd-year-season of calving, age at calving, and parity. Residual variance was varied by MCC. Months carried calf and week of lactation were both significant predictors of TDFAT ($P<0.001$). A second analysis was done for TDFAT with TDMILK added to the model as a covariable. Months carried calf remained a significant predictor of TDFAT, and week of lactation and TDMILK were also significant in this model ($P<0.001$). Least-squares-means for TDFAT increased as MCC increased in both models. Test day milk fat percent increased from 3.88% to 3.98% between MCC 3 and MCC 8 in the first model, and from 3.78% to 3.84% between MCC 2 and MCC 8 in the model that included TDMILK as a covariate. Results indicated that increasing duration of pregnancy may influence milk fat percentage of dairy cows.

Key Words: milk fat percent, duration of pregnancy

T241 Effect of rumen protected niacin (NiaShure®) supplementation during summer on milk production, and composition in lactating dairy cows. S. Emanuele*[1] and D. Schoenbaum[2], [1]*Balchem*, *New Hampton, NY*, [2]*Akey*, *Lewisburg, OH*.

Previous studies feeding 12 g/d of rumen-protected niacin (NiaShure®) reported that supplementation of niacin to lactating cows during periods of heat stress increased milk fat, milk protein percent and energy corrected milk. The objective for this trial was to determine the effect of supplementation of rumen-protected niacin (NiaShure®) at 6 g/d on milk yield and composition in cows producing greater than 45 kg of milk. The trial was conducted on a commercial dairy in central NY. Two groups of early lactation cows (n= 185/group) were balanced for milk yield, DIM, and parity and assigned to either a control or rumen-protected niacin (RPN) diet (6 g/d, NiaShure®). Diets were identical except for the addition of RPN. The diets contained whole cottonseed and tallow and dietary fat concentration was 5.8%. Diets were fed June through September. Milk yield and composition was measured monthly by DHIA. Milk yield and composition was analyzed using the mixed model procedure of SAS. Pen was the experimental unit used for statisitical analysis. Fixed effects were treatment, month and treatment X month. Milk yield was not different between treatments, 48.6 kg/d and 48.3 kg/d. Milk true protein percent was increased 4.8% by supplementation of NiaShure® ($p<0.02$). Milk true protein percent was 2.59% and 2.72% for control and NiaShure® diets. Milk fat percent was not different for control and NiaShure® diets (3.27% and 3.34%). There was a trend for a reduction in milk fat to protein ratio ($p<0.09$) on the NiaShure® diet compared to the control diet (1.23 versus 1.27). Supplementation of NiaShure® during the summer increased the value of milk by increasing milk protein by 0.13 units.

Key Words: niacin, rumen-protected niacin, NiaShure

T242 Effect of mixing before on-farm milk sampling on milk fat percent. M. Vazirigohar* and M. Dehghan Banadaki, *University of Tehran*, *Karaj, Tehran, Iran*.

Adequate air bubbling through the milk in an on-farm weigh jar is required to ensure homogeneity before sampling. Samples (n=960) were taken from 120 lactating Holstein cows at second meal of milking during 2 sequential days. The vacuum is left on and the sampler valve opened to allow air to enter and mix the milk to collect four samples at 0, 10, 20 and 30 seconds air bubbling from the same weigh jar at each milking. Least square means of milk fat percentage was lower ($p<0.01$) without air bubbling (2.58±0.076%) compare to 10, 20 and 30 seconds (3.5±0.074%, 3.57±0.074% and 3.66±0.074%, respectively). There was no differences between 10, 20, 30 seconds air bubbling through the milk on milk fat percentage. There were no differences between air bubbling times when a weigh jar contains lower than 6 kg milk.

Key Words: milk sampling, air bubbling, milk fat percentage

T243 Agreement between fat and protein measurements from DHIA and the AfiLab™ real time milk analyzer. A. De Vries*, M. J. Hayen, E. J. Diepersloot, A. H. Sanders, D. W. Webb, and D. R. Bray, *University of Florida*, *Gainesville*.

Objective of this study was to assess the degree of agreement between measurements of %fat and %protein from DHIA and the AfiLab™ real time milk analyzer. The AfiLab™ milk analyzer measures milk components for each cow at each milking in real time. The AfiLab™ milk analyzer is based on light scattering off matter. One milk analyzer was installed in each stall of the double-12 milking parlor at the University of Florida Dairy Unit in 2007. In 2008, approximately 400 Holstein cows were milked 2X daily in 12-hour intervals. Standard DHIA testing was performed each month alternating between the morning and evening milking. The AfiLab™ method was calibrated after each test day with the DHIA test day results for %fat and %protein. For this study, all available data from the test days in July through December 2008 were used (6 test days). Pairs of measurements by the DHIA and AfiLab™ methods were available for %fat and %protein (n=2,324). Mean and standard deviation (SD) were 3.66 ± 0.87% for DHIA %fat, 3.72 ± 0.70% for AfiLab™ %fat, 3.10 ± 0.36% for DHIA %protein and 3.07 ± 0.37% for AfiLab™ %protein. The unadjusted concordance correlation coefficients were 0.59 for %fat and 0.70 for %protein. Differences were calculated as DHIA measurement minus AfiLab™ measurement. Mean and SD of the unadjusted differences between both methods were -0.054 ± 0.716 percentage points (PP) for %fat and 0.036 ± 0.273 PP for %protein. The 1-, 50-, and 99-percentile unadjusted differences were -1.73, -0.08, and 2.14 PP for %fat and -0.63, 0.03, and 0.79 PP for %protein. The 95% limits of agreement were -1.36 and 1.46 PP for %fat and -0.61 and 0.54 PP for %protein. Variance components for these limits were obtained with a mixed model for each trait with the random effects of method x cow and cow x test day following the standard approach in method comparison studies. In conclusion, there can be considerable discrepancies between the 2 methods and the degree of agreement is moderate. Either method could contribute to the lack of agreement because the true %fat and %protein are not known.

Key Words: fat, protein, agreement

T244 Imprinting effects of lactational performance from dam to calf during gestation. V. A. Absalón Medina*, R.W. Everett, M. E. Van Amburgh, and W. R. Butler, *Cornell University*, *Ithaca, NY*.

The objective of this research was to investigate effects associated with the dam′s milk production during gestation on female offspring′s birth weight and first lactation milk production. The database consisted of 415 heifer calves born between 2001 and 2005 in a single herd. Milk production data was obtained using a test day model (TDM) that adjusts for the effects of calving year, season, management and environment on lactation performance reported as residual values (deviations from the grand mean). A two-level cow effects model was used to assess the effect of the dam′s lactation residual milk production (Lac Res) during gestation on the offspring′s birth weight (BWT). A second model estimated the effect of the same independent variable (Lac Res) on the offspring′s first lactation milk yield, also assessed by test day residuals. The model used was $Y_{i\,j} = \gamma_{00} + \gamma_{01}(x_j) + u_{0\,j} + r_{i\,j}$, where Y=BWT (or first Lac Res in the second model) of the *i*th heifer calf of the *j*th dam, $\gamma_{0\,0}$ is the intercept, $\gamma_{0\,1}$ is the slope times the *j*th dam Lac Res; $u_{0\,j}$ represents the variation in intercepts between cows and $r_{i\,j}$ represents the variation within cows. There was a positive relationship between the dam′s Lac Res and the heifer calf′s BWT (p=0.01). Parameter estimates are represented as: BWT= (42.9 kg) + (0.000455)*Dam Lac Res. Thus for every 450 kg of increased milk production by the dam, the resulting calf would weigh 0.205 kg more at birth when compared to the average. In addition, restricted maximum likelihood (REML) variance components estimates of offspring′s BWT accounted for 48.4% variation between cows and 51.6% variation among calves within cows. The second model was: Offspring Lac Res = (-390 kg) + (0.15364)*Dam Lac Res. Thus a 450 kg increase in dam Lac Res resulted in a 69 kg increase in the offspring′s first Lac Res (p=0.014). REML variance components estimates indicated that there is more variation among calves within dams (73.5%). These data suggest that higher milk production by the dam results in greater offspring birth weight and increased milk yield in the first lactation.

Key Words: milk residuals, multilevel model, test day model

T245 Deviation of reticular temperatures in association with mastitis and estrus. J. M. Bewley*[1,2], M. E. Einstein[1], M. W. Grott[1], and M. M. Schutz[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*University of Kentucky*, *Lexington*.

Reticular cow temperatures were collected using the Phase IV Cattle Temperature Monitoring System (Phase IV Engineering Inc., Boulder, CO) immediately after each milking from 298 Holstein cows at the Purdue Dairy Research and Education Center. Raw reticular temperatures were edited to remove erroneous reads and temperatures potentially influenced by water intake by removing temperatures (1) < 35.6°C or > 42.2°C, (2) < 3 SD from the overall mean temperature for the entire data set, and (3) < 3 SD from each individual cow's two-week rolling temperature average. The unadjusted mean of the remaining 131,181 temperatures was 38.77°C (±0.44). Temperatures were then adjusted for the impact of milking time, parity, temperature humidity index, housing system, DIM, and milk yield. Breeding and illness events were recorded by herd managers. Only events with a matching temperature recording on the day of the event were retained for analysis. Eighty-one distinct natural estrus events and 91 distinct mastitis events were used in all subsequent analyses. A rolling mean temperature was calculated using the 5 most recent recorded temperatures. The number of standard deviations (NUDEV) from which each respective temperature varied from this baseline was then calculated. The maximum temperature and NUDEV among the last 14 temperatures was used as a baseline to assess whether a temperature deviation was observed for mastitis events. Mean maximum temperature and NUDEV were 39.78 (± 0.83) and 4.99 (± 4.30), respectively. The NUDEV was more than 3 in 57.14% of mastitis events and MAXTEMP was greater than 39.44°C for 58.24% of mastitis events. The maximum temperature and NUDEV among the last 4 temperatures was used as a baseline to assess whether a temperature deviation was observed for breeding events. Mean maximum temperature and NUDEV were 39.04 (± 0.50) and 2.03 (± 1.52), respectively. The NUDEV was more than 3 in 24.69% of breeding events and MAXTEMP was greater than 39.44°C for 17.28% of breeding events. Natural variation in cow body temperatures may limit the utility of a reticular-based temperature monitoring system with twice-daily recordings.

Key Words: temperature monitoring, reticular temperature

T246 Effect of Gammulin supplementation in milk of dairy calves during the first 24 d of life on growth and health. G. Lopes Jr.*[1], L. G. D. Mendonça[1], S. Hayes[2], and R. C. Chebel[1], [1]*Veterinary Medicine Cooperative Extension, University of California Davis*, *Tulare*, [2]*APC Inc.*, *Ankeny, IA*.

Objectives were to evaluate the effect of adding Gammulin (GAM) to milk fed to calves from 2 to 24 d of age. All calves were fed colostrum twice, at 2 and 12 h after birth. Calves were randomly assigned to one of two treatments after balancing for gender, body weight (BW), and serum total protein (TPTN). Calves supplemented (GAM=263) received 25 g of Gammulin divided in 2 feedings from 2 to 24 d of age and control calves (CON=255) did not. From enrollment to 25 d of age calves were fed pasteurized waste milk (WM) and from 26 to 60 d of age calves were fed WM plus replacer (WMR). Calves were weighed at 23 and 60 d of age. Daily, starter intake (SI), attitude and fecal score, and anti-biotic (ATB), anti-inflammatory (AIN), and oral electrolytes (OE) treatments were recorded. Blood was sampled at 8, 15, and 24 d of age for measurement of TPTN and hematocrit (HMT). At enrollment, BW was 40.4±0.2Kg and TPTN 6.5±0.1 and 6.3±0.1mg/dL (P=0.05) for CON and GAM calves, respectively. During supplementation, treatment did not affect HMT, but GAM calves had greater TPTN (CON=5.3±0.03, GAM=5.4±0.03mg/dL; P=0.03). Attitude score was not affected by treatment, but on week 2 of age GAM calves had smaller fecal scores (3.2±0.03 vs. 3.3±0.03; P=0.04) and on week 3 CON calves tended to have smaller fecal scores (2.2±0.04 vs. 2.3±0.04; P=0.07). Average SI was greater for CON calves (400.1±8.8 vs. 375.2±8.7g/d; P=0.04) and BW did not differ at 23 d of age (48.1±0.2Kg; P=0.21), but CON calves were heavier at 60 d of age (69.9±0.5 vs. 68.3±0.5Kg; P=0.01), because from 23 to 60 d of age CON calves gained more weight (577.8±17.3 vs. 544.5±16.8g/d; P=0.05). Treatment did not affect mortality (5.2%) and incidence of diarrhea (99.6%) or fever (23.2%), but GAM calves were less likely to have diarrhea and fever (1.5 vs. 4.7%; P=0.05). Consequently, treatment did not affect number of d calves received ATB (1.3±0.1d) and AIN (0.3±0.0 d), but GAM calves received OE for fewer days (5.1±0.2 vs. 5.5±0.2d; P=0.02). Gammulin reduced severity of diarrhea, but did not improve performance of dairy calves under the conditions of this trial.

Key Words: Gammulin, dairy calve, health

T247 Genetics and environmental effects which influence reproduction and milk production traits in goats in Rio de Janeiro State, Brazil. L. F. D. Medeiros[1], D. H. Vieira[2], C. A. Oliveira[1], L. Shikasho[1],

V. L. Tierzo[3], J. P. F. Silveira[3], T. F. Silveira[3], P. Persichetti Junior[3], and J. L. C. B. Reis*[4], [1]*Rural Federal University of Rio de Janeiro, Seropedica, RJ, Brazil*, [2]*Center of Creation of Animals of Laboratory, Rio de Janeiro, RJ, Brazil*, [3]*São Paulo State University, Botucatu, SP, Brazil*, [4]*University of Agrarian Sciences - University of Marília, Marília, SP, Brazil*, [5]*Agricultural Municipal School Adolfo Alves Rezende, Campina Verde, MG, Brazil*.

This study was carried out in Rio de Janeiro State of Brazil on three farms, using data of 1875 parturitions. The objective was to evaluate genetic and environmental effects, which influenced the reproduction and milk production of Saanen, Toggenburg and Parda Alpine, between 2004 and 2006. The data were analyzed using SAS (Statistical Analysis system, GLM procedures) and heritability was estimated using MTDFREML with an Individual Animal Model. The analyzed traits were gestation length (GL), age at first kidding (AFK), kidding interval (KI), total milk production (TMP) and lactation length (LL). The statistical model included fixed effects: farm, breed, month of kidding, parturition type, sex of kid; and the covariate, goats weight at matting time. The Parda Alpine breed had the lowest AFK. The Saanen breed had the highest TMP, while the Toggenburg breed had the highest KI. The heritability was low magnitude and dependent of breed. The KI was affected by farm, breed, month of kidding and sex of the kid. The breed and parturition type affected the AFK. The TMK was influenced by breed. The results of this study evidenced that there is a possibility to improve the goat performance in Rio de Janeiro State. The improvement on general management can be a faster option for the reduction of AFK and KI and increase the production levels in the study herd.

Key Words: age at first kidding, gestation length, kidding interval

T248 Environmental effects and variance components of birth weight in dairy goats in Rio de Janeiro state, Brazil. L. F. D. Medeiros[1], D. H. Vieira[2], C. A. Oliveira[1], J. P. F. Silveira[3], V. L. Tierzo[3], M. V. Fonseca[1], T. F. Silveira[5], P. R. C. Cordeiro[6], and R. Belintani*[4], [1]*Rural Federal University of Rio de Janeiro, Seropedica, RJ, Brazil*, [2]*Center of Creation of Animals of Laboratory, Marília, SP, Brazil*, [3]*São Paulo State University, Botucatu, SP, Brazil*, [4]*University of Agrarian Sciences - University of Marília, Marília, SP, Brazil*, [5]*Agricultural Municipal School Adolfo Alves Rezende, Campina Verde, MG, Brazil*, [6]*Celles Lamb Foods, Nova Friburgo, RJ, Brazil*.

This study was aimed at the avaluating the environmental effects on birth weight (BW) of 1175 Saanen, Parda Apine and Toggenburg, males and females, born in 2004 to 2006. The mean was 3.60kg. There were not found significant differences among contemporary groups of birth, breeds or genetic compositions. Sex, twinning and their interaction were significant ($P<0.01$). Linear and quadratic affects of age of doe at kidding were also significant ($P<0.01$). Estimates were obtained using the Restricted Maximum Likelihood Method, with the MTDFREMIL program, assuming an animal a model. The estimatives of direct additive genetic, maternal, residual variance component and heritability for BW obtained were 0.175, 0.158, 0.288 and 0.25, respectively. Kidding BW studied showed moderate magnitude of heritability. Thus, it can be genetically improved.

Key Words: birth weight, dairy breeds, animal model

Ruminant Nutrition: Additives

T249 Effects of capsicum extract on intake and performance of feedlot calves. A. L. Cardillo[1], A. D. Garciarena[1], C. Faverin[1], G. A. Gagliostro[1], J. M. Hernandez Vieyra[4], and D. Colombatto*[2,3], [1]*INTA, Balcarce, Buenos Aires, Argentina*, [2]*Universidad de Buenos Aires, Buenos Aires, Argentina*, [3]*CONICET, Buenos Aires, Argentina*, [4]*Pancosma, Geneva, Switzerland*.

Capsicum extract (CAP) has the potential to influence intake and performance of calves fed on high concentrate diets. Thirty two Aberdeen angus calves (160 kg initial weight) were separated in four groups and randomly allocated to 16 pens of 2 animals each. Treatments were no additive (CON), 133 mg/d of CAP (CAP133), 399 mg/d of CAP (CAP399), and 665 mg/d of CAP (CAP665), added into a mineral mixture. Diets were fed once a day and consisted (DM basis) of 33.6% whole corn grain, 33.6% coarsely ground corn grain, 26.2% pelleted sunflower meal, 5.1% corn silage and 2% mineral mixture. Animals had ad libitum access to water. After 15 days of adaptation to the diets, the experimental period lasted for 98 days. Dry matter intake (DMI), average daily gain (ADG), feed conversion ratio (FCR), rib eye area (REA) and subcutaneous fat deposition (SFD)were determined throughout the study. The REA and SFD deposition rates were determined by ultrasound. Data were analyzed using PROC MIXED, and repeated measures were used for DMI and FCR. Contrasts were also performed, and differences declared at $P < 0.05$. Addition of CAP did not alter ($P = 0.52$) daily DMI (14.8, 15.3, 16.2, and 14.4 kg/pen for CON, CAP133, CAP399, and CAP665, respectively), ADG (1.50, 1.44, 1.47, and 1.49 kg/d, respectively, $P =0.60$), final live weight (295.9, 289.2, 293.5, and 293.9 kg, respectively, $P = 0.44$), and FCR (5.23, 4.94, 5.08, and 4.84, respectively, $P = 0.69$). Likewise, addition of CAP did not alter final SFD (10.68, 9.75, 10.03, and 10.73 mm for CON, CAP133, CAP399, and CAP665, respectively, $P = 0.52$), rate of SFD (2.87, 2.45, 2.53, and 2.98 mm/month, respectively, $P = 0.21$), REA (53.97, 49.76, 47.65, and 49.29 cm^2, respectively, $P = 0.16$) and rate of REA growth (8.05, 6.71, 6.32, and 6.91 cm^2/month, respectively, $P = 0.31$). These observations suggest that capsicum extract, applied at commercial doses, does not affect intake or performance of calves fed on high concentrate diets. It is yet to be determined whether addition of CAP affects initial rate of DMI or the ingestive behavior of the animals, measured through video images (data not shown).

Key Words: capsicum, feedlot, calves

T250 Effect of a mixture of eugenol and cinnamaldehyde on milk production and composition of goats during the first five months of lactation. D. Bravo*[1], N. Manteaux[2], P. H. Doane[3], Y. Senlis[2], and M. Cecava[3], [1]*Pancosma, Geneva, Switzerland*, [2]*Sanders Nutrition Animale, Bruz, France*, [3]*ADM Research, Decatur, IL*.

Prior meta-analysis of results with a mixture of eugenol and cinnamaldehyde (Xtract 6965, XT) has documented improvements in milk yield and DMI for mid-lactation dairy cows. The intent of this trial was to evaluate XT during earlier lactation, for a more extended period. Milk production and composition of dairy goats was monitored during the first 5 months of lactation. Seventy six pregnant Alpine goats receiving a common diet were selected for the experiment. Fifteen days after kidding, goats were separated in 2 groups balanced by parity and kidding date, multiparous goats were balanced for prior lactation performance. Group 1 received the control diet (CTR, no additive)

and group 2 received the same diet with 100 mg.animal^{-1}.d^{-1} of XT. Individual milk yield and composition (fat, protein, urea, somatic cell count) were recorded twice a month during 4 months (week 3 to 18 of lactation). GLM procedure of SAS with repeated measures was used to analyze the results. XT did not alter average milk yield (3.36 kg/d CTR and 3.43 kg/d XT, P = 0.49) or milk protein content (30.4 g/kg CTR and 30.9 g/kg XT, P = 0.33). The effect of time was significant, where XT improved average milk fat content (40.9 g/kg XT vs 39.4 g/kg CTR, P = 0.05), with particular improvements for 12th (+1.8 g/kg, P = 0.08), 14th (+3.5 g/kg, P < 0.001) and 16th weeks of lactation (+2.2 g/kg, P = 0.031). There was also a time interaction for milk protein content with improvements between the week 8 and 12. XT tended to decrease milk urea (559 mg/L XT vs 577 mg/L CTR, P = 0.067), with the difference becoming significant after the 12th week. Finally a lower average somatic cell count (909 x 10^3 cells/mL XT vs 1725 x 10^3 cells/mL CTR, P = 0.02) was associated with XT, again particularly later in the experiment. These results agree with the earlier studies with dairy cattle, and support the continued development and use of eugenol and cinnamaldehyde for lactating animals.

Key Words: essential oil, goat, milk production

T251 Synergy of cinnamaldehyde, eugenol and garlic for reduction of methane production in vitro. S. Cavini[1], D. Bravo*[2], S. Calsamiglia[1], M. Rodriguez[1], and A. Ferret[1], [1]*Universitat Autonoma de Barcelona*, *Bellaterra, Spain*, [2]*Pancosma*, *Geneva, Switzerland*.

The effect of combination of eugenol (E), cinnamaldehyde (C) and a garlic botanical standardized for propyl propyl thiosulfonate (G) on in vitro microbial fermentation was determined using a simplex centroid experimental design of degree 3 with 3 components. Treatments were mixtures between the 3 extracts totalling 250 mg/L and composed of (doses in mg/L) 1) 125G + 125C + 0E; 2) 0G + 250C + 0E; 3) 250G + 0C + 0E; 4) 41.7G + 41.7C + 166.7E; 5) 41.7G + 166.7C + 41.7E; 6) 0G + 0C + 250E; 7) 0G + 125C + 125E; 8) 166.7G + 41.7C + 41.7E; 9) 125G + 0C + 125E; and 10) 83.3G + 83.3C + 83.3E. Two controls were also used: negative control (CTR) and 500 mg/L of monensin (MON). Each treatment was tested in duplicate and in two periods. Fifty millilitres of a 1:1 ruminal fluid-to-buffer solution were introduced into polypropylene tubes supplied with 0.5 g of DM of a 60:40 forage:concentrate diet and incubated for 24h at 39C. Samples were collected for VFA and methane concentrations (CH4). Results were analysed with SAS using a special cubic model. Total VFA were unaffected by the 3 extract combinations. The molar proportion of acetate was decreased by C*G (P = 0.015) and by C*G*E (P = 0.023) whereas the molar proportion of butyrate was increased by C*G (P = 0.004) and by E*C*G (P = 0.024). The molar proportion of valerate was decreased by E*C (P = 0.042), by E*G (P = 0.116) and increased by C*G (P = 0.081) and E*C*G (P = 0.021). Concentration of CH4 for treatments 10, 5 and 4 were lower than CTR (17.96, 18.46, 18.49 and 22.2, respectively; P < 0.001) and higher than MON (5.81, P < 0.001). Concentratino of CH4 was affected by the combination E*C (P = 0.033) and decreased by E*C*G (P = 0.012). The regression predicting CH4 concentration with the 3 compounds is: CH4 = 0.078 E + 0.077 C + 0.096 G + (0.000356 E*C) - (0.000012 E*C*G) (P = 0.012, RSD = 1.61, R2 = 0.79). Results demonstrate that there is a synergy between the 3 extracts for the reduction of methane in vitro.

Key Words: essential oils, rumen fermentation, methane

T252 Effect of feeding eugenol on ruminal fermentation and carbohydrate digestion in the digestive tract of beef cattle fed finishing ration. W. Z. Yang*[1], C. Benchaar[2], B. N. Ametaj[3], M. L. He[1], and K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*, [3]*University of Alberta*, *Edmonton, AB, Canada*.

Eugenol (4-allyl-2-methoxyphenol; $C_{10}H_{12}O_2$) is a phenolic compound with wide-spectrum antimicrobial activity against gram-positive and gram-negative bacteria, and it is one of the main active components in clove bud and cinnamon oils. A study was conducted to evaluate the effects of supplementing eugenol on feed intake, rumen fermentation and feed digestibility in beef cattle fed finishing ration. Four spayed beef heifers with ruminal and duodenal cannulas were assigned in a 4 × 4 Latin suqare design with treatments: control (no eugenol), low, medium and high eugenol supplementation of 400, 800 and 1600 mg/head/day, respectively. The diets consisted of 15% barley silage, 80% barley grain, and 5% supplement (DM basis). Feed intake (averaged 9.6 kg/d) was not affected by eugenol supplementation. However, ruminal digestibility tended to linearly (P < 0.10) reduce from 40 to 31% for ADF, and 83 to 78% for starch with increasing eugenol supplementation, although ruminal digestibility of OM was not affected. Supplementation of eugenol had no effect on nutrient digestion in the intestine, whereas dietary inclusion tended to linearly reduce digestibility of NDF from 56 to 49% (P < 0.10), and that of ADF from 51 to 43% (P < 0.08) in the total digestive tract. Rumen pH (range of 6.12 to 6.23) was not affected by eugenol. However, VFA concentration numerically reduced (P < 0.15) from 122 to 115 m*M* and the proportion of acetate numerically reduced (P < 0.13) from 65 to 62%. In contrast, proportion of propionate tended to linearly increase (P < 0.09) from 17 to 21% with increasing eugenol supplementation. The results indicate that supplementation of a feedlot finishing diet with eugenol was detrimental to ruminal microbial activity, thus reducing digestion in the rumen.

Key Words: eugenol, digestibility, beef cattle

T253 Effects of eugenol supplementation on ruminal fermentation, protozoa counts, and in situ ruminal degradation of soybean meal, grass/legume hay, and corn grain in dairy cows fed high- or low-concentrate diets. C. Benchaar*[1], W. Z. Yang[2], H. V. Petit[1], and P. Y. Chouinard[3], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R&D Centre*, *Sherbrooke, QC, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [3]*Université Laval, Département des Sciences Animales*, *Québec, QC, Canada.*

Four ruminally primiparous lactating cows (BW=568 kg; DIM=67) were used in a 4×4 Latin square design (28-d periods) with a 2×2 factorial arrangements of treatments to determine the effects of eugenol (EUG) supplementation (0 vs. 50 mg/kg of DMI) and concentrate level (high: H vs. low: L; 65% vs. 35%, DM basis) on ruminal fermentation, protozoa counts, and in situ ruminal degradation (16 h incubation) of soybean meal, grass/legume hay, and corn grain. Orthogonal contrasts (MIXED procedure; SAS) were used to test the main effects of EUG supplementation, concentrate level, and their interaction. Significance was declared at $P \leq 0.05$. Average ruminal pH was lower for H than for L (6.04 vs. 6.23) while NH_3-N concentration was similar for H and L diets (6.00 m*M*). Total VFA concentration tended (P=0.09) to increase in cows fed H diets as compared to those fed L diets (134.7 vs. 127.0 m*M*). Molar proportion of acetate was lower (59.7 vs. 63.7%) and that of propionate was higher (23.3 vs. 19.5%) for H than for L. Proportions of butyrate (13.2%) and BCVFA (2.06%) remained unaffected by concentrate level. Total protozoa numbers were higher for H than for L diet (4.1 vs. 2.6

× 10^5/mL). Supplementation with EUG had no effect on ruminal pH, concentrations of total VFA and NH_3-N, and protozoa numbers. The effect of EUG on VFA profile was only limited to BCVFA proportion, which was higher in cows fed EUG as compared to those fed diets without EUG (2.19 vs. 1.93%). Ruminal degradation of hay DM was lower (45.1 vs. 53.7%) and that of soybean meal DM tended to be lower (71.1 vs. 76.7%; *P*=0.08) for H than for L. Ruminal degradation of corn DM was unaffected (68.9%) by the concentrate level. Supplementation with EUG had no effect on ruminal degradation of any of the feed ingredients tested. Results from this study show that at the concentration evaluated (50 mg/kg of dietary DM), eugenol supplementation had minor effects on fermentation, protozoa numbers, and feed degradation in the rumen of cows fed high- or low- concentrate diets.

Key Words: essential oil, concentrate level, rumen

T254 Effects of eugenol supplementation on feed intake, nutrient digestibility, nitrogen retention, milk production, and milk composition of dairy cows fed high- or low-concentrate diets. C. Benchaar*[1], W. Z. Yang[2], H. V. Petit[1], and P. Y. Chouinard[3], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R&D Centre, Sherbrooke, QC, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [3]*Université Laval, Départements des Sciences Animales, Québec, QC, Canada*.

Four ruminally primiparous lactating cows (BW = 568 kg; DIM = 67) were used in a 4 × 4 Latin square design (28-d periods) with a 2 × 2 factorial arrangements of treatments to determine the effects of eugenol (EUG) supplementation (0 vs. 50 mg/kg of DMI) and concentrate level (high: H vs. low: L; 65% vs. 35%, DM basis) on nutrient digestibility, N retention, milk production, and milk composition. Orthogonal contrasts (MIXED procedure; SAS Inst., Inc., Cary, NC) were used to test the main effects of EUG supplementation, concentrate level (CON) and their interaction (CON × EUG). Significance was declared at $P \leq 0.05$. No interaction of CON × EUG was observed for any of the variables measured. Intake of DM was higher for H than for L (20.0 vs. 16.9 kg/d). Apparent total tract digestibilities of DM (66.8 vs. 69.4%), OM (68.2 vs. 70.8%), N (66.0 vs. 68.8%), and ADF (57.3 vs. 60.6%) were lower for H than for L. Retention of N was not affected by concentrate level (59 g/d; 11% of N intake). Milk production (32.2 vs. 30.8 kg/d) and milk protein content (3.31 vs. 3.02%) were higher whereas milk fat content was lower (3.64 vs. 3.92%) and milk lactose concentration tended to be lower (4.67 vs. 4.61; $P = 0.08$) for cows fed H than for those fed L. Milk urea N was unaffected by concentrate level (9.52 mg/dL). Yield of 4% FCM was similar for H and L diets (30.1 kg/d). Yield of milk fat was not affected by concentrate level (1.17 kg/d) whereas milk yields of protein (1.05 vs. 0.93 kg/d) and lactose (1.51 vs. 1.37 kg/d) were higher for cows fed H than for those fed L. Feed efficiency (kg 4% FCM/kg DMI) was lower for cows fed H than for those fed L (1.51 vs. 1.79). Neither DMI nor nutrient apparent total tract digestibility, N retention or milk performance was affected by EUG supplementation. Results of this study show that adding EUG at the concentration of 50 mg/kg of dietary DM to a high- or low-concentrate diet had no effects on nutrient digestibility, N retention, milk production and milk composition of dairy cows.

Key Words: essential oil, concentrate level, dairy cow

T255 Assessment of the potential of cinnamaldehyde, condensed tannins, and saponins to modify milk fatty acid composition of dairy cows. C. Benchaar*[1] and P. Y. Chouinard[2], [1]*Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada*, [2]*Université Laval, Département des Sciences Animales, Québec, QC, Canada*.

Recently, plant secondary metabolites such as essential oils have been suggested as potential means to manipulate bacterial populations involved in ruminal biohydrogenation of unsaturated fatty acids and modify the fatty acid composition of ruminant-derived food products such as milk. This study was conducted to determine whether feeding cinnamaldehyde (CIN; main component of cinnamon bark essential oil; *Cinnamon cassia*), condensed tannins from quebracho trees (QCT; *Schinopsis balansae*) or saponins from *Yucca schidigera* extract (YSE) alters milk fatty acid profile of dairy cows. For this purpose, four lactating cows (BW = 730 kg; DMI = 87) were used in a 4 × 4 Latin square design (28-d periods) and fed a total mixed ration containing no additive (control), or supplemented with CIN (1 g/d), QCT (150 g/d; 70% of tannins), or YSE (60 g/d; 10% of steroidal saponins). The fatty acid profile was determined on milk pooled samples collected from four consecutive milkings (d 22 to 23). Data were analyzed as a 4 × 4 Latin square design (MIXED procedure; SAS Inst., Inc., Cary, NC). Differences between treatments and the control were determined using the Dunnett's comparison test. Significance was declared at $P \leq 0.05$ and tendency at $0.05 < P \leq 0.10$. Results revealed no effects of feeding CIN or QCT on milk fatty acid profile. Supplementation with YSE resulted in some modifications of milk fatty acid profile as suggested by the reduced proportions of C6:0 (2.71 vs. 2.95%; $P = 0.10$), C8:0 (1.66 vs. 1.89%; $P = 0.08$), and *trans*-11 C18:1 (0.92 vs. 1.01%; $P = 0.05$). Results show that at the feeding rates used in this study, the potential of cinnamaldehyde, condensed tannins, and saponins to alter ruminal biohydrogenation process and modify the fatty acid profile of milk fat is low.

Key Words: plant extract, milk fatty acid profile, dairy cow

T256 Screening the activity of medicinal plants or spices on in vitro ruminal methane production. H. Jahani-Azizabadi[1], M. Danesh Mesgaran*[1], A. R. Vakili[1], A. R. Heravi Moussavi[1], and M. Hashemi[2], [1]*Ferdowsi University of Mashhad, Mashhad,Khorasan Razavi, Iran*, [2]*Research and Petroleum Engineering Center of Kermanshah, Kermanshah, Iran*.

The objective of the present study was to evaluate the in vitro effect of medicinal plants or spices powder on ruminal methane and total gas production. In vitro incubation was carried out based gas production method. Approximately 300 mg of dried alfalfa hay (as control) (NDF= 537 and CP= 150 g/kg DM) or plus 12 mg of garlic, cinnamon, cumin, nutmeg or rosemary powder as treatments were placed in a 100 ml glass syringes (n= 3) containing 40 ml of buffered rumen fluid (ratio of buffer to rumen fluid was 2:1), and incubated for 24 h at 38.5°C. Rumen fluid was obtained from three adult ruminally fistulated sheep (49.5 ± 2.5 kg body weight), before the morning feeding, and immediately strained through four layers of cheesecloth. After 24 h of incubation, gas which was accumulated in the headspace of each syringe was measured, and a sample of the gas was collected into a 10 ml vacuum tube. Methane content of the produced gas was determined using gas chromatography procedure (GC, Sri 8610, and Column: 6% cyanopropylphenyl, 94% dimethylpolysiloxane). Volumes of gas and methane (ml) were converted to mmol assuming one mol is equivalent to 22.4l L of gas (Table1). Data were applied to the completely randomized design model of SAS

(V. 9/1) and Duncan test was used to compare the means (P< 0.05). The results of the present study indicated that all medicinal herbs or spices, expect Nutmeg, reduced significantly (P< 0.05) in vitro methane and total gas production from alfalfa hay compared with the control. These finding confirmed the ability of Rosemary to decrease methane production, which may help to improve the efficiency of energy used in the rumen.

Table 1. Effect of medicinal herbs or spices on in vitro methane and total gas production (mmol/g DM incubated for 24 h)

Items	alfalfa	alfalfa + Garlic	alfalfa + Cinnamon	alfalfa + Cumin	alfalfa + Nutmeg	alfalfa + Rosemary	S.E
Total gas	11.97 a	11.13 b	12.72 c	10.81b	12.00 a	10.17	0.22
Methane	3.59 a	3.34 b	3.82 c	3.24 b	3.63 a	3.05	0.07

a, b, c: Means with difference letter in each row were significant (P< 0.05).

Key Words: methane, gas production, medicinal herbs

T257 Effects of cinnamaldehyde on in vitro methane production and ruminal fermentation of medium and high-concentrate diets. C. Kamel[1], H. M. R. Greathead[1], M. L. Tejido[2], M. J. Ranilla*[2], M. E. Martínez[2], C. Saro[2], and M. D. Carro[2], [1]*Faculty of Biological Sciences, University of Leeds*, *Leeds, United Kingdom*, [2]*Departamento de Producción Animal, Universidad de León*, *León, Spain*.

The effects of five doses (0 (control), 20, 60, 180 and 540 mg/L incubation medium) of cinnamaldehyde (CIN) on in vitro fermentation of a medium concentrate (MC; 50:50 alfalfa hay:concentrate) or a high concentrate (HC; 15:85 barley straw:concentrate) diet were evaluated in batch cultures of mixed rumen micro-organisms from the rumen of sheep fed the same diets. Previous in vitro studies have shown that CIN supplementation leads to reduced rumen ammonia levels but since this effect depends on microbial populations, it may be expected to relate to the incubated diet and the diet fed to donor sheep. After 16 h of incubation, the main fermentation variables were determined. Differences among treatments were declared at P < 0.05. CIN at 20 mg/L did not modify rumen fermentation, and at 60 mg/L only decreased ammonia-N concentrations for MC diet. For both diets, the 540 mg/L dose inhibited rumen fermentation, as indicated by the decrease in the production of volatile fatty acid (VFA), gas and methane, with the effects being more pronounced for HC diet than for MC. In addition, CIN at 540 mg/L increased total lactate concentrations by 22 and 11 times compared to control for MC and HC diets, respectively. The 180 mg/L dose increased acetate proportions and acetate:propionate ratio without reducing VFA production, decreased ammonia-N concentrations, and tended (P = 0.06) to reduce methane production for the MC diet, whereas only a reduction in acetate proportion and a tendency (P = 0.10) to lower ammonia-N concentrations were observed for the HC diet. These results would indicate that CIN dietary supplementation does show effects on lowering ammonia-N but that responses may differ depending on the administered dose and the diet composition and microbial populations in the inoculum, which could help to explain the controversial results obtained in different studies.

Key Words: cinnamaldehyde, microbial fermentation, methane

T258 Evaluation of plant extracts in natural-fed finishing cattle. N. A. Pyatt*[1], D. Bravo[2], and P. H. Doane[1], [1]*ADM Research*, *Decatur, IL*, [2]*Pancosma Research*, *Geneva, Switzerland*.

Performance data from British-cross steers (n = 35) were used to evaluate the effects of a blend of plant extracts (XT) in natural-fed feedlot diets without ionophores. Steers were adapted to a high-energy diet prior to allotment to the finishing trial. The basal diet consisted of 62% cracked corn, 25% wet distillers grains with solubles, 10% hay, and 3% supplement (DM basis). Cattle were blocked by weight to one of two treatments (2 pens per treatment; 8 or 9 head per pen); 1) negative control (CON) or 2) CON + XT (266 mg•steer^{-1}•d^{-1} eugenol + cinnamaldehyde and 133 mg•steer^{-1}•d^{-1} capsicum, XT 6965 and XT 6933, respectively; Pancosma). Steers were fed ad libitum using the GrowSafe automated feeding system (one unit per pen). Steers (initial BW 398.2 kg) were fed (on average) 103 d and harvested in two groups based on weight and condition. The model included treatment and animal nested within pen as fixed variables. There were no differences (P > 0.05) in animal performance or carcass merit parameters. Cattle fed XT tended to have greater cumulative ADG (P = 0.20; 1.74 vs. 1.88 kg/d, respectively) and feed efficiency (P = 0.16; 16.24 vs. 17.47 kg x 100/kg, respectively). Similarly, cattle fed XT tended to have greater HCW (P = 0.20; 364.2 vs. 379.8 kg, respectively), LMA (P = 0.09; 86.3 vs. 91.3 cm^2, respectively), and less KPH fat (P = 0.12; 2.0 vs. 1.8%, respectively). Cattle fed XT tended to have a greater proportion of YG 2 carcasses, while CON cattle had more (P = 0.13) YG 3 carcasses. Resulting carcass value was $27.10/hd greater for steer fed XT ($1010.13 vs. $1027.23/hd, respectively). Rumen fluid was collected by rumenocentesis from five animals per treatment on d 100. Total VFA (mM), acetate, and butyrate concentrations were lower for cattle fed XT. However, steers consuming XT had numerically greater propionate (%) and lower acetate:propionate ratio. These data suggest XT improved feedlot ADG (8.1%), feed efficiency (7.5%), HCW (4.3%), and carcass leanness. Including a blend of eugenol, cinnamaldehyde, and capsicum in natural-fed beef finishing diets without ionophores may increase finishing performance and profit potential.

Key Words: beef cattle, plant extracts, performance

T259 Effect of yellow mustard glucosinolates on ruminal fermentation *in vitro*. R. A. Hristova*[1], A. N. Hristov[2], S. Zaman[1], and V. Borek[2], [1]*Pennsylvania State University*, *University Park*, [2]*University of Idaho*, *Moscow*.

The objective of this study was to evaluate the effect of glucosinolates from mustard meal on ruminal fermentation, total gas and methane production, and protozoal counts *in vitro*. Ruminal inoculum was incubated with 1% (w/v) ground alfalfa hay and 0, 0.1, 0.2, and 0.4% (w/v) of cold-pressed yellow mustard (*Brassica juncea*, variety Pacific Gold) meal (NM). The meal contained 236 µmol/g total glucosinolates (97% of which was 2-propenyl glucosinolate). A portion of the meal was incubated with deionized water at room temperature for 48 h to inactivate the glucosinolates (IM). Monensin-Na was used as a positive control at 5 ppm final medium concentration. Incubations were continued for 24 h and repeated 3 times (n = 3). Gas pressure within the incubation vessels was recorded at 6, 12, 18, and 24 h. Gas samples for methane and carbon dioxide analyses were collected at 6 and 12 h. Compared with the blank (0% mustard meal), monensin slightly decreased (by 4%; *P* = 0.01) 24-h cumulative gas production. Increasing the inclusion of mustard meal linearly increased (*P* < 0.001) gas production, but there was no difference (*P* = 0.58) between NM and IM. Cumulative gas production per gram of substrate linearly decreased (*P* < 0.001) with

increasing the amount of mustard meal. Treatment had no effect (P = 0.24 to 0.85) on methane and carbon dioxide production. Monensin did not affect (P = 0.22 to 0.65) total or individual VFA concentrations, except propionate tended to be higher (P = 0.09) compared with the blank. Glucosinolates had no effect (P = 0.14 to 0.20) on VFA. Monensin decreased (P = 0.002 to 0.01) total protozoal counts, but NM or IM had no effect (P = 0.77 to 0.94). Inclusion of mustard meal increased linearly (P < 0.001) ammonia concentration in the incubation medium. Monensin and glucosinolates did not affect (P = 0.39 and 0.35) ammonia concentration. In the conditions of this experiment, *B. juncea* glucosinolates had no effect on ruminal fermentation, protozoal counts, and methane production.

Key Words: mustard meal, glucosinolate, rumen fermentation

T260 Effects of *Saccharomyces cerevisiae* on ruminal pH and fermentation of Holstein dairy cows. Y.-H. Chung*[1], L. Holtshausen[1], N. Walker[2], and K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [2]*Lallemand Animal Nutrition, Montréal, QC, Canada*.

Ten ruminally cannulated, nonlactating, and nonpregnant Holstein dairy cows were used to measure the effects of active dried yeast (*Saccharomyces cerevisiae*) on ruminal pH and fermentation. Cows were blocked by ruminal pH and DMI and randomly assigned to the control or yeast treatment. The yeast was Levucell SC (Lallemand Animal Nutrition, Montréal, QC) provided at 1×10^{10} cfu/head/d and dosed via the rumen cannula daily at the time of feeding (1× feeding/d). Cows were fed a barley-based total mixed ration (50:50 forage to concentrate ratio) formulated to meet the nutrient requirements of a dairy cow producing 30 kg/d of milk. The experiment consisted of a 28-d yeast feeding period and ruminal pH was measured continuously every 60 s using an indwelling system during the last 7 d of the experimental period. Rumen contents were sampled on 2 d (d 22 and 26) at 0, 3, and 6 h after feeding. Dry matter intake and BW were not affected (P > 0.10) by yeast feeding and averaged 14.1 kg/d and 820 kg, respectively. Supplementing the diet with yeast did not affect (P > 0.10) the minimum pH (5.67 vs. 5.63), mean pH (6.35 vs. 6.27), maximum pH (6.88 vs. 6.86), and the time that the ruminal pH was below 5.8 (0.95 vs. 2.81 h/d) or 5.5 (0.12 vs. 0.64 h/d) compared with the control. Rumen VFA profiles and lactic acid concentrations were similar between the control and yeast treatment. It is concluded that supplementing diet with yeast had no effect on ruminal pH or ruminal fermentation in nonlactating Holstein dairy cows.

Key Words: yeast culture, ruminal pH , fermentation

T261 Multiple study analysis of the effect of live yeast (*Saccharomyces cerevisiae* CNCM I-1077) on milk and milk component production and feed efficiency. M. B. de Ondarza*[1], C. J. Sniffen[2], L. Dussert[3], E. Chevaux[3], J. Sullivan[3], and N. Walker[3], [1]*Paradox Nutrition, LLC, West Chazy, NY*, [2]*Fencrest, LLC, Holderness, NH*, [3]*Lallemand Animal Nutrition, Milwaukee, WI.*

A dataset with diet information and production responses was compiled from fourteen research trials conducted internationally (160 observations representing 1615 cows) that tested the effect of dietary inclusion of live yeast (Levucell SC®). Diet and feed analysis data for each study was entered into CPM Dairy 3.0.8 to estimate dietary nutrient parameters. Mean milk yield was 31.56 kg (SD=6.45) with 3.75% milk fat (SD=0.34) and 3.02% true protein (SD=0.15). Mean DMI was 19.22 kg (SD=3.67). Mean diet CP was 17.32%DM (SD=1.93) with 32.65% RUP (%CP) (SD=2.43). Mean diet NDF was 34.91% DM (SD=5.04) and mean diet starch was 22.82% DM (SD=8.39). Mixed model analysis was conducted using JMP statistical software (SAS, Cary, NC) with CPM nutrients as main effects with no interactions. Number of cows per treatment was included as a weighting factor and experiment was included as a random effect. Live yeast significantly improved 3.5% FCM production (35.54 vs. 34.58 kg/d for live yeast and control) (P<0.0001) with the effect being greater for cows <100 DIM (36.06 vs. 34.93 kg) (P<0.01) but still highly significant for cows >100 DIM (33.81 vs. 32.83 kg) (P<0.005). Feed Efficiency (kg 3.5% FCM/ kg DMI) was improved with live yeast (1.75 vs. 1.70 for live yeast and control) (P<0.001). Yeast effects on feed efficiency were greater for cows producing >38 kg milk/d (1.85 vs. 1.78 for live yeast and control) (P<0.05). There was no overall effect of live yeast on DMI (P>0.10). Although milk fat and protein content were slightly lower with the inclusion of live yeast, both milk fat yield (1.28 vs. 1.25 kg/d; P<0.01) and milk true protein yield (1.02 vs. 1.00 kg/d; P<0.0001) increased with live yeast. The improvement in 3.5% FCM yield and feed efficiency, with the inclusion of live yeast, could be a consequence of improved rumen function. Further investigations should provide opportunities to design optimized diets.

Key Words: live yeast, 3.5% FCM, feed efficiency

T262 Potential of yeast-supplemented barley based dairy cow diets. L. Holtshausen* and K. A. Beauchemin, *Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*.

Active dry yeast products, based on *Saccharomyces cerevisiae*, are widely used in corn based diets in North America to improve milk yield. However, diets fed to dairy cows in western Canada are primarily barley based and the objective of this study was therefore to determine the potential benefits of supplementing barley based diets with yeast. Forty lactating Holstein dairy cows were randomly assigned to one of two treatments: 1) control diet (no yeast) and 2) yeast supplemented diet. All cows were fed the control diet for 3 weeks followed by a 6-week period on their assigned diet. The control diet TMR consisted of 23% barley silage, 23% alfalfa silage, 6% alfalfa hay and 48% of a ground barley based concentrate (DM basis). For the treatment diet Levucell® SC-1077 (Lallemand Animal Nutrition, Milwaukee, WI) was added to the concentrate to provide 0.5 g Levucell®/head/day (10 billion CFUs/head/day). There was no difference in final body weight (623 vs. 621 kg, P = 0.82), average daily gain (0.533 vs. 0.368 kg/d, P = 0.30), net energy output (8.76 vs. 8.75 MJ/d, P = 0.98) and efficiency of net energy output (0.38 vs. 0.38 MJ/kg DMI, P = 0.20) for cows on the control diet compared to those on the yeast-supplemented diet. There was no difference (23.1 vs. 22.9 kg/d, P = 0.58) in DMI for cows on the control diet, but 3.5% fat corrected milk yield (FCM) was numerically 1 kg/d higher (35.6 vs. 36.7 kg/d, P = 0.31) for yeast-supplemented cows. This resulted in a numerically higher (5.8% increase) efficiency of milk production (1.55 vs. 1.64 kg FCM/kg DMI, P = 0.26) for yeast-supplemented cows. Although milk yield was only numerically higher with yeast supplementation to a barley-based diet, the improvement in milk production efficiency could lower the cost of feeding.

Key Words: yeast, barley based diets, dairy cows

T263 The effect of enzymatically hydrolyzed yeast on feeding behavior and immune function in early lactation dairy cows. K. Proudfoot*[1], J. Nocek[2], and M. von Keyserlingk[1], [1]*University of*

British Columbia, Vancouver, BC, Canada, [2]*Spruce Haven Research Center, Auburn, NY*, [3]*University of British Columbia, Vancouver, BC, Canada*.

An experiment was conducted to determine the effects of enzymatically hydrolyzed yeast (EHY) on eating behavior, milk production and immune function in early lactation cows. Twenty-two multiparous Holstein cows were monitored for 12 wk after calving. Experimental pens were equipped with electronic feed and water bins that controlled which cows had access and monitored cow attendance, and intake. Stocking density was 2 cows/feeding bin and 1 cow/lying stall. Group composition in all pens was dynamic; as one cow left a pen, another cow took her place. Cows were balanced for parity and previous 305 milk production. At calving cows were assigned to a TMR with or without (control) supplemental EHY(Celmanax, 1oz/d, Varied Industries Corporation, IA, USA). Treatments were alternated in space across, and cows were assigned to treatment. Blood was collected at -1,0,1,2,3,4 and 8 wk post calving for hematology and metabolic profiling. Treatment effects were tested using a mixed model with cow as a random effect. EHY had no effect (P>0.05) on DMI, feeding time and feeding rate. There was no effect (P>0.05) of EHY on milk yield or composition, although the average yield for cows consuming EHY was numerically higher (by 1.8 kg/d) than non-supplemented cows. Over the study, EHY cows exhibited 1 new case of clinical mastitis compared to 4 for control cows. Sub clinical cases (SCC > 200,000) were 1 and 3 for EHY and control cows, respectively. EHY had no effect on total WBC throughout the experiment (P>0.05). However, a trt*wk interaction for the proportion of lymphocytes and granulocytes (P = 0.008 and P = 0.01) was detected where control cows had a lower percentage of granulocytes at wk 1 and wk 4 after calving and a lower granulocyte count at wk 4 after calving (P=0.01). EHY supplementation showed a strong numerical increase in milk yield and reduced cases of mastitis compared to control: its effect on immune function appears to show some promise.

Key Words: hydrolyzed yeast, milk production, mastitis

T265 Repeated ruminal acidotic challenges in sheep : Effects on pH and microbial ecosystem and influence of active dry yeasts. M. Silberberg*[1], F. Chaucheyras-Durand[2,1], L. Commun[1], M. M. Richard-Mialon[1], C. Martin[1], and D. P. Morgavi[1], [1]*INRA, Saint Gens Champanelle, France*, [2]*Lallemand Animal Nutrition, Toulouse, France*.

In ruminants, the use of readily fermentable carbohydrates is known to increase the risk of rumen acidosis. Animals may encounter several acidotic episodes, lasting for long periods of time. The decrease in rumen pH has been reported to be linked to changes in the fermentative profile and shifts in the balance of microbial communities. The aim of this work was to follow the evolution of pH and microbial ecosystem during repeated acidotic challenges, and also to investigate the effects of Active Dry Yeasts (ADY). Rumen-cannulated sheep (n=12) were divided into one control group and one receiving the ADY CNCM I-1077. They were fed during 3 weeks with a basal diet (hay:wheat, 80:20), then they received an acidotic diet (hay:wheat, 40:60) during 5 days. This sequence was repeated 3 times. Throughout the experiment, rumen pH was continuously monitored using indwelling probes. Rumen samples were collected for determination of bacterial and protozoal counts, quantification by qPCR of specific bacterial populations, and VFA concentrations. The 1st acidotic challenge induced sharp decline in pH. Subsequent acidotic bouts led to a significant increase in time spent under pH 5.6 in the control group, whereas pH was stabilized in the ADY group from the 2nd episode. The 1st acidotic bout deeply modified the microbial balance (increase in lactate-producing bacteria, decrease in cellulolytic bacteria and protozoa numbers) and probably selected the more acidotic-resistant microbes. Moreover, ADY induced a sharp decline in streptococci and lactobacilli, and in Streptococcus bovis during the last acidotic episode. VFA profile shifted from propionate, during the 1st challenge, to butyrate during the 2nd and the 3rd challenges. As intended, ADY appears a useful tool to limit the onset of acidosis, but also to help recovery from repeated acidotic bouts. The dietary history of the animal appears important to partly explain differences observed between animals, with the same potential in feeding practices including high levels of readily fermentable carbohydrates.

Key Words: ruminal acidosis, microbiota, active dry yeast

T266 Effects of live yeast on growth performances and meat quality of beef cattle fed fast or slow fermentable diets. A. Agazzi[1], G. Invernizzi[1], M. Ferroni[1], V. Vandoni[1], C. A. Sgoifo Rossi[1], G. Savoini*[1], V. Dell'Orto[1], and E. Chevaux[2], [1]*University of Milan, Milan, Italy*, [2]*Lallemand, Blagnac, France*.

The aim of the trial was to evaluate the effects of the administration of *Saccharomyces cerevisiae* (CNCM I–1077) on growth performance and meat quality in beef cattle fed slow (SF) or fast (FF) fermentable diets. Eighty three male Charolaise cattle were divided in four homogenous groups: SF–C=n 24, FF–C=n 17, SF–T=n 21 and FF–T=n 21, and fed slow (SF; RUP 30.60%, NDF 31.20%, NFC 44.60, starch 34.20 on DM) or fast (FF; RUP 26.90%, NDF 30.60%, NFC 44.70, starch 32.40 on DM) fermentable diets with (T) or not (C) *S. cerevisiae* (8×10^9 cfu/d). ADG (evaluated at day 70 and 98 of the trial), and *longissimus dorsi* colour characteristics, chemical composition, pH at 24h post mortem, tenderness and fatty acid composition were compared using the GLM of S.A.S. with contrasts. SEUROP classes frequencies in the groups were analyzed by a PROC FREQ of S.A.S. with a chi-square test. Improved ADG was highlighted in SF–T and FF–T vs. FF–C (1.61 kg/d, 1.57 kg/d and 1.49 kg/d respectively; $P\leq0.05$). An increased lightness (L*) was recorded in SF–T vs. other groups (41.3 vs. 39.3 SF–C, 38.9 FF–C and 37.4 FF–T; $P\leq0.01$) and a decreased yellowness (b*) was observed in FF–C (8.3 vs. 10.0 SF–C, 10.3 SF–T and 9.8 FF–T; $P\leq0.01$). No differences were found in meat chemical composition, carcass characteristics, meat pH, cooking losses, or fatty acid composition of the meat except for a lower EPA content in FF–T. Tenderness was increased independently from slow or fast fermentable diets when live yeast was fed to cattle (SF–T 3.7 kgF, FF–T 3.6 kgF, SF–C 4.1 kgF, FF–C 4.1 kgF; $P\leq0.05$). The inclusion of live yeast in both slow and fast fermentable cattle diets affected positively performance and meat tenderness, while the use of slow fermentable rations in association with *S. cerevisiae* (CNCM I–1077) determined increased lightness and yellowness of the meat.

Key Words: beef cattle, live yeast, fermentable diet

T267 Effect of live yeast *Saccharomyces cerevisiae* (strain Sc 47) on ruminal nitrogen degradation in relation with varying levels of protein solubility. C. Julien[1], J. P. Marden[1,2], E. Auclair[2], R. Moncoulon[1], and C. Bayourthe*[1], [1]*Université de Toulouse, INRA, Castanet-Tolosan, France*, [2]*Lesaffre Feed Additives, Marquette-Lez-Lille, France*.

The aim of the study was to evaluate the effects of live yeast on crude protein (CP) degradability of protein sources in dairy cows. Ruminal CP degradability of raw (R) and formaldehyde-treated (F) soybean meal (SBM), and raw (R) and extruded (E) lupin seeds (LS) were studied by means of *in sacco* technique. Two lactating and ruminally cannulated

Holstein cows were assigned in a 2 × 2 Latin square design. They were fed a TMR (23 kg/d DMI) as control diet or TMR supplemented with 20 g (8×10^9 CFU/g) /d of live yeast, during a 28-d experimental period (21 d of diet adaptation, 7 d of measurements). Ruminal degradation rate of CP was estimated as percent nitrogen degradability (DgN) from polyester bags incubated in rumen for 2, 4, 8, 16, 24 and 48 h. Data were fitted to the nonlinear regression equation: $DgN(t) = a + b(1 - e^{-ct})$ where DgN is percentage disappearance of N at time *t*, *a* the soluble fraction and *b* the less rapidly degradable fraction which disappears at the constant fractional rate *c* per time *t*. Live yeast significantly reduced DgN from 61.3 and 41.9% to 51.2 and 35.1% for RSBM and FSBM respectively, and from 92 and 60.9% to 91.4 and 48.3% for RLS and ELS respectively. For any protein source, live yeast did not significantly influence *a* and *b* fractions while it reduced similarly the breakdown rate (*c*) of the fraction *b*. It diminished the DgN values by 9.4 and 4.8 points for protected and raw protein sources respectively. The effect of live yeast could be quantified by the ΔDgN (DgN measured with control diet – DgN measured with live yeast supplemented diet). The ΔDgN values were correlated at $P = 0.066$ with DgN measured with the control diet ($r = -0.602$). It can be put forward that the lower the DgN, the more pronounced is the yeast effect.

Key Words: degradability, crude protein, live yeast

T268 Effect of live yeast dietary supplementation on growing calves performance and health. V. Bontempo*[1], A. Agazzi[1], E. Chevaux[2], V. Dell'Orto[1], and G. Savoini[1], [1]*Dept Veterinary Science and Technologies for Food Safety, University of Milan*, *Italy*, [2]*Lallemand SAS*, *France*.

A trial was carried out to evaluate the effects of live yeast (*S. cerevisiae* CNCM I-1077 - Levucell SC20, Lallemand SAS) dietary supplementation on performance and health status of calves. Generally researches on yeast indicate positive effects of increasing rumen pH and VFA concentration, and reducing lactic acid production on rumen development. Ninety six male Italian Friesian calves (14 to 21 d age, 59.4 + 1.76 kg BW), were assigned by weight to one of two dietary treatments (Ctr and T). Animals were housed in pens of 16 animals each (3 replicates per group). Treatments differed only in the live yeast supplementation of milk replacer and starter. After a 5 d-rehydration period, calves were fed 4 l/d of milk replacer at 12.5% DM from 0 to 60 d; calf starter and ryegrass hay were provided ad libitum from the beginning to the end of the study. Live yeast was included in milk replacer from 0-21 d (0.03% in milk powder, 4x109 CFU/kg) and starter (0.02%, 4x109 CFU/kg from 0 to 60 d; 0.01%, 2x109 CFU/kg from 61-90 d) of treated calves. Starter consumption per pen was recorded daily. Calves were weighted at 0, 30, 60, 90 d of study. Blood samples were withdrawn at the beginning and at the end of the study. Body weight of calves fed S. cerevisiae was greater both at 60 d (115 vs 124 + 2.49 kg) ($P < 0.01$) and 90 d (134 vs 145 + 2.48 kg) ($P < 0.01$). Calves fed live yeast showed a greater daily gain from 0 to 30 d (0.85 vs 1.00 + 0.019 kg/d) ($P < 0.01$), from 30 to 60 d (0.93 vs 1.08 + kg/d) ($P < 0.01$), and during overall trial (0.91 vs 1.04 + 0.035 kg/d) ($P < 0.01$). Calves in both treatments presented similar total DMI and gain to feed ratios. No differences were detected between the two groups for total protein, creatinine, glucose, CPK, total bilirubin, γ-GT, AST, and urea plasma content. The inclusion of live yeast both in milk replacer and starter feed improved growth performance of calves and may be of great importance during transition from liquid to solid feed.

Key Words: calves, *S. cerevisiae*, growth performance

T269 Reduced carriage of *Escherichia coli* O157:H7 in cattle fed yeast culture supplement. L. Liou[1], H. Sheng[1], W. Ferens[1], C. Schneider[2], A. N. Hristov*[3], I. Yoon[4], and C. J. Hovde[1], [1]*Department of Microbiology, Molecular Biology and Biochemistry, University of Idaho*, *Moscow*, [2]*Department of Animal and Veterinary Science, University of Idaho*, *Moscow*, [3]*Department of Dairy and Animal Science, Pennsylvania State University*, *University Park*, [4]*Diamond V Mills, Inc.*, *Cedar Rapids, IA*.

Effect of yeast culture on cattle carriage of *Escherichia coli* O157:H7 (O157) was assessed using eight, one-year-old Charolais heifers equipped with ruminal cannulae in a 74 d trial. Animals were confirmed negative for O157 prior to initiation of the trial and until bacterial challenge and fed alfalfa hay and grain twice daily with *ad libitum* access to drinking water. Animals were randomly assigned to either Control (200 g/d ground barley without yeast culture) or YC (56 g/d Diamond V XP™ Yeast Culture mixed with 144 g ground barley) treatments. Animals were challenged with 10^{10} CFU O157 (ATCC 43895) through the rumen cannula on d 30 of the trial. Rumen samples were collected at 2, 6, and 12 h post-challenge with O157. Recto-anal junction mucosal swab (RAMS) samples and ruminal digesta were collected on d 1, 4, and then twice a week post-challenge and cultured for O157. On the day of inoculation, O157 in the rumen of the YC heifers was lower ($P = 0.043$) than in Control heifers (averages 5.40×10^2 vs. 2.43×10^3 CFU/ml, respectively). On d 4 post-challenge, rumen samples from all heifers that received YC were O157 culture-negative, while 2 of 4 Control heifers still harbored the bacteria. On d 4 post challenge, O157 from RAMS culture was lower ($P = 0.021$) in YC than Control heifers (averages 9.23×10^4 vs. 5.93×10^5 CFU/swab, respectively). By d 11 post-challenge, 2 of 4 YC heifers were culture negative for O157 while all Control heifers remained culture-positive through d 24 post-challenge. Thus, the cattle fed Diamond V XP™ Yeast Culture carried fewer O157 for a shorter duration than the Control heifers. The mechanism of action of YC was not investigated.

Key Words: yeast culture, *Escherichia coli* O157:H7, recto-anal junction mucosal

T270 A meta-analysis of the effect of monensin or live yeast or a combination thereof on performance of beef cattle. L. J. Erasmus*[1], R. F. Coertze[1], M. N. Leviton[1], and E. Chevaux[2], [1]*Dept. Animal and Wildlife Sciences, University of Pretoria*, *Pretoria, South Africa*, [2]*Lallemand SAS*, *Blagnac Cedex, France*.

A meta-analysis of the effect of monensin, live yeast (Saccharomyces cerevisiae CNCM I-1077, Levucell, SC) or a combination of the two feed additives on production in beef cattle was conducted using 15 trials that contained eligible data. The database included data from 1875 animals for the average daily gain (ADG) analysis and 222 replicates for the feed conversion ratio (FCR) analysis. The GLM procedure of SAS was used. All main effects (study, yeast, monensin and the interaction between yeast and monensin) were included in the initial models. The effect of different parameters (DMI, dietary CP%, dietary NDF %) as covariates and first order interactions were fitted according to a step down procedure and included if significant ($P < 0.05$). Least square means and SE were calculated and the significance of difference between means was determined by Fichers test. Average daily gain of cattle that received no supplement was lower (1.45 kg /d) than those supplemented with live yeast only (1.54 kg /d) and ADG of cattle receiving monensin only (1.54 kg/d) was lower compared to cattle supplemented with both additives (1.57 kg /d) ($P < 0.05$). The FCR of cattle supplemented with live yeast only (6.40kg DM/kg weight gain) was better than

unsupplemented cattle (6.61kg DM/kg weight gain) ($P < 0.05$) but did not differ from cattle supplemented with monensin only (6.32kg DM/kg weight gain) or a combination of additives (6.13kg DM/kg weight gain) ($P > 0.05$). Results suggest similar effects of either live yeast or monensin on performance of feedlot cattle. Further research is needed on potential complimentary effects between ionophores and live yeast when supplemented to beef cattle.

Key Words: beef cattle, live yeast, monensin

T271 Feed additives (monensin or yeast cultures) for finishing Nelore cattle. C. T. Gomes, F. A. P. Santos, J. T. das N. Neto, L. F. Greco, J. R. R. Dórea, L. R. D. A. Neto, M. C. Moscardini, G. B. Mourão, A. M. Pedroso*, A. D. Pacheco Jr., and M. A. C. Danes, *University of Sao Paulo, Piracicaba, São Paulo, Brazil*.

The objective of this trial was to study the feeding of monensin or yeast cultures for finishing cattle. Eighty non-implanted Nelore steers with an average initial shrunk BW (SBW) of 391 kg were used in a 60-d feeding trial after a period for adaptation to high concentrate diets. Animals were blocked by SBW and randomly allotted to 16 pens. Experimental diets were isonitrogenous and contained 15% sugar cane silage and 85% concentrate (DM basis), containing dried citrus pulp, finely ground sorghum, urea, and minerals and vitamins. Treatments were: 1) Control, 2) Saccharomyces cerevisiae (YEA-SAAC®1026 - 10g/animal/day), 3) Saccharomyces cerevisiae (BIOSAF SC 47 heatstable® - 10g/animal/day), 4) monensin (RUMENSIN®- 30ppm of diet DM). Data were analyzed based on a randomized complete experimental design, with pens as the experimental units, using the PROC GLM of Statistical Analysis Systems (SAS Inst. Inc., Cary, NC). Least square means were compared using the PDIFF procedure. Dry matter intake was lower ($P<0.05$) for animals fed monensin compared to other treatments. Neither ADG nor G:F ratio were improved by feed additives.

Table 1.Intake and performance of finishing Nelore bulls fed different feed additives

Variables	T1	T2	T3	T4	SEM	P value
ADG (kg/d)	1.126a	1.004ab	0.984b	1.020ab	0.917	0.0488
DM Intake (kg/d)	9.45a	9.46a	9.38a	8.77b	0.318	0.0393
G:F ratio	0.119	0.106	0.105	0.116	0.101	0.2416

Key Words: monensin, probiotics, cattle

T272 Digestibility and ruminal parameters in beef steers fed different additives. J. P. I. S. Monneratt, P. V. R. Paulino*, S. C. Valadares Filho, M. S. Duarte, N. K. P. Souza, L. D. Silva, and P. D. B. Benedeti, *Universidade Federal de Viçosa, Viçosa, MG, Brazil*.

The present experiment aimed to evaluate the effects of yeast culture supplementation in comparison to monensin and a control treatment on feed intake and nutrient digestibility, ruminal volatile fatty acids (VFA), pH and ammonia ($N\text{-}NH_3$) concentration in beef steers fed high-concentrate diets (80% of DM) with two levels of starch. Eight crossbred steers (489 kg average BW) fitted with rumen cannulae were used. The animals were allotted into two groups of four steers each; each group received one of the two diets (23 and 38% starch). The experiment was evaluated following a two-by-two Latin square design. Within each square, four treatments were implemented: control (no additive), monensin (250 mg/kg of DM), yeast low dose (*Saccharomyces cerevisae*) – 1.0 g/100 kg BW/day and yeast high dose – 2.5 g/100 kg BW/day. The diets with different levels of starch were applied independently in each Latin square. Intakes of non-fiber carbohydrates, starch and dry matter, expressed as % of BW and metabolic body size, were lower ($P < 0.10$) for the low dose of yeast when compared to the other treatments. Ruminal pH was not influenced ($P > 0.10$) by the inclusion of the additives in the diets, with a mean value of 6.48. Ruminal VFA concentrations were higher ($P < 0.10$) in the animals receiving the lowest starch level, monensin and yeast, at the dose of 1 g/100 kg of BW. Lower lactate concentrations ($P < 0.10$) were observed in the treatments which had monensin added to the diet and for the diet with the highest starch level. The ruminal concentrations of propionate and $N\text{-}NH_3$ were not influenced ($P > 0.10$) by any of the additives used in this study, with mean values of 5.61 and 16.50 mg/dL, respectively. However, propionate concentration tended to be higher ($P < 0.10$) in animals fed the low starch level than those fed the high starch diet. Lower ruminal $N\text{-}NH_3$ concentrations and higher NDF digestibility coefficients were observed in the treatment with the lowest starch level. All the additives used in this study improved ($P < 0.10$) the digestibility of ether extract.

Key Words: ruminal pH, ruminal ammonia, volatile fatty acids

T273 Feedlot performance of Nellore and Brangus cattle fed monensin or polyclonal antibody preparation against lactate-producing rumen bacteria. D. D. Millen*[1,2], R. D. L. Pacheco[1], M. D. B Arrigoni[1], C. L. Martins[1], T. M. Mariani[1], J. P. S. T. Bastos[1], L. M. N. Sarti[1], R. S. Barducci[1], and S. R. Baldin[1], [1]*FMVZ/Unesp, Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP, São Paulo, Brazil*.

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria on feedlot performance of Brangus (BR) and Nellore (NE) cattle. The experiment was designed as a 2 × 2 factorial arrangement using repeated measures over time, replicated 6 times (4 bullocks/pen), in which 48 9-mo-old bullocks (284.4 ± 23.4 kg) of each of two breeds evaluated were fed diets containing either monensin (MO) at 300 mg•animal^{-1}•d^{-1} or PAP at 3g•animal^{-1}•d^{-1} for 116-d. Measures over time were taken according to the level of concentrate (LOC) fed during the study: 70, 80 and 85%. These diets were named growing 1 (G1), growing 2 (G2) and final (FN), respectively. BR had greater ($P < 0.01$) ADG (1.42 vs. 1.14 kg), HCW (251.09 vs. 206.08 kg), DMI (8.31 vs. 6.38 kg) and DMI as percentage of BW (DMIBW, 2.11 vs 1.97%) than NE cattle. But in terms of G:F, it was observed ($P > 0.10$) similar efficiencies (BR = 0.171; NE = 0.178). Similar dressing percentages (DP) were found ($P > 0.10$) among breeds as well (BR = 52.8, NE = 52.9%). Interactions between breeds and LOC were found ($P < 0.05$) for DMIBW and G:F. BR and NE showed similar DMIBW when fed G1, however BR had greater DMIBW when fed G2 and FN. On the other hand, G:F was similar when breeds were fed G1 and G2, but NE showed better G:F when fed FN. No significant ($P > 0.10$) FA main effects were observed for any of the feedlot performance parameters (ADG, HCW, DP, DMI and G:F) with the exception ($P < 0.05$) of DMIBW (PAP = 2.08; MO = 2.00%). Interaction between FA and LOC were found ($P < 0.05$) for ADG and G:F. Cattle fed PAP and MO had similar ADG and G:F when fed G1 and G2, however, feeding MO led to greater ADG (1.36 vs. 1.23 kg) and better G:F (0.175 vs. 0.159) when fed FN. No interaction between breeds and FA was found ($P > 0.10$). BR performed better than NE in the study. Cattle fed MO performed better than those fed PAP when fed FN, however over the study, no differences between FA tested were detected on feedlot performance, with the exception of DMIBW.

Key Words: feedlot, PAP, monensin

T274 The interaction of flaxseed hulls and monensin on feed intake, apparent digestibility, and milk composition of late-lactating dairy cows. C. Côrtes*[1], D. C. da Silva[1,2], R. Kazama[1,2], N. Gagnon[1], C. Benchaar[1], G. T. dos Santos[1,3], L. M. Zeoula[1,3], and H. V. Petit[1], [1]*Agriculture and Agri-Food Canada, Quebec, Canada*, [2]*Universidade Estadual de Maringa, Parana, Brazil*, [3]*CNPq, Brazil*.

The objective of the experiment was to determine the effect of feeding a combination of flaxseed hulls and monensin on DMI, apparent digestibility, and milk composition of dairy cows. Four primiparous Holstein cows (BW = 665 kg; DIM = 190 d) fitted with ruminal cannulae were used in a 4 x 4 Latin square. Each experimental period consisted of 21 d of adaptation and 7 d of data collection. Cows were milked and fed twice a day. Treatments were: control with no flaxseed hulls and monensin (CO), 20% (DM basis) flaxseed hulls (FH), control with monensin (16 ppm; MO); and 20% (DM basis) flaxseed hulls and 16 ppm of monensin (HM). Results were analyzed using the MIXED procedure of SAS (2000) within a 2 x 2 factorial arrangement of treatments. Significance was declared at $P < 0.05$. There was no interaction between flaxseed hulls and monensin. DMI was higher for CO and MO than for FH and HM and monensin had no effect. Flaxseed hulls had no effect on DM digestibility however monensin tended to increase it. Apparent digestibility of CP was higher for cows supplemented with monensin compared to those not receiving monensin. Digestibility of ADF was higher for CO and MO than for FH and HM while the inverse was observed for digestibilities of CP and EE. Milk production was decreased by flaxseed hulls supplementation. Concentrations of milk fat, CP, and lactose were similar among treatments.

Table 1. Dry matter intake, apparent digestibility, and milk composition

						P-value		
	CO	FH	MO	HM	SE	Flaxseed hulls	Monensin	Interaction
DMI, kg/d	20.1	19.0	20.0	18.6	0.4	0.04	0.56	0.72
Digestibility								
% DM	65.0	65.1	66.4	65.8	0.4	0.64	0.08	0.45
% CP	65.7	70.0	66.6	71.9	0.4	0.002	0.05	0.35
% ADF	55.3	44.0	57.6	47.2	1.5	0.01	0.17	0.78
% NDF	46.2	43.9	49.7	45.9	2.1	0.24	0.27	0.75
% EE	77.1	91.4	75.7	91.7	1.0	0.001	0.63	0.45
Milk								
kg/day	27.5	26.0	26.8	23.3	0.7	0.03	0.09	0.21
% CP	3.7	3.5	3.6	3.6	0.05	0.11	0.18	0.10
% fat	3.0	3.6	3.3	3.3	0.06	0.15	0.94	0.17
% lactose	4.7	4.8	4.8	4.9	0.38	0.14	0.17	0.57

Key Words: dairy cows, flaxseed hulls, monensin

T275 Feeding behavior of Nellore and Brangus cattle fed monensin or polyclonal antibody preparation against lactate-producing rumen bacteria. T. M. Mariani[1,2], D. D. Millen*[1], R. D. L. Pacheco[1], M. D. B. Arrigoni[1], C. L. Martins[1], J. P. S. T. Bastos[1], R. S. Barducci[1], L. M. N. Sarti[1], S. R. Baldin[1], D. Tomazella[1], E. S. Ogawa[1], F. S. Parra[1], and J. R. Ronchesel[1], [1]*FMVZ/Unesp, Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP, São Paulo, Brazil*.

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria on feeding behavior of Brangus (BR) and Nellore (NE) cattle. The experiment was designed as a 2 × 2 factorial arrangement using repeated measures over time, replicated 4 times (4 bullocks/pen), in which 32 9-mo-old bullocks (279.4 ± 21.5 kg) of each of two breeds evaluated were fed diets containing either monensin (MO) at 300 mg•animal^{-1}•d^{-1} or PAP at 3g•animal^{-1}•d^{-1} for 116-d. Measures over time were taken according to the level of concentrate (LOC) fed during the study: 55, 70, 80 and 85%. These diets were named adaptation (ADP), growing 1 (G1), growing 2 (G2) and final (FN), respectively. Visual appraisal was made 15-d after introduction of a new diet, and then every five minutes during 24-h, feeding behavior data was collected as follows: time spent eating (EAT), ruminating (RUM), resting (RES) expressed in minutes and number of meals per day (MEA). The meal length (MLE) in minutes was calculated as follows: EAT/MEA. Feeding MO led to longer ($P < 0.05$) RUM than PAP (421.58 vs. 397.05 min), however no differences ($P > 0.10$) among feed additives (FA) were observed for EAT and RES. Interaction between FA and LOC was found ($P < 0.05$) for RUM and RES. Feeding PAP and MO led to similar RUM and RES when fed ADP and G1, however, cattle fed PAP had shorter RUM and longer RES than MO when fed G2 (RUM: PAP = 291.9, MO = 340.5 min) and FN (RUM: PAP = 292.6, MO = 337.1 min). MEA was greater for cattle fed MO when compared to those fed PAP (17.0 vs. 15.9; $P < 0.05$), whereas feeding PAP led to longer MLE (15.3 vs. 13.8 min; $P < 0.05$). No significant ($P > 0.10$) breed main effects were observed for any of the feeding behavior parameters (EAT, RUM, RES and MEA) with the exception ($P < 0.05$) of MLE (BR = 15.1; NE = 14.0 min). No interaction was observed ($P > 0.10$) between breeds and FA. Feeding MO reduced the MLE and led to greater MEA and RUM compared to PAP. BR and NE presented similar MEA, however BR had longer MLE.

Key Words: behavior, PAP, monensin

T276 Feedlot performance of Brangus cattle fed monensin or polyclonal antibody preparation against lactate-producing rumen bacteria. R. S. Barducci[1,2], L. M. N. Sarti[1], M. D. B. Arrigoni[1], R. D. L. Pacheco*[1], D. D. Millen[1], C. L. Martins[1], S. R. Baldin[1], F. S. Parra[1], J. R. Ronchesel[1], D. Tomazella[1], T. Leiva[1], H. D. Rosa[1], T. M. Mariani[1], J. P. S. T. Bastos[1], T. C. Putarov[1], [1]*FMVZ/Unesp, Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP, São Paulo, Brazil*.

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test the effects of polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria or monensin (MO) on feedlot performance of Brangus cattle fed high concentrate diets. Seventy-two 9-mo-old bullocks (285.9 ± 38.7 kg) were assigned to 24 pens (3 bullocks/pen) and used in a completely randomized design with 2 × 2 factorial arrangement of treatments, replicated 6 times. Factors were inclusion or not of PAP or MO, at a dose of 4.5g•animal^{-1}•d^{-1} or 300 mg•animal^{-1}•d^{-1}, respectively. Animals were adapted for 21-d to the high concentrate diet fed. Diet contained 47.5% high moisture corn, 20% citrus pulp, 12.8% soybean meal, 13.7% sugarcane bagasse, 4.6% *Cynodon* hay and 1.5% supplement. Bullocks were weighed every 28-d to calculate ADG and G:F, and DMI was recorded every day and expressed in kilos (DMIKG) and as percentage of BW (DMIBW). No significant ($P > 0.10$) PAP main effect or interactions between PAP and MO were observed for any of the feedlot performance parameters (final BW, ADG, HCW, G:F, DMIKG, DMIBW and dressing percentage). However, feeding MO led to greater final weight (with MO = 474.86, without MO = 459.61 kg; $P < 0.05$), ADG (with MO = 1.68, without MO = 1.57 kg; $P < 0.05$), HCW (with MO = 248.46, without MO = 240.20 kg; $P < 0.08$) and G:F (with MO = 0.180, without MO = 0.173;

P < 0.10). Feeding MO did not affect (P > 0.10) dressing percentage (with MO = 52.27, without MO = 52.23%), DMIKG (with MO = 9.33, without MO = 9.01 kg) and DMIBW (with MO = 2.42, without MO = 2.39%). Cattle fed MO performed better than those animals not fed MO. On the other hand, feeding PAP did not improve feedlot performance of Brangus cattle in this study.

Key Words: PAP, performance, monensin

T277 Rumen papillae measurements of feedlot cattle fed monensin or polyclonal antibody preparation against lactate-producing rumen bacteria. L. M. N. Sarti[1,3], R. S. Barducci[1], D. D. Millen*[1], R. D. L. Pacheco[1], M. D. B. Arrigoni[1], C. L. Martins[1], S. F. Costa[2], L. Q. Melo[2], F. S. Parra[1], J. R. Ronchesel[1], D. Tomazella[1], H. D. Rosa[1], T. Leiva[1], S. R. Baldin[1], N. R. B Cônsolo[4], [1]*FMVZ/Unesp*, *Botucatu, São Paulo, Brazil*, [2]*UFLA*, *Lavras, Minas Gerais, Brazil*, [3]*Apoio FAPESP*, *São Paulo, Brazil*, [4]*UD/Unesp*, *Dracena, São Paulo, Brazil*.

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test the effects of polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria or monensin (MO) on rumen wall absorptive surface area of feedlot cattle fed high concentrate diets. Seventy-two 9-mo-old bullocks (285.9 ± 38.7 kg) were assigned to 24 pens (3 bullocks/pen) and used in a completely randomized design with 2 × 2 factorial arrangement of treatments, replicated 6 times. Factors were inclusion or not of PAP or MO, at a dose of 4.5g•animal^{-1}•d^{-1} or 300 mg•animal^{-1}•d^{-1}, respectively. Diets contained 47.5% high moisture corn, 20% citrus pulp, 12.8% soybean meal, 13.7% sugarcane bagasse, 4.6% *Cynodon* hay and 1.5% supplement. After slaughter the entire rumens were washed and a fragment of 1 cm^2 of one of three animals from each pen was harvested from cranial sac. Manually, the number of papillae per square centimeters of rumen wall (NOP) was determined. Consequently, 12 papillae were randomly collected from each fragment, scanned on Petri plates, and the mean papillae area (MPA) was determined using the Image Tool software for image analysis (UTHSCSA, 2002). Absorptive surface area per square centimeters of rumen wall (ABS) was calculated as follows: 1 + (NOP×MPA) – (NOP×0.002), where number 1 represents the 1 cm^2 fragment collected, and 0.002 is the estimated basal area of papillae. Participation of rumen papillae in the absorptive surface area (PAB) was calculated as follows: (NOP×MPA/ABS)×100. No significant (P > 0.10) PAP main effect or interactions between PAP and MO were observed for any of the rumen papillae measurements. Nevertheless, feeding MO led to greater ABS (with MO = 24.92, without MO = 19.45 cm^2; P < 0.05) and PAB (with MO = 96.07, without MO = 94.30%; P < 0.10), without altering NOP and MPA (P > 0.10). Greater ABS and PAB for cattle fed MO could indicate greater VFA absorption and lesser extent of rumen lesions.

Key Words: monensin, PAP, papillae

T278 Influence of virginiamycin supplementation on ruminal fermentation and microbial populations of steers. T. J. Guo[1,2], J. Q. Wang*[1], D. P. Bu[1], J. P. Wang[1], K. L. Liu[1], D. Li[1], S. Y. Luan[1], and X. K. Huo[1], [1]*Institute of Animal Science, State Key Laboratory of Animal Nutrition, Chinese Academy of Agricultural Science*, *Beijing, China*, [2]*Xinjiang Agricultural University*, *Urumqi, China*.

Influence of virginiamycin (VM) supplementation on ruminal fermentation parameters and microbial populations was studied in steers. Four ruminally cannulated steers (BW 559.4±30.1 kg) were used in a crossover design experiment. Each period was of 28 d. The basal diet had a forage-to-concentrate ratio of 35:65 (DM basis). The experimental treatments were (1) control; (2) control diet plus VM 30 mg/kg concentrate. Ruminal fluid was collected at 0730 h prefeeding, at 1130 h and 1730 h post-feeding on 27 and 28 d of each period. Part of the pooled samples of rumen fluid were transferred to anaerobic culture by roll-tube technique and extract 11 procaryotic taxa DNA for Real-time PCR analysis. Remaining pooled rumen fluid samples were analyzed for pH, VFA, ammonia-N, and L-lactic acid. Data were analyzed by the MIXED procedure of SAS 9.0. Compared with the control, steers receiving VM had higher ruminal pH (6.70 vs 6.63; P<0.05) and lower ammonia nitrogen (4.94 vs 6.19 mg/dL; P<0.01), and had lower mean counts of amylolytic bacteria and proteolytic bacteria (P<0.01) by roll-tube technique. The L-lactic acid concentrations in rumen fluid of control and VM receiving steers were not different (1.39 vs 1.26 mmol/L). Compared to control, the steers receiving VM had no influence on the following bacterial species (log10 copies per μL): *Selenomonas ruminantium* (5.55 vs 4.46), *Anaerovibrio lipolytica* (8.12 vs 7.93), *Ruminococcus albus* (6.95 vs 7.39), *Streptococcus bovis* (6.67 vs 7.74), *Lactobacillus spp.* (4.57 vs 5.22), *Butyrivibrio fibrisolvens* (4.44 vs 4.74), Genus-level Ruminococcus (8.36 vs 8.45), *Ruminococcus flavefaciens* (3.77 vs 4.00), Genus Prevotella (9.99 vs 10.04), *Megasphaera elsdenii* (2.26 vs 2.27), and *Prevotella ruminicola* (4.79 vs 4.32). Feeding VM to steers raised ruminal pH, reduced ammonia-N with no influence on major microbial species in the rumen fluid.

Key Words: virginiamycin, beef steer, microbial populations

T279 Effects of increasing levels of monensin on dairy cows in early lactation. G. F. Schroeder*[1], B. D. Strang[1], M. A. Shah[1], M. A. Messman[1], and H. B. Green[2], [1]*Cargill Animal Nutrition, Innovation Campus*, *Elk River, MN*, [2]*Elanco Animal Health*, *Greenfield, IN*.

A previous analysis of 966 cows from nine trials suggested that the rate of increase in DMI during the first 8 weeks of lactation increased as monensin dose increased. This may indicate that monensin may have a different effect on DMI depending on stage of lactation and energy status of the cows. To evaluate this hypothesis, 44 Holstein cows (including both primiparous and multiparous cows) were blocked according to BW and milk yield from the previous lactation and randomly assigned to 1 of 4 treatments: 0 (Control), 300 (M300), 450 (M450), or 600 (M600) mg/d of monensin during the first 9 weeks of lactation. Cows were housed in a tie-stall barn and individually fed the same diet (17% CP, 34% NDF, 38% NFC, 3.7% Fat, and 1.7 Mcal/kg NEL), with monensin treatments top-dressed twice daily. Milk production and DMI was measured daily and milk composition and urine ketone body were determined twice weekly. Data were averaged by week and model included repeated measures. Treatment by week interaction was not significant for any of the variables analyzed (P > 0.05). A quadratic increase in milk yield and a linear increase in DMI was observed with increasing monensin levels. Concentration of ketone body (Acetoacetic acid) in urine tended to be lower at higher levels of monensin feeding. Efficiency of 3.5% fat-corrected milk (FCM) yield (2.0 kg FCM/kg DMI) was not affected by treatments (P > 0.05). Milk fat concentration linearly decreased with increase levels of monensin. Although milk true protein concentration was not affected, milk protein yield was quadratically increased as dose of monensin increased. Overall, the results of this study support the hypothesis that monensin seems to increase intake right after calving, reduce ketone body formation and increase milk yield in early lactating cows.

Table 1.

	Treatments						P<		
	Control	M300	M450	M600	SEM	Monensin	Linear	Quad	Cubic
Milk, kg/d	41.5	43.5	49.3	43.2	1.94	0.12	0.22	0.05	0.09
DMI, kg/d	19.0	20.4	21.9	21.0	0.79	0.03	0.04	0.16	0.52
3.5% FCM, kg/d	42.9	42.4	49.3	41.4	2.00	0.62	0.80	0.08	0.02
Fat, %	3.78	3.45	3.52	3.36	0.14	0.05	0.06	0.57	0.33
Fat, kg/d	1.53	1.45	1.72	1.40	0.08	0.84	0.72	0.12	0.01
Protein, %	2.78	2.84	2.82	2.78	0.05	0.33	0.93	0.30	0.75
Protein, kg/d	1.14	1.21	1.38	1.18	0.05	0.06	0.26	0.01	0.06
Ketone bodies, mg/dL	7.11	1.88	3.07	4.21	1.97	0.09	0.36	0.08	0.43

Key Words: early lactation, intake, monensin

T280 Field study to investigate the risk factors for milk fat depression (MFD) in dairy herds feeding Rumensin®. D. V. Nydam*[1], T. R. Overton[1], D. E. Bauman[1], T. C. Jenkins[2], and G. D. Mechor[3], [1]*Cornell University*, *Ithaca, NY*, [2]*Clemson University*, *Clemson, SC*, [3]*Elanco Animal Health*, *Greenfield, IN*.

Commercial dairy herds (n=79) in the Northeastern and Upper Midwestern U.S. were enrolled in a cross-sectional observational study to investigate herd-level factors related to bulk tank milk fat percentage in herds feeding Rumensin®. Data collection consisted of a herd survey, samples of high group TMR for wet chemistry nutrient analyses (Cumberland Valley Analytical Services, Maugansville, MD) and fatty acid (FA) profiling (Clemson) and samples of bulk tank milk for FA profiling (Cornell). Unconditional univariable associations of continuous predictor variables and herd milk fat percentage were evaluated using simple regression, categorical analyses using the 3rd quartile as a cut-point were conducted and compared using t-tests, and multivariate analyses with backward stepwise elimination of variables was conducted using PROC GLM. The median milk fat percentage was 3.45% (range 2.70 to 4.30) and Rumensin® dose was 250 mg/d (range 150 to 410 mg/d). Milk fat content of *trans*-10, C18:1 was correlated negatively (R^2= 0.53) in a curvilinear manner with milk fat percentage. Variables related to TMR composition (Rumensin® dose, CP, ADF, NDF, starch, sugar, ether extract, total FA) did not have univariate relationships with herd milk fat percentage (P > 0.50). Increased proportions of TMR particles on the middle screen of the Penn State separator were positively associated to herd milk fat (R^2=0.09; P < 0.01) and increasing proportions of TMR particles in the bottom pan were negatively associated to herd milk fat percentage(R^2=0.11; P < 0.01). Increased dietary intake of monounsaturated FA (C16:1 and C18:1) was negatively related (P < 0.07) to herd milk fat. Overall, results suggest that altered ruminal biohydrogenation of dietary FA occurs in commercial dairy herds with lower herd level milk fat percentage. Furthermore, the lack of univariate relationships of most TMR variables with herd milk fat supports multiple factors contributing to MFD.

Key Words: milk fat, Rumensin®

T281 Effect of monensin and propylene glycol on volatile fatty acid and rumen parameters in early lactation Holstein cows. H. Bahrami-Yekdangi, K. RezaYazdi, and M. Dehghan-Banadaky*, *Universsity of Tehran*, *Karaj, Tehran, I.R., Iran*.

We evaluated the effects of monensin and propylene glycol on volatile fatty acid, rumen NH3-N concentration and Rumen pH of 16 lactating Holstein cows (60±30 DIM, Milk production 33±3 Kg/day) between September and November 2007. Cows were used in a completely random design with 4 rations and 4 replicates (cows). Basal ration were formulated according to CNCPS with (60% concentrate and 40% forages). Cows in group I were fed basal ration without additive (control), cows in group 2 were fed basal ration with 335 mg/head/day monensin, cows in group 3 were fed basal ration with 400 ml/head/day propylene glycol and cows in group 4 were fed basal ration with 335 mg/head/day Monensin and 400 ml/head/day propylene glycol. Data were analyzed on mixed models for repeated measurement. Results showed that ration propylene glycol an monensin (group 4) significantly decreased acetate and butyrate concentration of cows (p<0.05) but propionate N-NH3 concentration and pH were not different between groups.

Table 1. Effects of monensin and/or propylen glycol on rumen parameters

SEM 4 3 2 1* variable	1	2	3	4	SEM
Total VFA	121.2	119.5	113.8	105.8	9.12
acetate (mmol/lit)	78.6[a]	75.2[ab]	64.3[b]	59.9[b]	9.90
propionate (mmol/lit)	23.8	27.5	27.4	28.7	4.87
acetate/propionate	3.3[a]	2.7[b]	2.6[b]	2.1[b]	0.23
butyric (mmol/lit)	14.1[a]	12.6[ab]	9.9[ab]	7.4[b]	2.77

Ration 1 without additive (control), ration 2 with 335 mg/head/day, ration 3 with 400 ml/head/day propylene glycol, and ration 4 TMR with 335 mg/head/day monensin and/or 400 ml/head/day propylene glycol.

Key Words: propylene glycol, monensin, rumen parameters

T282 The interaction of flaxseed hulls and monensin on milk fatty acid composition of late-lactating dairy cows. C. Côrtes*[1], D. C. da Silva[1,2], R. Kazama[1,2], N. Gagnon[1], C. Benchaar[1], G. T. dos Santos[2,3], L. M. Zeoula[2,3], and H. V. Petit[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*, [2]*Universidade Estadual de Maringa*, *Parana, Brazil*, [3]*CNPq*, *Brazil*.

The objective of the study was to determine the effect of feeding a combination of flaxseed hulls and monensin on milk fatty acid (FA) profile of dairy cows. Four primiparous Holstein cows (BW = 665 kg; DIM = 190 d) fitted with ruminal cannulae were used in a 4 x 4 Latin square. Each period consisted of 21 d of adaptation and 7 d of data collection. Cows were milked and fed twice a day. Diets were: control with no flaxseed hulls and monensin (CO), 20% (DM basis) flaxseed hulls (FH), monensin (16 ppm; MO), and 20% (DM basis) flaxseed hulls and monensin (HM). Results were analyzed using the MIXED procedure of SAS (2000). Significance was declared at $P < 0.05$. There was no interaction between flaxseed hulls and monensin for milk FA profile. Concentrations (% of total FA) of saturated (SFA), short-chain (SCFA), and medium-chain (MCFA) FA were significantly lower and those of monounsaturated (MUFA), polyunsaturated (PUFA), and long-chain (LCFA) FA were higher for cows supplemented than unsupplemented with flaxseed hulls. Concentrations of n-3 FA (*cis*9,12,15-18:3, *cis*5,8,11,14,17-20:5 and 22:5) and n-6 FA (*cis*9,12-18:2, *cis*6,9,12-18:3, *cis*11,14-20:2, *cis*8,11,14-20:3 and *cis*5,8,11,14-20:4) were significantly higher and lower, respectively, with flaxseed hulls supplementation. Feeding flaxseed hulls decreased the n-6 to n-3 FA ratio in milk fat and changed favourably milk FA profile for better human health.

Table 1. Fatty acids concentrations (% of total FA)

							P-value	
	CO	FH	MO	HM	SE	Flaxseed hulls	Monensin	Interaction
MUFA	22.44	37.02	24.36	39.69	1.80	0.004	0.29	0.85
PUFA	3.92	6.73	4.42	6.92	0.46	0.01	0.51	0.76
SFA	73.63	56.25	71.23	53.40	2.20	0.004	0.32	0.92
SCFA	17.83	11.69	16.34	8.99	0.92	0.01	0.11	0.56
MCFA	48.92	29.73	47.57	31.49	1.17	0.001	0.87	0.28
LCFA	33.24	58.59	36.13	59.52	1.92	0.001	0.40	0.65
n-3	0.80	2.02	1.00	1.96	0.14	0.004	0.88	0.23
n-6	2.58	2.41	2.66	2.33	0.05	0.01	0.98	0.20
n-6: n-3	3.14	1.10	2.73	1.17	0.22	0.004	0.50	0.36

Key Words: flaxseed hulls, milk fatty acids, monensin

T283 Combined use of ionophore and virginiamycin in Nellore steers fed high concentrate diets. A. J. C. Nuñez*[1,2], M. Caetano[1], A. Berndt[3], J. J. A. A. Demarchi[3], P. R. Leme[2], and D. P. D. Lanna[1], [1]*ESALQ/USP, Piracicaba, SP, Brazil*, [2]*FZEA/USP, Pirassununga, SP, Brazil*, [3]*APTA Regional Extremo Oeste, Andradina, SP, Brazil*.

The objective of this work was to evaluate the effects of adding virginiamycin to a high concentrate diet containing an ionophore. Performance, carcass traits, liver abscess incidence and fecal starch content were evaluated in 72 Nellore steers, with initial BW of 379 ± 27 kg. Animals were blocked by initial weight, randomly allocated to individual pens and fed for 61 days (once daily at 0800 h). Diets had two concentrate levels (73%C and 91%C had 73 and 91% concentrate in the DM respectively) and two virginiamycin levels (Control and VM had 0 and 15 mg/kg DM respectively) in a 2x2 factorial arrangement. The 73%C diet had 16% CP, 30.5% NDF, 69% TDN and 29.7% starch (52% dry ground corn), and the 91%C diet had 16% CP, 16.9% NDF, 80% TDN and 45.3% starch (70% ground corn). All diets had the ionophore salinomycin at 13 mg/kg DM. Statistical analyses were conducted using the GLM procedure of SAS. There were no interactions between concentrate and virginiamycin levels for any variable. Dry matter intake (DMI) was higher (P<0.01) for the 91%C treatment (9.0 ± 0.2 vs. 7.8 ± 0.2 kg/day), as was average daily gain (ADG) (1.79 ± 0.06 vs. 1.43 ± 0.06 kg/day; P<0.01). There was a trend for increased feed efficiency (FE) in the 91%C treatment (202.7 ± 6.7 vs. 185.9 ± 6.7 g/kg; P=0.08). DMI was lower for the VM treatment (7.98 ± 0.2 vs. 8.76 ± 0.2 kg/day; P<0.01), however, ADG did not differ from Control (P=0.66). Hence, virginiamycin fed animals had increased FE (206.0 ± 6.71 vs. 182.6 ± 6.71 g/kg; P=0.02). Animals fed 91%C diet had higher dressing percentages (55.3 ± 0.3 vs. 54.4 ± 0.3%; P=0.02) and heavier kidney and pelvic fat (8.1 ± 3.1 vs. 7.2 ± 3.0 kg; P=0.04). Virginiamycin levels did not affect carcass traits and no liver abscesses were found. Fecal starch content was higher (P<0.01) for the 91%C treatment (19.3 ± 1.1 vs. 13.9 ± 1.1%), but did not change due to virginiamycin (17.3 ± 1.1 vs. 15.9 ± 1.1% for Control and VM, respectively; P=0.40). These results suggest that adding virginiamycin to a diet containing an ionophore is an efficient tool to improve efficiency in high concentrate diets for Nellore cattle.

Key Words: antibiotics, beef cattle, salinomycin

T284 Effects of an amylase inhibitor on rumen pH and feed intake of young Holstein heifers fed a 100% concentrate diet. A. Bach*[1,2], M. Devant[2], A. Serrano[2], and A. Aris[2], [1]*ICREA, Barcelona, Spain*, [2]*IRTA-Ruminant Production, Caldes de Montbui, Spain*.

Sixteen rumen-cannulated Holstein heifers (BW = 258±53.7 kg) were used in a replicated 4x4 Latin square design to evaluate the effects of 3 doses (35, 52.5, and 70 ppm) of an amylase inhibitor (acarbose) on rumen pH and feed consumption. The heifers received a non-acidotic ration ad libitum for the first 14 d of each period, feed was withdrawn for one day, and then animals received a 100% concentrate ration ad libitum for 6 d to induce rumen acidosis. During these 6 d of each 21-day period, rumen pH was determined every 15 min in all 16 animals simultaneously. Total feed intake during the 6-d acidotic challenge was recorded. Rumen samples were obtained from all heifers in periods 2 and 3 to determine VFA concentrations and amounts of cDNA from S. ruminantium, M. elsdenii, and S. bovis using real-time PCR. Rumen pH data were analyzed using a model that accounted for the fixed effects for treatment, day, and treatment by day interaction and the random effects for animal and period. All data from 4 heifers were removed from the study due to respiratory and digestive upsets. Concentrate intake was affected by treatment and period and their interaction. Inclusion of acarbose allowed heifers to increase feed intake and maintain number of hours that ruminal pH was <5.5 at the same level as for control animals. Feed intakes for 0, 35, 52.5 and 70 ppm acarbose supplementation were 3.5, 4.6, 4.6 and 5.5 kg/d with the two lower doses being different at P < 0.05 from the control and the high doses. Number of hours that ruminal pH was <5.5 were 7.6, 11.3, 5.0 and 8.5 for 0, 35, 52.5 and 70 ppm, respectively and only the 35 ppm dose differed (P<0.05) from control. Thus, acarbose supplementation greater than or equal to 52.5 ppm resulted in increased intake while maintaining ruminal pH. There were no differences among treatments in area under the curve of pH 5.5 or ruminal VFA concentrations. There were no change in counts of the studied bacteria with addition of acarbose. It is concluded that supplementation with as little as 52.5 ppm of acarbose improves feed consumption under acidogenic conditions, while avoiding a decrease in rumen pH.

Key Words: acidosis, intake, pH

T285 Effect of *Bacillus subtilis* natto on milk performance, ruminal fermentation, and microbial profile of dairy cows. L. F. Deng[1], J. Q. Wang*[1], D. P. Bu[1], K. L. Liu[1], Y. M. Jiang[1], Q. Chen[1], P. Yu[1], H. T. Zhang[1], and J. K. Drackley[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*University of Illinois, Urbana*.

Two experiments were conducted to evaluate effects of *Bacillus subtilis* natto (BSN2) initially isolated from fermented soybeans on dairy cow performance, ruminal fermentation and microbial profile. In Exp 1, thirty-six dairy cows (DIM, 54 ± 23 d) were randomly assigned into 3 groups: Control (Cont), basal diet; Group 1, basal diet plus 0.5×10^{11} cfu/d of BSN2 cow^{-1} and Group 2, basal diet plus 1.0×10^{11} cfu/d cow^{-1}. During treatment (70 d), daily milk production and weekly milk composition were determined on individual cows. For cows in Group 2, uncorrected milk yield, 4% fat- corrected milk (FCM), and energy-corrected milk (ECM) were 14.7, 17.0, and 17.4% higher (P<0.05) than cows fed Control, but Log_{10} somatic cell count (SCC) was 5.5% lower (P<0.05). There was no difference (P>0.05) between Cont and Group 1 and 2 for milk fat, protein and lactose concentration. In Exp 2, four rumen-cannulated dairy cows fed Cont diet for 0-7 d and rumen samples were collected on d 5 and 6, the same cows then were fed BSN2 (1.0×10^{11} cfu/d) 8-21 d and rumen samples were collected on d 20 and

21. Compared with Cont period, during the treatment period ruminal pH decreased (6.64 vs. 6.46, $P<0.05$), and NH_3-N, total VFA and molar proportion of propionate increased 37.7, 47.4, 6.4% ($P<0.05$) respectively. Molar proportion of acetate decreased 1.9% ($P<0.05$), and the A/P ratio was lower (3.23 vs. 3.02, $P<0.05$). No difference ($P>0.05$) for 24-h DM digestibility were detected between treatments. Total ruminal bacteria, proteolytic and amylolytic bacteria and protozoa in rumen increased ($P<0.05$) in treatment groups. These results demonstrate that BSN2 improved milk production and milk components yield, decreased SCC, and promoted the growth of some ruminal microorganisms. Thus, BSN2 has potential to be used as a probiotic for dairy cows.

Key Words: *Bacillus subtilis* natto, milk performance, ruminal fermentation

T286 Probiotic effect of *Bacillus subtilis* (natto) on rumen bacterial diversity of weaning Holstein calves. P. Yu[1], J. Wang*[1], D. Bu[1], K. Liu[1], D. Li[1], and C. McSweeney[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing,China*, [2]*CSIRO Livestock Industries, Queensland, Australia*.

The purpose of the present study was to investigate the probiotic effect of *Bacillus subtilis* (natto) on the rumen bacterial diversity of weaning calves. Eight calves were randomly assigned into two groups, a control group fed a starter diet, and a treatment group supplemented with *Bacillus subtilis* (natto), which was mixed with the diet at a concentration of 5×10^6 CFU per gram of the average daily feed intake. Calves were slaughtered eight weeks after weaning. Rumen contents were taken from the perforated rumen immediately. DNA was extracted using the Beater-Bead method and used for 16S rDNA library construction. Results showed that feeding *Bacillus subtilis* (natto) decreased the concentration of volatile fatty acids in the rumen of the treatment group compared with the control group (67.9 vs.73.5 mmol/L). The vast majority of the two 16S rDNA clone libraries were represented by sequences related to the *Bacteroidetes* and *Firmicutes*. Members of *Bacteroidetes* accounted for about 39% and 25% of the total clones in control and treatment group, respectively, while *Firmicutes* increased from 46% in control to 57% in the treatment group. Clones affiliated to *Ruminococcus* and *Prevotella* accounted for 5% and 32% in control while 10% and 17% in the treatment animals respectively. These differences were confirmed by real-time PCR quantification using genus-specific primers. The numbers of *R. albus* ($\log_{10}$ 7.7 per mL) and *R. flavefaciens* ($\log_{10}$ 8.1 per mL) were higher in the rumens of the treatment group than in that of control group ($\log_{10}$ 7.3 per mL and $\log_{10}$ 7.7 per mL, respectively). These results indicated that supplementation of *Bacillus subtilis* (natto) on weaning calves could promote the establishment of the rumen microbial community, especially the growth of fibrolytic bacteria in the rumen of weaning calves.

Key Words: *Bacillus subtilis* (natto), weaning calves, rumen bacteria diversity

T287 Effect of an exogenous phytase on *in vitro* dry matter degradation, phosphorus balance and growth performance of finishing lambs. G. Buendía-Rodríguez[1], S. S. González-Muñoz*[1], G. D. Mendoza-Martínez[2], J. M. Pinos-Rodríguez[3], E. Aranda-Ibañez[1], L. A. Miranda-Romero[4], and L. M. Melgoza-Contreras[2], [1]*Colegio de Postgraduados, Montecillo, Edo. de México, México*, [2]*UAM Xochimilco, México D.F., México*, [3]*UASLP, San Luis Potosí, SLP, México*, [4]*Universidad Autónoma Chapingo, Chapingo, Edo. de México, México*.

The objective of this experiment was to determine the effect of a phytase (Natuphos 5000G, BASF Mexicana) on finishing lambs. Phytase was added (0, 150, 300 and 450 mg/kg diet; treatments) to a sorghum (70%) based diet and *in vitro* DM degradation was evaluated; data was analyzed using a Gompertz model and the DM remaining at each incubation time was used to fit a nonlinear regression model with the NLIN option of SAS. Additionally, DM, NDF and P total tract digestion, growth performance, and P balance were determined in 32 finishing Suffolk x Creole lambs (21.5±2.2 kg initial BW) during a 60 d feeding period. The experimental design was completely randomized; data collected over time was analyzed as repeated measurements using the MIXED option of SAS, and means were compared with the Tukey test. Inclusion of phytase in the diet had not effect ($P\geq0.05$) on *in vitro* DM degradation. There was a linear ($P\leq0.01$) improvement in total tract digestion of DM (741, 769, 773 and 799 g/d), NDF (527, 552, 564 and 624 g/d), and P (37.3, 40.5, 42.3 and 49.5 g/d) as phytase level in the diet increased. Phosphorus intake and excretion (urine and feces) and plasma P were not affected ($P\geq0.05$) by the inclusion of phytase in the diet. Retention of P, calculated using P values of feed, feces and urine, was linearly ($P\leq0.01$) increased (0.62, 0.72, 0.78 and 1.17 g/d) as phytase level was added in the diet. Feed intake, final BW, ADG and carcass dressing percentage of finishing lambs were not changed ($P\geq0.05$) by phytase. It is concluded that an exogenous phytase improved digestion of DM, NDF and P, as well as retained P, but it did not affect growth performance of finishing lambs.

Key Words: phytase, lambs, P balance

T288 Effect of fibrolytic enzymes on ruminal fermentation and digestibility in steers fed a diet with sodium bicarbonate. O. D. Montañez-Valdez*[1], J. M. Tapia Gonzalez[1], G. Rocha-Chavez[1], E. O. Flores-García[2], and J. H. Avellaneda-Cevallos[3], [1]*Centro Universitario del Sur de la Universidad de Guadalajara, Ciudad Guzmán, Jalisco, México*, [2]*Centro Universitario de la Costa Sur de la Universidad de Guadalajara, Autlán de Navarro, Jalisco, México*, [3]*Universidad Técnica Estatal de Quevedo, Quevedo, Ecuador*.

The objective of this study was to evaluate the effect of exogenous fibrolytic enzymes (ENZ; 0.3% of total diet) on ruminal fermentation and disappearance in steers fed a diet with or without sodium bicarbonate (SB, 3% of total diet). Six steers (450 ± 15 kg body weight) were randomly assigned to a replicated 3 × 3 Latin square with 2 different squares for balancing carryover effects. Both squares had 3 steers and squares were conducted simultaneously. The ruminal cannulas measured 7.5 cm center diameter (Bar Diamond, Parma, ID). Steers were housed in individual dry lot pens and offered the experimental diets twice a day at 0700, 1800 h for 90% of intake to allow no refusal. Steers were offered 1 of 3 diets (treatment), which were chemically very similar with 70% concentrate and 30% forage as follow: control; fibrolytic enzymes (ENZ; 0.3% of total diet); and ENZ + sodium bicarbonate (SB; 3% of total diet). The fibrolytic enzyme preparation containing xylanase and cellulase activities (Fibrozyme, Alltech Inc., Nicholasville, KY, USA). Sodium bicarbonate was a feed grade ruminal buffer (BS; Arm & Hammer, Church and Dwight Co., Inc.). Three days before the beginning of the feeding period the enzyme mixture was first mixed with alfalfa hay and then with the rest of the feed ingredients. Each experimental period consisted of 11 d of adaptation to diets and 4 d of experimental measurements. The buffer capacity was 67.8 for control, 67.9 for ENZ, and 128 for ENZ+BS. Ruminal pH values and ammonia N concentration were increased ($P \leq 0.05$) with ENZ+BS (6.8; 95.75 mg/l), but not with ENZ (6.6; 75.25 mg/l) as compared to control diet (6.2; 55.75 mg/l).

Ruminal disappearance of DM and NDF were not affected (P≥ 0.05) by ENZ and ENZ+BS. We fail to show significant effect of EZN+SB on ruminal disappearance. The hypothesis that EZN+SB would have significant effect on ruminal disappearance was not confirmed. Perhaps, the ruminal pH found was not low enough for the ENZ+SB to alleviate the drop in digestibility that occurs in presence of low ruminal pH.

Key Words: fibrolytic enzymes, sodium bicarbonate, digestibility

T289 Effects of feeding a mixed enzyme on performance in Varamini male lambs. H. Baghershah*, K. Rezayazdi, and M. Dehghan-banadaky, *Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran*.

Twenty-four varamini male lambs (with 22±1.5 kg initial body weight) were used to evaluate the effects of feeding a mixed enzyme on performance in sheep. The mixed enzyme contained: phytase, alpha-amylase, beta-glucanase, cellulase, hemicellulase, pectinase, amylogycosidase, xylanase, protease and pentosanase. The animals were fed basal diet with three level of mixed enzyme (0, 0.05 and 0.1% in kg ration) according to a completely randomized design (CRD) with 3 rations and 8 lambs (replicate) for 84 days. The basal diet had 50:50 forage to concentrate ratio and were formulated according to CNCPS for sheep. Dry matter intake was recorded per day and lambs were weighted bi weekly. Nutrients digestibility were measured with internal marker (acid insoluble ash). The results were showed that average daily gain of lambs 144, 157 and 152 gram per day, dry matter intake 1.132, 1.147 and 1.137 kilogram per day and feed conversion ratio 7.94, 7.38 and 7.57 that were not significantly different among rations. Digestibility of crude protein, ether extract, dry matter, organic matter, neutral detergent fiber and acid detergent fiber did not different between rations. Therefore the use of 0.05 and 0.1% of this mixed enzyme were not suitable for performance of varamini male lambs.

Table 1. Effect of feeding a mixed enzyme on performance and nutrients digestibility in sheep with its SE

	Diet *		
Trial	0	0.5	1
Dry matter intake (g/day)	1132±50a	1147±12a	1137±25a
Average daily gain (g/day)	144±19a	157±21a	152±21a
Final weight (kg)	34.68±1.39a	34.90±1.86a	34.87±1.47a
Feed conversion ratio	7.94±1.02a	7.38±0.96a	7.57±0.96a
Digestibility (%)			
Dry matter	85.03±2.73a	83.63±7.01a	80.10±8.56a
Organic matter	77.36±4.10a	75.80±3.86a	75.45±2.19a
Crude protein	76.77±3.97a	74.64±5.46a	74.65±1.95a
Ether extract	84.10±6.7a	75.13±10.13a	77.18±7.67a
Neutral detergent fiber	69.05±5.37a	69.09±6.17a	67.06±3.42a
Acid detergent fiber	64.41±6.33a	63.17±5.21a	62.24±3.88a

* Level of complex enzyme (g/kg asfed) **Values with the same superscripts within rows are not significantly different (P>0.05).

Key Words: mixed enzyme, performance, nutrient digestibility

T290 Feruloyl and acetyl esterase production of an anaerobic rumen fungus *Neocallimastix* sp YQ2 and its potential in the hydrolysis of fibrous feedstuffs. Q. Yue[1], H. J. Yang*[1], Y. C. Cao[1], Y. H. Jiang[1], and J. Q. Wang[2], [1]*Department of Animal Nutrition and Feed Science, College of Animal Science and Technology, China Agricultural University,, Beijing, P.R. China*, [2]*State key Laboratory of Animal Nutrition, Institute of Animal Science, China Academy of Agricultural Sciences, Beijing, P.R., China*.

A 2×3×4 factorial experiment of ten-day pure culture was applied in *Neocallimastix sp* YQ2 with two levels of glucose (G+: glucose added at a level of 1.0 g/L and G-: without glucose), three insoluble carbon sources (C1: corn stalk; C2: Chinese wildrye grass hay; and C3: alfalfa hay) and four levels of nitrogen source (N1: 1.4 g/L yeast extract, 1.7 g/L tryptone; N2: 2.8 g/L yeast extract and 0.5 g/L $(NH_4)_2SO_4$; N3: 1.6 g/L tryptone and 0.5 g/L $(NH_4)_2SO_4$; N4: 1.0 g/L yeast extract, 1.0 g/L tryptone and 0.5 g/L $(NH_4)_2SO_4$. The optimal combinations of carbon and nitrogen sources for Neocallimastix sp YQ2 to produce ferulic acid esterase (FAE), acetyl esterase (AE), xylanase (XYL), carboxymethyl cellulosase (CMC) and avicelase (AVI) were G+C1N4, G-C2N3, G-C3N3, G+C1N2, and G+C2N4, respectively. The FAE, AE, CMC and AVI activities reached their peak at day 1, 2, 8 and 10 of the incubation. Growth performance indicated by the yield of volatile fatty acids (VFAs) showed that C1 was beneficial to the growth of Neocallimastix sp YQ2 grown on whatever nitrogen source either glucose added or not in pure culture. The fungus produced more total volatile fatty acids (VFAs) and less propionic acid (HPr) when C1 was used as growth substrate as well as more acetic acid (HAc) when C2 was used than the situation when C3 was used (P<0.05). As for the enzymological characteristics of FAE and AE, Km and Vmax of FAE against methyl ferulate (MFA) were 90 uM and 1.15 mU, and the Km and Vmax of AE were 2.97 mM and 2.94 U with substrate of p-nitrophenyl acetate. The crude enzyme preparation of the fungi grown on substrate of G+C1N4 combination showed significantly higher potential in the release of ferulic acid (FA) and p-coumaric acid (CA) in corn stalk up to 129.8 g/kg the alkali-extractable FA and 87.9 g/kg the alkali-extractable CA, respectively. The strong capability to hydrolyse plant materials presented by the fungus can be used to deeply understand the degradation of fibre-rich feedstuffs in rumen and also open up prospects for the development of feed enzyme products for ruminants.

Key Words: rumen, anaerobic fungus, plant cell wall degradation

T291 Use of *Megasphaera elsdenii* NCIMB41125 as a probiotic for early-lactation dairy cows: Effects on rumen pH and fermentation patterns. P. C. Aikman*[1], P. H. Henning[2], C. H. Horn[2], and D. J. Humphries[1], [1]*University of Reading, UK*, [2]*KK Animal Nutrition, South Africa*.

Multiparous rumen-fistulated Holstein cows were fed, from d 1 to 28 post-calving, an ad libitum TMR containing (g/kg DM) grass silage (196), corn silage (196), wheat (277), soybean meal (100), and other feeds (231) with CP, NDF, starch and water soluble carbohydrate concentrations of 176, 260, 299 and 39 g/kg DM respectively and ME of 12.2 MJ/kg DM. Treatments consisting of a minimum of 10^{10} cfu *Megasphaera elsdenii* NCIMB 41125 in 250 ml solution (MEGA) or 250 ml of autoclaved *M. elsdenii* (CONT) were administered via the rumen cannula on d 3 and 12 of lactation (n=7 per treatment). Mid-rumen pH was measured every 15 minutes and eating and ruminating behavior was recorded for 24 h on d 2, 4, 6, 8, 11, 13, 15, 17, 22 and 28. Rumen fluid for VFA and lactic acid (LA) analysis was collected at 11 timepoints on each of d 2, 4, 6, 13 and 15. Data were analysed as repeated measures using the Glimmix (LA data) or Mixed (all other data) procedures of SAS with previous 305 d milk yield and d 2 measurements as covariates where appropriate. Milk yield was higher (CONT 43.0 vs MEGA 45.4

±0.75 kg/d, P=0.051) and fat concentration was lower (CONT 45.6 vs MEGA 40.4 ±1.05 g/kg, P=0.005) in cows that received MEGA. Time spent eating (263 ±15 min/d) and ruminating (571 ±13 min/d), DM intake (18.4 ±0.74 kg/d), proportion of each 24 h period with rumen pH below 5.6 (3.69 ±0.94 h) and LA concentrations (2.00 mM) were similar (P>0.327) across treatments. Ruminal total VFA concentration (104 ±3 mM) was similar (P=0.404) across treatments, but a shift from acetate (CONT 551 vs MEGA 524 ±14 mmol/mol VFA, P=0.161) to propionate production (CONT 249 vs MEGA 275 ±11 mmol/mol VFA, P=0.099) meant that the acetate:propionate ratio (CONT 2.33 vs MEGA 1.94 ±0.15) was reduced (P=0.072) in cows that received MEGA. This study provides evidence that supplementation of early lactation dairy cows with MEGA alters rumen fermentation patterns in favour of propionate, with potential benefits for animal health and productivity.

Key Words: *Megasphaera elsdenii*, VFA, dairy cow

T292 Prebiotic performance in the prevention of acidosis of different substances using the 'gas-*in-vitro*' methodology in ruminal acidosis-like condition. A. R. Aldrovandi[1], A. Britos[1], S. Paz[1], A. Molina[1], C. Cajarville*[1], and P. Zunino[2], [1]*Universidad de la República, Montevideo, Uruguay*, [2]*Instituto de Investigaciones Biológicas Clemente Estable, Montevideo, Uruguay*.

The aim of this study was to test the prebiotic performance in the prevention of acidosis of different substances through the 'gas-*in-vitro*' methodology. Substrates were chosen to mimick subacute ruminal acidosis (SARA) with 50% forage and 50% barley grain ground. Four prebiotic substances were added at 3 doses (3, 9, and 15% of total substrate) and were: *Saccharomyces cerevisiae* (strain ATCC-18824) inactivated (SC), sorbitol (SO), inulin (IN) and malic acid (MA). Fementation flasks of 125 mL of capacity, hermetically closed with rubber stoppers and aluminium cases were used by triplicate. Each one contained 500 mg of substrate + prebiotic, 40 mL of artificial saliva and 10 mL of fresh ruminal liquor. There were 2 more treatments, one without substrate (blank) and other withouth any prebiotic (control). Gas production was measured at 2, 4, 6, 8, 10, 12, 18, 24, 48, 72, and 96 h after the beginning of fermentation. Data were fitted, by a non linear regression to a bicompartimental model where Vol (mL/g DM incubated) means total volume and it is the response variable, Vfr and Vfl (mL/g DM incubated) are fast and slow pool volume respectively, Kdr and Kdl (h-1) are specific rates of Vfr and Vfl. Parameters were compared by 2 way ANOVA. One way of variation was the prebiotic used and the other way was the level of prebiotic. No differences were observed between levels. Comparation between prebiotics showed that Kdr (minimum, MA=0.088; maximum, IN=0.152; control=0.096) and Kdl (minimum, MA=0.018; maximum, SC=0.033; control=0.020) had differences at $p < 0.01$, while Vfr $p = 0.015$ (minimum, IN=23.38; maximum, SC=33.67; control=35.90) and Vfl $p = 0.059$ (minimum, MA=22.06; maximum, IN=33.59; control=21.35). Some of the selected substances had a prebiotic effect on the modulation of the ruminal microbiota and then they acted as prebiotics, decreasing the Vfr and the rate of gas production.

Key Words: SARA, ruminal flora modulation, statical fermentation systems

T293 Effect of a prebiotic (AgriMOS) and a probiotic (Levucell SB) on performance, health and fecal microflora of veal calves. K. Chong*[1], L. Phillip[1], R. Cue[1], and N. Walker[2], [1]*McGill University, Montreal, QC, Canada*, [2]*Lallemand, Animal Nutrition, Montreal, QC, Canada*.

Probiotics and prebiotics have been used in many areas of animal husbandry for their beneficial effects on health and growth performance; however, the effect of these products in veal calf production has received little attention. The aim of the study was to determine the role of these products in improving health and performance of veal calves, and to assess their effect on the fecal microflora. Sixty-eight Holstein calves (approx. 7 d old) were randomly assigned, in a 2 month study, to 3 treatments: probiotic (0.5g/d of Levucell SB); live yeast (*S. cerevisiae*, spp. *boulardii* (SB); prebiotic (3g/d of AgriMOS, a specific combination of manno-oligosaccharides and glucose extracted from the yeast cell walls of *S. cerevisiae*); control (no additive). The products were added to the milk replacer (MR) which was consumed until d53; calf starter (CS) was offered ad lilbitum until the end of the study. Body weight, feed consumption, fecal pH and fecal score were recorded. Performance data (n=48; SB n=11, AgriMOS n=12, control n=25) were analyzed using mixed model SAS. The only significant effect on performance was on MR intake. Calves fed SB consumed more than those on AgriMOS ($p<0.05$). To assess the effect on the gut flora, fecal samples were collected on d0, 7, 13, 28, 41 and 57, and selective growth medium was used to enumerate *E. coli*, *Lactic acid bacteria*, *Campylobacter*, *Clostridia* and *Salmonella* in these samples. Animals fed the additives showed a reduction in *E. coli* over time, whereas *E. coli* counts in the control group remained static. *Clostridia* numbers were also reduced in the SB group. DNA was extracted from fecal samples and PCR-TTGE was used to generate a DNA fingerprint of the fecal bacterial community which was analyzed using GelComparII. Similarity indices were calculated using Pearson coefficient and dendograms were constructed by UPMGA. Different banding patterns were observed on different days and treatments, indicating differences in the composition of the gut flora. Although fecal pathogens were reduced indicating a health benefit, this did not translate into any significant improvement on performance.

T294 Effect of rumen-protected lysine (AminoShure™-L) on milk production and composition in dairy cows fed diets containing distillers dried grains. S. Emanuele*[1], P. Doane[2], D. Putnam[1], and M. Cecava[2], [1]*Balchem, New Hampton, NY*, [2]*ADM, Decatur, IL*.

Objective for the trial was to test the effect of supplementing rumen-protected lysine on milk yield and composition when cows were fed a low lysine diet. A 3x3 Latin Square design was replicated twice with cows producing greater than 41 kg of milk. Periods were 3 weeks with the last week for sample collection. Diets contained 16.5% crude protein, 10% RDP, 34% NDF and NEL concentration of 1.8 Mcal/kg. Treatments were control (no supplemental lysine), LYS-1 (30 g/d AminoShure™-L), and LYS-2 (60 g/d AminoShure™-L). The control diet contained 6.0% lysine as a percent of metabolizable protein (MP). The LYS-1 and LYS-2 diets contained 6.3% and 6.6% lysine as a percent of MP. All diets contained 2.2% methionine as a percent of MP. Based on actual dry matter intake, the control, LYS-1 and LYS-2 diets were predicted to supply 163, 180 and 192 g of metabolizable lysine, respectively. All statistical comparisons were performed at $p< 0.05$. Supplementing rumen-protected lysine increased DMI by 1.3 kg/d and milk yield by 2.6 kg (Table 1.). Milk fat and protein yields were also increased by supplementing rumen-protected lysine. Milk casein yield was increased ($p=0.06$) by 4.2% as the supply of metabolizable lysine was increased in the diet. Results indicate that supplementation of rumen-protected lysine to diets with low levels of lysine will increase the yield of milk and milk components.

Table 1. Effect of rumen-protected lysine on milk yield and milk components

Variable	Control	LYS-1	LYS-2	SE
DMI, kg/d	23.5[a]	24.8[b]	25.0[b]	0.30
Milk yIeld, kg/d	38.6[a]	41.2[b]	40.9[b]	0.50
Milk fat yield, g/d	1112[a]	1272[b]	1273[b]	37.0
Milk protein yield, g/d	1194[a]	1238[b]	1249[b]	17.0
Milk casein yield, g/d	973	997	1014	14.0
MUN, mg/dl	14.7	14.8	14.8	0.40

[ab] means within a row without a common superscript differ p<0.05

Key Words: rumen-protected lysine, milk protein, milk casein

T295 In vivo determination of lysine bioavailability of rumen protected lysine in lactating dairy cows. M. D. Hanigan*[1], C. Vanderhoof[1], S. Garbade[1], O. Becvar[1], C. A. Umberger[1], and M. J. de Veth[2], [1]*Virginia Polytechnic Institute and State University, Blacksburg*, [2]*Balchem Corporation*, *New Hampton, NY*.

Lysine and methionine have been identified as the two amino acids most limiting milk production in lactating dairy cows. Presently there are no rumen protected lysine (RPL) products commercially available that have reported in vivo lysine bioavailability. The objective of this study was to determine the plasma lysine response to two RPL products and compare with a plasma lysine response curve developed from known amounts of abomasally infused lysine. This approach was recently validated as a reliable approach for determining lysine bioavailability. The two RPL products (RPL-1 and RPL-2) were protected by proprietary lipid encapsulation (Balchem Corporation) and contained 47 and 46% lysine-HCl. In vitro rumen testing of both products indicated a rumen bypass of 75 and 87%, respectively (estimated passage rate of 11%/h). The study was designed as two consecutive 4 X 4 Latin square experiments and used 4 ruminally fistulated Holstein cows. In the first Latin Square, 0, 25, 50 and 75 g/d of raw lysine-HCl were abomasally infused for 3 d periods and plasma samples were used to generate a blood lysine response curve. In the second Latin Square, RPL-1 and RPL-2 were fed each at two doses (50 and 100 g lysine-HCl) for 7 d periods. Throughout the study cows were fed a TMR diet that contained 19% CP to ensure all amino acids, including lysine, were not limiting. Blood was sampled every 2 h over the last 24 h of each period and amino acids were determined by isotope dilution using a GC-MS. Abomasal infusion of graded levels of lysine resulted in a linear increase in plasma lysine concentration ($P < 0.001$; $R^2 = 0.72$) with an intercept of 68 μM (SE = 4.2) and slope of 0.52 μM per gram of infused lysine-HCl (SE = 0.09). Based on this response curve and the plasma lysine concentration when feeding RPL the bioavailability of RPL-1 and RPL-2 (averaged across both RPL doses) was estimated to be 46 and 56%, respectively, but did not differ significantly from each other ($P = 0.62$). The results from this study indicate that this lipid encapsulation provides a means to effectively supply bioavailable lysine to the lactating dairy cow.

Key Words: lysine, ruminal protection, lactation

T296 Supplementation of RuMin 8™ and urea on microbial crude protein, ammonia and volatile fatty acid concentrations *in vitro*. D. P. Bu[1], X. Y. Li[1], J. Q. Wang*[1], H. Y. Wei[1], L. Y. Zhou[1], and R. R. Rastani[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*MSC*, *Carpentersville, IL*.

The objective of this study was to examine the effect of ruminal supplementation of RuMin 8™ (a lactose based sugar product, MSC) and urea on microbial crude protein (MCP), ammonia (NH_3 H) and volatile fatty acid (VFA) concentrations. An in vitro batch culture system was used with a 3×3 factorial design: with RuMin 8 (0%-R0, 1.5%-R1.5, 3%-R3 on a DM basis) and Urea (0%-U0, 0.5%-U0.5, 1%-U1 on a DM basis) and 500 mg Chinese wildrye as the substrate. The experiment was repeated twice, and three flasks without substrate (only rumen fluid) were used to adjust for error between the two periods. Mixed ruminal fluid from three lactating Holstein cows fed with 20 kg DM/day (forage to concentrate = 60:40) was withdrawn via the cannula 3 h after feeding and was mixed with buffer in a ratio of 1:4. After mixing, 60 ml of buffered rumen fluid were dispensed into 120-ml flasks containing 500 mg of the substrate, according to treatment assignment. The flasks were sealed (CO_2 atmosphere) and placed in an incubator at 39°C, without shaking. The pH value, VFA, NH_3 H and MCP were measured from fermentation fluid after 6, 12, 30, 48 and 96 h incubation at 39°C. The data were analyzed using the PROC MIXED with incubation time as the repeated measure. There were no significant effects with varying levels of urea and no RuMin 8*urea interactions. Supplementation of increasing levels of RuMin 8 resulted in increased MCP, acetate, propionate, and butyrate concentrations ($P < 0.001$). Thus, RuMin 8 supplementation may improve utilization of Chinese wildrye in ruminant diets.

Table 1- Effect of RuMin 8 on fermentation parameters

	RuMin 8		
Item	0	1.5	3
MCP, gN/dL	3.55[a]	4.11[b]	4.88[c]
NH^3 N, mg/dL	15.38	14.37	13.40
Acetate, mmol/L	31.43[a]	38.91[b]	50.84[c]
Propionate, mmol/L	8.27[a]	12.19[b]	17.92[c]
Butyrate, mmol/L	5.43[a]	7.05[b]	8.96[c]

[a,b,c]Means in a row with different superscripts differ ($P < 0.001$).

Key Words: lactose, urea, rumen fermentation

T297 Effect of Optigen® on milk yield, composition, and component yields in commercial Wisconsin dairy herds. J. F. Inostroza*[1], R. D. Shaver[1], V. E. Cabrera[1], and J. M. Tricarico[2], [1]*Department of Dairy Science, University of Wisconsin*, *Madison*, [2]*Alltech Inc.*, *Brookings, SD*.

The objective of this field trial was to determine the effect of Optigen® (blended, controlled-release urea), as a source of dietary nitrogen, on milk yield, composition and component yields in commercial Wisconsin dairy herds. The number of lactating cows within herd averaged 148 cows ranging from 58 to 550 cows across the 16 trial herds. Within herd, cows were fed a single-diet TMR. Control TMR (CON) for each herd was formulated by the herd nutritionist according to production level. The treatment TMR (OPT) for each herd contained 114 g/cow/d Optigen® replacing an equivalent amount of supplemental CP, primarily from soybean meal, to provide iso-nitrogenous control and treatment TMR. Diet formulation space created by the use of Optigen® was filled with DM from either corn grain or corn silage at the discretion of the herd nutritionist in the treatment TMR. Across the 16 trial herds, TMR contained 56±3% forage comprised of 43±9% corn silage and were formulated for 17.1±0.4% CP and 30.5±1.7% NDF (DM basis). Herds were randomly assigned to either OPT-CON or CON-OPT treatment

sequence in a cross-over design with two 30-d feeding periods. Records of weight and composition (fat, protein and MUN) of bulk tank milk shipments were obtained for each herd over the 60-d trial. The numbers of cows with milk in the bulk tank for each shipment were recorded for each herd over the 60-d trial. Average per cow daily milk yield and component yields for each treatment period for each herd were then calculated. Data were analyzed using the mixed model procedure of SAS with period, sequence and treatment as fixed effects and herd as a random effect. Least squares mean results are presented in the table. Milk yield was 0.5 kg/d/cow greater (P < 0.01) for OPT than for CON.

Table 1. Least squares means for lactation performance.

Item	CON	OPT	SEM	(P <)
Milk Yield, kg/d	35.4	35.9	0.2	0.01
Fat, %	3.72	3.69	0.02	0.07
Fat Yield, g/d	1317	1322	8	NS
Protein, %	2.98	2.97	0.01	NS
Protein, g/d	1055	1065	6	0.13
MUN, mg/dl	12.4	13.2	0.3	0.01

NS=Not significant.

Key Words: milk yield, dairy cows, controlled-release urea

T298 Supplementation of grazing dairy cows with isopropyl ester of 2-hydroxy-4-methylthiobutanoic acid (HMBi). L. F. Greco*[1,2], J. T. Neves Neto[1], A. Moreira[1], M. A. Penatti[1], C. M. M. Bittar[1], G. B. Mourao[1], and F. A. P. Santos[1], [1]*University of Sao Paulo, Piracicaba, Sao Paulo, Brazil*, [2]*University of Florida, Gainesville*.

Objectives were to evaluate the supplementation with HMBi in the concentrate fed to cows grazing elephant grass. Sixteen Holstein (Ho) and 12 crossbred Ho/Jersey (Cr) cows (150d in milk) were randomly assigned to receive a concentrate supplemented or not with HMBi in a crossover design with 2 periods of 28d each. HMBi was supplemented to achieve a lys:met ratio of 3:1 of the metabolizable protein. Elephant grass was managed under rotational grazing with varying rest periods to achieve a canopy height of 1m when cows had access to the pasture. The grazing area, was divided into 28 pastures of 0.2 ha each. Pastures were fertilized with 80kg of N/ha following each grazing period, which lasted 1 to 2d, the residual grass was at a height of 40cm. The forage selected by cows had 22% CP, 66% NDF, and 71.5% in vitro digestibility of the DM. Concentrate was offered individually at 1kg for each 3kg of milk, which was established at the beginning of the study. The concentrate was the same in both treatments, except the HMBi, which was added at 2g/kg of concentrate DM. The concentrate contained 30% ground corn, 20% soybean meal, 46% citrus pulp, and 4% mineral/vitamin supplement, and had 18% CP, 17% NDF, and 2.4% ether extract. Yields of milk and milk components were measure in the last 14d of each 28-d period. Data are presented in the following sequence, control and HMBi. Supplementing grazing cows with 2g of HMBi for every 3kg of milk produced did not influence (P>0.10) yields (kg/d) of milk (16.2 vs. 16.5) and 3.5% fat-corrected milk (16.3 vs. 16.6), or the concentrations (%) of fat (3.57 vs. 3.57), protein (3.12 vs. 3.13), lactose (4.30 vs. 4.32), and milk urea N (11.3 vs. 11.5 mg/dL). Ho and Cr had similar yields of milk and 3.5% fat-corrected milk, and fat concentration in milk, but milk protein was greater (P=0.02) for Cr than Ho (3.23 vs. 3.02). Mid-lactation dairy cows grazing tropical grass with a high CP content and producing 16 kg/d do not benefit from an improved amino acid balance by supplementing HMBi.

Key Words: amino acid, grazing, methionine

T299 Effects of feeding 2-hydroxyl-4-methylthio butanoic acid (HMTBa) and HMTBa chelated trace minerals on dairy cattle production. M. Gallardo[2], G. Conti[3], G. Castillo[1], and S. Toffano*[1], [1]*Novus International Inc., Capital Federal, Buenos Aires, Argentina*, [2]*EEA- Inta Rafaela, Rafaela, Santa Fe, Argentina*, [3]*Universidad del Litoral, Esperanza, Santa Fe, Argentina*.

Primiparous and multiparous mid to late lactation cows were selected to evaluate the effect of feeding a mixture (MINTREX® MIN; Novus International, St. Charles, MO, USA) that contained the calcium salt of 2–hydroxy–4-methylthio butanoic acid (HMTBa) as a source of methionine and Zn–, Cu–, and Mn– $(HMTBa)_2$ as a source of chelated trace minerals plus methionine on dairy cattle production. During the autumn of 2008 in Nuevo Torino (Castellanos County), Sante Fe province in Argentina, 100 cows (50 control; 50 treatment) were selected from a herd of 160 lactating dairy cattle. Cows were acclimated to the experimental period for 24 d and measurements were taken over a 19 d treatment period. Diets were formulated with 30% of dietary dry matter as alfalfa pasture and 70% as a TMR containing corn silage, alfalfa hay, high moisture corn, a soybean meal pellet (expeller), sunflower meal, and an inorganic trace mineral (ITM) and vitamin premix. Minerals were formulated to meet NRC (2001) requirements for Zn (47 ppm), Cu (11 ppm), and Mn (40 ppm) from feedstuffs and inorganic mineral supplements. For the treated group, diets were top-dressed with the MINTREX® MIN providing 320 mg of Zn, 300 mg of Cu, 260 mg of Mn and 1310 mg HMTBa per head per day plus 8400 mg HMTBa as the calcium salt of HMTBa. Group fed cows receiving the mixture averaged 7.4% more milk and 8.2% more milk fat yield .On average milk protein yield, lactose, and total solids were similar in both treatments. Supplementing dairy cows on alfalfa pasture with a combination of HMTBa and Zn–, Cu–, and Mn– $(HMTBa)_2$ chelates (MINTREX®) improved milk performance.

Key Words: organic trace mineral, methionine, HMTBa

T300 The impact of a blend of synthetic antioxidants (AGRADO® Plus) on milk fatty acids in dairy cows fed a high rumen unsaturated fatty acid load (RUFAL) diet. C. L. Preseault*[1,3], J. Kraft[1], G. R. Bowman[2], H. M. Dann[3], and A. L. Lock[1], [1]*University of Vermont, Burlington*, [2]*Novus International Inc., St. Charles, MO*, [3]*William H. Miner Agricultural Research Institute, Chazy, NY*.

A risk factor for the production of specific biohydrogenation intermediates (BHI) known to cause milk fat depression (MFD), is an increase in rumen unsaturated fatty acid load (RUFAL). Previous work has indicated that antioxidants have potential to maintain 'normal' biohydrogenation pathways thus, reducing the production of BHI that cause MFD. This study evaluated the impact of a blend of synthetic antioxidants, AGRADO® Plus (Novus International, Inc.), on milk fatty acid (FA) profile in cows fed a high RUFAL diet. Sixteen lactating Holstein cows (163±47 DIM), in a crossover design with two 21-d periods, were individually fed a high RUFAL diet designed to induce MFD, primarily through feeding distillers grains (15% DM). Cows were fed the diet without supplementation (Control; CON) or supplemented with 0.02% (DM basis) of AGRADO® Plus (AP). Milk samples were collected at the start of the study (baseline) and the end of each period (d 20-21) and analyzed for milk fat and FA. The high RUFAL diet induced MFD in both treatments, although milk fat content and yield were further reduced by 3 (P<0.01) and 4% (P<0.05), respectively, in CON vs. AP. Compared to baseline, decreases in milk fat were primarily a result of lower yields (g/d) of saturated FA (SFA) with a smaller decrease in *cis* monounsaturated FA (MUFA). There were, however, no differences in

FA yields between CON and AP at the end of treatment periods (P>0.05). Compared to baseline the high RUFAL diets had a twofold increase in total *trans* 18:1 FA and *trans*-10 and *trans*-11 18:1. A similar increase in *cis*-9, *trans*-11 18:2 in both CON and AP was also observed. Examination of treatment sequence revealed possible carry over effects across periods. At the end of periods 1 and 2 the content of *trans*-10 18:1 in milk fat (g/100 g FA) was 1.06±0.31 and 0.81±0.37 for the CON-AP sequence and 1.44±0.31 and 1.73±0.37 for the AP-CON sequence. Data indicate possible carry over effects of AP requiring further research to examine any long term effects on rumen BHI production and their consequences on milk fat synthesis.

Table 1. Effect of CON and AP treatments on milk fatty acid yields

FA Yield (g/d)	Baseline ± SEM	CON	AP	SEM
SFA	996 ± 34	852	864	31
C16:0	462 ± 18	370	387	17
MUFA *cis*	379 ± 26	357	351	14
C18:1 *trans*	58 ± 2	94.2	89.8	5.0
C18:1 10*t*	7 ± 0.4	19.0	15.2	3.7
C18:1 11*t*	18 ± 1	34.7	35.0	2.4
PUFA	40 ± 2	45.5	44.0	1.6

Key Words: milk fat, dietary antioxidants, fatty acids

T301 The effect of malic acid supplementation on diet digestibility and methane production by beef cattle fed a forage diet. S. M. Cobb, J. J. Michal, and K. A. Johnson*, *Washington State University*, *Pullman*.

The effect of malic acid (MA) supplementation to a forage diet on ruminal fermentation and methane (CH_4) production by beef cattle was examined using four ruminally fistulated animals in a 4x4 Latin square design. Animals were fed at maintenance a 75% bluegrass straw (BGS) and 25% alfalfa hay diet and MA treatment levels were 0, 200, 400, and 600 g/d. Malic acid was supplemented via rumen fistula in two equal portions immediately after animals were fed at 0700 and 1900 h. Ruminal fluid samples were collected at 0, 4, 8, 12, 16, and 20 h after feeding and immediately analyzed for pH and frozen for later volatile fatty acid analysis. Bluegrass straw and alfalfa hay dry matter (DM), neutral detergent fiber (NDF), acid detergent fiber (ADF), and organic matter (OM) in situ digestibilities were determined at 0, 8, 16, 24, and 48 h after feeding. Daily methane emissions were measured for 3 d. The mean ruminal fluid pH level was 6.4 ± 0.04, changed over time (P≤0.0001), and was unaffected by MA treatment. Bluegrass straw in situ NDF, ADF, and ash disappearance was unaffected by MA treatment, although extent of DM and OM disappearance decreased (P≤0.0001) with the highest level of MA supplementation. Alfalfa hay DM, NDF, ADF, OM, and ash disappearance was also unaffected by MA treatments. CH_4emissions averaged 299.1 ± 0.11 g/d and were not affected by treatment. In addition, CH_4 loss as a percent of gross energy intake averaged 7.6% across all treatments and was not affected by treatment. These data indicate that supplementation of forage diets with malic acid does not appear to reduce methane emissions unlike the impact observed with higher concentrate diets, and may negatively affect the digestibility of poor quality forages.

Key Words: beef cattle, malic acid, methane

T302 Effects of DeOdorase® on fermentation and digestion in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech Biotechnology*, *Nicholasville, KY*.

With increasing interest in feeding strategies to reduce methane production, additives with ability to alter ruminal populations are being investigated for their potential to lower methane production in the rumen. Effects of three levels of DeOdorase® (*Yucca schidigera* extract) were investigated in single-flow rumen-simulating fermenter cultures. Cultures were fed diets formulated in CPM (version 3.08) with 0, 3, or 8 g DeOdorase (equivalent at 22.7 kg DM intake). Twelve cultures were used in a completely randomized design with 3 dietary treatments and 4 replicates. Cultures were fed 12.5 g as fed of experimental diets twice daily for 2 days. On day 2, culture pH was measured and samples collected for ammonia determination at 0, 1, 2, 4, 6, and 8 h postfeeding. An effluent sample from each fermenter was used for DM and NDF disappearance and volatile fatty acid (VFA) analyses. Methane concentration was estimated from VFA concentrations based on a theoretical fermentation balance (Wolin. 1960. J. Dairy Sci. 43:1452). Data were analyzed for effects of treatment using the GLM procedure of SAS. DeOdorase did not affect culture pH (P>0.10). Culture ammonia was lower in cultures fed either DeOdorase level than those fed control diets (P<0.05). Molar proportions of volatile fatty acids were not affected by dietary treatment (P>0.10). Total VFA concentration was lower in cultures fed either DeOdorase level (P<0.05). Methane production (mmoles/d) was lower in cultures fed DeOdorase (P<0.05). Digestion of DM and NDF were not affected by treatment (P>0.10). Compared to controls, mean ammonia concentration was 22% lower in cultures fed the DeOdorase 3 g treatment and 35% lower in cultures fed the higher DeOdorase level (8 g). DeOdorase was also effective in lowering methane concentration and production (-5.2% and -8.1%, respectively for 3 g treatment compared to control). DeOdorase has the potential to shift ruminal fermentation in a manner that results in lower ammonia concentrations and lower methane production.

Key Words: DeOdorase®, ammonia, methane

T303 Effect of saponin extract supplementation on ruminal fermentation in continuous culture. J.-S. Eun*, C. M. Dschaak, F. H. Bhushan, Y.-M. Kim, and A. J. Young, *Utah State University*, *Logan*.

This study examined whether supplementing saponin extract (SAE) was beneficial on in vitro ruminal fermentation when added to a lactating dairy TMR diet. We were particularly interested in the effects of SAE on ruminal pH, N utilization, methane production, and VFA profiles. A dual-flow continuous culture system was used in a randomized complete block design. Three fermentor vessels with working volume of 700 mL were fed 20 g of dry feed per day (divided equally between a.m. and p.m. feedings). Experimental diet consisted of 33% alfalfa hay, 7% corn silage, 40% rolled barley grain, and 20% concentrate mix. Source of SAE was *Yucca schidigera* (DK sarsaponin 30, containing 10% of steroidal saponins) by Desert King International (San Diego, CA). Dietary treatments were as follows: 1) TMR without SAE, 2) TMR with low SAE (1% SAE), and 3) TMR with high SAE (2% SAE). Following an adaptation period of 5 d, culture samples were taken on d 6, 7, and 8 of each period for analysis. A second run of the fermentors followed the same treatment sequence to provide replication. Data were analyzed using the MIXED procedure of SAS. Culture pH did not differ between treatments (average pH 6.14). In addition, methane production (average 7.28 mmol/d) and ammonia-N concentration (average 8.3 mg/dL) were not affected by the treatments. Total VFA production tended to decrease (P = 0.15) with supplementing SAE regardless of its level,

whereas molar proportions of acetate, propionate, and butyrate and acetate to propionate ratio were not influenced by supplementing SAE. The use of SAE caused an inhibition of the microbial activity, based on the decreased VFA, but it did not shift microbial fermentation patterns reflected on no effects on methane production and individual VFA proportions. At the doses tested in this study, SAE supplementation had minor impact on in vitro fermentation of the barley-based dairy TMR diet without any beneficial effect.

Key Words: saponin extract, ruminal fermentation, continuous culture

T304 The effect of combinations of Acid Buf and sodium bicarbonate on milk production, milk composition and ruminal pH profiles. C. W. Cruywagen*[1], S. J. Taylor[2], and T. Calitz[1], [1]*Dept. Animal Sciences, Stellenbosch University*, *Stellenbosch, South Africa*, [2]*Celtic Sea Minerals*, *Carrigaline, Co. Cork, Ireland*.

Eight lactating Holstein cows, fitted with rumen cannulae, were used in a Latin square experiment to compare different buffer combinations. A high concentrate TMR was used to construct four dietary treatments in which Acid Buf (AB), the skeletal remains of the seaweed Lithothamnium calcareum, was used alone or in combination with sodium bicarbonate (BC). The diets contained 3.5 g/kg of AB (Treatment 1) or 1.75 g/kg of AB and 1.75 g/kg of BC (Treatment 2) or 3.5 g/kg of AB 3.5 g/kg of BC (Treatment 3) or 3.5 g/kg of AB and 5.2 g/kg of BC (Treatment 4). The total experimental period was 100 days in which every cow received each diet for a period of 18 days prior to a data collection period of 7 days. Rumen pH was monitored continuously over 2 days and samples of rumen fluid were collected for VFA and rumen ammonia analyses. During each data collection period, milk production was recorded twice daily for 7 d, whereas milk was sampled twice daily for five consecutive days for component analysis. Treatment had no significant effect on milk production, milk composition or feed intake. Ruminal pH profiles of all the treatments indicated that the diets were well buffered. Average pH over 24 hours was 6.1, 6.1, 6.2, and 6.3, for Treatments 1, 2, 3 & 4, respectively. The pH did not go below 5.8 for any of the treatments and increasing levels of sodium bicarbonate increased the diurnal profile such that at the highest level (Treatment 4), the pH profile ranged from 6.1 to 6.5. Although not significant, Treatment 1 (Acid Buf alone) numerically resulted in the highest milk output without compromising milk quality. It is proposed that high rumen pH may impact negatively on milk output by increasing acetate:propionate ratio to the detriment of rumen efficiency. The use of buffers which react to increasing acid load in the rumen may therefore provide an efficient, safe solution to rumen acidosis. The current study confirmed previous results indicating that a daily intake of 80 g of Acid Buf by cows receiving high concentrate diets would support high milk production without compromising milk solids content.

Key Words: buffers, milk production, rumen metabolism

T305 Effect of ractopamine on whole body and splanchnic energy balance in holstein steers. A. F. Koontz*, S. W. El-Kadi, D. L. Harmon, and K. R. McLeod, *Department of Animal and Food Sciences, University of Kentucky*, *Lexington*.

This study was designed to examine the influence of ractopamine (RAC) on whole-body and splanchnic energy balance. Six growing Holstein steers (BW= 402kg ±39.5) surgically fitted with an arterial and portal, hepatic, and mesenteric venous indwelling catheters were used in a repeated measures study. Treatments were a basal diet of alfalfa cubes fed at 1.5x ME requirements (d 1-21; CON) and basal plus RAC (430mg/hd•d^{-1}; d 22-42). On d 14 of each period splanchnic and portal-drained viscera (PDV) energy balance was determined as the product of arteriovenous O2 difference and blood flow. Blood flow was determined using down-stream dilution of *p*-aminohippuric acid. Whole-body energy balance was determined on d 15-21 of each period, which included 7 d total excreta collection and 3 d of respiratory gas exchange measurements. Bodyweight and DM intake were greater ($P < 0.05$) for steers receiving RAC compared with those receiving CON, however, no difference was observed in either BW or DMI when expressed on a $BW^{.75}$ basis. Similarly, as a function of $BW^{.75}$, whole-body heat production (691 kJ/kg $BW^{.75}$•d^{-1}; $P = 0.96$) and retained N (0.85 g/kg $BW^{.75}$•d^{-1}; $P = 0.34$) and energy (298 kJ/kg $BW^{.75}$•d^{-1}; P = 0.71) were unaffected by RAC. In contrast, RAC tended to decrease ($P = 0.09$) energy use by splanchnic tissues (191 vs. 156 kJ/kg $BW^{.75}$•d^{-1}), largely due to a reduction ($P = 0.12$) in energy use by the PDV (100 vs. 86 kJ/kg $BW^{.75}$•d^{-1}). These data indicate that although whole-body energy use is not affected by RAC, energy use by splanchnic tissues is decreased, thereby increasing energy use by peripheral tissues.

Key Words: bovine, ractopamine, energy

T306 Zilpaterol hydrochloride impact on core body temperature, performance, and carcass characteristics of finishing steers. J. L. Wahrmund*[1], B. P. Holland[1], C. R. Krehbiel[1], M. N. Streeter[2], D. A. Yates[2], J. P. Hutcheson[2], W. T. Nichols[2], C. L. Goad[3], and C. J. Richards[1], [1]*Department of Animal Science, Oklahoma State University*, *Stillwater*, [2]*Intervet/Schering-Plough*, *DeSoto, KS*, [3]*Department of Statistics, Oklahoma State University*, *Stillwater*.

Beta agonists have been shown to increase heart and respiration rates in finishing beef cattle. The objective of this study was to determine the effect of zilpaterol hydrochloride (ZH) on core body temperature of finishing beef steers. Forty one d prior to slaughter (d 0) 68 crossbred steers (initial BW = 530 ± 8.7 kg) were randomly assigned to 12 pens and administered a remote temperature monitoring ruminal bolus, which transmitted rumen temperature data at a rate of once every 11 ± 8 min. Pens were then randomly assigned to one of two treatments: 0 (control) or 8.3 mg/kg (100% DM basis) ZH fed for 20 d. ZH was fed beginning on d 16 and control diets resumed for all steers on d 36. Temperature monitoring began on d 7. Temperatures were compared across treatments and during 3 time periods of 9 d prior to ZH feeding, 20 d during ZH feeding, and a 5-d withdrawal period. Feeding ZH increased ADG by 21.5% ($P = 0.01$). However, final live BW (mean = 588 ± 11.1 kg) did not differ ($P = 0.18$) between treatments. Inclusion of ZH resulted in 15 kg greater ($P = 0.01$) HCW, 3.5 percentage units greater ($P = 0.01$) dress, and 6.7 cm^2 greater ($P = 0.002$) LM area. Additionally, ZH inclusion decreased internal fat by 17.5% ($P = 0.03$) and yield grade by 9.95% ($P = 0.02$). There were no treatment × time period interactions ($P = 0.52$) for rumen temperature. Average and maximum daily rumen temperatures did not differ ($P > 0.46$; 39.81 and 40.27°C, respectively) between treatments. Average and maximum daily rumen temperatures were not different ($P > 0.17$; 39.76 and 40.27°C, respectively) during the first two periods. Average daily rumen temperatures were 0.11°C greater ($P = 0.005$) in period 3 compared to period 1, and tended ($P = 0.08$) to be 0.06°C greater in period 3 compared to period 2. During period 3, maximum daily rumen temperatures were 0.08°C greater ($P = 0.04$) compared to period 2, and 0.13°C greater ($P = 0.005$) compared to period 1. These data indicate that when fed for 20 d, ZH improves

performance and carcass traits, and has no impact on daily average and maximum core body temperature of finishing beef steers.

Key Words: Beta agonist, bovine, body temperature

T307 The effect of substituting fish oil in cow diets with DHA-micro algae on milk composition and fatty acids profile. R. B. Potu*[1], A. A. AbuGhazaleh[1], and S. Ibrahim[2], [1]*Southern Illinois University, Carbondale*, [2]*North Carolina A&T University, Greensboro*.

Fish oil (FO) in the cow diet has been shown to function as a modifier for ruminal biohydrogenation to maximize the production of vaccenic acid (VA; trans-11 C18:1), the precursor of conjugated linoleic acid (cis-9, trans-11 CLA). It also has been shown that the FO stimulatory effect on VA production is attributed to docosahexaenoic acid (DHA)'s ability to inhibit the reduction of VA to C18:0 in the rumen. In this experiment, the effect of substituting FO with DHA-micro algae on milk fatty acid composition was examined. Twenty-four Holstein cows in mid lactation (165 ± 22 DIM) allowed to graze on an alfalfa-based pasture were divided into four treatment groups (6 cows/treatment) and supplemented with 7 kg/d grain mix supplements containing 350 g soybean oil and either 150 g FO (FO), 100 g FO plus 50 g algae (2/3FO), 50 g FO plus 100 g algae (1/3FO), or 150 g algae (ALG). Cows were fed treatment diets for 3 wks and milk samples were collected from each cow during the last 3 days of the study. Grain supplement intake, milk production (17.96, 17.56, 17.55, and 19.26 kg/d for treatments 1 to 4, respectively), milk fat percentages (3.17, 3.49, 3.74, 3.43 for treatments 1 to 4, respectively) and yield, and milk protein percentages (3.35, 3.50, 3.71, and 3.42 for treatments 1 to 4, respectively) and yields were not affected ($P > 0.05$) by the treatment diets. Concentrations (g/100g fatty acids) of milk cis-9, trans-11 CLA (3.51, 3.69, 4.47, and 4.21 for treatments 1 to 4, respectively) and VA (11.80, 12.83, 13.87, and 13.53) were not affected ($P > 0.05$) by treatment diets. The results suggest that DHA-micro algae can substitute for FO in a cow's diet without any adverse effects on milk production, milk composition or milk cis-9, trans-11 CLA content.

Key Words: fish oil, algae, CLA

Ruminant Nutrition: Efficiency

T308 Residual feed intake and feeding behavior of Nellore bulls selected for post-weaning weight. T. L. S. Corvino*[1], R. H. Branco[2], A. Polizel Neto[1], S. F. M. Bonilha[2], L. A. Figueiredo[2], and A. G. Razook[2], [1]*Programa de Pós-gradução emZootecnia - UNESP, Botucatu, São Paulo, Brazil*, [2]*CAPTA Pecuária de Corte - Instituto de Zootecnia, Sertãozinho, São Paulo, Brazil*.

Residual feed intake (RFI) is the difference between DMI observed and predicted based on metabolic BW and ADG. Feeding behavior influences RFI, however the relationships between these traits are not well known. The objective of this research was to evaluate the differences in feeding behavior of low and high RFI Nellore bulls selected for post-weaning weight. The experiment was conducted at CAPTA Pecuária de Corte - Instituto de Zootecnia, Sertãozinho - São Paulo/Brazil. Sixty one Nellore bulls had RFI evaluated (112 d in individual pens) and were classified in: low RFI (<0.5 SD; more efficient; n=21), medium RFI (<0.5SD<; n=22), and high RFI (>0.5 SD; less efficient; n=18). Feeding behavior was evaluated at 10 min intervals, during 24 h, in two random d, to determine feeding and chewing categories. Measured traits were feeding duration (FD), chewing time (CT) and bunk attendance (BA). FD/DMI had significant difference for RFI levels, being more efficient bulls (low RFI) those with lesser intake and greater time spent on feeding than less efficient ones (high RFI). Low RFI bulls used food with higher efficiency, eating slowly and retaining more nutrients than high RFI bulls.

Table1. Feeding behavior of low and high RFI Nellore bulls

	RFI			
	Low	Medium	High	P
n	21	22	18	
RFI	-0.346[c]	-0.009[b]	0.415[a]	<0.001
DMI, kg/d	5.72[b]	5.94[b]	6.63[a]	0.007
FD, min/d	217[a]	225[a]	214[a]	0.609
FD/DMI, min/kg DM	39.1[a]	38.7[a]	32.6[b]	0.009
BA, event/d	9.3[a]	9.9[a]	9.8[a]	0.155
DMI/event, kg DM/event	0.62[a]	0.62[a]	0.68[a]	0.266
FD/event, min/event	23.5[a]	23.2[a]	22.4[a]	0.174
CT, min/d	477[a]	477[a]	504[a]	0.080
CT/DMI, min/kg DM	86[a]	82[a]	77[a]	0.150

Within a row, means without a common superscript letter differ ($P < 0.05$) by Student Newman-Keuls test.

Key Words: efficiency, nutrition, selection

T309 Effects of residual feed intake on carcass characteristics of Nellore bulls. S. F. M. Bonilha*[1], R. H. Branco[1], G. F. Alleoni[2], A. M. Castilhos[3], L. A. Figueirdo[1], and A. G. Razook[1], [1]*Instituto de Zootecnia, Agência Paulista de Tecnologia dos Agronegócios, Sertãozinho, SP, Brazil*, [2]*Instituto de Zootecnia, Agência Paulista de Tecnologia dos Agronegócios, Nova Odessa, SP, Brazil*, [3]*Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu, SP, Brazil*.

Residual feed intake (RFI) is an efficiency measurement calculated as the difference between actual feed intake and predicted DMI based on metabolic BW and ADG. Some studies, using *Bos taurus* breeds, have found differences on carcass characteristics, mainly those related to fat content, on animals selected for low RFI, but there is no information about relationships between RFI and carcass traits on Nellore breed. Therefore, the objective of this work was to evaluate carcass characteristics of Nellore bulls classified in low and high RFI levels. Thirty three young Nellore bulls, with minimum RFI -0.640 and maximum RFI

0.690, were slaughtered and had their carcasses evaluated. Table bellow shows the least-square means of DMI; ADG; empty BW (EBW); HCW; dressing percentage (DP); hindquarter percentage (HQP); edible fraction percentage (EFP); rib-eye area (REA); and fat thickness (FT). Low RFI bulls had lesser DMI than high RFI bulls. No differences were detected for ADG, EBW, and HCW indicating that low and high RFI bulls had the same body size. For yield measurements (DP; HQP; and EFP) no differences were detected, but there is a tendency of low RFI (more efficient) bulls to have greater HQP than high RFI (less efficient) ones. No differences were found for REA and FT. Low RFI bulls ate less than high RFI bulls and had carcasses of the same size and fat content.

Table 1. Carcass characteristics of low and high RFI bulls

	LOW RFI	HIGH RFI	P
	(n=18)	(n=15)	
DMI, kg	6.55[a]	7.51[b]	0.0485
DMI, %BW	1.76[a]	2.05[b]	0.0079
ADG, g	721[a]	756[a]	0.6954
EBW, kg	368[a]	362[a]	0.7210
HCW, kg	245[a]	242[a]	0.7938
DP, %	62.3[a]	62.3[a]	0.9689
HQP, %	46.5[a]	45.1[a]	0.0611
EFP, %	80.1[a]	80.3[a]	0.5715
REA, cm^2	74.8[a]	75.6[a]	0.8467
FT, mm	3.56[a]	3.22[a]	0.3658

Within a row, means with a common superscript letter do not differ ($P < 0.05$) by least-square means adjusted for Pdiff.

Key Words: development, efficiency, selection

T310 Relationships between residual feed intake and internal organs of Nellore bulls. S. F. M. Bonilha*[1], R. H. Branco[1], T. L. S. Corvino[2], G. F. Alleoni[3], L. A. Figueiredo[1], and A. G. Razook[1], [1]*Instituto de Zootecnia, Agência Paulista de Tecnologia dos Agronegócios, Sertãozinho, SP, Brazil*, [2]*Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu, SP, Brazil*, [3]*Instituto de Zootecnia, Agência Paulista de Tecnologia dos Agronegócios, Nova Odessa, SP, Brazil*.

Residual feed intake (RFI) is an alternative measurement of feed efficiency, which is theoretically independent of production level and body size, calculated as the difference between actual feed intake and predicted DMI based on metabolic BW and ADG. The objective of this work was to identify the relationships between RFI and size of important internal organs in Nellore bulls classified in low and high RFI levels. Thirty three young Nellore bulls, with minimum RFI -0.640 and maximum RFI 0.690, were slaughtered and had their internal organs weighted. Table bellow shows the least-square means of final BW (FBW); empty BW (EBW); liver (LIV); kidney (KID); gastrointestinal tract (GIT); KPH; and other internal organs (IOR). No differences were detected in body size between low and high RFI bulls. Low RFI bulls had smaller important internal organs (LIV, KID, and GIT) than high RFI bulls. For KPH, no differences were detected. Low RFI bulls ate less than high RFI bulls, had smaller internal organs and the same fat content.

Table 1.

	LOW RFI	HIGH RFI	P
n	18	15	---
FBW, kg	374[a]	391[a]	0.1148
EBW, kg	343[a]	357[a]	0.1797
LIV, kg	4.16[b]	4.63[a]	0.0043
KID, g	673[b]	786[a]	0.0389
GIT, kg	21.8[b]	24.3[a]	0.0411
KPH, kg	5.25[a]	5.38[a]	0.8018
IOR, kg	10.4[a]	11.1[a]	0.0711

Within a row, means with a common superscript letter do not differ ($P < 0.05$) by least-square means adjusted for Pdiff.

Key Words: development, efficiency, selection

T311 Genetics of feed conversion efficiency: Using a dynamic metabolic model to investigate the patterns of nutrient flux in the most efficient dairy animals. C. Shachtschneider, J. L. Vierck, and J. P. McNamara*, *Washington State University, Pullman*.

In dairy cattle, measures of efficiency take into account not only feed intake and milk production, but also metabolic flux in body tissues, primarily in visceral, muscle, and adipose tissues. Metabolic processes are affected by genotype, phenotype, and intake, processes that are usually under control of hormonal and neural systems. In continued work with the objective of identifying the patterns of metabolic flux in the most efficient dairy cattle, an existing mechanistic metabolic model (Molly, UC Davis) was used. Data were collected from 2nd to 4th parity cows over several experiments (approximately 150 animals) that measured nutrient intake, milk component output, changes in adipose tissue lipid and visceral and body protein and lipid, and metabolism rates and gene expression in adipose tissue. Explicit inputs into the model included nutrient intake, initial body fat and protein, milk production, fat and protein output. Each cow was simulated separately. Body fat, body protein and visceral protein all varied ($P< 0.05$) in daily flux and overall change in direct relation to their milk productive efficiency. Intake energy ranged from 89 to 139 Mcal/d; from 19.9 to 41.9 for maintenance; from -1.74, to -0.015) for change in body energy (to 120 DIM); and from 0.826 to 0.862 for (milk energy/(energy absorbed - maintenance E)). Nitrogen intake varied from 0.52 to 0.81 kg/d; milk N from 0.16 to 0.27), change in body N from -0.06 to -0.004): urea N from 0.26 to 0.37); and N balance from -0.032 to -0.008 kg/d. The model identified ($P <0.05$) differences in use of energy and nitrogen in body tissues of the most efficient versus less efficient dairy cattle, the rates of adipose tissue metabolism were directly related to overall efficiency. Feed intake was a major component of overall feed efficiency ($P < 0.01$), while the ability of body tissue to support milk production and recover after peak production was another major contributor ($p < 0.01$). Integrating all the biological process in the dairy animal will help us speed improvement of overall efficiency.

Key Words: effiiciency, integrative biology, metabolic models

T312 Associations between feed efficiency and gut microbial ecology and fermentation parameters in feedlot cattle. W. K. Krueger[1,2], G. E. Carstens[1,2], Z. D. Paddock[1,2], T. R. Calloway[3], R. C. Anderson[3], N. A. Krueger[3], V. Gontcharova[4], S. E. Dowd[4], R. R. Gomez*[2], and W. E. Pinchak[5], [1]*Intercollegiate Faculty of Nutrition, Texas A&M University*,

College Station, [2]*Department of Animal Science, Texas A&M University*, *College Station*, [3]*USDA, ARS, Food and Feed Safety Research Unit*, *College Station, TX*, [4]*Medical Biofilm Research Institute*, *Lubbock, TX*, [5]*Texas AgriLife Research, Texas A&M University*, *Vernon*.

The objective of this study was to examine the relationships between feed efficiency (residual feed intake; RFI) and gut microbial ecology and rumen and fecal fermentation parameters in feedlot cattle. Crossbred steers (N = 170; initial BW = 378 ± 30kg) were fed a high-corn finishing ration (ME = 3.0 Mcal/kg DM), and individual feed intake recorded for 70 d using GrowSafe feeding system. RFI was calculated as the difference between actual and expected DMI from linear regression of DMI on mid-test $BW^{0.75}$ and ADG. Rumen fluid and fecal samples were collected from the 6 most (low RFI) and 6 least efficient (high RFI) steers and assayed for VFA and pH, and in vitro procedures used to determine 24-h methane producing activity (MPA) and ammonia producing activity (APA). Initial BW (381 ± 27 kg) and ADG (1.5 ± 0.5 kg) were similar for steers with low and high RFI; low RFI steers consumed 24% less DMI (9.1 vs. 11.9 ± 0.3 kg) and had 26% lower feed:gain ratios than high RFI steers. No differences were observed between phenotype groups for ruminal 24-h MPA; however, steers with low RFI had higher (P = 0.02) fecal MPA (10.4 vs. 3.8 ± 1.7 µmol CH4/ml) than steers with high RFI. Ruminal and fecal APA, VFA, and pH were similar for sampled steers. Intestinal microbial ecology was examined using bacterial tag-encoded FLX 16s rDNA amplicon pyrosequencing methodology. There were no differences detected in the rumen or fecal Firmicute:Bacteriodetes ratio between steers with divergent RFI. Low RFI steers tended to have higher (P = 0.09) percentage of fecal Prevotella spp. and had lower (P < 0.05) fecal Spirochaetes and ruminal Cyanobacteria. These results indicate that there are no inherent differences in ruminal MPA, APA, VFA, and pH or gross microbial ecology between steers with divergent RFI. Subtle microbial shifts in fecal Prevotella, Spirochaetes, and ruminal Cyanobacteria, and fecal MPA due to divergent RFI may be evident. Further research into the potential associations between gut microbiota and inter-animal variation in RFI of beef cattle is warranted.

Key Words: feed efficiency, microbial ecology, residual feed intake

T313 Proteomic analyses in beef cows with low and high maintenance energy requirements. M. J. Prado-Cooper*[1,2], R. D. Madden[1], J. W. Dillwith[1], C. L. Bailey[1], E. C. Wright[1], C. R. Krehbiel[1], D. L. Step[1], and R. P. Wettemann[1], [1]*Oklahoma Agricultural Experiment Station, Stillwater*, [2]*Universidad Centroccidental, Barquisimeto, Lara, Venezuela*.

Spring-calving Angus x Hereford cows were used in two replications (rep 1, n = 32; rep 2, n = 37) to describe muscle proteome and evaluate protein abundance in beef cows with different maintenance energy requirements (MR). Gestating cows (4 to 7 yr of age) in the second to third trimester of gestation with a BCS of 5.0 ± 0.3 and BW of 576 ± 41 kg, were individually fed a complete diet to determine their MR based on achievement of constant BW. Cows were classified as having low (> 0.5 SD less than mean, LMR) or high (> 0.5 SD more than mean, HMR) MR. Greatest differences in MR for all cows were 24% and 25% in rep 1 and 2, respectively. Muscle biopsies from LM of LMR (n = 12) and HMR (n = 12) cows were taken after cows were on actual maintenance diets for 28 d, immediately frozen in liquid nitrogen, and stored at -80°C for proteomic analyses. Proteins were separated by two-dimensional gel electrophoresis and identified using mass spectrometry (MALDI-TOF and orbitrap). Protein abundance was quantified by two-dimensional, fluorescent, difference gel electrophoresis (2-D DIGE) to separate proteins, and DeCyderTM software (version 5.0, GE Healthcare Bio Sciences) for image analysis. From a total of 103 dissected spots, 78 proteins corresponding to 52 gene products were identified; the proteins were related to metabolism (33%), contractile apparatus (19%), cell structure (10%), cell defense (13%), and other processes (25%). Protein abundance tended to be greater in HMR cows for cofilin-2 (P = 0.11), and glyceraldehyde-3-phosphate dehydrogenase (P = 0.16). Identification of biomarkers for maintenance energy requirements will allow selection of cows that require less energy to maintain BW and may increase efficiency of beef production.

Key Words: beef cattle, maintenance energy requirements, proteomics

T314 Forage intake, rumen and blood variables, ultrasound and body measurements and behaviour in pregnant beef heifers differing in phenotypic residual feed intake. P. Lawrence*[1,2], M. McGee[1], D. Kenny[2], D. H. Crews, Jr.[3], and B. Earley[4], [1]*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*, [2]*UCD School of Agriculture, Food Science and Veterinary Medicine, Belfield, Dublin, Ireland*, [3]*Department of Animal Sciences, Colorado State University, Fort Collins*, [4]*Teagasc, Animal Bioscience Centre, Dunsany, Co. Meath, Ireland*.

The objective of this study was to characterise productivity-related variables in pregnant beef heifers differing in phenotypic residual feed intake (RFI), an alternative measure of feed efficiency. Seventy-three, pregnant (mean (SD) gestation day 169 (28 d)) Simmental and Simmental × Friesian-Holstein heifers (mean (SD) initial body weight (BW) 548 (47.1 kg)) were offered grass silage *ad libitum*. Dry matter intake (DMI), BW, body condition score (BCS) and measurements (withers height, chest depth, back length, pelvis width and girth), ultrasound fat (13^{th} rib), and fat and muscle (3^{rd} lumbar) depth, visual muscularity score, rumen fluid pH, blood variables (albumin, creatinine, beta-hydroxy butyrate, globulin, glucose, non-esterified fatty acids, total protein, triglycerides, urea, aspartateaminotransferase, alkaline phosphate, creatine kinase, fibrinogen, haptoglobin, anti-oxidant status and total bilirubin), feeding and activity behaviour, calf birth weight and calving difficulty were measured. Expected DMI was calculated by regressing average daily DMI on average daily BW gain (ADG), mean $BW^{0.75}$ and calving day over an 84-d period, for each breed separately. Within breed, heifers were ranked by RFI into low (efficient), medium and high (inefficient) groups. Overall mean (SD), ADG (kg/d), DMI (kg/d), and RFI (kg DMI/d) were 0.46 (0.17), 7.93 (0.88), 0.07 (0.70), respectively. Heifers with high RFI had 0.14 and 0.21 higher (P<0.001) DMI than medium and low RFI groups, respectively. The RFI groups did not differ in the variables measured, with the exception that bilirubin concentration (P<0.01) and muscularity score (P<0.05) were higher in low RFI, and rumen pH was higher (P<0.05) in high RFI, than the other two RFI groups. In conclusion, differences in phenotypic RFI in pregnant beef heifers were not noticeably associated with appreciable differences in the other traits measured.

Key Words: pregnant beef heifers, residual feed intake, grass silage

T315 Fatty acid profiles and meat quality of steers finished in feedlot or on pasture. H. O. Patino*[1], F. S. Medeiros[1], K. C. Swanson[2], and M. A. Sierra[1], [1]*Dep. Zootecnia, UFRGS, Porto Alegre, RS, Brazil*, [2]*Dept. Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*.

Thirty crossbreed steers were used in a completely randomized design to evaluate the effect of different feeding systems on the performance, meat quality and fatty acid profile of intramuscular fat. The experimental treatments were levels of feeding (0, 0.4, 0.8 and 1.2% BW) of a corn based supplement in a winter pasture of annual ryegrass (*Lolium multiflorum L*) and oats (*Avena strigosa Schreb*), or a feedlot, using a 50:50 concentrate/silage diet. Steers were slaughtered at 24 months of age at similar levels of subcutaneous fat (ultrasound evaluation). No differences were observed in tenderness (3.15 kg/cm^2), marbling (5.72 points), pH (5.64), Color L* (36.84), Color b* (12.89) and in cooking (14.34%) and drip losses (4.33%) in the *Longissimus dorsi* samples (p>0.05). The level of lipids in meat of steers finished in feedlot was 29% greater than steers supplemented on pasture (13.28 vs 9.38%;p<0.01). Supplementation level did not influence lipid concentration (p>0.05). Concentrations of myristic, palmitic, stearic and linoleic acid did not differ among treatments averaging 3.08, 25.80, 20.15 and 1.87%, respectively (p>0.05). Supplementation up to the level of 0.8% BW increased CLA (0.473%) and linolenic (0.798%) FA levels in the intramuscular fat, in relation to the highest level of supplementation and the feedlot, which didn´t differ from each other, with average levels of CLA and linolenic acid of 0.292 and 0.600, respectively (p<0.05). Treatments on pasture had higher n-3 FA compared to feedlot (p<0.05) but didn´t differ in the content of n-6 FA (p>0.05), producing lower n-6:n-3 of 1.89, 2.31, 2.50 and 2.89 for the levels of supplementation compared to feedlot (4.11; p<0.05). Supplementation level linearly reduced n-3 FA and CLA and linearly increased n-6:n-3 (P<0.05). Fattening animals on winter pastures using increasing levels of energy supplementation doesn´t result in differences in meat quality but results in changes in FA profile.

Key Words: winter pasture, feedlot, energy supplementation

T316 Nutrient digestibilities of Holstein steers fed diets containing different levels of nonforage fiber in a low forage diet. M. Mojtahedi, M. Danesh Mesgaran*, A. R. Heravi Moussavi, and A. Tahmasbi, *Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran*.

The aim of this study was to investigate the effect of diets containing barley grain and/or dried sugar beet pulp (SBP) on total tract apparent nutrient digestibilities in Holstein steers. Four Holstein steers with initial body weight of 368±8 kg fitted with ruminal fistulae were used in a 4×4 Latin square design (28 days of each period). Basal experimental diet consisted of 15% corn silage, 20% alfalfa hay, 33% barley grain, 17% soybean meal, 13.8% wheat bran, 0.5% calcium carbonate, 0.2% salt, and 0.5% mineral and vitamin premix on dry matter basis. Barley grain was substituted with SBP as 0.0%, 33%, 66% or 100% (SBP0, SBP33, SBP66, and SBP100, respectively). Steers were fed 9.5 kg of diet DM as total mixed ration twice daily at 0800 and 1600 h. Fecal samples were collected during the last 7 d of each period. Acid insoluble ash (AIA) was used as an internal marker to determine the digestibility. Data were analyzed using the mixed model procedure of SAS (Y = Mean + Treatment + Animal + Period + Residual) and the means compared by the Duncan test (P< 0.05). Results are presented in table 1. Apparent total tract digestibility coefficients for dry matter (DM) and neutral detergent fiber (NDF) increased by inclusion of SBP in the diet (p< 0.05), but was similar for SBP0 and SBP100 (p> 0.05). Total tract digestibility of organic matter (OM), crude protein (CP) and acid detergent fiber (ADF) were not different among treatments (p> 0.05). Results from this study suggested that the substituting SBP at low and medium inclusion rates can improve diet DM and NDF digestibility in Holstein steers fed high level of concentrate.

Table 1. Effects of substitution of sugar beet pulp for barley grain on total tract nutrient digestibility.

Items						
Treatments †	SBP0	SBP33	SBP66	SBP100	SEM	P
Apparent digestibility (g/Kg)						
DM	696.0^{b}	717.0^{a}	722.0^{a}	709.0^{ab}	5.2	0.03
OM	779.5	781.7	773.2	772.5	6.4	0.68
CP	730.0	740.2	723.0	726.5	11.2	0.72
NDF	611.2^{b}	634.2^{a}	636.7^{a}	620.2^{b}	4.0	0.04
ADF	536.5	529.7	540.7	551.7	9.4	0.42

† Barley grain was substituted with SBP as 0.0%(SBP0), 33%(SBP33), 66%(SBP66) or 100%(SBP100) a, b, c Means in row with different superscript letter are different

Key Words: sugar beet pulp, nutrients digestibility, dteers

T317 Adjustment of physically effective fiber sources in diets for beef cattle. R. Goulart*, J. Daniel, V. Santos, R. Amaral, G. Muraro, S. Toledo Filho, L. Nussio, and A. Pires, *University of Sao Paulo-ESALQ, Piracicaba, SP, Brazil*.

The physical effectiveness factor (fef) from forage and nonforage fiber sources was evaluated in a 6 × 6 Latin square trial using Nellore steers with six 19–d periods. After the 10–d adaptation period samples were collected from d 11 through 19. The six diets were composed of fiber sources: basal (low fiber content) with 10% NDF from corn silage (DM basis); high fiber (20% NDF from corn silage); and four diets containing 10% NDF from corn silage, and 10% NDF from each of the following sources: sugarcane, sugarcane bagasse, soybean hulls and high oil – cottonseed meal. All diets were formulated in order to provide a response function relating total chewing time (min/kg DMI) to fef value. This response was calculated assuming that corn silage NDF was completely effective (effectiveness factor = 1) and that the NDF from concentrate (corn and protein supplement) was completely ineffective (effectiveness factor = 0). Chewing activities were monitored and the feeding behavior from the steers was recorded every 5 min over one 24–h period during each sampling period. The fef values observed were: 1.19, 2.46, 0.41 and 0.00 for sugarcane, sugarcane bagasse, high oil – cottonseed meal and soybean hulls, respectively. Greater total chewing time (min/kg DMI) was observed for the diet which contained sugarcane bagasse (94.51 min/kg DMI) and the lowest mean for the diet whith soybean hulls (51.64 min/kg DMI) (P < 0.05). The soybean hulls diet showed a fef value equals to zero, resulting in lower ruminal pH (6.00) when compared to the sugarcane bagasse diet (6.31) (P < 0.05). These results suggested that soybean hulls appeared to be poorer stimulator of chewing than the high oil cottonseed meel and therefore, not suitable to maintain adequated mean ruminal pH. Moreover, the sucargane and sugarcane bagasse, showed higher fef than corn silage (p < 0.05).

Key Words: effectiveness factor, ruminal pH, Nellore steers

T318 Effect of infrequent roughage delivery on digestion and ruminal pH of beef steers fed concentrate diets. J. I. Arroquy*[1,3], J. Cervetto[2], M. Avila[1], and D. Daviu[2], [1]*INTA Santiago del Estero, Santiago del Estero, Argentina*, [2]*Univ. Nacional de Santiago del Estero-Fac. Agronomía y Agroindustrias, Santiago del Estero, Argentina*, [3]*CONICET, Santiago del Estero, Argentina*.

The objective of this experiment was to evaluate the effect of feeding a total mixed ration compared to feeding the roughage portion of the diet once every two days and separated of the daily delivered concentrate mix on digestibility and ruminal pH. Four ruminally fistulated beef steers (Braford; BW = 259 kg; SEM = 27 kg) were used in a factorial, four treatments by two periods (4 × 2) experiment. Treatment structure was 2 × 2 factorial, where first factor consisted of two diets: D1) 14% roughage: 86% concentrate; D2) 7% roughage: 93% concentrate. Roughage source of the diets was ground hay (Setaria italica); and concentrate portion had dry ground corn, cottonseed, and urea plus mineral-salt mix supplement. The second factor was roughage delivery in a total mixed ration (TMR) or the same proportion of ingredients but roughage offered once every 2-d and separated of the daily delivered concentrate portion of the diet (roughage every other day, REOD). Steers had continuous access to fresh water and were limit-fed daily at 2.9% BW (DM basis). There were not diet × roughage delivery system interaction for intake and digestion (e.g., OM, CP, NDF, and starch). Both diets were similar in intake and digestion. Roughage delivery system did not significantly affect intake and digestion of OM, CP, NDF, and starch. Intake means were 89.7 g/kg0.75 BW (SEM = 11.1), 8.7 g/kg0.75 BW (SEM = 0.6), 28.0 g/kg0.75 BW (SEM = 4.2), and 38.2 g/kg0.75 BW (SEM = 4.6) for OM, CP, NDF, and starch respectively. Average digestibility were 653 g/kg OM (SEM = 24), 576 g/kg CP (SEM = 56), 458 g/kg NDF (SEM = 80), and starch 877 g/kg starch (SEM = 28) for OM, CP, NDF, and starch respectively. Diet × roughage delivery system interaction tended to be significant for ruminal pH (P = 0.06). On average D2-REOD tended to have lower pH (P = 0.06) ruminal pH than the other treatments (e.g., D1-TMR, D2-TMR, and D1-REOD). In conclusion, under the conditions of this study, digestibility and ruminal pH was not affected in response to infrequent roughage delivery either in 7% or 14% roughage diet.

Key Words: roughage delivery, digestion, ruminal pH

T319 Ruminal pH profile of feedlot steers during a 3-week transition from a high-forage to high–concentrate diet. L. Holtshausen*, K. A. Beauchemin, and K. S. Schwartzkopf-Genswein, *Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*.

Ruminal pH profile, as an indicator of ruminal acidotic condition, of 16 cannulated crossbred beef steers (431 ± 25 kg BW) was measured during a diet transition period. Steers were transitioned from a 45 to 90% concentrate diet (DM basis) in 3 steps over 3 wk (+15% concentrate/wk). The diet consisted of barley grain, wheat distillers grain, corn silage and a mineral-vitamin supplement, with increasing amounts of corn silage replaced with barley grain. Ruminal pH was measured for 4 consecutive 24-h periods each week with indwelling ruminal pH electrodes. Minimum and mean ruminal pH were lower ($P < 0.05$) in wk 3 compared to the first 2 wk (minimum pH: 5.28, 5.20, 5.01; mean pH: 6.24, 6.10, 5.80 for wk 1, 2 and 3, respectively). Week × d interactions ($P < 0.01$) were observed. In wk 1, minimum and mean pH were higher on d 1 than on d 2, 3 and 4; in wk 2 and 3 it was similar or lower. The ruminal pH remained longer under 5.8 and 5.5 ($P < 0.05$) in wk 3 compared to the other wk (pH < 5.8: 5.4, 7.1, 12.6 h/d; pH < 5.5: 3.2, 4.7, 8.9 h/d for wk 1, 2 and 3, respectively), and there was a wk × d interaction ($P < 0.01$). In wk 1, duration under pH 5.8 and 5.5 were lower on d 1 than on d 2, 3 and 4; in wk 2 and 3 it was similar or higher. Alternate transition diet protocols such as more diet steps with smaller grain increments or shorter initial and longer final steps may aid in reducing the incidence of sub-clinical and clinical acidosis.

Table 1. Ruminal pH profile for steers transitioning from 45 to 90% (+15% concentrate/wk) concentrate (DM basis)

		Day					
pH	wk	1	2	3	4	SE	P
Min	1	5.40^{a}	5.21^{b}	5.18^{b}	5.34^{ab}	0.084	0.15
	2	4.81^{a}	5.30^{bc}	5.50^{b}	5.21^{c}	0.092	<0.01
	3	4.85^{a}	4.94^{a}	5.12^{b}	5.11^{b}	0.051	<0.01
Mean	1	6.39^{a}	6.12^{b}	6.20^{b}	6.25^{ab}	0.074	<0.01
	2	5.90^{a}	6.09^{b}	6.24^{b}	6.16^{b}	0.079	0.01
	3	5.78^{ab}	5.72^{a}	5.81^{ab}	5.91^{b}	0.071	0.05
Duration (h) under							
5.8	1	3.4^{a}	6.8^{b}	5.5^{ab}	6.0^{ab}	1.09	0.01
	2	10.8^{a}	7.1^{b}	4.6^{b}	5.8^{b}	1.29	<0.01
	3	13.1^{ab}	14.1^{a}	12.0^{ab}	11.1^{b}	1.25	0.09
5.5	1	1.9^{a}	4.4^{b}	3.4^{ab}	3.2^{ab}	0.93	0.07
	2	8.2^{a}	4.4^{b}	2.9^{ab}	3.2^{ab}	1.09	<0.01
	3	10.4	9.9	8.0	7.3	1.35	0.29

Key Words: ruminal pH, transition, feedlot cattle

T320 Influence of processing method on comparative digestion of white corn vs. conventional steam-flaked yellow dent corn in finishing diets for feedlot cattle. A. Plascencia*[1], M. Cervantes[1], M. A. Lopez-Soto[1], D. May[1], and R. A. Zinn[2], [1]*Universidad Autonoma de Baja California, Mexicali, Baja California, Mexico*, [2]*University of California, Davis, El Centro*.

Four Holstein steers (143 ± 3 kg) with cannulas in the rumen and proximal duodenum were used in a 4x4 Latin square design to evaluate the influence of processing method on comparative digestion of white corn. Treatments consisted of a basal finishing diet containing 80% corn grain (DM basis) as: 1) dry-rolled white corn (DRWC), 2) steam-flaked white corn, 0.36 kg/L flake density (SFWC-36) 3) steam-flaked white corn, 0.31 kg/L flake density (SFWC-31), and 4) steam-flaked yellow corn, 0.31 kg/L flake density (SFYC-31). Characteristics of ruminal, posruminal and total tract digestion of OM, starch, and N were similar (P > 0.20) for SFYC-31 and SFWC-31 treatments. Decreasing flake density (0.36 to 0.31 kg/L) of white corn did not affect (P = 0.23) ruminal OM digestion, but tended to increase (1.9%, P= 0.07) total tract OM digestion. Compared with dry rolling, steam flaking WC increased ruminal (9.4%, P = 0.05), posruminal (14.4%, P<0.01) and total tract OM digestion (8.2%, P<0.01) of OM, reflecting a corresponding increase in ruminal (13.3%, P <0.01), posruminal (43%, P<0.01) and total tract (12.3%, P<0.01) starch digestion. Apparent total-tract N digestion also was greater (5.5%, P = 0.04) for SFWC than DRWC. There were no treatments effects on ruminal pH (P > 0.10). We conclude that compared with dry rolling, steam flaking markedly enhances the feeding value of white corn, optimal flake density being less than 0.36 kg/L. Although white corn has greater horny endosperm content, characteristics of site and extent of OM, starch and N digestion are similar to that of conventional yellow dent corn when processed to a similar flake density (0.31 kg/L).

Key Words: steer, white corn, digestion

T321 Use of whole oats in feedlot diets. D. J. Gibb*, Y. Wang, K. S. Schwartzkopf-Genswein, and T. A. McAllister, *Agriculture & Agri-Food Canada Research Centre, Lethbridge, Alberta, Canada*.

One hundred twenty steers (353 ± 3 kg) were utilized to assess the impact of including 15% whole oats (DM basis) in barley-based backgrounding and finishing diets, in place of 9% silage and 6% barley. Control and treatment diets included barley silage at 55 and 46%, respectively, in the backgrounding period, and at 9 and 0% during finishing. Supplement was included at 5% of DM and included monensin sodium at levels to provide 33 mg/kg in diet DM. One of the five pens per treatment was equipped with GrowSafe technology that monitored feeding behaviour of individual animals. Oat samples (n = 12) contained 35% NDF, which resulted in similar NDF levels between control and oat-based backgrounding (35%) and finishing diets (18%). Feeding whole oats during the backgrounding period increased average meal size (982.6 vs. 671.2 g; P = 0.03) and DMI (8.94 vs. 8.39 kg/d; P = 0.0001) but did not affect ADG (1.31 kg/d; P = 0.48), resulting in reduced gain/feed (0.147 vs. 0.160; P = 0.008). During the finishing period, feeding oats increased eating rate (156.7 vs. 142.2 g/min; P = 0.04) without affecting DMI (11.96 kg/d; P = 0.27) or meal size (1336 g; P = 0.11). However, both ADG (1.90 vs. 1.73; P = 0.002) and gain/feed (0.158 vs. 0.145; P = 0.003) were improved when oats were included in the finishing diet. Dressing percentage was reduced (58.1 vs. 58.7; P = 0.03) with the inclusion of oats, but carcass weight (377.6 kg; P = 0.61), back fat (11.8 mm; P = 0.69), ribeye area (92.4 cm^2; P = 0.27) and quality grade (38.7% AAA; P = 0.13) were not affected by diet. Although similar rates of total (16.5%; P = 0.50) and severely abscessed livers (10.2%; P = 0.95) indicate similar digestive health between diets, the impact of more rapid eating of finishing diets on variables such as bloat is uncertain.

Key Words: oats, feedlot, eating behaviour

T322 Performance of steers fed a high energy oat as a replacement for barley or corn in growing and finishing diets. G. R. Zalinko*[1], B. G. Rossnagel[2], V. J. Racz[1], D. A. Christensen[1], and J. J. McKinnon[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*, [2]*Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada*.

Two trials were conducted to evaluate performance and carcass traits of steers fed a low lignin hull, high oil groat oat as a replacement for barley or corn in feedlot diets. In trial 1, 400 steers (275.4 ±20.8 kg) were fed one of two diets (37.8% barley or oat grain, DM basis). DMI was lower (P<0.05) (7.49 vs. 7.72 kg/d) and gain to feed improved (P<0.01) (0.171 vs. 0.159 kg) for steers fed the oat-based diet. Calculated NE_m (1.80 and 1.71 Mcal/kg) and NE_g (1.17 and 1.09 Mcal/kg) values were higher for the oat-based diet. In trial 2, 240 steers (341.7 ±18.1 kg) were fed one of three finishing diets with barley, corn or oat grain as the cereal grain. Target slaughter weight was 650 kg. Steers fed the oat diet had lower (P<0.01) ADG than barley or corn-fed cattle (1.40, 1.69 and 1.84 kg/d, respectively) reflecting lower (P<0.01) DMI (9.56, 10.84 and 11.56 kg/d, respectively). Calculated NE_m (1.93 ±0.01) and NE_g (1.29 ±0.01) values were similar between diets indicating that the poorer performance of the oat-fed cattle was due to reduced DMI. Carcass weight and dressing percentage was lower (P<0.01) for steers fed the oat diet. Rib composition did not differ (P>0.05) between treatments although the corn-fed cattle had higher (P<0.05) extractable fat in the *l. dorsi*. Stearic acid (C18:0) content of the *l. dorsi* of oat-fed cattle was higher (P<0.01) than that of the barley or corn-fed cattle. The ratio of polyunsaturated to saturated fatty acids in the muscle of oat and corn-fed cattle was higher (P<0.05) than barley-fed cattle. Results indicate that the energy value of this oat is equivalent or superior to that of barley for growing cattle, however further research is required to identify factors limiting feed intake of finishing cattle fed this new oat cultivar.

Key Words: low lignin hull, cattle performance, carcass traits

T323 Effects of replacing barley with corn grain in finishing diets on VFA concentration and ruminal ammonia nitrogen of Holstein male calves. F. Fatehi, M. Dehghan-Banadaky*, K. Reza-Yazdi, M. Moradi-Shahrbabak, and H. Bahrami, *The University of Tehran, Karaj, Tehran, Iran*.

Twenty five Holstein Male calves (body weight: 276±79 kg) were used to determine the effects of five different ratios of barley to corn grain (100:0, 25:75, 50:50, 75:25, 0:100) in finishing diets on rumen parameters for 110 days. Calves were allotted by weight to 5 groups and used in a completely randomized design. rumen liquor were sampled every 30 days. There were no differences among concentration of Butyrate and Isovalerate among calves. When the proportion of barley in diets decreased, the ruminal total VFA, propionate and valerate concentration decreased (P<0.05). inversely, acetate concentration and acetate to propionate ratio incrased (P<0.05). The postfeeding ruminal pH was more stable for animals fed the higher proportion of corn, then declined at a lower rate up to 3 h for this animal. It is notable that for all diets, ruminal pH was â‰¥ 5.7, which Van Houtert (1993) suggested was required to maximize growth of ruminal bacteria. Diets with higher proportion of Barley had greater (P < 0.05) at 0 h and lower (P < 0.05) concentrations at 3 and 6 h than Diets with higher proportion of Barley. Finally Regardlees to time, When the proportion of barley in diets decreased, the ruminal NH3 N concentrations in rumen increased (P<0.05).

Key Words: barley, corn, finishing diets

T324 The effect of dietary protein on immune response in receiving steers. E. P. Lane*, E. S. Vanzant, K. R. McLeod, and M. N. Steinman, *University of Kentucky, Lexington*.

Growing, crossbred steers (n = 192; initial BW = 259 ± 0.4 kg) from central Kentucky markets were used to study effects of protein level and source on growth and immune response of newly received steers in a 30-d receiving period. Steers were lotted by weight to 24 pens which were assigned randomly within weight blocks to receive one of four experimental diets (n=6): two metabolizable protein (MP) levels (80% or 100% of NRC MP requirements for 1.13 kg/d gain) and one of two protein sources, differing in ruminal protein degradability (SBM or SoyPlus, West Central, Ralston, IA), in a 2 × 2 factorial arrangement of treatments. Formulated degradable intake protein levels were: 62%, 57%, 68%, and 68% of CP for SoyPlus 80%, Soyplus 100%, SBM 80%, and SBM 100%, respectively. Steers were weighed on d 0 and 30. On day 0, steers were vaccinated (Vista Once-SQ, 20/20 Vision 7 with SPUR, Intervet, Madison, NJ; *Moraxella ovis*, Novartis, Greensboro, NC) and drenched with an oral anthelmintic (Safe-Guard, Intervet). Additionally, to assess humoral immune response to a novel antigen, steers were inoculated on d 0 and 30 with a Leptospirosis vaccine (L5-SQ, Intervet). Blood samples were collected on d 0, 30, and 58 for measurement of antibody titers to Leptospira serovar hardjo (LSH). On day 30, all steers were removed from treatments and placed on fescue pastures. Residual effects of treatments on immunological status were evaluated in 160 of the steers (evenly representing treatments and blocks) by measuring the antibody titer at d 58. Only DMI had a protein source

x level interaction (P<0.01). Steers fed the 100% MP diet had higher (P<0.01) ADG (1.22 vs 1.02 kg/d), gain:feed (0.19 vs 0.16) and 30-d LSH titers than steers fed the 80% MP diet. Treatments did not affect 56-d LSH titers (P>0.63). Dry matter intake was lower (P<0.03) with the SBM 100 treatment than with any of the other treatments. Gain:feed tended (P=0.10) to be greater with SBM than with SoyPlus. Both gain and immunological status of the steers responded to increasing levels of MP showing that immunological function can be depressed when dietary protein is limited.

Key Words: protein, immunological, beef

T325 Feeding soybean meal, urea or slow release urea (Optigen®) to finishing Zebu cattle. R. Carareto*[1], F. A. P. Santos[1], G. B. Mourão[1], D. F. A. Costa[2], A. M. Pedroso[1], J. A. D. Pacheco Junior[1], and J. C. Martinez[3], [1]*University of Sao Paulo, Piracicaba, Sãão Paulo, Brazil*, [2]*University of Queensland, St. Lucia, Brisbane, Australia*, [3]*Faculdade de Ciencias Agrarias e Veterinarias, Jaboticabal, São Paulo, Brazil*.

The objective of this trial was to compare 3 supplemental N sources, conventional soybean meal (SBM), urea (U) or slow release urea (SRU) (Optigem®) in diets for finishing cattle. One hundred Nelore bulls with an average initial SBW of 389 kg were used in a 90-d feeding trial after a 21 days period for adaptation to high concentrate diets. Animals were blocked by SBW and randomly allotted to 20 pens. Experimental diets were isonitrogenous and contained (%DM) 8% hay, 59.5 to 63.5% dried citrus pulp, 10% ground sorghum, 12% corn co-product with 17% oil, 3% cane molasses, 1.6% mineral mix with monensin, and the respective supplemental N sources. Treatments were: 1) 5% SBM + 0.9% U; 2)1.7% U; 3)2.5% SBM + 0.5% SRU + 0.8% U; 4) 1% SRU + 0.8% U; 5) 1.5% SRU + 0.3% U. Data were analyzed based on a randomized complete experimental design, with pens as the experimental units, using the Proc. Mixed of SAS (1999) version 9.2 for Windows. Dry matter intake, ADG and feed efficiency (DMI/ADG) were not affect by treatments (P>.05) (Table 1). Finishing Nelore bulls performance was not improved by feeding SBM or SRU compared to conventional urea.

Table 1. Dry matter intake (DMI), average daily gain (ADG) and feed efficiency (DMI/ADG) of finishing Nelore bulls fed 3 different supplemental N sources.

Variables	T1	T2	T3	T4	T5	Standard Error	Pr>F
ADG (Kg /day)	1.48	1.50	1.49	1.48	1.50	0.064	0.953
DMI (kg DM/day)	10.35	10.64	10.76	10.47	10.62	0.132	0.227
DMI/ADG	7.20	7.55	7.44	7.31	7.14	0.378	0.936

Key Words: soybean, urea, finishing cattle

T326 The effects of crude protein concentration and urea source on nitrogen metabolism in Holstein steers. V. B. Holder*[1], S. Elkadi[1], J. M. Tricarico[2], E. Vanzant[1], K. M. McLeod[1], and D. L. Harmon[1], [1]*Department of Animal and Food Sciences, University of Kentucky, Lexington*, [2]*Alltech Biotechnology, Nicholasville, KY*.

The objective of the study was to compare the effects of a slow release urea and regular feed grade urea on whole animal nitrogen metabolism when fed at two different concentrations of protein intake. The experiment was conducted utilizing 8 growing Holstein steers (BW = 265±18kg) in a replicated 4 × 4 Latin square experimental design with a 2 × 2 factorial treatment structure. Treatment factors included dietary crude protein (CP) concentration (10.9 vs. 12.1%) and urea source (slow release vs. regular feed grade). The higher crude protein diets were formulated to provide sufficient metabolizable protein to allow 800g of daily live weight gain. The lower CP diets were formulated to supply 82% of the metabolizable protein requirement for 800g of daily live weight gain. All diets were formulated to contain equivalent concentrations of non protein nitrogen (NPN) as a percentage of CP (20.5%). Intake was adjusted at the beginning of each period to be 2.28% of body weight. Experimental animals were adapted to each diet for 14 days before being transferred to metabolism stalls for 7 days of total urine and fecal collection. Total nitrogen efficiency was calculated as the difference between intake and excretion expressed as a percentage of nitrogen intake, and urinary N excretion was expressed as a proportion of total N intake. There was no effect of CP concentration, urea source or their interaction on total nitrogen efficiency (30%). There was no significant CP concentration x urea source interaction or urea source effect on urinary nitrogen excretion; however, the proportion of urinary nitrogen excretion was greater for the 12.1% crude protein diets (37% vs. 31%, P < 0.05). Thus, the proportion of nitrogen excreted in urine can be reduced by reducing the total nitrogen content of the diet. However, no further benefits of changing urea source were detected.

Key Words: nitrogen balance, nutrient synchrony

T327 Feed intake by Nellore and Red Norte bulls finished in feedlot. O. R. Machado Neto[1], M. M. Ladeira*[1], T. M. Gonçalves[1], L. S. Lopes[1], R. L. Oliveira[2], M. S. Bassi[1], D. M. Oliveira[1], J. S. Ribeiro[1], and E. O. S. Saliba[3], [1]*Federal University of Lavras, Lavras, MG, Brazil*, [2]*Federal University of Bahia, Salvador, BA, Brazil*, [3]*Federal University of Minas Gerais, Belo Horizonte, MG, Brazil*.

The objective of this work was to determinate the dry matter intake (DMI) in Nellore (NE; *Bos indicus*) and Red Norte (RN; *Bos taurus $times; Bos indicus*) bulls finished in feedlot, and the prediction of this traits by NRC (2000), CNCPS 5.0 and BR-CORTE systems. Forty one animals feedlot in collective pens were used, 19 NE and 22 RN with 361±31 and 367±30 kg of initial live weight, respectively. The animals had an adaptation period of 28 days. The experimental period lasted 56 days when individual intake was measured using the hidroxy phenil propan LIPE® (rich extracted lignin), chromic oxide and indigestible dry mater (iDM) markers. The diet chemical composition was 14.3% of CP, 30.1% of NDF and 70.3% of TDN. Predicted intakes by the systems NRC, CNCPS and BR-CORTE were compared with the actual, using the procedure PROC REG by software SAS (1999). There was no difference (P>0.05) in DMI between the genetics groups when expressing in kg/day (10.66 versus 10.44). When expressed as percentage of live weight (%LW) it was observed higher DMI (P<0.05) for the NE (2.55 versus 2.39%). It's possible to observe, because the slope and intercept of regression analysis, that all systems evaluated showed low accuracy in DMI (Table 1). In conclusion, Nellore bulls presented more intake than Red Norte, and the requirement systems haven't accuracy in intake prediction for Nellore, and Red Norte bulls.

Table 1. Regression analysis of the actual dry mater intake (DMI) values and predicted by systems NRC, CNCPS e BR-CORTE to Nellore and Red Norte

	Nellore						
		Slope			Intercept		
System	r^2a	Value	SEM	P	Value	SEM	P
NRC	-0.0301	-0.09011	0.130	<0.01	9.807	1.401	<0.01
CNCPS	-0.0390	-0.07674	0.134	<0.01	10.318	1.444	<0.01
BR-CORTE	-0.0513	-0.07212	0.206	<0.01	10.433	2.213	<0.01
	Red Norte						
		Slope			Intercept		
System	r^2a	Value	SEM	P	Value	SEM	P
NRC	0.0116	0.12409	0.111	<0.01	7.95	1.164	<0.01
CNCPS	0.0060	0.12703	0.119	<0.01	8.56	1.253	<0.01
BR-CORTE	-0.0443	0.05078	0.153	<0.01	9.010	1.607	<0.01

Key Words: *Bos indicus*, crossbreed, requirements systems

Ruminant Nutrition: Grass Cattle

T328 Nutrient balance and fermentive parameters of continuously cultured rumen fluid maintained with bermudagrass hay and supplied with additional soybean hulls and(or) corn. A. I. Orr* and B. J. Rude, *Mississippi State University*, *Mississippi State*.

Ruminal fluid was continuously cultured using the BioFlo® 110 fermentation system to evaluate the *in vitro* fermentive parameters of ground moderate-quality bermudagrass hay either alone (HAY; 20 g DM L^{-1} d^{-1}) or supplemented (7 g DM L^{-1} d^{-1}) with corn (CORN), soybean hulls (SBH), or both (25:75; MIX). Each of 4 vessels were maintained at 2L and 39°C while under constant agitation and N_2 sparging. Every 3h (between 0700 and 1900) fresh mineral-buffer was added. Culture pH did not to exceed 6.5 by automated addition of 2*N* H_2SO_4. Data was analyzed as a Randomized Complete Block, blocked by week (n=5). Each week, fresh ruminal cultures were grown for 9 d with sampling d 7, 8, and 9. Addition of hay DM was uniform ($P = 0.34$) among cultures (ranging from 39.07 to 39.14 g). Total DM added was slightly greater ($P < 0.0001$) for CORN (53.78 g) than SBH or MIX (53.61 and 53.58 g, respectively), and all 3 received more DM than HAY (39.07 g). Nutrient balance indicated DM disappearance was greatest ($P < 0.0001$) for MIX and least for HAY (0.0045 and -0.0058 g, respectively). No differences ($P = 0.10$) were observed for CP (-0.24 to -0.17 g), NDF (-0.04 to -0.01 g), or ADF (-0.001 to 0.02 g) disappearance. Culture pH was least ($P < 001$) for CORN from 2 to 6 h post-feeding (5.94 to 6.18). Ruminal ammonia-N was least ($P < 001$) for CORN 0 thru 12 h post-feeding (from 13.3 to 17.33 mg/dL) with MIX resulting in the next lowest ($P < 001$), 6 thru 12 h post-feeding (ranging from 16.59 to 18.55 mg/dL). Ammonia-N concentrations were evaluated as polynomial functions over time revealing a weak fit to the model for CORN (quartic; $P < 0.01$; Adj-$R^2 = 0.1135$), SBH (cubic; $P < 0.01$; Adj-$R^2 = 0.1024$), and MIX (quadratic; $P < 0.01$; Adj-$R^2 = 0.0849$). Data for HAY did not adequately fit any of the polynomial models. Analysis of VFA is forthcoming. Fermentive characteristics indicate a more complete and efficient utilization of nutrient DM and ammonia-N by cultures provided CORN and MIX. Additional evaluation is needed to assess nutrient disappearance under each ascribed diet.

Key Words: continuous culture, rumen, soybean

T329 Effects of dietary energy source in late gestation diets on pre- and post-partum beef cow performance. A. E. Radunz*, H. N. Zerby, F. L. Fluharty, and S. C. Loerch, *The Ohio State University*, *Wooster*.

Mature Angus-cross (n = 180) beef cows (initial body weight = 573 ± 5 kg) were used to determine the effects of late gestation dietary energy source on pre- and post-partum cow performance. Cows were blocked by location (n = 3) and stratified by body weight (BW), body condition score (BCS) and age (5 pens/treatment). Cows were adapted to diets starting at approximately 200 d of gestation and fed until 1 wk prior to expected calving date. Cows were fed 1 of 3 energy sources: hay (HAY); corn (LFC); and dried distiller grains (DDGS). Cows allotted to HAY were allowed ad libitum access to round-bale grass hay and averaged 12.2 kg DMI/d. Limit-fed corn and DDGS diets provided 4.8 kg whole corn or 4.0 kg DDGS, plus 2.2 kg hay, and 1.0 kg supplement to meet nutritional needs during late gestation. Following parturition, cows were fed a common diet and managed as one group per location. Milk production was measure by weigh-suckle-weigh at an average of 31, 100, and 164 d postpartum. At 2 locations, cows were synchronized for estrus and bred 81 ± 4 d postpartum. Cows fed DDGS gained more BW than either HAY or LFC (1.6, 1.1, and 1.1 ± 0.8 kg/d, respectively; $P < 0.01$) and had improved ($P = 0.02$) BCS as compared to HAY at the end of gestation. However, at the end of lactation (164 &polusmn; 7 d) BW ($P = 0.23$) and BCS ($P = 0.13$) were not different between treatments. Prepartum energy source did not affect first service conception rates ($P = 0.31$) or overall pregnancy rates ($P = 0.79$) postpartum. Milk production and composition were not different ($P > 0.2$) among treatments. Daily feed costs during late gestation were less for DDGS as compared to LFC and HAY. Limit-feeding DDGS as an alternative energy source in late gestation diets can improve cow BCS and BW gain and reduce daily feed costs; however these differences in weight gain and BCS at the end of gestation did not impact postpartum reproduction performance, milk production, or cow performance. Calf data are presented in a companion abstract.

Key Words: prepartum nutrition, beef cattle, energy source

T330 Growth performance and metabolism of cow-calf pairs receiving a high or low total non-structural carbohydrate diet with or without folic acid and vitamin b_{12} supplementation of the dams. J. Mercier*[1], C. L. Girard[2], D. Cinq-Mars[1], and R. Berthiaume[2], [1]*Département des Sciences Animales, Pavillon Paul-Comtois, Université Laval, Québec, QC, Canada*, [2]*Agriculture et Agroalimentaire Canada, Centre de Recherche sur le Bovin Laitier et le Porc, Sherbrooke, QC, Canada*.

Our objective was to study the effects of a maternal supplementation of folic acid and vitamin B_{12} (v+ vs. v-) and of dietary total non structural carbohydrates (HTNC vs. LTNC) on milk production, cow and calf weights and cow plasma concentrations of glucose and non-esterified fatty acids (NEFA). Thirty-two spring calving cows (723 ± 92 kg) and calves (77.8 ± 19.5 kg) were blocked according to parity and calving date (8 blocks of 4 cows) and randomly assigned to each treatment according to a randomised complete block design. Within each block, 2 cows were fed a LTNC diet, whereas the 2 other cows were fed a HTNC diet. Within each diet, cows received either no vitamins (v-) or weekly intramuscular injections of 160 mg of folic acid plus 10 mg of vitamin B_{12} (v+). During the first 100 days of lactation, the cows were fed daily grass silage ad libitum with (HTNC) or without 1 kg of dried molasses (LTNC). From day 100 to 200, cow-calf pairs were allotted new pasture every day at 0630h (LTNC) or 1830h (HTNC). During days 200 to 300, cow-calf pairs were fed ad libitum silage cut at 0600h (LTNC) or 1800h (HTNC). All calves were weaned at 300 d and slaughtered within 30 d. Treatments had no effect on milk yield (P=0.17) or cow plasma NEFA (P=0.41) but v+ cows tended to lose less BW than v- cows (+12.8 vs. -10.1 ± 9.9 kg; P=0.10). A TNC x vitamin interaction (P=0.02) was observed as the combination v+ and LTNC increased cow plasma glucose concentrations (3.95 vs. 3.80 ± 0.06 μM; P=0.03) and calf weights (246 vs. 223 ± 6.2 kg; P=0.01) whereas it had no effect on HTNC (P=0.26 and P=0.47 for plasma glucose and for calf weight, respectively). Our results suggest an interaction between dietary TNC levels and dam folic acid and B_{12} supplementation. The latter seems to have a beneficial effect when a LTNC diet is fed.

Key Words: beef, total nonstructural carbohydrates, B-vitamins

T331 Camelina meal and crude glycerin as feed supplements for developing replacement beef heifers. P. Moriel*, E. P. Goncalves, P. L. Price, V. Nayigihugu, and B. W. Hess, *University of Wyoming*, *Laramie*.

Ninety-nine Angus × Gelbvieh rotationally crossed heifers were used in a randomized complete block designed experiment to determine the effect of feeding camelina biodiesel co-products (meal and crude glycerin) on serum thyroid hormone concentrations as well as growth and reproductive performance. Heifers were stratified by initial BW (300 ± 2.1 kg) and randomly assigned to receive 1 of 3 experimental supplements (12.6% dietary CP): control (50% ground corn and 50% soybean meal, as-fed); camelina meal; and glycerin (50% soybean meal, 33% ground corn, 15% crude glycerin, 2% corn gluten meal; as-fed). Bromegrass hay and supplements were offered daily at 2.40% and 0.3% of BW (as-fed) for the first 30 days and at 2.26% and 0.29% of BW (as-fed) for last 30 days, respectively. Blood samples were taken from the coccygeal vein or artery at the beginning, after 30 days, and at the end of the 60-d experimental feeding period. Serum concentrations of T3 and T4 were determined by RIA. On d 60, heifers were synchronized for estrus using a 1-shot PGF2α protocol and any heifer showing estrus was bred via AI 12 hours after standing heat. Heifers not detected in estrus were bred via AI 14 days after the end of the experimental feeding period. No treatment effect was observed for ADG (P = 0.978), final BW (P = 0.967), heifers detected in estrus before timed AI (P = 0.787), first conception rate to timed AI (P = 0.541), overall first conception rate (P = 0.945), initial (P = 0.392), mid- (P = 0.499), and final (P = 0.498) serum concentration of T4, or initial (P = 0.731) and mid- (P = 0.905) serum concentrations of T3. Final concentrations of T3 in serum (P = 0.034) were 79.54, 83.30 and 92.95 ng/dL for heifers fed control, glycerin and camelina meal, respectively. These preliminary results indicate that camelina biodiesel co-products are acceptable dietary supplements for developing replacement beef heifers.

Key Words: camelina, glycerin, heifers

T332 Growth performance and breeding soundness of Angus bulls fed FlaxLic®. A. C. Pesta* and J. S. Drouillard, *Kansas State University*, *Manhattan*.

We evaluated growth performance and semen attributes of Angus bulls fed molasses-based block supplements containing ground flaxseed and linseed oil. Yearling bulls (n=120; initial BW=507 kg) were allocated equally among three feeding pens equipped with GrowSafe feeders and fed *ad libitum* amounts of a forage-based total mixed ration (TMR) for 70 d. Treatments consisted of the TMR only (Control); TMR plus a block supplement containing linseed oil and ground flaxseed (FlaxLic; 15% ether extract and ~8% alpha linolenic acid [ALA]); or a similar supplement in which a portion of molasses was replaced with corn steep liquor (CSL). Feed intakes of individual animals were monitored using the GrowSafe system. Blood serum and semen samples were retained from a random subset of bulls in each treatment on d 70. Compared to control bulls, FlaxLic and CSL increased serum and decreased semen concentrations of omega-3 fatty acids (P <0.05). Supplements had no effect (P > 0.10) on percentages of normal or motile sperm compared to Control bulls, and breeding soundness scores were similar among treatments (P>0.10). FlaxLic increased ADG by 11 and 19% compared to Control and CSL treatments, respectively (P < 0.05), and improved gain efficiency by 18% (P < 0.05) compared to bulls fed Control and CSL treatments. Supplementation with sources of alpha linolenic acid can increase serum concentrations of omega-3 fatty acids, but increases do not necessarily manifest as improvements in semen quality. Additionally, ingredient composition of supplements (though similar in nutrient content) can impact growth performance.

Table 1. Performance, Serum, and Semen Attributes of Yearling Bulls

Item	Control	FlaxLic	CSL	SEM
DMI, kg	12.2[a]	1.7[b]	11.6[b]	0.14
ADG, kg	1.33[a]	1.48[b]	1.24[a]	0.046
Gain:feed	0.11[a]	0.13[b]	0.11[a]	0.003
Serum ALA, ug/g	126[a]	147[b]	140[a,b]	5.1
Semen ALA, ug/g	11.9[a]	7.3[b]	8.9[b]	1.08

[a,b]Means without common superscripts are different, P <0.05.

Key Words: omega-3 fatty acid, semen

T333 A meta-analysis of dry matter intake in Nellore and Zebu-crosses cattle. J. A. G. Azevedo[1,2], S. C. Pina[2], M. L. Chizzotti[3], and O. G. Pereira*[2], [1]*Universidade Estadual de Santa Cruz, Ilheus, Bahia, Brazil*, [2]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*, [3]*Universidade Federal do Vale do São Francisco, Petrolina, Pernambuco, Brazil*.

This experiment was carry out aiming develop and evaluate new equations for dry matter intake (DMI) prediction in Nellore cattle and Zebu-crosses using meta-analysis. The data used for parameter estimation were collected from independent performance experiments with growing and fattening Nellore and crossbred (Nellore × Bos taurus), compiled from 27 thesis (study) and 561 of N experimental units. Prior to propose an equation to DMI predict was observed that the genetic group was a significant (P<0.15) source of variation. Therefore, different equations to predict DMI in the Zebu-Crosses e Nellore cattle were independently developed. The model used included terms for body weight (BW or BW^0.75^), average daily gain (ADG) and average daily gain quadratic (ADG^2^). Equation development was conducted in PROC MIXED using mixed-model regression techniques. In the Validation of the DMI predict equation were utilized independent experiments published between 2005 and 2008 in the Brazilian Journal of Animal Science and one thesis with independent datasets. The predictions of the fitted equations for Nellore cattle overestimated DMI, when the DMI were smaller than 7 and more than 10 kg d^-1^, however, the predicted DMI for the both equation fitted were next the tendency line. For Zebu-Crosses cattle dispersions of 3 kg d^-1^ was observed when extreme intakes were appraised. While for the prediction equation that includes BW^0.75^ the intercept did not differ of zero and the slope did not differ of 1, beyond the largest coefficient of determination values were for equations with Zebu-Crosses cattle. According to the statistics from regression, both, Zebu-Crossed and Nellore cattle, the prediction equation that includes BW0.75, were more precise and with a slight advantage than the equation with BW, when the values of mean square prediction error, mean absolute error and mean bias were evaluated. Fitted equations DMI = -2.6098 + 0.08844BW^0.75^ + 4.4672ADG – 1.3579ADG^2^ and DMI = -2.7878 + 0.08789BW^0.75^ + 5.0487ADG – 1.6835ADG^2^ they should be targeted at alternate to predict DMI of Zebu-Crosses and Nellore beef cattle, respectively, in tropical conditions.

Key Words: beef cattle, feed intake, meta-analysis

T334 Dry matter intake and performance of steers fed sugar cane ensiled with different levels of calcium oxide. F. H. M. Chizzotti[1], O. G. Pereira*[1], S. C. Valadares Filho[1], M. L. Chizzotti[2], and R. T. S. Rodrigues[2], [1]*Universidade Federal de Viçosa, Viçosa, MG, Brazil*, [2]*Universidade Federal do Vale do São Francisco, Petrolina, PE, Brazil*.

A trial was conducted with thirty-five crossbred steers (Holstein x Nellore), averaging 350 kg BW, distributed in seven randomized blocks to evaluate levels of calcium oxide (CO) as additive of sugar cane silage. Diets consisted of 50% roughage and 50% concentrate, formulated to be isonitrogenous (12% CP, DM basis). The five treatments consisted of sugar cane ensiled with four CO levels (0, 0.5, 1.0, and 1.5%) and a standard diet with corn silage. The experiment lasted 99 d and steers were fed individually. DMI was measured daily and individually. A mixed model with random effect of blocks was used. There was a negative linear effect (P<0.01) of CO levels on intake of DM (kg/d), while DMI as % of the BW had a quadratic effect with maximum intake of 2.15%BW at 0.53% of CO in sugar cane silage. Quadratic effects of levels of CO were observed on ADG and gain efficiency. Steers fed sugar cane silage with 0.5% of CO or corn silage had similar DM intakes. However, the ADG of steers fed corn silage diets was higher than those fed sugar cane silages. The addition of up to 0.5% of calcium oxide in sugar cane ensilage improves sugar cane silage quality and animal performance.

Table 1. Effect of calcium oxide (CO) in sugar cane silage on DMI, ADG, gain efficiency and dressing percentage (DP)

	CO levels in sugar cane silage, %					*P*[1]	
Item	0	0.5	1	1.5	Corn silage	L	Q
DMI, kg	8.83^{b}	9.5^{ab}	8.48^{cd}	7.73^{d}	9.92^{a}	0.01	0.03
DMI, %BW	2.04^{ab}	2.19^{a}	2.03^{b}	1.87^{c}	2.19^{a}	0.03	0.01
ADG, kg	0.89^{c}	1.13^{b}	0.89^{c}	0.71^{c}	1.34^{a}	0.04	0.01
G:F, g/kg	101^{bc}	120^{ab}	106^{bc}	90^{c}	134^{a}	0.17	0.02
DP, %	53.1^{bc}	54.3^{ab}	53.2^{bc}	52.3^{c}	55.6^{a}	0.17	0.09

[1]Linear, quadratic effect of CO in sugar cane silage; ^{a,b,c,d}Means within a row differ, Tukey 5%

Key Words: additive, feedlot, roughage supplementation

T335 Effects of protein or fat supplements for finishing beef cattle grazing tropical grass during dry season. A. A. Souza*[1], T. I. Ferreira[2], C. F. Martins[1], and J. C. Hadlich[3], [1]*UNIDEP/ANHANGUERA, Campo Grande, Mato grosso do Sul, Brazil*, [2]*IAGRO, Campo Grande, Mato grosso do Sul, Brazil*, [3]*UNESP, Botucatu, Sao Paulo, Brazil*.

This study has evaluated the effects of additional fat or protein supplements on animal performance and carcass characteristics of Nellore cattle grazing tropical pastures during the dry season. The trial was conducted at University for development of State and Pantanal Region, Mato Grosso do Sul, Brazil. Thirty-six Nellore steers were divided and evaluated in 3 treatments as follows: Control = *Brachiaria brizantha* + mineral supplement; Supl. Fat = *Brachiaria brizantha* + commercial supplement with 10% fat (soybean oil); Supl. Prot = *Brachiaria brizantha* + commercial supplement with 40% protein. The quantities of supplements fed daily were 0.3% of liveweight/animal. The initial and final live weight were 424-463; 415-487; and 415-471 kg for Control, Supl Fat and Supl Prot, respectively. After 130 days on trial, all animals were slaughtered at a commercial plant and backfat thickness measured. The average daily gains were 0.35; 0.50; and 0.57 kg/animal/day for control, Supl. Fat and Supl. Prot, respectively (Table 1). Higher carcass yield was observed for both groups fed supplemented feed. Backfat results were similar to carcass yield results (table 1). The use of fat or protein as grazing supplement had benefitial effects in animal performance and carcass characteristics, finishing grazing animals with higher backfat thickness and carcass yield. The use of supplements for increased nutrient intake during dry season is a necessary step to improve carcass and meat quality of animals finished on tropical pastures.

Table 1. Average daily gains and backfat and carcass yield after chilling

Treatments	Daily Gains (kg)	Backfat (mm)	Carcass Yield (%)
Control	0.35^{a} ± 0.05	2.67^{a} ± 0.20	51.5^{a}
Supl. Fat	0.57^{b} ± 0.04	3.01^{b} ± 0.31	53.3^{b}
Supl.Prot	0.50^{b} ± 0.03	3.42^{b} ± 0.33	53.1^{b}

*means with different superscripts are statistically different (P< 0.05)

Key Words: beef cattle, carcass characteristics, meat quality

T336 Effect of supplemental energy level on performance, blood parameters and carcass characteristics of steers finished on pasture. H. O. Patino*[1], F. S. Medeiros[1], K. C. Swanson[2], and M. A. Sierra[1], [1]*Dep. Zootecnia, UFRGS, Porto Alegre, RS, Brazil*, [2]*Dept. Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*.

To evaluate the effect of supplemental energy levels on performance, blood parameters and carcass characteristics, 24 Aberdeen Angus × Charolais steers were used. The experimental treatments were levels of feeding (0, 0.4, 0.8 and 1.2% BW) of a corn based supplement in a winter pasture of annual ryegrass (*Lolium multiflorum L*) and oats (*Avena strigosa Schreb*) managed in order to avoid constraints to animal performance. Animals were supplemented daily (14:00 – 16:00) in individual pens and slaughtered when they achieved 4.5 mm of fat cover on the rump point. No differences were observed in fat deposition, measured in live animals with ultrasound at the end of the performance period, and in live weight gain, which had average values of 3.9 mm and 1.54 kg/d, respectively (p>0.05). Blood serum levels of urea were linearly decreased (p<0.01) and cholesterol linearly increased (p<0.01) by energy supplementation, with no differences in the serum levels of glucose and triglycerides (p>0.05). Energy supplementation linearly increased dressing percent (p<0.06) and carcass weight gain (p<0.05), but no differences were observed for rib eye area, slaughter weight and hot carcass weight, which averaged 67.85 cm^2, 438.95 kg and 227.75 kg (p>0.05). Increasing the levels of energy supplementation resulted in greater dressing percent and greater carcass daily gains, without changes in performance and carcass parameters.

Key Words: blood parametrs, energy supplementation, winter pasture

Small Ruminant: Lactation, Physiology, Reproduction, Health

T337 Long-term effects of lipid supplementation on milk concentration of conjugated linoleic (CLA) and vaccenic acid (VA) in dairy goats. G. A. Gagliostro*[1], M. A. Rodriguez[2], V. I. Cejas[2], M. Martinez[3], A. V. Cano[1], P. Gatti[2], G. Muset[2], R. A. Castañeda[3], and Y. Chilliard[4], [1]*Instituto Nacional de Tecnología Agropecuaria, Balcarce, Buenos Aires, Argentina*, [2]*Instituto Nacinal de Tecnología Industrial, PTM San Martín, Buenos Aires, Argentina*, [3]*Instituto Nacional de Tecnología Agrpecuaria, Salta, Salta, Argentina*, [4]*Institut National de la Recherche Agronomique, Theix, Ceyrat, France*.

The objective of the study was to test the persistency in milk of fatty acids (FA) that have potential benefits to human health over 150 d after lipid supplementation in Saanen goats. Six animals/treatment grazed a grass based pasture and were individually supplemented with : T1) 1 kg/d cracked corn grain, T2) 1 kg/d corn grain + 30 g/d fish oil (FO) + 109 g/d soybean oil (SO), and T3) 0.5 kg/d corn grain + 0.5 kg/d cracked soybean grain (SG) + 30 g/d FO. Milk samples were collected every 15 d. Data were analyzed using a model including treatment, sampling time, and the interaction. Concentrations of individual FA in milk were expressed as g/100 g of total FA. Protein and lactose concentrations in milk were not affected. Milk fat content increased (P < 0.06) by 8.3 g/kg in T2 compared to T1 and T3. In T2, pre-treatment basal concentrations of de novo FA (C4:0-C15:1), C12:0, and C14:0 decreased (P < 0.01) after lipid supplementation, but C16:0 concentration did not change. The basal atherogenicity index (AI) decreased (P < 0.01) from 2.91 to 1.30 in T2, and from 2.57 to 1.53 in T3. Supplementary lipids decreased C12:0 (-1.31) and C14:0 (-1.74) in T3 (P < 0.01). Compared to T1 (2.29 g/100 g)concentrations of VA increased (P < 0.01) in T2 (+11.9) and T3 (+9.15) and remained high throughout the experiment. Trans-10 C18:1 ranged from 0.21 to 0.24 g/100 g FA in T1, and from 0.98 to 1.10 in T2 and T3. Basal 9-cis 11-trans CLA averaged 1.27 g/100 g (T1), 1.03 (T2), and 1.26 (T3). The average increase in CLA after 150 d was 4.28 g/100 g in T2 and 3.75 in T3. In T1, CLA concentrations ranged from a minimum of 0.83 g/100 g FA in samples taken at d 135 to a maximun of 1.84 at d 15. SO combined with FO were the most effective to increase milk concentration of trans-11 C18:1 but differences between effects of SO or SG on milk CLA contents were not observed. Feeding SG or SO combined with FO reduced the concentrations of FA linked to cardiovascular risk disease and the AI of milk, and increased the concentrations of CLA and VA over an extended period after lipid supplementation.

Key Words: goat milk, conjugated linoleic acid, vaccenic acid

T338 Effects of mechanical processing of sugarcane on performance and milk composition of dairy goats. V. P. Santos*, L. G. Nussio, G. B. Muraro, S. G. Toledo Filho, R. C. Amaral, J. L. P. Daniel, R. S. Goulart, I. Susin, G. B. Mourão, R. S. Gentil, and C. Q. Mendes, *Universty Of Sao Paulo/ESALQ, Piracicaba, SP, Brazil*.

The experiment was conducted to evaluate the effects of mechanical processing of sugarcane on milk production and composition in dairy goats. Twelve Sannen × Boer goats (20 ± 5 d in milk) were assigned to a three latin square 4×4 design. Experimental diets were formulated to meet the AFRC (1998) requirements for energy, protein, Ca, and P, and consisted of four treatments (diets). Treatment 1 contained corn silage (C) in a 50:50 (concentrate:roughage ratio) total mixed ration, and the three other treatments were based on sugarcane chopped to mean particle size 0.52, 6.53, 12.40 mm, mixed in a 44:56 ration. Each period consisted of a 10–d period of adaptation followed by 4–d for sample collection. The goats were fed ad libitum individually once daily at 0800 h to allow at least 5 to 10% orts and milked twice daily at 0730 and 1530 h. Milk weight was recorded for each goat and samples were collected for composition during the morning and afternoon across the last 3–d of each sampling period. There were no differences (P > 0.05) for intake of DM (kg/d) and DMI (%BW), where the values found for C were 1.63 and 2.73% BW, DM animal/d, and mean values for other treatments (chopped sugarcane) were 1.55, and 2.5% BW, respectively. Differences between treatments were not observed for milk yield (kg/d). However, the percentage of milk fat (%) and 3.5% milk corrected yield (3.5 FCM; kg/d) was higher for C treatment (4.32 and 2.57, respectively) when compared with treatments containing sugarcane. It might be related to the smaller particle size of sugarcane when compared to the corn silage. For the treatments containing sugarcane processed in sizes 0.52, 0.63, 12.4 mm, the observed values for 3.5 FCM and milk fat were 2.09, 2.24, and 2.07 kg/d and 3.92, 3.82, and 3.75%, respectively.

Key Words: silage corn, roughage, fat

T339 Thyroid hormones and blood metabolites of dairy goats supplemented with dietary iodine. A. Nudda[1], G. Battacone[1], G. Bomboi[2], B. Floris[2], and G. Pulina*[1,3], [1]*Dipartimento di Scienze Zootecniche, University of Sassari, Italy*, [2]*Dipartimento di Biologia Animale, University of Sassari, Italy*, [3]*Agricultural Research Agency of Sardinia - AGRIS Sardegna, Sassari, Italy*.

The supplementation of dairy animals with iodine should be a valuable method to increase iodine content in milk. Aim of this work was to determine if long-term potassium iodide (KI) supplementation to dairy goats, used to increase milk iodine content, can influence important metabolic and hormonal parameters. Thirty crossbreed dairy goats were divided into 3 groups and each goat was supplemented with 0 (control; group 0), 450 (group 1), or 900 (group 2) μg of KI/d. The dose of KI (76.5% of iodine) was administered every day for 8 wk as iodized salt dissolved in water. Blood contents of nonesterified fatty acids (NEFA), urea, glucose, insulin, free triiodothyronine (FT3) and free thyroxine (FT4) were determined. Data were analyzed with a GLM procedure including iodine level, week and the interaction in the model. There was a significant effect of the increasing iodine intake on the level of FT3 hormone, which represents the biologically active form of thyroid hormones. Iodine supplementation had no effects on plasma FT4 levels and NEFA. The blood urea nitrogen (BUN) and insulin were significantly lowered by iodine supplementation (groups 1 and 2), whereas blood glucose concentration was decreased only by low iodine supplementation (group 1). In conclusion, the daily supplementation of low doses of KI can influence the level of T3 and BUN in dairy goats.

Table 1 - Concentration of glucose, insulin, NEFA, urea and thyroid hormones (T3, T4) in goats supplemented with KI

	group			P value		
	control	1	2	group	sampling	Inter
glucose, mg/dL	63.3A	60.0B	64.0A	**	**	**
NEFA, mmol/L	0.13	0.14	0.14	ns	**	*
UREA, mg/dL	7.5A	6.3B	6.7B	**	**	ns
FT3, pg/mL	4.2A	4.5A	5.4B	**	**	ns
FT4, pg/mL	10.8	9.1	11.2	ns	ns	ns
Insulin, mU/L	29.9A	11.1B	17.4B	**	**	ns

Means within a row with different superscripts differ (P<0.01)

Key Words: iodine, thyroid hormones, goat

T340 Effect of duodenal soybean small peptides infusion on lactation performance, peptide-bound amino acid and free amino acid metabolism in lactating goats. H. Liu, Z.-J. Cao, L. Wang, and S.-L. Li*, *College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The objective of the study was to determine the effect of soybean small peptides infusion on lactation performance, peptide-bound amino acid (PBAA) and free amino acid (FAA) metabolism. Eight Chinese Saanen lactating goats were used in crossover design. Four treatments were control, duodenal infusion of 0.9% sodium chloride solution (700 mL/d), duodenal infusion of 60 g/d, 120 g/d and 180 g/d of soybean small peptides which was dissolved in 700 mL/d of 0.9% sodium chloride solution through duodenal fistulas, respectively. Data were analyzed by the one–way ANOVA procedure using SPSS 10.0. Multiple comparisons were done by Duncan's test. Concentrations of arterial amino acids increased by soybean small peptides infusion ($p < 0.05$) except Thr, Arg, Gly, and Ala. Total essential amino acid (TEAA) and total nonessential amino acid (TNEAA) concentrations in arterial plasma were increased ($p < 0.01$). Except for PB-Ile, PB-Thr, and PB-Ala, concentrations of all PBAA were increased ($p < 0.05$) and those of total peptide-bound amino acids (TPEAA) and total peptide-bound nonessential amino acids (TPNEAA) were increased ($p < 0.05$) with grade soybean small peptides infusion. The mammary uptake (MU) of the PB-AA increased with the increase of soybean small peptides infused except for PB-Gly and PB-Glu; the uptake of most FAA were increased in 60 and 120 g/d treatment and unchanged in the 180 g/d treatment. The mammary uptake of TPEAA and TPNEAA were increased by soybean small peptides infusion. PB-His and PB-Lys were extracted more efficiently ($p < 0.05$). PB-Ser and PB-Pro extraction efficiency had significant differences. Milk protein yields were slightly increased and mRNA expression of β-casein, αs1-casein and κ-casein in mammary gland were obviously increased ($p < 0.05$). Based on the current data, small peptides can be efficiently utilized by mammary gland.

Key Words: soybean small peptides, mammary metabolism, duodenal infusion

T341 The effects of shearing on milk production traits and milk fatty acid profile in Sarda dairy ewes. S. P. G. Rassu, M. G. Manca, R. Boe, R. Rubattu, A. H. D. Francesconi, and A. Nudda*, *Dipartimento di Scienze Zootecniche, University of Sassari, Italy.*

The present study aimed to investigate the metabolic response of dairy ewes to shearing by monitoring their milk yield, milk fat content and milk fatty acid (FA) profile. Twelve 2-4-year-old Sarda ewes, in mid-late lactation, were used. The trial lasted from 30th May to 9th June 2006. The pre-experimental period (pre-shearing, PrS) was from 30th May to 5th June (shearing day), being followed by the experimental period (post-shearing, PoS) until 9th June. Four milk samplings during PrS and another four during PoS periods were performed. Daily milk production was recorded and daily milk samples were collected for analysis of fat content and FA profile. Shearing did not influence milk yield but increased milk fat content (6.37 *vs.* 6.94% for PrS and PoS, respectively; P<0.01). Shearing modified the FA profile of milk (Table 1). The concentration of C8, C10, C12 and C16 increased from PrS to PoS. On the other hand, the content of long-chain FA (>C18:0) did not change between PrS and PoS. These results suggest that the increase of milk fat after shearing was related to the increase of the main FA synthesized by the mammary gland. However, the mechanism involved in the modification of the FA profile caused by shearing in dairy ewes needs further investigation.

Table 1 - Fatty acid profile in milk of dairy ewes before and after shearing

Fatty acid (g/100 g of FAME†)	pre-shearing	post-shearing	P level
C8	1.2	1.54	**
C10	4.9	5.5	**
C12	3.0	3.3	*
C14	10.1	10.0	ns
C16	27.9	26.7	**
C18	13.9	13.9	ns
>C18	42.3	46.4	ns

†FAME = fatty acid methyl ester; **P<0.01; *P<0.05; ns = not significant

Key Words: shearing, dairy sheep, fatty acids

T342 Goat colostrum chemical composition evolution during 7 h postpartum. D. Sanchez-Macias[1], N. Castro[1], J. Capote[2], I. Moreno-Indias[1], and A. Argüello*[1], [1]*Las Palmas de Gran Canaria University, Arucas, Las Palmas, Spain*, [2]*Instituto Canario de Investigaciones Agrarias, La Laguna, Tenerife, Spain*.

As a consequence of the extreme importance of the quality of colostrum in dairy goat production when goat kids are separated from their dam at birth, the objective of present work was to study the evolution of the chemical composition of colostrum for 7 h postpartum. Forty Majorera breed goats were milked at birth and once an hour until 7 h postpartum. Colostrum production was recorded and the chemical composition was analyzed for protein, fat and lactose using a MIRIS® device. An ANOVA was performed using time as an independent variable on SAS (V9.0). Colostrum production was higher at 0 h postpartum than the following hours and no significant differences were shown after 0 h. A tendency of decreasing colostrum secretion was observed (see table). The percentage of colostrum protein fell between 0 and 4 h (45%) and subsequently stabilized, whereas colostrum fat percentage increased postpartum and then decreased, remaining stable from 4 to 7 h postpartum. The percentage of colostrum lactose increased from 0 to 4 h postpartum, and remained stable from 5 to 7 h postpartum. The chemical composition of the colostrum changed drastically in a few hours, therefore to ensure the passive immune transfer it is incorrect management when kid goats do not receive first milking colostrum within the first few hours of life (whether through stored first milk colostrums or suckling directly).

Table 1. Colostrum chemical composition during the 7 h postpartum

h PP	0	1	2	3	4	5	6	7	SEM
Colostrum production (g)	2505.7^{a}	174.3^{b}	169.3^{b}	165.1^{b}	165.1^{b}	132.7^{b}	115.7^{b}	117.9^{b}	116.9
Protein (%)	10.4^{a}	9.7^{a,b}	7.8^{b,c}	6.9^{c,d}	5.7^{d}	5.1^{d}	5.4^{d}	5.3^{d}	0.3
Fat (%)	8.7^{a,b}	10.3^{a}	9.7^{a,b}	8.6^{a,b}	7.3^{b}	6.8^{b}	6.9^{b}	6.9^{b}	0.3
Lactose (%)	2.1^{a}	2.2^{a}	2.7^{a,b}	3.1^{b,c}	3.3^{b,c}	3.6^{c}	3.6^{c}	3.5^{c}	0.1

^{a,b,c,d}Means within a row with different superscripts (P<0.05)

Key Words: goat, colostrum, chemical composition

T343 Somatic cell count in milk of goats enrolled in Dairy Herd Improvement Program in 2007. L. Zhang[1,2], G. R. Wiggans[3], J. Clay[4], R. LaCroix[5], J. Z. Wang[1], T. Gipson[1], and S. S. Zeng*[1], [1]*Langston University, Langston, OK*, [2]*Agricultural Research Center of China, Changchun, Jilin, China*, [3]*Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD*, [4]*Dairy Records Management Systems, North Carolina State University, Raleigh*, [5]*AgSource Cooperative Services, Verona, WI*.

The effects of breed, parity, stage of lactation (mo), herd size, and regions/states on somatic cell count (SCC) and production of milk from dairy goats enrolled in the Dairy Herd Improvement (DHI) program in the United States in 2007 were investigated to monitor the current status of SCC and to help goat producers improve their herd management and receive premiums for high quality goat milk. Statistical analysis of composite DHI data (n = 29,000) indicated that SCC and production of goat milk were affected by many non-infectious factors. Significant variations ($P < 0.05$) in SCC were found among breeds, with Toggenburg and Nubian being the highest, and Pygmy and Nigerian Dwarf being the lowest. The mean SCC of milk from Toggenburg and Nubian goats were near the current regulatory limit of 1.0×10^6 /mL for Grade "A" goat milk. As parities increased, SCC in milk increased steadily ($P < 0.05$). Significant differences ($P < 0.05$) in both SCC and milk production were discovered among regions. Large herds of goats tended to have higher milk production and SCC than the small herds ($P < 0.05$). The above findings suggest that consideration be given to culling goats with high somatic cell score (SCS) in their 5th lactation as SCS is expected to increase as they age, that year-round breeding and lactation programs be practiced, if dairy goat producers in the United States are to meet the Grade "A" goat milk requirements. All factors that contributed to variations in SCC and production of goat milk should be taken into consideration when establishing price incentive systems for goat milk.

Key Words: goat milk, somatic cell count, DHI

T344 Excretion pattern of aflatoxin M1 in milk of goats fed a single dose of aflatoxin B1. G. Battacone*[1], A. Nudda[1], M. Decandia[2], A. Mazzette[1], M. Acciaro[2], and G. Pulina[1,2], [1]*Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italy*, [2]*Agenzia AGRIS Sardegna, Sassari, Italy*.

A single dose (0.8 mg/head) of aflatoxin B1 (AFB1) was administered per os to five Saanen goats in mid lactation in order to investigate the consequent excretion of aflatoxin M1 (AFM1) in milk. In all goats, the AFM1 was detected at the first milking performed 1 h after the AFB1 intake. The highest concentrations of AFM1 were reached in milk collected 3 and 6 h after the AFB1 administration. After the maximum concentration of AFM1 was reached, the pattern of clearance in milk was fitted by a decreasing exponential function. The coefficient of determination of the equation was quite high ($R^2 = 0.90$), despite the great individual variability observed. AFM1 values were below 50 ng/L, that is the maximum allowed level by EU, in milk collected 36 h after the AFB1 administration. The AFM1 in milk sampled at 72 h after dosing was near the LOD value (0.04 ng/mL) of our analytical method. The mean percentage ratio of AFM1 excreted in milk within the 72 h to the amount of AFB1 ingested was 0.17%, with a high individual variability (st.dev. = 0.064). About the 85% of AFM1 was excreted in milk collected within 24 h after the AFB1 administration. The hypothesis that the transfer of AFM1 from blood into milk is due to a passive permeability is confirmed by the pattern of concentrations of main milk constituents.

Key Words: aflatoxin M1, goat, milk

T345 Lamb production in the Northern Patagonia with or without winter supplementation. L. Villar*[1], E. Pavan[2], M. Zimerman[1], C. Giraudo[1], and F. Santini[3], [1]*INTA-EEA Bariloche, Bariloche, Rio Negro, Argentina*, [2]*INTA-EEA Balcarce, Balcarce, Buenos Aires, Argentina*, [3]*INTA-CIA Castelar, Hurlingham, Buenos Aires, Argentina*.

Lamb meat is the main ingredient of a variety of traditional dishes in the Patagonia region of Argentina. In recent years, tourism increase has boosted its demand. Sheep production systems in the Hills and Plateaus of Northern Patagonia are mainly aimed at producing fine wool; secondarily lambs are slaughtered at light weights (11 kg) and marketed as whole or half carcasses. If a heavier slaughter weight were reached, total meat production could be increased, and meat could be marketed as commercial cuts. The objective of this study was to evaluate winter supplementation effects on performance, carcass traits, meat and wool quality of heavy lambs on extensive grazing conditions. Forty-six Merino male lambs (8 mo of age) were randomly divided into two

groups; one group was not supplemented (CTRL), whereas the other one (SPPL) received 200 g alfalfa pellet and 150 g oat grain daily for 95 d. Each group had free access to a 70 ha plot of shrub grass steppe; groups switched plots every 15 d. Lambs were sheared and wool samples taken. When the mean LW of each group reached 35 kg, 12 lambs from the group were randomly selected for carcass and meat evaluation. At 24 h postmortem, carcass traits and longgisimus muscle (LM) pH, color and water holding capacity (WHC) were determined and LM samples were taken for Warner-Bratzler shear force (WBSF) evaluation. Data were analyzed by ANOVA using GLM procedure of SAS software; LW at slaughter was used as a covariate when significant. Animals from the SPPL group were slaughtered after 130 d on grazing, while those of the CTRL group, 27 d later. ADG for SPPL was greater ($P < 0.001$) than for CTRL during the first 95 d and the overall grazing period, but lower ($P < 0.05$) from the end of supplementation to slaughter. CTRL had greater ($P = 0.04$) ribeye area and L* value than SPPL. No differences ($P > 0.05$) were observed for wool quality traits, HCW, dressing percentage, carcass and leg compactness, fat thickness, pH, WHC, WBSF. Our data suggest that a low level of winter supplementation would allow marketing heavy lambs in advance without major changes in wool traits or carcass and meat quality.

Key Words: performance, carcass traits, meat quality

T346 Relationship between body condition score and fertility of Saanen goats under intensive conditions. A. Ata*[1], M. Saatci[2], and M. S. Gulay[3], [1]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Department of Reproduction and Artificial Insemination, Burdur, Turkey*, [2]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Department of Animal Science, Burdur, Turkey*, [3]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Department of Physiology, Burdur, Turkey*.

The present study was undertaken to investigate the relationship between body condition score (BCS) and some fertility parameters of goats kept under intensive conditions. The data were obtained from brucellosis-free Saanen goats (61 primiparous and 71 multiparous). All goats were housed in a free-stall barn allowing 2 m^2 spaces for an individual goat. The goats were fed a commercial diet that provided 88% dry matter, 9% ash, 18% crude protein, 14% crude fiber, and 2700 kcal/kg of metabolizable energy. Water was given *ad libitum*. Body weight (BW), BCS and presence of horns were recorded at mating. Does were grouped according to their BCS (thin BCS = 2-2.5; normal BCS = 3-3.5; and fat BCS = 4.0-4.5) and BW [thin BW<30 kg (primiparous) and 45 kg (multiparous); normal BW = 30-40 kg (primiparous), 45-60 (multiparous); and fat BW > 50 kg (primiparous), 60 kg (multiparous)]. Primiparous and multiparous does were analyzed separately by proc FREQ and LOGISTIC procedure. The pregnancy rates (PR; number of pregnant does/number of does inseminated) for primiparous and multiparous does were 90.16 and 86.66%, respectively. BCS or BW at mating did not affect the PR. Similarly, no effects of BCS or BW were detected on abortion rates (AR; number of observed aborting goats/number of goats pregnant) in primiparous does. However, the AR for multiparous does were significantly affected by BCS ($P < 0.02$). Thin (25%) and fat (39.1%) does had higher AR than normal (6.7%) does. Kidding rate did not affect reproductive losses negatively in primiparous or multiparous does. Likewise, AR were similar for polled goats when compared with horned goats in primiparous group. On the other hand, polled goats were more likely to abort (33.3%) compared with horned goats (9.4%) in multiparous group ($P < 0.02$). In conclusion, it is clear that does are able to conceive even when their body energy reserves are too low or too high. However, inadequate BCS are expected to have a dramatic impact later on the abortion, especially in multiparous does. Thus, it is necessary to establish a target BCS at mating (3-3.5; 5-point scale) for goats under intensive conditions.

Key Words: intensive management, Saanen goat, BCS

T347 Preliminary results of a comparison between Texas Rambouillet sheep and Australian Merino F1 crosses. C. J. Lupton[1], F. A. Pfeiffer*[1], W. S. Ramsey[2], M. Salisbury[3], D. F. Waldron[1], J. W. Walker[1], and T. D. Willingham[1], [1]*Texas AgriLife Research, San Angelo, TX*, [2]*Texas A&M University, College Station*, [3]*Angelo State University, San Angelo, TX*.

The objectives of the study were to produce a smooth-bodied sheep that is well adapted to western ranges and capable of growing more and finer wool than the Rambouillet (R) without compromising lamb production. Commercial R ewes (n = 187, 2-5 yr of age, BW = 61.5 ± 6.9 kg, average fiber diameter [AFD] = 21.3 ± 2.1 μm) were bred to selected Australian Merino (M) rams (n = 5) via laparoscopic artificial insemination (LAI) in June 2007. Purebred lambs were produced by exposing similar R ewes (n = 115) to highly productive, performance-tested R rams (n = 4) for 3 wk prior to and 3 wk after the LAI date. Lambs were born and raised under range conditions. Their paternity was confirmed by DNA analysis of blood. Lambs were weighed at 5 (BW1) and 10 (BW2) mo of age. Three fiber characteristics (AFD, average staple length [ASL], and average fiber curvature [AFC]) were determined using an OFDA2000 on mid-side samples shorn at 7 mo of age. Data were analyzed using PROC MIXED of SAS. The model included fixed effects of genotype and sex and a random effect of sire within genotype. The low number of lambs weaned was attributed to conception rate (LAI, 75%; naturally bred, 84%), subsequent fetal losses, and predation. Least squares means are presented in Table 1. Female lambs had lower BW than males but produced longer wool. BW at 5 mo of age and ASL at 7 mo of age were not different between the 2 genotypes. R lambs were heavier than M X R lambs at 10 mo of age. The crossbred lambs produced finer wool than R lambs. Thus, preliminary data indicate that at least one of the 5 objectives appears to be attainable with this approach.

Table 1. Fiber characteristics and BW of lambs

	Genotype			Sex		
Dependant variable	M X R (n = 47)	R (n = 44)	P	Female (n = 45)	Male (n = 46)	P
BW1, kg	27.8	29.3	0.357	27.0	30.0	0.011
BW2, kg	44.0	48.4	0.049	41.7	50.7	0.001
AFD, μm	18.1	19.5	0.005	18.8	18.8	0.896
ASL, mm	51.6	49.3	0.596	54.8	46.2	0.001
AFC, deg/mm	73.4	80.8	0.042	75.6	78.6	0.124

Key Words: Merino, Rambouillet, wool

T348 Two seasonal lambing in spring and fall increases reproductive efficiency of range sheep flock. T. Wuliji*[1], H. Glimp[1], and T. Filbin[2], [1]*University of Nevada, Reno*, [2]*Rafter 7 Ranch, Yerington, NV*.

Although ewes can complete a lambing and lactation cycle within 8 mo, they are normally bred only once a year in the fall or spring. While feed, forages, labor, facilities and other resources are available, seasonality constitutes a major waste in productive opportunity. Therefore, program-

ming a two-seasonal lambing regime in spring and fall will increase sheep production efficiency and farm profits. We have initiated a spring and fall two-seasonal lambing program since 2006 on Rafter 7 ranch (Yerington, Nevada). Two-seasonal lambing system was experimented for three consecutive years in 2006, 2007 and 2008. Spring lambing range ewes (n = 850, 1100, 1319) were bred during late November to December in 15, 21 and 23 single sire mating groups (1 ram: 50 ewes) for 2 estrus cycles (35 d). All fall bred ewes were ultrasound scanned for pregnancy diagnosis during the second trimester of gestation. The non pregnant, non lamb rearing ewes and a selected number of yearling ewes were separated from spring lambing flocks and scheduled for spring breeding flock (n = 350, 476, 500) and mated in 6, 8, 10 single sire groups for one estrus cycle in late May to early June of 2006, 2007 and 2008 respectively. Data were analyzed with chi-square statistics. For spring lambing, 714, 703 and 1081 ewes lambed with lambing percentage of 131%, 130% and 129%, and weaned 1.2 ± 0.2, 1.0 ± 0.1 and 1.1 ± 0.2 lambs/per ewe in 2006, 2007 and 2008 respectively. While fall lambing, 315 (1.35 ± 0.3 lamb/ewe lambed), 185 (1.29 ± 0.2 lamb/ewe lambed) and 218 (1.33 ± 0.3 lamb/ewe lambed) lambs were weaned correspondingly in 2006, 2007 and 2008 fall born crops. These experiments indicate that two-seasonal lambing reduce reproductive waste in the sheep flock, and advance the reproduction by a season for the first breeding yearling ewes, and increase the total number of lambs weaned per ewe/year ($P < 0.05$). The two seasonal lambing systems should reduce the product turn over time, spread the labor intensity on farm, and provide an extra opportunity to market lambs at a premium price, and increase farm profit margin over one seasonal lambing practice.

Key Words: sheep, lambing, breeding

T349 A daily exposure for 4 hours to the male effect is sufficient to induce ovulatory activity in goats. J. A. Delgadillo*[1], M. Bedos[1], J. A. Flores[1], G. Fitz-Rodriguez[1], and B. Malpaux[2], [1]*Centro de Investigacion en Reproduccion Caprina, Universidad Autonoma Agraria Antonio Narro*, *Torreon, Coahuila, Mexico*, [2]*Physiologie de la Reproduction et des Comportements, UMR 6175 INRA-CNRS-Universite de Tours-Haras Nationaux*, *Nouzilly, France*.

The objective of the current study was to determine whether 4, 8, 12 or 16 h of presence of males rendered sexually active by exposure to long d stimulate the ovulatory activity in anovulatory goats. Males were exposed to 2.5 mo of long d (16 h of light by d) from November 1 to stimulate their sexual activity during the non-breeding season. One group of does remained isolated from males. Four other groups were exposed for 4, 8, 12 or 16 h per d to the long-day treated males during 15 d. Ovulation was inferred from plasma progesterone levels and transrectal ultrasonography. The proportion of does having ovulations, the proportion of does displaying normal or short ovulatory cycles were all compared using the χ^2 test. Ovulation rates were compared using the Mann-Whitney U test. The proportion of females that ovulated at least once during the whole experiment were greater in all groups exposed to sexually active bucks compared to the control group ($P < 0.001$). However, the proportion of females that ovulated did not differ ($P > 0.05$) between does exposed daily for 4 (100%), 8 (100%), 12 (100%) or 16 h (94%) to the males. Moreover, the proportion of females that displayed short or normal ovulatory cycles and the ovulation rates at the second male-induced ovulation were similar between groups exposed to long-day treated bucks. These results indicate that a reduction of the daily contact between sexes does not modify the ovulatory response of female goats exposed to the male effect.

Key Words: goats, teasing, duration of contact

T350 Estrus and mating response after estrus synchronization protocols in meat goats. J. L. Eierman*[1], D. J. O′Brien[1], E. K. Crook[1], R. A. Barczewski[1], and N. C. Whitley[2], [1]*Delaware State University*, *Dover*, [2]*North Carolina A&T State University*, *Greensboro*.

The objective of the present study was to examine the effectiveness of using melengestrol acetate (MGA) or a controlled internal drug releasing device (CIDR) in combination with the buck effect and PMSG, when compared to no hormonal priming before buck introduction in synchronizing estrus during the breeding season in goats. Fifty–eight Boer and Boer–crossbred meat–type does and 4 bucks located at Delaware State University were used in the experiment. To facilitate the use of the buck effect, males were removed from sight, sound and smell of females for 3 wk prior to the beginning of the study. All goats were housed in dry lot areas and separated into 3 groups. The MGA group (n = 20) were fed an 8% CP diet with MGA to provide 0.25 mg MGA/d each for 9 d (first d of feeding = d–9). Both the control (CON; n = 20) and CIDR (n = 18) groups received a similar ration without MGA daily. On d–9, CIDRs were inserted vaginally into females in the CIDR group. At progesterone removal (d 0), both MGA and CIDR groups received 300 IU of PMSG i.m., and all females were grouped for mating with 4 mature bucks wearing marking harnesses for 13 d. Females were checked twice daily for mating and number of does marked was recorded to determine day to first mating and percentage mated. Data were analyzed using the FREQ and GLM procedures of SAS with means separated using LSMEANS. There was no effect of treatment on percentage of females mated, averaging 60.0 ± 0.1%, 66.7 ± 0.1%, and 70.0 ± 0.1% for CON, CIDR and MGA-treated females, respectively. In addition, of the females mated, the MGA-treated does (3.8 ± 0.3 d) came into heat later ($P < 0.001$) than both the CON (1.41 ± 0.3 d) and CIDR–treated (2.3 ± 0.3 d) does. Females mated in the CON group tended ($P < 0.06$) to come into heat earlier than the CIDR–treated group. In conclusion, under the conditions of this study, neither hormonal estrous synchronization protocol tested was as effective as the buck effect alone in synchronizing estrus.

Key Words: buck effect, estrus synchronization, goat

T351 Complement system activity on goats, hemolytic assay possibilities. I. Moreno-Indias*[1], A. Argüello[1], N. Castro[1], J. Capote[2], A. Morales-delaNuez[1], and B. Sim[3], [1]*Las Palmas de Gran Canaria University*, *Arucas, Las Palmas, Spain*, [2]*Instituto Canario de Investigaciones Agrarias*, *La Laguna, Tenerife, Spain*, [3]*Oxford University*, *Oxford, United Kingdom*.

Usually complement system hemolytic assays in human and veterinary species are performed with sheep red blood cells (SRBC), but goats and sheep are closed phylogenetically. The objective of the present study was to evaluate the best combination between the red blood cells species and presence or absence of antibodies for complement system hemolytic assay in dairy goats. Both goat plasma (GP) and goat serum (GS) samples (n = 10) from Majorera breed were used to develop the hemolytic assays. SRBC, SRBC plus rabbit antibody (RA), SRBC plus human antibody (HA), SRBC plus RA plus goat antibody, human red blood cells (HRBC) and HRBC plus RA were used as substrate of goat complement system on the hemolytic assays. An ANOVA procedure was performed. In a scale from 0 to 100%, the best results of hemolysis were observed when GP and HRBC plus RA were used (82.4 ± 0.8%). Medium hemolytic activity was displayed when GP and HRBC or GS and HRBC plus RA were used (38.85 ± 0.6 and 37.26 ± 0.5%, respectively). Low hemolytic activity was observed when GS and HRBC were used (7.53 ± 0.2%), and no activity was observed in the other

combinations. In conclusion, SRBC is not a useful tool for hemolytic assay in dairy goats, being HRBC an adequate option.

Key Words: complement system, goat

T352 The use of internet-based tools in establishing scrapie resistant sheep flocks in Canada. D. G. Bishop and A. Farid*, *Nova Scotia Agricultural College, Truro, Nova Scotia, Canada*.

Genotypes of Canadian purebred sheep at the prion protein gene from various laboratories are assembled into a national database and are linked with pedigree information regularly obtained from the Canadian Livestock Record Corporation. Breeders have had password protected access to their flock data through a web-interface (genenovas.ca) since early 2005. The system is designed 1) to provide breeders with a fast and secure way of obtaining the genotypes of their sheep, 2) to be the depository of the official genotype of animals, 3) to establish a convenient system that breeders can use to manage their genotype results, 4) to detect genotype inconsistencies and measure the accuracy of the data when the genotypes of parents and offspring are available, 5) to allow flock owners to display the genotype of any number of their sheep to in a 'Marketplace', which is accessible by all prospective buyers free of charge, thus facilitating the purchase of sheep with a desired genotype, and 6) to determine the genotype of progeny of tested parents, when possible, thus avoiding unnecessary testing and reducing the cost of establishing resistant flocks. To date (1 Feb 2009), genotypes of approximately 18,000 sheep of 41 breeds from 490 farms have been added to the database. The genotypes of an additional 1,291 sheep (7.1% of animals tested) were predicted and added to the database. As the frequency of homozygous resistant animals increases by selection, the number of such animals is expected to increase. The proportion of breeders who never visited their page on the website was 46.0%, while others logged into their website between one and 144 times. The results show that the use of the Internet by the Canadian sheep breeders is reasonably high.

Key Words: prion protein gene, scrapie, internet-based tools

T353 Comparison of raw versus post-differentially corrected GPS collar fixes in free-ranging goats. T. A. Gipson*[1], S. P. Hart[1], and R. Heinemann[2], [1]*American Institute for Goat Research, Langston University, Langston, OK*, [2]*Kiamichi Forestry Research Station, Oklahoma State University, Idabel*.

Even though selective availability of GPS signals was discontinued on May 1, 2000, there remains some debate as to whether GPS fixes need to be post-differentially corrected. The objective of this study was to determine the effect of post-differential correction on fixes of GPS collars worn by free-ranging goats. Twenty-one wether goats (46 ± 4.7 kg) were fitted with GPS collars that recorded a fix every 5 min and released into a novel environment (35°53'40"N, 94°45'21"W) of 4.6 ha. Collars were downloaded after 1 wk and 41,744 raw (R) GPS fixes were post-differentially corrected (C). For fix status, C decreased 3-D fixes and increased 2-D fixes and No-fix compared with R fixes (R: 95.8, 4.0, and 0.2%; C: 69.1, 28.4, and 2.5% for 3-D, 2-D, and No-fix status, respectively; χ^2 = 10,270, P < 0.01). A higher percentage of C fixes were located within the boundary of the study area compared with R (89.7 vs. 86.3%, P < 0.01). The correcting distance between R and C fixes was greater in daylight hours than at night (23.4 vs. 16.9 m; P < 0.01). With distance calculations restricted to fixes within the boundary, the minimum (straight-line) distance traveled between consecutive fixes was greater for R than for C (29.5 vs. 27.6 m, P < 0.01). Therefore, the calculation of daily total minimum distance traveled per goat was greater for R than for C (4.16 vs. 3.82 km, P < 0.01). Inter-goat distance was greater for R than for C (19.9 vs. 15.4 m, P < 0.01). Analysis using R vs. C fixes may affect conclusions because more C than R fixes were within study area boundary, corrections were greater during daylight hours when animals were most active, and intra/inter-animal distance calculations were greater for R than for C. These differences may be especially important for researchers studying spatial distribution of grazing animals or calculating distance traveled such as in energy expenditure experiments.

Key Words: goats, GPS, post-differential correction

T354 Garlic as an anthelmintic for goats. Z. Wang*, A. L. Goetsch, S. P. Hart, and T. Sahlu, *American Institute for Goat Research, Langston University, Langston, OK*.

A previous experiment (J. Anim. Sci. 86 (E-Suppl. 2):292) showed that feeding garlic to Spanish goat wethers infected with *Haemonchus contortus* reduced fecal egg count (FEC). The present experiment was conducted to determine the anthelmintic effect of garlic in mature does. Twelve Spanish does (7 yr of age; 39 ± 2.2 kg BW) naturally infected with *H. contortus* were allocated to two treatments (six per treatment) and housed individually. Does were fed diets (ME = 8.7 MJ/kg and CP = 10% DM) of coarsely ground grass hay (73%) and concentrate (primarily corn and soybean meal) at a level of intake for BW maintenance without or with 2% garlic powder hand-mixed with concentrate for 28 d. Fecal samples were collected on d 0, 2, 4, 8, 11, 15, 18, 21, and 24 and blood was collected on d 0, 14, and 28; d-0 values were used as covariates in the mixed model. Statistical analysis of FEC entailed log transformation. Initial FEC averaged 6,167/g (SEM = 2,319; range = 600 to 13,050) for Control and 13,800/g (SEM = 5,301; range = 2,050 to 38,650) for Garlic. Average daily gain during the experiment was greater (P < 0.02) for Garlic vs. Control (74 vs. -42 g). Average FEC was decreased (P < 0.02) by garlic supplementation (6,395 vs. 1,290/g), although there was a trend for an interaction between treatment and day (P < 0.06). Effects of garlic on FEC on d 2 and 4 were nonsignificant (P > 0.43), whereas differences occurred on d 8 (5,819 vs. 912/g; P < 0.03), 11 (7,368 vs. 605/g; P < 0.01), 15 (6,114 vs. 658/g; P < 0.01), 18 (5,783 vs. 745/g; P < 0.02), 21 (8,571 vs. 1,777/g; P < 0.07), and 24 (9,362 vs. 1,720/g; P < 0.05). Serum concentrations of IgA, IgM, and IgG and the number of blood eosinophils were not influenced by feeding garlic (P > 0.10). However, the number of white blood cells tended (P < 0.08) to be greater for Garlic than for Control (11,153 vs. 8,783/μL). In conclusion, garlic appears to possess anthelmintic activity against *H. contortus* via cell mediated immunity, which requires a feeding period of at least 4 d for expression.

Key Words: goat, garlic, parasite

T355 Comparison of copper sulfate and copper oxide wire particles as an anthelmintic for goats. S. P. Hart* and Z. Wang, *E Kika de la Garza American Institute for Goat Research, Langston, OK*.

Gastrointestinal nematodes are the leading cause of morbidity and mortality in small ruminants, especially those raised in warm humid environments. The overuse of anthelmintics has resulted in anthelmintic resistance of gastrointestinal nematodes to most of the available anthelmintics. Copper sulfate has been used as an anthelmintic early

in the previous century and more recently has been shown efficacious in sheep. Copper oxide wire capsules have been recently shown to be effective as an anthelmintic in both sheep and goats. The objective of this study was to compare copper sulfate at two dose levels as an anthelmintic to copper oxide wire particles. This study was conducted with Angora does that were two years of age or older. Fecal samples were taken for three consecutive days before treatments were administered and goats stratified by fecal egg count (FEC) and randomly assigned to treatments, 10 goats per treatment. Goats were fasted overnight prior to treatment administration. Four treatments were administered: N, negative control administered a water drench; C, 4 g of copper oxide wire particles administered in a gelatin capsule; L, low dose of copper sulfate (16.5 mg/kg bw); H, high dose of copper sulfate (33 mg/kg bw). Copper sulfate treatments were administered as a 1.5% drench. Fecal samples were taken at 7,8 and 9 d post- treatment and fecal egg count reduction (FECR) calculated. Fecal egg counts were conducted by the McMaster procedure. Data were analyzed by the SAS NPAR1WAY procedure for non-parametric tests. Mean FEC for the group before treatment was 5,350 eggs/g (range 200-29,900). FEC was not reduced by N (FECR = 44%; $P > 0.10$). FEC was reduced ($P < 0.05$) by L (FECR = 83%), C (FECR = 77%) and H (FECR = 67%). Copper sulfate drench at both dose levels was equally effective to copper oxide wire capsules in reducing FEC of Angora goats.

Key Words: copper, anthelmintic, gastrointestinal nematodes

T356 Performances of kids and calves grazing together and separately. S. Gebrelul*, R. Marshall, Y. Ghebreiyessus, and V. Bachireddy, *Southern University Ag. Center*, *Baton Rouge, LA*.

A mixed-grazing project was designed to determine the performance of calves and kids grazing together and separately. In a 3x2 factorial, 100 Spanish goats and 28 Brangus cows were randomly assigned to continuous or rotational grazing systems and three grazing schemes: goat-alone (4 ha), cattle-alone (11 ha) or mixed (16 ha). Kid's preweaning records of 1200 and 384 of calves were available. Body weights, condition scores (BCS), FAMACHA scores (FS), fecal egg counts (FEC), packed cell volume (PCV), fresh (FFY) and dry (DFY) forage yields, plant height (PHT), crude protein (CP), acid (ADF) and neutral (NDF) detergent fibers, and dry matter (DM) were obtained every 28 d for 3 yr. Data were analyzed using mixed procedure of SAS and stepwise regression. Chi-square analysis was used for BCS and FS. All fixed effects were significant ($P < 0.05$) sources of variation for kid measurements. Kids in mixed grazing weighed more (16.9 ± 0.3 vs 13.2 ± 0.3 kg, $P < 0.01$) than kids grazing alone. PCV values were negatively correlated with FS ($P < 0.05$) but positively correlated with BCS. BCS had a high negative correlation with FAMACHA scores (-0.54, $P < 0.01$) and FEC (-0.23, $P < 0.01$). Kids that grazed alone on rotational pastures had higher PCV percentages (30.1%) than those grazing on continuous pastures (27%). Kids grazing alone averaged 2.03 ± 0.03 in BCS while those in mixed averaged 2.36 ± 0.04 ($P < 0.01$). Calves grazing alone were heavier (171.8 ± 2.6 vs. 156.0 ± 2.6 kg) than those grazing mixed with kids ($P < 0.10$). Calves grazing alone under continuous grazing were similar in weight (170.2 ± 3.5 vs 173.4 ± 3.8 kg) to those in rotation, but both were heavier ($P < 0.05$) than calves in mixed grazing in continuous (162.5 ± 3.8 kg) or in rotation (149.4 ± 3.4 kg). For calf weight, the order of variables that entered the regression model at $P < 0.05$ were ADF, PHT, NDF, FDY, and CP; and PHT, DFY, FFY and NDF for kid weights. Results indicated that calves required more time to adjust and perform when mixed with kids, but kids could graze with calves to efficiently utilize available forage resources. More information is needed to evaluate mixed grazing systems under Louisiana conditions.

Key Words: mixed-grazing, goats, forages

T357 Small ruminant producer gastrointestinal nematode (GIN) management survey. N. C. Whitley*[1], R. M. Kaplan[2], J. M. Burke[3], T. H. Terrill[4], J. E. Miller[5], W. R. Getz[4], S. Mobini[4], E. Valencia[6], and M. J. Williams[7], [1]*North Carolina A&T State University*, *Greensboro*, [2]*University of Georgia*, *Athens*, [3]*USDA, ARS*, *Booneville, AR*, [4]*Fort Valley State University*, *Fort Valley, GA*, [5]*Louisiana State University*, *Baton Rouge*, [6]*University of Puerto Rico*, *Mayaguez, PR*, [7]*NRCS*, *Gainesville, FL*.

The objective was to determine, by survey, sheep and goat producer GIN management methods. Respondents from GA (n = 62), FL (n = 30), PR (n = 7), LA (n = 14) and other southern states (n = 11) had a total of 4434 goats (67.4 ± 3.9% of responders) and 2821 sheep (35.4 ± 3.9% of responders). New (non-sire) animals were brought to the farm by 71.4 ± 3.5% of responders. A moderate to severe parasite problem was indicated by 77.9 ± 3.5% of responders with 59.1 ± 4.3% indicating increased or no change in problem severity over the past 3 yr. For 87.2 ± 4.3, 50.4 ± 2.9, 60.1 ± 3.7, 97.7 ± 3.9, 23.5 ± 1.9, 15.0 ± 3.1 and 18.0 ± 2.4% of respondents, anthelmintics used were benzimidazoles, imidazothiaoles, moxidectin, ivermectin, Eprinex or Dectomax, Rumatel and/or herbal/natural products, respectively. The following parasite management methods were reported by respondents: estimating individual animal BW for anthelmintic treatment (54.2 ± 4.6%); treating new animals (77.4 ± 5.2%) with the same routine as for existing animals (65.0 ± 4.9%); rotating anthelmintics (42.9 ± 3.5%); rotating pastures (68.5 ± 4.1%); treating at pre-set times (24.1 ± 3.7%), as needed (35.3 ± 4.2%) or both (38.3 ± 4.2%); moving weaned offspring to a new pasture (55.8 ± 4.7%) or back to the same pasture (53.3 ± 4.6); testing for fecal GIN egg at least once/yr (36.4 ± 2.6%) and treating every 4, 8 or 12 wk (16.7 ± 4.1, 17.9 ± 4.2 and 19.0 ± 4.3%, respectively). Respondents reported treating animals 4.8 ± 0.4 times/yr. Factors influencing anthelmintic usage for greater than 75% of respondents included cost, ease of use, technical meetings, journal articles, producer and veterinarian recommendations, and good effects. Parasite management education can be developed to address issues determined by this and similar surveys.

Key Words: goat, sheep, parasites

T358 Leg bands and rumen boluses for the long-term electronic identification of goats. S. Carné, G. Caja, M. A. Rojas-Olivares, and A. A. K. Salama*, *G2R, Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

A total of 220 Murciano-Granadina dairy goats were used to assess the performance of electronic identification by half-duplex ISO transponders: 1) leg bands (LB) placed in the shank of the right hind leg (metatarsus), and consisting of plastic bands (181×39 mm, 21 g; n = 220) closed with 2 types of button electronic ear tags (LB1, 26.5 mm o.d. open female, 3.9 g, n = 90; LB2, 25 mm o.d. closed female, 5.5 g, n = 130); 2) rumen boluses (RB, 68×21 mm, 75 g, n = 220) containing 32×3.8 mm transponders. Shank perimeter of a sample of 6 mo of age (n = 47) and adult goats (n =103) was measured to decide on the inner perimeter of fastened LB. Total time for tagging, reading and recording was measured using an ISO handheld reader. Readability [(read/readable) × 100] was monitored monthly during 1 yr using the

handheld reader in the milking parlor. Data from dead or culled goats were excluded (n = 23). Perimeter and readability data were analyzed using the GLM and CATMOD procedures of SAS, respectively. Shank perimeters of young (70 ± 1 mm) and adult goats (88 ± 1 mm) were lower (P < 0.001) than the inner perimeter of the fastened LB (110 ± 1 mm). Young 6-mo goats were considered inadequate for LB application. Time for LB tagging and data recording was 53 ± 3 s, similar to the time reported for RB (49 s). After 1 yr, 2.5% RB (n = 5) were lost; 3.6% LB (n = 7) were open and unreadable due to the breakage of the electronic ear tags, and 1.5% (n = 3) had to be removed because of limping (1 leg was inflamed and the LB constricted the metatarsus, and 2 LB were too loose and got blocked on the pastern). Readability of LB transponders, excluding the LB removed, was 93.6 and 98.3% (P = 0.11) for LB1 and LB2, respectively. In total, no readability difference between LB and RB was detected (98.5 vs. 97.5%, respectively; P = 0.48). In conclusion, leg bands were not adequate for the identification of replacement goats although, adequately sized and closed, they may be an efficient method for adult goats. In our conditions, electronic ear tags placed on leg bands and rumen boluses were unable to achieve the ICAR reference value for official identification (>98%).

Key Words: electronic identification, transponder, goat

T359 Natural plant anthelmintic fails to reduce internal parasites in meat goat kids. D. J. O'Brien[1], K. K. Mathews*[1], J. E. Miller[2], N. C. Whitley[3], E. K. Crook[1], and J. L. Eierman[1], [1]*Delaware State University, Dover*, [2]*Louisiana State University, Baton Rouge*, [3]*North Carolina A&T State University, Greensboro*.

Worldwide reports of drug resistance in small ruminant gastrointestinal nematodes (GIN) have led producers to seek alternative parasite control strategies such as the use of natural plants. Anecdotal evidence exists supporting feeding pumpkin as a possible GIN control method, so 22 mixed–sex, crossbred goats averaging 185.1 ± 1.9 d of age were used to evaluate the effect of pumpkin seeds on GIN indicators. Goats were placed in individual pens on solid concrete floors (d 0) and received pre-weighed rations of a commercially pelleted 15% CP meat goat feed daily for 21 d. Animals were supplemented with ground pumpkin seeds (PUM; n = 11) mixed into feed at a rate of 170 g/34.1 kg BW or were not supplemented (CON; n = 11). Goat BW was measured on d 0, 7, 14 and 21. Fecal samples were collected rectally from individual animals to determine fecal egg counts (FEC) using the Modified McMasters technique and blood samples were collected by venipuncture to determine packed cell volume (PCV) on d 0, 7, 14 and 21. Fecal samples were collected on d 0 and 21 and pooled by treatment for larval identification. Body weight was similar between the two groups at all time points measured and averaged 24.1 ± 1.0 kg for all animals. Goat PCV was not influenced by treatment and averaged 37.8 ± 1.2, 30.8 ± 1.8%, 34.1 ± 1.7 and 33.6 ± 1.7% for d 0, 7, 14 and 21, respectively. Goat FEC was also not influenced by treatment, averaging 5965 ± 796, 6411 ± 1823, 3425 ± 413, and 3655 ± 631 eggs/g on d 0, 7, 14, and 21, respectively. On d 0, CON group fecal samples consisted of 6% Haemonchus contortus (HC) and 94% Trichostrongylus (Tric) while the PUM group had 2% HC and 98% Tric. By d 21, the CON group had 46% HC and 54% Tric while the PUM group had 28% HC and 72% Tric. In this study, feeding pumpkin seeds did not impact FEC or PCV in meat goat kids. More studies are needed to evaluate the use of natural plant dewormers in small ruminants.

Key Words: goat, satural anthelmintic, parasites

SYMPOSIA AND ORAL SESSIONS

Animal Health: Emerging Foreign Animal and Zoonotic Diseases

272 Potential threat of foreign animal diseases to US agriculture. T. Beckham*, *Texas Veterinary Medical Diagnostic Laboratory, Texas A&M University System, College Station*.

Homeland Security Presidential Directive 9 designated agriculture as a US critical infrastructure. Protection of the agricultural industries is critical to protecting the nation's economy. Agriculture in the United States contributes approximately one-trillion/year towards the gross domestic product. Furthermore, fifteen percent of Americans are employed in food production and US agricultural industries export approximately 50 billion dollars worth of products annually. The US agricultural and livestock industries today face very real threats from foreign, emerging and/or zoonotic diseases. In particular, the past decade and more specifically the past year alone has demonstrated that the numbers of new and emerging diseases affecting our industries are on the rise. For example, new serotypes of Bluetongue virus continue to move through the European communities and Ebola virus was recently isolated from an atypical host (swine) in the Phillipines. While many of these examples do not originate in the United States, the disease threats that face our industries are still large. These threats stem in part from the globalization of commerce, the consolidation of our industries into larger commercial units and the interactions between humans, livestock and wildlife. Protection of our livestock industry will require state-of-the art diagnostic tools that enable us to conduct broad-level surveillance. This surveillance effort will be largely conducted in our state-veterinary diagnostic laboratories and will be a coordinated effort between veterinarians (our first line responders), state animal health authorities and the federal government.

Key Words: foreign animal disease, agricultural threats, national security

273 Preventing and detecting foreign animal diseases. T. McKenna*, *Wisconsin Veterinary Diagnostic Laboratory, Madison*.

The threat of a foreign animal disease introduction into the United States is very real. What can be done to prevent an introduction, and what is the role of detection in controlling an outbreak? We all have a part to play in the prevention of foreign animal disease introduction. Biosecurity on the farm and at the borders is paramount. Being able to identify an introduction early is crucial to limiting the impact of a foreign animal disease. Current diagnostic tools and surveillance approaches will be described.

Key Words: foreign animal disease, diagnosis, prevention

274 Responding to a foreign animal disease incident. M. Cochran*, *Texas Animal Health Commission, Austin*.

The devastating economic and animal health impacts of foreign animal diseases mandate an efficient response by animal health authorities, requiring the simultaneous coordination of local and national resources. The Incident Command System, well-tested in emergency responses of all types, allows for quick establishment of a chain of command and expansion as necessary for response to the foreign animal disease. Foreign animal disease investigations often start when a veterinarian or producer discovers a suspicious lesion or other symptoms in an animal or a herd. After this incident is reported to state or federal animal health authorities, a foreign animal disease diagnostician, a veterinarian trained in disease identification and specimen collection techniques, is dispatched to the premises in question. Careful laboratory analysis is required before confirmation is reported to the animal health authorities. Already on alert, animal health authorities quickly establish an incident command post in proximity to the first detected case. The incident commander and his or her team then work to determine the scope of the outbreak and establish quarantines and issue stop-movement orders as the situation requires. The approximate scope of the foreign animal disease outbreak will translate into establishment of an infected zone and a buffer surveillance zone around the infected zone. Coordination and control, coupled with cooperation at the local level, help minimize the spread of the disease. The end goal of a foreign animal disease response is disease eradication. With this goal in mind, laboratory diagnostics, strict biosecurity controls in both specimen collection and animal movement, analysis of the disease agent and environmental conditions, and selective culling of animals are required to eradicate a foreign animal disease with the least negative impact on animal health and production.

Key Words: animal health, incident command center, quarantine zones

Breeding and Genetics: Genomic Evaluation

275 Opportunities for genomic delection with redesign of breeding programs. J. C. M. Dekkers*[1], H. H. Zhao[2], D. Habier[3], and R. L. Fernando[1], [1]*Iowa State University, Ames*, [2]*Pioneer Hi-Bred Int., Johnston, IA*, [3]*Christian-Albrechts University of Kiel, Kiel, Germany*.

Genomic Selection (GS) using EBV from dense marker data is promising for genetic improvement but may require a complete redesign of breeding programs. Our objective was to develop and compare GS programs that capitalize on opportunities to reduce generation intervals and program sizes using layer chickens as an example. Assuming GS allows a reduction in generation intervals from 1 y to 6 mo, our goal was to develop a GS program that nearly doubles response but with a similar rate of inbreeding per y. Comparison was to a standard program with selection of the top 60 and 360 out of 1000 males and 3000 females based on BLUP EBV for a sex-limited trait with heritability 0.3. Using analytical predictions by selection index, a GS program with selection of the top 50 males and females out of 250 candidates per sex based on GS EBV was predicted to achieve this goal. These standard and GS programs were then evaluated by stochastic simula-

tion. A GS training population of 1000 individuals with phenotype for a trait with 200 segregating QTL and genotypes on 6000 SNPs on a 7.5 Morgan genome was used. Linkage disequilibrium was based on historical population sizes of 500 and 100 for 900 and 100 generations. GS EBV were predicted by Bayes-B, without or with retraining each generation after adding 250 females with phenotype from the previous generation. Assuming a generation interval of 6 mo versus 1 y, results showed that GS indeed achieved similar rates of inbreeding per year as the standard program. Responses for GS without and with retraining were 61 and 68% greater than for the standard program after 1 y of selection and 31 and 70% greater after 4 y. Variance of response was, however, greater for GS than for standard selection. These results demonstrate that with substantial redesign of breeding programs, GS can maintain or increase response to selection while controlling rates of inbreeding and achieve that with substantially reduced program sizes in terms of the number of individuals raised and phenotyped. *Financial support from Hy-Line Int., PIC-Genus and Monsanto Co.*

Key Words: genomic selection, breeding strategies

276 Computing procedures for genetic evaluation including phenotypic, full pedigree and genomic information. I. Aguilar*[1,2], I. Misztal[1], and A. Legarra[3], [1]*University of Georgia, Athens*, [2]*Instituto Nacional de Investigación Agropecuaria, Las Brujas, Uruguay*, [3]*INRA, SAGA, Castanet-Tolosan, France*.

The purpose of this study was to evaluate computing procedures to solve mixed models equations with additive relationship matrix H modified to account for genomic information. It is assumed that H=A+Δ, where A is a numerator relationship matrix based on pedigrees and Δ includes deviations due to the genomic information. To avoid computing H^{-1}, mixed model equations due to the additive effect, say $[Z'X\ Z'Z + kH^{-1}]$ can be expressed in an alternate Henderson form as [H Z'X H Z'Z + Ik]. The modified equations have a nonsymmetric left-hand side where H may be poorly conditioned numerically. Expressions involving A can be computed efficiently with conjugate gradient algorithms. Data included 4539 records of final score and 2697 pedigrees. Comparisons involved a repeatability animal model with simulated changes due to genomic relationships in a random sample of fifteen percent of the animals. Changes were simulated as Δ={UN(-b,b)} for different values of b (0, 0.01, 0.05). Solutions were Preconditioned Conjugate Gradient (PCG), which only works with symmetric matrices, and by Conjugate Gradient Squared (CGSQ) and Bi-Conjugate Gradient Stabilized (BiCGSTAB), which work with nonsymmetric matrices. With the original equations, PCG converged in 46 rounds, CGSQ in 33, and BiCGSTAB in 36 rounds. With the alternate equations and b=0, CGSQ converged in 36 rounds while BiCGSTAB converged in 29 rounds. With nonzero b, the change in convergence did not exceed two rounds despite some H being non positive definite. The cost of one round in CGSQ and BiCGSTAB was similar and approximately twice that cost in PCG. CGSQ and particularly BiCGSTAB are suitable for the alternative equations even if H is poorly conditioned. If computation of terms with Δ can be done efficiently, it may be possible to modify the existing evaluation to incorporate the genomic information at approximately double the cost of the original evaluation.

Key Words: BLUP, genomic selection, genetic evaluation

277 Genetic evaluation including phenotypic, full pedigree and genomic information. I. Misztal*[1], A. Legarra[2], and I. Aguilar[1], [1]*University of Georgia, Athens*, [2]*INRA SAGA, 32326 Castanet-Tolosan, France*.

Currently the genomic evaluations use multiple step procedures, which are complicated and prone to errors. For many traits, predictions involving estimation of SNP effects or BLUP using a genomic relationship matrix are equivalent. A single step procedure may be applicable by modifying the numerator relationship matrix A in a regular evaluation to H= A+Δ, where Δ includes deviations from original relationships. However, the traditional mixed model equations require H-1, which is difficult to obtain for large pedigrees. The computations with H are feasible when the mixed model equations are expressed in an alternate form given by Henderson that also applies for singular H, and when those equations are solved by the conjugate gradient techniques. Then the only computations involving H are in the form of Aq or Δq, where q is a vector; the product Ac can be calculated efficiently in linear time using Colleau's indirect algorithm. The alternative equations have a nonsymmetric left-hand side. Several alternative H are possible. A naïf possibility is to substitute the relationships of genotyped animals with the genomic relationship matrix. However, this results in incoherencies because the genomic relationship matrix includes information on relationships among ancestors and descendants. Another possibility is to condition the genetic value of ungenotyped animals on the genetic value of genotyped animals via the selection index (e.g., pedigree information), and then use the genomic relationship matrix for the latter. This results in a joint distribution of genotyped and ungenotyped genetic values, with a pedigree-genomic relationship matrix H. In this matrix genomic information is transmitted to the covariances among all ungenotyped individuals. Both possibilities allow for an efficient computing in the form of Δq. The proposed methodology may allow upgrading of an existing evaluation to incorporate the genomic information.

Key Words: genomic selection, genetic evaluation, SNP

278 Transition of genomic evaluation from a research project to a production system. G. R. Wiggans*[1], P. R. VanRaden[1], L. R Bacheller[1], F. A Ross[1], T. S Sonstegard[1], G. te Meerman[2], and C. P. Van Tassell[1], [1]*ARS, USDA, Beltsville, MD*, [2]*University Medical Center Groningen and University of Groningen, Groningen, the Netherlands*.

Genomic data began to be included in official USDA genetic evaluations of dairy cattle in January 2009. Numerous changes to the evaluation system were made to enable efficient management of genomic information, to incorporate it in official evaluations, and to distribute evaluations. Artificial-insemination and breed organizations can use an online query to designate animals to be genotyped, to determine if the animal has already been nominated, and to check for the reason if a genotype was rejected. Four commercial laboratories provide genotypes. A genomic sample scanner generates large files of intensity data, which are used to determine the genotype of each single-nucleotide polymorphism (SNP). A technique to adjust jointly for sample and SNP effects may improve call rate and allow automation of adjustment for differences among scanners and reagent batches. Genotypes for 58,336 SNP are stored in a database table with 1 row per animal genotype. Genotypes rejected from evaluation because of parentage conflicts are stored to allow easy recovery if the conflict is resolved. For evaluation, genotypes for new animals and those with pedigree changes are extracted, combined with verified genotypes from the previous evaluation, and searched for conflicts. Validated genotypes are shared with Canada. Data for all ancestors of genotyped animals are collected, and missing pedigrees and foreign cow evaluations prior to addition of genomic data are obtained. The most recent evaluations from the Interbull Centre

(Uppsala, Sweden) are combined with genomic data into a single evaluation that includes all available information. The US Jersey and Brown Swiss breed associations have sought additional animals to genotype, and the Brown Swiss association has arranged to share genotypes with European countries. The evaluation system is being streamlined to provide genomic evaluations that meet industry needs and can be produced with available resources.

Key Words: genomic evaluation, genotype, single-nucleotide polymorphism

279 Can you believe those genomic evaluations for young bulls? P. M. VanRaden, M. E. Tooker*, and J. B. Cole, *USDA Animal Improvement Programs Laboratory*, *Beltsville, MD*.

Breeders began selecting on official genomic tests for U.S. Holstein and Jersey bulls, cows, and heifers in January 2009. Statistical properties of genomic evaluations, traditional evaluations, and parent averages were validated using data from November 2004 to predict January 2009 daughter merit, weighted by reliability of 2009 data. The validation used 1,611 young and 4,422 proven Holstein bulls in 2004. The top 20 young and top 20 proven bulls were selected based on 2004 traditional or genomic net merit. To determine if selection was effective, means from 2004 and 2009 data were compared after subtracting $155 for the 2005 base change. Mean 2009 daughter merit was $395 for the young bulls selected on parent average, $516 for young bulls selected on genomic evaluation, $381 for proven bulls selected on traditional evaluation, and $463 for proven bulls selected on genomic evaluation. Thus, actual merit was highest for genomic tested young bulls and lowest for traditionally evaluated proven bulls. Evaluations in 2004 were higher than average daughter merit in 2009 for all 4 selected groups, with respective biases of $278, $130, $96, and $30. Regressions of 2009 daughter deviations on 2004 evaluations were expected to be 1.0 across all bulls but were 0.63, 0.74, 0.91, and 1.10 for the 4 groups. Thus, evaluations of young bulls are biased, but the bias is less with genomic tests than with parent average. Adjustments are needed such as further limits on phenotypic deviations or decreases in heritability to decrease bias, particularly for traditional parent average. Selection using traditional or genomic evaluations had only small effects on average relationships among selected animals. The correlation with expected future inbreeding was slightly higher for young bull parent average than for the genomic evaluation (0.21 vs. 0.13). Breeders should greatly increase use of the best young Holstein bulls because their merit already exceeds that of the best proven bulls, and advantages of young bulls over proven bulls will increase as more young animals are tested.

Key Words: genomic selection, net merit

280 Application of kernel partial least squares to estimate genomic breeding values of crossbred beef cattle. G. Vander Voort*[1], M. Kelly[1], T. Caldwell[1], D. Lu[1], Z. Wang[2], J. Mah[2], G. Platstow[2], S. Moore[2], and S. Miller[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph*, *Guelph, Ont., Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta*, *Edmonton, Alberta, Canada*.

A relatively small number of beef cattle are genotyped for a 50k SNP panel, leading to a data structure with a larger number of independent variables (SNP) relative to the number of dependent variables (phenotypes). Kernel partial least squares (KPLS) have been used in analysis of data with this structure to improve the accuracy of prediction. Data for a single trait analysis included adjusted phenotypes for a measure of beef tenderness, shear force in the longissimus dorsi 7 days post mortem (LM7D) of 783 crossbred cattle genotyped for a 50k SNP panel. Data was divided into a training data set of 632 records for estimation of SNP effects and a validation dataset of 151 records to test the predictive accuracy of SNP effects estimated with the training data. The training dataset included two University of Guelph research herds with alternate herds included in the validation data. Kernel matrices elements used in the analysis were a polynomial function of the dot product of 33800 SNP codes (0,1,2) included (low frequency SNP excluded) in the design matrix. KPLS predicted LM7D were correlated with observed LM7D at a high of 0.99 in the training data, but dropped to 0.45 in the validation dataset or 20% of the phenotype variation. This proportion of phenotypic variation translates to explaining most of the genetic variance, given LM7D heritability was estimated to be 0.23. By comparison, genomic selection using BLUP predicted LM7D in the validation data with a correlation of 0.08. Increase in accuracy of prediction of KPLS relative to BLUP estimates supports the utility of applying KPLS to estimate genomic breeding values. Current research focus is on expansion to a multivariate analysis and effect of kernel structure

Key Words: genomic selection, single nucleotide polymorphism, marker assisted selection

281 Visualization of results from genomic predictions. J. B. Cole*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Genomic predictions of estimated breeding values (EBV) include effects of tens-of-thousands of markers distributed over thirty chromosomes for many traits. There are so many numbers that data are difficult to compare, levels of detail are obscured, and data cannot easily be tabulated. Graphics can present data with higher density than text or tables and provide additional insight into the data. Estimates of marker effects are not currently exchanged between countries but plots of results can be shared without disclosing sensitive information. Genomic data can be visualized at several levels, such as the distribution of marker effects across the genome, proportions of additive genetic variance explained by markers on a chromosome, and relationships among markers on the same chromosome. Ratios of actual to expected genetic variance can be plotted as bar graphs, making it easy to identify chromosomes that deviate from expectations; stacked bar graphs allow for simultaneous comparisons of methods of estimating variance ratios. All markers affecting a trait can be plotted on the same ordinate to visualize the distribution of marker effects across the genome, colors or textures can be used to differentiate between chromosomes, and stacked graphs can be constructed to compare interesting groups of traits. Chromosomal EBV can be presented as sparklines, high-resolution graphics embedded in text, to provide an overview of individual animals for comparison to potential mates. Small multiples of chromosomal genetic correlation matrices can be used in conjunction with edge exclusion graphs to identify interesting patterns of association among traits, such as that on chromosome 18 associated with calving traits, conformation, and economic merit. Line plots of marker effects for autosomal recessives can be used to quickly locate chromosomal regions in which causative mutations are probably located, identifying areas of interest for further study. These graphics are easily produced automatically and add to online query systems, providing users with novel information at little cost.

Key Words: genomic prediction, quantitative trait loci, visualization

282 Comparison of Student's *t*, LASSO, and multiple shrinkage methods for the prediction of genomic breeding values. C. Maltecca* and J. P. Cassady, *North Carolina State University*, *Raleigh*.

The objective was to compare 4 different approaches for predicting genomic breeding values (GEBV). First an implementation of the Bayes-A (M1) was used. The second method was an extension of Bayes-A (M2) with scale and degrees of freedom of the mixing inverted Chi-square distribution treated as unknown and estimated from the data. Third (M3) a Laplace prior was employed to obtain LASSO estimates of SNPs effects. Finally a semi-parametric approach was investigated (M4) which allowed shrinkage of each coefficient toward multiple prior means with unknown location. A Dirichlet process prior was put on the mean and scale parameters in order to create few groups with different degree of shrinkage. Hierarchical modeling was employed for all the methods. We simulated 8000 SNPs and 12 QTL. Genotypes for 2000 individuals were generated in age order over 4 generations with the first 500 representing the training generation. All individuals were assigned a phenotypic value by adding a random residual to the true breeding value obtained as the sum of each marker effect. This was done in order to mimic estimated breeding values with different accuracies. Two different average levels of accuracy (0.95, 0.85) of the phenotypes were simulated. Five replicates of each scenario were performed. On average M2, M3, and M4 performed better that M1 in estimating markers effects and predicting GEBV in subsequent generations. The average increase in accuracy (measured as correlation between true and estimated GEBV in the next generation) was of .031(±0.004), .034(±.008) and .036(±.011) (M1 prediction accuracy 0.85 ±.011); .042(±.012), .048(±.009), .051(±.014) (M1 prediction accuracy 0.78 ±.013); .052(±0.015), .051(±0.018), .048(±0.017) (M1 prediction accuracy 0.71 ±.012) for M2, M3 and M4 over M1 for the first, second and third generation after training, respectively for phenotypes accuracy of 0.95. M3 and M4 performed on average better than M2 at higher phenotypic accuracy but failed to converge in some replicates at lower phenotypic accuracy. M2 was the least computationally demanding, and M4 was the most computationally demanding.

Key Words: GEBV, Bayesian methods, multiple shrinkage

283 Equivalent mixed model for joint genetic evaluation considering molecular and phenotypic information. N. Gengler*[1,2] and F. Colinet[1], [1]*Gembloux Agricultural University*, *B-5030 Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *B-1000 Brussels, Belgium*.

Currently efforts are underway to introduce molecular information into genetic evaluation systems. A particular situation is genomic selection however simpler cases exists where major genes are known and used by breeders. A new alternative strategy for the prediction of gene effects and especially their smooth integration into genetic evaluations based on an equivalent method was developed from existing theory. Underlying hypothesis were based on the idea that knowledge of genotypes will not affect overall additive genetic variance but only change expected values of genetic effects for animals with known genotypes. The developed equations were modified to allow that not all animals were genotyped. As the underlying mixed model is open a very large range of models can be used in situations including random regression models, multiple-trait, maternal effects and multiple-across-country-evaluation models. Computations involved successive solving of two mixed models, with the use of an linear extrapolation to speed up convergence of gene effects. The method was tested for several known major genes and QTL, e.g. for the mh gene in the dual-purpose Belgian Blue population in Belgium. Modifications of the method could also be developed to be useful in the context of genomic selection.

Key Words: molecular Information, joint estimation, genomic selection

284 Effect of estimation approach and number of QTLs in accuracies of genomic breeding values for simulated data. G. Gaspa[1], E. L. Nicolazzi[2], R. Steri[1], C. Dimauro[1], and N. P. P. Macciotta*[1], [1]*Dipartimento di Scienze Zootecniche, Università di Sassari*, *Sassari, Italia*, [2]*Istituto di Zootecnica, Università Cattolica del Sacro Cuore*, *Piacenza, Italia*.

Accuracies of estimated genomic breeding values (GEBVs) in simulated data depends both on the relative efficiency of the methodology used but also on the assumptions made for the simulation. A key issue is represented by the number of QTLs related to the genome length and to the density of SNP markers. In this study two scenarios of number of QTLs, 10 or 20, for a genome size of 1 M length and with 1000 SNPs were tested. Initial allelic frequencies for both SNPs and QTLs were sampled from a uniform distribution. QTL effects were sampled from a gamma distribution (shape parameter 0.42). After 50 generations of random mating, two training (2,000 individuals) and three prediction (3,000 individuals) generations were created. Phenotypes of training individuals were generated by adding random noise to the true breeding value (TBV). Heritability was set at 0.5. The estimation step was performed by fitting phenotypes of training individuals with a mixed linear model that included the fixed effect of the mean and the random effect of: i) the genotype of all 1,000 SNP markers (ALL); or ii) the scores of the first 200 principal components extracted from the correlation matrix of the SNP genotypes (PCA). Estimates were then used to predict GEBVs in the prediction generations. Accuracy of prediction was evaluated as correlation between TBVs and GEBVs. Each scenario was replicated 10 times. Average accuracy of prediction for the training generations was 0.90 (standard deviation 0.04) and 0.86 (0.03) for BLUP or PCA calculations, respectively, when 10 QTLs were simulated. Values raise to 0.94 (0.02) and 0.87 (0.01) in the scenario with 20 QTLs. In the prediction generations, the PCA approach resulted in a higher accuracy of prediction in both scenarios: 0.66 (0.09) vs 0.53 (0.07) and 0.72 (0.06) vs 0.61 (0.07) for 10 and 20 QTLs respectively. Moreover, the decreasing trend of accuracy in the prediction generations was less pronounced reduced in the PCA approach. Both the number of QTLs considered and the mathematical approach used had an influence in the accuracy of GEBVs.

Key Words: genomic selection, number of QTLs, principal component analysis

285 Protein quality differences exist among high quality mammalian, avian, and marine protein sources evaluated using avian assays. T. A. Faber*[1], D. C. Hernot[1], C. M. Parsons[1], K. S. Swanson[1], S. Smiley[2], P. J. Bechtel[2,3], and G. C. Fahey, Jr.[1], [1]*University of Illinois, Urbana*, [2]*University of Alaska, Fairbanks, Alaska*, [3]*Agricultural Research Service, Fairbanks, Alaska*.

Meat and fish serve as important protein sources in the human and companion animal diet, but limited information is available on quality differences among high quality protein sources. Beef loin, pork loin, chicken breast, pollock fillet, and salmon fillet were evaluated for protein quality and amino acid bioavailability using the cecectomized rooster and protein efficiency ratio (PER) assays. Pollock contained the highest concentration of protein, total essential amino acids (TEAA), and total non-essential amino acids (TNEAA; 96.9, 38.6, and 50.3%, respectively, dry matter basis). Salmon contained the next highest concentrations (92.8, 36.4, and 44.6%) followed by chicken (90.3, 36.1, and 43.2%). Beef had the lowest protein content (82.7%), but higher TEAA and TNEAA (33.9 and 42.0%) than pork (86.2, 33.6, and 41.3%). Twenty cecectomized roosters were crop-intubated and dosed with one of the five test protein substrates. All excreta were collected, freeze-dried, and analyzed for amino acids. Amino acids in pollock fillet were more digestible (90.4%) ($P<0.05$) compared to other test substrates, whereas chicken breast and salmon fillet had the lowest ($P<0.05$) amino acid digestibility (86.9 and 87.5%, respectively). Protein efficiency ratio was evaluated using one hundred 8-d old male chicks fed one of five diets containing 10% protein provided by each of the five test protein substrates. The assay was conducted as a completely randomized design: five treatments with five chicks per treatment and each treatment with four replicated pens. No differences were noted for beef loin, pork loin, salmon fillet, or pollock fillet; however, chicken breast had a lower ($P<0.05$) PER than other substrates. Among test protein sources, pollock fillet was the highest quality substrate and chicken breast the lowest based on standardized amino acid digestibility and PER data.

Key Words: amino acid bioavailability, protein quality, meat

286 Total tract nutrient digestibility, fecal characteristics, and blood chemistry profiles of dogs as affected by alpha-cyclodextrin supplementation. M. A. Guevara*[1], K. A. Garleb[2], and G. C. Fahey[1], [1]*University of Illinois, Urbana*, [2]*Abbott Nutrition, Columbus, OH*.

The objective was to examine nutrient digestibility, fecal characteristics and blood chemistry profiles of dogs as affected by alpha-cyclodextrin (ACD) supplementation. Five mixed-breed hounds were used in a Latin square design with 5 periods of 14 d each, including 10 d for diet adaptation and 4 d for fecal collection. Dogs were fed twice a day a diet with poultry by-product meal and brewer's rice as the main ingredients, and chromic oxide (0.2%) was included as a digestion marker. Dogs were supplemented with either 0, 1, 2, 3, or 4 g of ACD diluted in 15 ml of water twice per day for a total of 0, 2, 4, 6, and 8 g of ACD per day. Average daily food intake, fecal production on a dry matter basis, fecal scores, and dry matter digestibility were not significantly different among treatments. Body weight and condition score, and blood triglycerides and cholesterol concentrations, remained unaltered throughout the duration of the experiment. Crude protein, and fat digestibility coefficients were lower ($p<0.05$) for treatment groups receiving 6 and 8 g of ACD compared to control. Alpha-cyclodextrin lowered fat and crude protein digestibility somewhat without affecting blood lipid concentrations or outcomes related to tolerance.

Key Words: dog, alpha-cyclodextrin, digestibility

287 Influence of dietary protein on fecal quality and colonic tight junction gene expression in Miniature poodles and German shepherds. J. Nery*[1,2], V. Leray[1], V. Biourge[3], L. Martin[1], H. Dumon[1], and P. Nguyen[1], [1]*École Nationale Vétérinaire de Nantes, France*, [2]*University of Turin, Italy*, [3]*Royal Canin, Aimargues, France*.

Large dogs are prone to producing feces of poorer quality than small dogs, partly due to a higher colonic permeability. Fermentation of undigested proteins would have deleterious effects on the colonic mucosa. The aim of the study was to assess the effect of dietary protein source and level on fecal quality and tight junction (TJ) proteins in the colon of small and large dogs. Five Miniature poodles (MP) and 6 German shepherds (GS) spayed dogs were fed 2 diets varying in main protein sources (wheat gluten: WG, and poultry meal: PM) and levels (LP: 21.4%, and HP: 34.8% CP as fed) in a 2x2 wk cross-over study design. Feces were scored daily (1=dry and hard to 5=liquid). Proximal and distal colonic biopsies were taken at the end of each 14-d period. mRNA expression of claudins 4 and 7 (CLN4 and CLN7), junctional adhesion molecule (JAM), occludin (OCLD) and zonula occludens 1 and 2 (ZO-1 and ZO-2) were measured by real time-PCR. Fecal score data was analyzed using Kruskal-Wallis test and gene expression using repeated-measures ANOVA. Fecal score was higher in GS dogs ($p<0.001$ for diet WG-LP, $p=0.006$ for PM-HP), and when feeding PM-HP ($p=0.010$ for MP, $p=0.003$ for GS). Protein digestibility was WG: 87.9% and PM: 83.4% ($p<0.001$). The expression of CLN4 and ZO-2 in the proximal colon was higher ($p=0.008$ and $p=0.088$) in GS than MP dogs. Higher expression of CLN7 was observed ($p=0.059$ in the proximal and $p=0.069$ in the distal colon) of GS than MP. The expression of OCLD was higher in GS than MP, in the proximal and distal colon ($p=0.002$ and $p=0.058$, respectively) and when feeding WG-LP and PM-HP ($p=0.046$ and $p=0.013$, respectively). No effects of diet, breed or biopsy location were found for JAM and ZO-1. Feeding highly digestible protein source WG at low level leads to an improvement of fecal score and moisture but it does not influence colonic TJ expression. Poorer fecal score in GS compared with MP would not be related to lower TJ expression in the colon of GS dogs.

Key Words: dog, protein, tight junction

288 Identifying relationships of urinary 5-hydroxyindoleacetic acid, homovanillic acid and cortisol with behavioural display during social isolation in the domestic dog. M. J. Toscano*, C. Basse, E. Blackwell, J. W. S. Bradshaw, and R. Casey, *DFAS, University of Bristol, Langford, UK*.

Separation related behaviour (SRB) of domestic dogs is a leading cause for returning dogs to shelters. The current effort served to develop a test to predict SRB using behavioural and physiological measures. Before testing, 52 shelter dogs were habituated to a single experimenter on a single day for 20 min. On the following day, urine was passively taken for the quantification of 5-hydroxyindoleacetic acid (5-HIAA), homovanillic acid (HVA), cortisol and creatinine. Creatinine was used as a corrective factor for the other physiological measurements. Following urine collection, the experimenter spent between one and 12 minutes with the animal and then left the room for five minutes. All interactions on the second day between the experimenter and dog as well as the dog in isolation were recorded on a video recorder and then analyzed for the occurrence of various behaviours that had been found in previous research to be predictive of SRB. Urine was analyzed for 5-HIAA and HVA using HPLC while a radioimmunoassay was used for cortisol and

creatinine. Linear regression was used to identify correlations between cortisol and neurotransmitter metabolites and SRB related behaviours. Neither 5-HIAA nor DOPA proved to be predictive of either the duration or latency to show SRB ($P > 0.1$). However, cortisol showed a weak positive correlation with the total duration of SRB shown (vocalisation and destruction combined; Pearson $r = 0.401$, $P<0.05$). The metabolites 5-HIAA and HVA displayed a weak positive correlation with the duration for which dogs remained standing at the door with a tense body posture (5-HIAA: Pearson $r = 0.383$, $P=0.05$; HVA: Pearson $r= 0.321$, $P=0.02$). Both also negatively correlated with the duration of interaction with the tester before being left alone (5-HIAA Pearson $r = -0.328$, $P=0.018$; HVA: Pearson $r = -0.278$, $P=0.046$). Our findings indicate a potential relationship between cortisol and neurotransmitter metabolites, and the manner in which domestic dogs respond to an anxiogenic situation, although more work is needed to identify the mechanisms of these correlations

Key Words: shelter, dog, 5-HIAA

289 Canine adipose tissue transcriptome changes following eight weeks of diet-induced obesity. R. W. Grant*, B. M. Vester, T. K. Ridge, T. K. Graves, and K. S. Swanson, *University of Illinois*, *Urbana*.

Changes that occur in organs and tissues over the course of obesity development are not well characterized. The purpose of this study was to characterize adipose tissue transcriptome changes occurring after 8 wk of diet-induced obesity and compare these changes to circulating metabolites. Intact female beagles were fed a commercially available high-fat diet and randomized to either ad libitum feeding (n=5) or weight maintenance (n=4). Subcutaneous adipose tissue biopsies and blood samples were collected at baseline and at 8 wk. At least .3g of subcutaneous adipose was collected after an incision was made over the latissimus dorsi and immediately frozen in liquid nitrogen. Total cellular RNA was extracted using Trizol. Transcriptome changes were assessed using Affymetrix Canine 2.0 microarrays and analyzed using the Limma package with an FDR = 0.05. After 8 wk, body fat mass (obese: 4.16±.15kg vs control:1.62±.08kg), BW, and blood leptin were elevated ($P<0.05$) in dogs fed ad libitum, but blood NEFA, triglyceride, insulin, glucose, adiponectin, CRP, and TNF-α concentrations were unchanged. 790 gene transcripts were differentially expressed in adipose tissue following 8 wk of diet-induced obesity. The majority of these changes were observed in seven functional classes: transcription/translation, metabolism, apoptosis/cell cycle regulation, transport, RNA/DNA processing, signaling and redox state. These results indicate that major changes associated with cell growth and metabolism occur during diet-induced obesity and adipocyte growth and proliferation prior to the onset of systemic low-grade inflammation.

Key Words: obesity, adipose, transcriptomics

290 Colonic protein metabolites and microbial populations are altered in adult cats by consumption of cellulose, fructooligosaccharides, or pectin. K. A. Barry*, B. J. Wojcicki, I. S. Middelbos, B. M. Vester, K. S. Swanson, and G. C. Fahey Jr., *University of Illinois*, *Urbana*.

Twelve young adult (1.5 y) male cats were used in a replicated 3 × 3 Latin square design to determine the effects of fiber type on nutrient digestibility, fermentative end-products, and microbial populations in feces. Three diets containing 4% cellulose, fructooligosaccharides (Synergy C, Beneo-Group, Tienen, Belgium; FOS), or pectin were evaluated. Nutrient digestibility; fecal output, pH, score, and fermentative end-products; and microbial populations were measured. No differences were observed in intake of dry matter (DM), organic matter (OM), or crude protein; DM digestibility; OM digestibility; or fecal output, pH, or concentrations of phenylalanine or histamine. Crude protein digestibility decreased ($P < 0.05$) in response to supplementation with pectin vs. cellulose. Both FOS and pectin supplementation resulted in higher ($P < 0.05$) fecal scores and concentrations of ammonia, butyrate, isobutyrate, isovalerate, valerate, total branched-chain fatty acids, phenol, tryptamine, and cadaverine. While fecal concentrations of putrescine and total biogenic amines increased ($P < 0.05$) with both FOS and pectin, the concentrations of these compounds were greater in cats supplemented with pectin than FOS. Fecal indole concentrations and Bifidobacterium spp. populations increased ($P < 0.05$), while tyramine concentrations and E. coli populations decreased ($P < 0.05$), in FOS-supplemented cats. Fecal concentrations of acetate, propionate, total short-chain fatty acids, and spermidine increased ($P < 0.05$) in pectin-supplemented cats. Fecal concentrations of Clostridium perfringens, E. coli, and Lactobacillus spp. also increased ($P < 0.05$) in pectin-supplemented cats. Despite increasing populations of protein-fermenting microbiota, pectin increased fermentative end-products associated with carbohydrate vs. protein fermentation. Pectin and FOS may be useful fiber sources in promoting intestinal health of the cat.

Key Words: cat, fiber, protein metabolites

291 Apparent macronutrient digestibility of four raw meat diets in African wildcats, jaguars, and Malayan tigers. K. R. Kerr*[1], A. Beloshpaka[1], C. Dikeman[2], S. Burke[2], L. G. Simmons[2], and K. S. Swanson[1], [1]*University of Illinois*, *Urbana*, [2]*Henry Doorly Zoo*, *Omaha, NE*.

Captive exotic felids in the US are traditionally fed horse-based raw meat diets, while those in the UK are usually fed beef–based diets. Little nutritional or metabolic information has been collected from captive exotic cats fed raw diets, and most have focused on horsemeat and beef-based diets with no attention paid to commercially available alternatives. With the closing of horse abattoirs in 2007, the availability of quality grade horsemeat for use in zoological institutions in the US has decreased, and there is a need for research on possible alternatives. The objective of this study was to evaluate the differences in apparent digestibility of four raw meat-based diets. Diets based on beef (BE), bison (BI), elk (E), and horse (H) meats were fed to three captive exotic felid species: African wildcats (AWC), jaguars (JAG), and Malayan tigers (MT). Four animals of each species were randomized to treatment individually. In general, the diets tested were highly digestible in all species. Apparent dry matter (DM) and organic matter (OM) digestibilities were lower ($P<0.05$) in cats fed BI (DM = 82.7%; OM = 85.5%) as compared to those fed BE (DM = 87.9%; OM = 90.3%) and E (DM = 86.9%; OM = 89.6%), and lower ($P<0.05$) for cats fed H (DM = 84.5%; OM = 87.4%) as compared to those fed BE. Apparent fat digestibility was lower ($P<0.05$) in cats fed E (87.9%) as compared to those fed BE (94.6%) and H (93.4%), and lower ($P<0.05$) for cats fed BI (90.2%) as compared to those fed BE. To conclude, our results suggest that all protein sources are highly digestible and may be suitable replacements for horse meat.

Key Words: digestiblity, feline

292 Response of the somatotropic axis and growth rate in mule deer (*Odocoileus hemionus*) fed three different diets from birth to 68 weeks of age. G. A. Comeau*[1], S. McCusker[2], J. P. Richmond[1], L. A. Shipley[2], E. A. Koutsos[3], and S. A. Zinn[1], [1]*University of Connecticut, Storrs*, [2]*Washington State University, Pullman*, [3]*Mazuri Exotic Animal Nutrition, St. Louis, MO*.

To examine the somatotropic axis in mule deer fed 3 distinct diets from birth (June) to 68 wk of age, mule deer (n=24) were randomly assigned to 1 of 3 dietary treatments [3 males (M); 5 females (F)/group). Before weaning (15 wk), animals were fed milk replacer and their experimental diet. Diets differed in starch and fiber [A: high starch (22%), low fiber (13%); B: medium starch (16%), medium fiber (15%); and C: low starch (3%), high fiber (29%); DM basis]. Animals were exposed to natural photoperiods. Blood samples and BW were taken at 0, 5, 15, 24, 33, 47, 58, 68 wk. From 24 to 68 wk, leg length, and loin (LT) and rump fat (RFT) thickness were measured. Plasma GH and IGF-I were determined using RIA and IGFBP-2 and -3 were quantified using ligand blot. Except for IGFBP-2, diet did not influence any variables measured and data were combined. Average BW increased (P<0.01) from birth (7.3±1.2 kg) to 68 wk (66.4±1.1 kg) and was greater (P<0.01) in M than F (36.2±1.2 vs. 30.5 ±0.9 kg). Leg length (42.8 to 48.5±0.3 cm) and LT (2.8 to 3.7±0.07 cm) increased (P<0.01) from 24 to 68 wk and were greater (P<0.01) in M than F (47.1 vs. 44.5±0.3 cm, 3.4 vs. 3.0±0.1 cm, respectively). Measures of RFT decreased (P>0.01) from 24 to 47 wk (0.5±0.06 to 0.05 ±0.07 cm) and then increased (P<0.01) until 68 wk (1.5±0.1 cm). In addition, RFT tended to be greater (P<0.09) in M than F (0.53 vs. 0.38±0.05 cm). Concentrations of GH decreased (P=0.01) from birth (9.4±1.7 ng/mL) to 68 wk (1.7±1.4 ng/mL). Plasma IGFBP-2 paralleled changes in GH, except IGFBP-2 was greater (P = 0.05) in fawns fed Diet A. From birth to 33 wk IGF-I declined (112 to 63±9.4 ng/mL; P<0.01), and then gradually increased (P<0.01) until 68 wk (133±9.4 ng/mL). Overall IGF-I was greater in M than F (135±7.7 vs 98±4.3 ng/mL). Concentrations of IGFBP-3 paralleled IGF-I. Developmental patterns of GH and IGFBP-2 are similar to domestic cattle, but the decline in IGF-I and IGFBP-3 from birth to 33 wk may indicate that season influences these hormones in mule deer.

Key Words: mule deer, somatotropic axis, insulin-like growth factor-I

293 Effects of zinc amino acid complex and iron amino acid complex on performance, health and pelt quality of weanling blue fox (*Alopex lagopus*). Y. Zhang[1], H. Wei[1], D. J. Tomlinson*[2], and T. L. Ward[2], [1]*Institute of Special Wild Animal and Plant Science, Jilin, China*, [2]*Zinpro Corporation, Eden Prairie, MN*.

Healthy 65-day old arctic blue foxes (60 male and 60 female) with similar body weight and near kinship were assigned randomly to one of four treatments with 30 replicates. Treatment diets were: (1) Control: 80ppm supplemental Zn from ZnSO4; (2) 40ppm Zn from ZnSO4+40ppm Zn from Availa-Zn zinc amino acid complex (AvZn) ; (3) 80ppm Zn from AvZn; (4) diet 2 +40ppm Fe from Availa-Fe iron amino acid complex (AvFe). Diets were similar in ingredient composition except for trace mineral supplement. Diets were offered in two phases: growth (0 to 60d) and pelting (61 to 147d). Foxes were fed and managed in individual cages. Body weight and size were recorded every two wk. Ten kits were sacrificed at the beginning of the study to establish liver trace mineral status. Blood was collected from 24 foxes per treatment at the beginning and end of the study to measure superoxide dismutase and lactate dehydrogenase activity. At the end of the study, liver samples were collected from 24 fox per treatment to determine trace mineral status. Pelt quality was assessed for length, width and total area. Fur quality was assessed for texture, uniformity, color, clarity, length and density. Results show that compared to inorganic zinc, supplementing with AvZn at 40 or 80ppm Zn resulted in greater weight gain (P < 0.05) and feed intake (P < 0.05); longer body length at 80 ppm AvZn (P < 0.05); better fur quality (skin length, width and area with AvZn at 80 ppm; length and amount of guard hair and fluff, and fur density – all AvZn treatments; P < 0.05); and higher scores in sensory assessment - all AvZn treatments; significant increase in liver zinc concentration at 80 ppm AvZn (P < 0.01); greater maintenance of serum SOD and LDH activity which increased with level of AvZn in diet. These findings indicate supplementing arctic blue fox with AvailZn and AvailFe had positive effects on growth, fur quality and sensory effects.

Key Words: fox, zinc amino acid complex, iron amino acid complex

CSAS Symposium: Nutrition – Behavior Interaction in Ruminants

294 Behavior and dairy cattle nutrition: Not just what she eats but how she eats it. M. A. G. von Keyserlingk* and D. M. Weary, *University of British Columbia, Vancouver, BC, Canada*.

One of the most important challenges that any animal faces is ensuring its daily food supply. In intensive dairy cattle production, cows are completely reliant on our ability and knowledge to provide them with food that supports growth, productivity, health and welfare. There has been great progress in the field of dairy cattle nutrition over the past years – we are now better able to estimate the dietary needs of dairy cattle, and meet these needs through carefully formulated diets. Research on behavior is now broadening our understanding of dairy cattle nutrition; the question is no longer just what do they eat, but how do they eat it, and this improved understanding of behavior is helping to avoid practical problems such as competition for feed. One of the main challenges for lactating dairy cows is a sudden increase in nutrient requirements to support the onset of lactation at a time when dry matter intake lags behind. Cows are also susceptible to a suite of diseases in these weeks immediately after parturition. Thus, a more sensitive method of continuously monitoring animal health or risk for disease during the transition period is needed. Recent work in our laboratory indicates that changes in feeding behavior and dry matter intake in the weeks before calving are valuable indicators of illness in dairy cows. An understanding of social behavior in cattle can help improve feed access and changes in these behaviours also can be used as an early indicator of ill health.

Key Words: behavior, nutrition, dairy cattle

295 Interactions of nutrition and behavior in dairy calves. J. K. Drackley*, *University of Illinois, Urbana*.

Raising dairy calves has too often been viewed as a nuisance on dairy farms rather than as a critical investment for the future of the business. That calves have remarkable growth potential in early life has been well-documented for decades, yet has been forgotten amid the convention of restricted calf feeding. Recent research has confirmed this unexploited growth potential and also demonstrated that improved early nutrition increases subsequent milk yield. These findings have resulted in widespread interest in early-life nutrition in calves, and how to provide it in practical on-farm systems. While behavioral research in calves has frequently been relegated by nutritionists to the category of

animal welfare interests, a large body of research has accumulated on the importance of animal behavior in promoting efficient early growth. Researchers have investigated such aspects as teat versus bucket feeding, temperature and consistency of liquid feeds, availability and use of water, ad libitum versus restricted feeding, feeder design, computer feeding systems, single versus pair or group housing, number of feedings daily, systems for introduction of starter, and weaning methods. Management systems that capitalize on various natural feeding behaviors are becoming more clearly defined. These systems offer the possibility to capture greater biological efficiencies of nutrient utilization at little if any additional net costs for capital or labor. With animal agriculture worldwide challenged to improve utilization of nutrients and decrease nutrient loss to the environment, these systems are increasingly attractive for reasons beyond just improving animal well-being. However, widespread adoption of behaviorally enhanced feeding programs will require a major paradigm shift within the industry. Extensive education about their proper implementation and benefits will be essential. In particular, the concept that the calf is an investment for the future, and is complex with variable nutrient and behavioral requirements, must continue to be reinforced throughout the dairy industry.

Key Words: calves, feeding systems, feeding behavior

296 Understanding the behavior of growing dairy heifers from a nutritional perspective. T. J. DeVries*, *University of Guelph, Kemptville Campus*, *Kemptville, Ontario, Canada*.

The primary goals of dairy replacement heifer rearing are to feed heifers for maximal production potential, while at a low economic and environmental cost, without compromising health or welfare. To meet these goals the feeding strategies utilized for dairy heifers are variable, including traditional high-fiber forage diets, higher energy diets to shorten the rearing period and reduce feed costs, and higher energy diets fed in a limited amount to control growth rate, while reducing feed costs and improving nutrient utilization. As with adult dairy cattle the feeding behavior of growing dairy heifers interacts with the feeding strategy utilized, as well as with the housing and management associated with those feeding strategies. For higher forage diets, with limited concentrate feeding, feeding method has a strong influence on feeding behavior. Component feeding results in the rapid consumption of concentrate after feed delivery, prior to forage consumption, and increases feed sorting across the day. Alternatively, provision of a TMR to growing heifers promotes feeding behavior patterns that result in a more balanced intake of nutrients across the day. Limit feeding dairy heifers caused changes in behavior, indicative of hunger and frustration. These behavioral changes include increased vocalization, increased standing while not eating, as well as aggressive `reaching' to acquire feed. Given that feed is only available for a limited amount of time, adequate bunk space is required to reduce competition for feed and thus allow for equal bunk access. This in turn will reduce between-heifer nutrient intake variability, and thus reduce within-pen variability in growth and improve overall animal health. Alternatives to limit feeding include provision of low-nutritive feedstuffs in the ration. Such rations have been shown to target nutrient intake without negatively affecting feeding behavior or growth potential. Future research is needed to further refine the feeding strategies of growing dairy heifers to meet the goals of rearing these animals, while maintaining their behavioral needs, health and overall welfare.

Key Words: dairy heifer, behavior, feeding strategy

297 Application of feeding behavior as an indicator of pain and morbidity in feedlot cattle. K. Schwartzkopf-Genswein*, L. González, D. Gibb, and T. McAllister, *Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*.

Studies exploring the utility of feeding and drinking behavior in the early detection of pain or sickness in feedlot cattle have shown great potential for identifying well-being and health issues before overt symptoms are displayed. Early detection of pain would allow for more targeted and effective pain mitigation, and improve welfare. Likewise, early detection of illness could improve an animals′ response to drug therapy and help reduce the negative effects of disease. The magnitude and direction of change observed in specific feeding behavior measures with the onset of health problems or painful events appears to depend on the tissue or system being affected. For example, some health disorders (i.e. bovine respiratory disease) reduce appetite and feed intake leading to a reduction in daily feeding duration. In contrast, pain associated with castration results in calves making fewer daily visits to the feeder while daily feeding duration remains unchanged between castrated and uncastrated calves. Documenting changes in feeding behavior will allow a better understanding of the mechanisms affected, and the development of specific strategies to improve management and monitor their effectiveness. Automated approaches for the detection of pain and illness, such as radio frequency technology, will aid in facilitating such research.

Key Words: feeding behavior, feedlot cattle, morbidity

298 Grazing preferences in sheep and cattle: Implications for production, the environment and animal welfare. S. M. Rutter*, *Harper Adams University College*, *Newport, Shropshire, United Kingdom*.

Given a free choice of grazing on adjacent monocultures of perennial ryegrass and white clover, sheep and cattle show a partial preference of approximately 70% for clover. They also show a consistent diurnal pattern of preference, with the proportion of grass in their diet increasing over the course of the day. Studies with lactating dairy cattle show they produce significantly more milk when they graze adjacent grass/clover monocultures compared with mixed swards. This is attributed to reducing the costs of selection i.e. the spatial separation of the monocultures makes it easier for the cattle to select their own diet without having to search through the mixed sward. In-vitro studies have shown that the optimal level of microbial protein synthesis in an artificial rumen is achieved with approximately 70% clover i.e. the same proportion as the animals select. This suggests that the animals are selecting a diet that optimizes their own feed conversion efficiency, so optimizing the use of nutrients. Although requiring further research, this could help to reduce the environmental impact of ruminant production. In ongoing research, high-yielding dairy cows given a free choice between eating a total mixed ration indoors or grazing grass outdoors showed a partial preference of approximately 91% to be indoors. When outdoors, cattle spent a significantly higher proportion of their time eating compared with indoors, even though a TMR with a higher potential intake rate was freely available indoors. The fact that high-yielding dairy cattle make this trade-off suggests that the choice to graze outdoors is of some importance to them, and, therefore, is also of importance to their welfare. Further research is needed to establish whether it is being able to graze that is important, or whether the important factor is simply having a choice. In conclusion, offering cattle and sheep separated feeds enables them to easily choose what to eat and can offer clear production benefits. It could also offer environmental and animal welfare benefits. The development of livestock feeding regimes that facilitate diet choice warrants further research.

Key Words: grazing, preference, behavior

Forages and Pastures: Symposium: Forage Management Strategies of Offset High Input Costs

299 Effects of biological N fixation and nutrient cycling on stocking strategies for cow-calf and stocker programs. F. Rouquette, Jr.* and G. Smith, *Texas AgriLife Research, Overton*.

Pasture and beef production costs for fuel, fertilizers, feed, and seeds increased from 2 to 3-fold between 2003 and 2009. With primarily grass-based pasture systems for cow-calf and stocker operations in the southeastern US, increased costs of nitrogen (N) fertilizer has caused shifts in management and stocking strategies. Incorporation of biological N-fixing clovers and other legumes into pastures presents challenges with seasonal and total DM production, sustainability of forage species, and maintenance of stocking rates. Nutrient cycling via animal excreta is the primary process of transferring N fixed in plants back to the soil for subsequent use by forages. Bermudagrass (BG) pastures at Overton which have received N and overseeded with ryegrass vs no N and overseeded with clovers (Trifolium sp.) have been stocked at three intensities with cows and calves for 24 years, 1985-2009, to assess forage species composition, cow-calf performance, and gain per unit area. Without N fertilization on Coastal Plain soils, bahiagrass invasion and an increase in BG ecotype diversity occurred at high stocking rates; however, at low stocking rates, both common and Coastal BG stands were maintained at about 80% of the pasture composition. At low stocking rates of 2.0 to 2.5 cow-calf units per ha, calf ADG was similar at 1.25 kg d^{-1} with gains of 450 kg ha^{-1} for N + ryegrass and 360 kg ha^{-1} for no N + clover. Angus x Brahman heifers (245 kg) had similar ADG of 1.3 kg d^{-1} stocked at 3.7 hd ha^{-1} or 0.6 kg d^{-1} when stocked at 10 hd ha^{-1}. Gain per unit area ranged from 970 kg ha^{-1} at 10 hd ha^{-1} to 580 kg ha^{-1} at 3.7 hd ha^{-1}. Pasture costs per kg gain must also include phosphorus, potassium, lime, etc. for sustained forage production. Management strategies which offset high input costs must be attentive to stocking rates, fertilizer regimens, forage utilization, hay requirements, and efficiency of animal production parameters.

Key Words: N-fixation, nutrient cycling, stocking strategies

300 Effects of N fertilization and supplementation strategies on forage intake, dietary selection, and performance of growing beef cattle. S. A. Gunter*, T. L. Springer, and J. A. Bradford, *USDA-ARS, Southern Plains Range Research Station, Woodward, OK*.

The N cycle on pasture is the movement of N through several pools found in the pastoral system. Except on a global scale, N cycles are generally not closed; that is, there are inputs to and losses from the system. Nitrogen is the most perplexing of all nutrients; moving in a variety of pathways-both biological and chemical; it has several oxidative states, can exist as a gas, a dissolved cation or anion, a precipitated salt, or a dissolved or solid organic molecule. There are 6 major pathways of N loss in grazed land: NH_3 volatilization, denitrification, wind and water erosion, NO_3^- leaching, and animal losses (export). Fecal pats of cattle contain the equivalent of 560 to 1,120 kg of N/ha, but plant recoveries of N from these pats rarely exceed 30%. Nitrogen fertilizers have been the tool most easily manipulated to affect herbage quality and available mass to grazing ruminants. Recently, the price of N fertilizers increased to a point where graziers are questioning the economics of adding N via chemical fertilizers. Nitrogen fertilizers increase herbage mass production, thereby impacting the optimal stocking rate for maximal net-return per unit of land. The net return of the stocker cattle enterprise is functions of ADG, BW gain/ha, production cost, and revenues. Supplementation practices that decrease herbage DMI can increase the carrying capacity of a pasture without placing greater demand on the herbage mass, except through trampling, and accelerate the N cycle. Supplements transport N into the pasture N cycle from an outside source and can make a significant contribution to nutrient pool. Nitrogen in excreta generated from supplemental grain, hay, silage, and product feeds enter the system and increase the quality and quantity of forage produced. Nitrogen in feces is mainly in organic forms, with one-third in microbial biomass. Fecal N degradation in the pat is usually slow, being limited by anaerobic conditions at first, then by dry conditions. There is a need to discover what management will optimize the relationship between plant growth and N cycling in the full range of climatic conditions.

Key Words: nitrogen, cattle, supplementation

301 Effects of grazing management on productivity of cow/calf and stocker cattle with an emphasis on utilization of stockpiled tall fescue. M. H. Poore* and M. E. Drewnoski, *North Carolina State University, Raleigh*.

Improved grazing management has potential to boost productivity of beef production systems. Despite active extension programs promoting improved grazing management, a low level of grazing management remains predominant on the majority of beef cattle operations. Increased adoption will depend on understanding more than the biological responses to changed management. More attention needs to be put on sociological barriers to adoption of new management techniques. Stockpiling late summer and autumn growth and then using the resulting forage for winter grazing with carefully controlled animal access can extend the grazing season and reduce winter feeding cost. Teaching producers to stockpile and intensively graze forage during winter appears to be a good entry point for those interested in improving their grazing management because of the direct economic impact and relative ease of management. Stockpiled summer growth along with a protein supplement has long been used to winter dry beef cows on native range in the high plains. Stockpiling and tightly controlling winter grazing is only recently gaining popularity in the eastern US. Any forage can be stockpiled for later grazing, but due to a number of positive agronomic attributes, tall fescue is the main forage of interest across much of the eastern US. Date to initiate the stockpile, nitrogen fertilization rate and source, and forage quality throughout the winter season are factors that have been researched at many locations. Recent research has shown that toxicity from the endophyte is reduced during the winter period, at least partially due to a large mid-winter decrease in ergot alkaloids. There are information gaps regarding the influence of grazing management style, responses to various supplementation strategies, and how stockpiled tall fescue fits into an optimal whole-farm forage system. More research on frequency and level of forage allowance, and supplementation strategies to meet various production goals would enhance our understanding of optimal management systems for use of stockpiled tall fescue.

Key Words: grazing management, stockpiled tall fescue, winter grazing

302 Economic analysis of cost, rewards and trade-offs of alternative forage management strategies. G. A. Benson*, *North Carolina State University, Raleigh*.

Farm financial performance and cost of production data show a wide variation in revenue, expense and net returns per for individual cattle operations within regions as well as among average performance among regions. In addition, the producers' goals likely vary among farms. Therefore, few general recommendations can be made about production practices. One general recommendation is that producers keep adequate records to measure animal performance, cost of production, revenue, and net income. Estimates of the amount of forage produced that is lost and wasted during harvesting, storage and feeding total as much as 50%. Changes in management practices can reduce losses. The adoption of rotational or strip grazing can increase utilization by half, allowing increases in animal performance or stocking rate. Added costs include increases in labor and equipment use. New investments in grazing infrastructure may be needed. The cost of stored forages includes harvesting, storage, feeding out, and losses. The effective cost can be double that of comparable grazed forages. Extending the grazing season through modifications to fertilizer applications and stockpiling can be profitable alternatives to stored forages in some circumstances. Risk is inherent to rainfed forage production systems and includes reduced forage production and livestock performance and input price risk. Risk management options include carrying reserves of stored forages, purchasing forages, and purchasing forage extenders, all of which incur cost. Budgeting tools, including partial and enterprise budgets and sensitivity analysis can be used to evaluate alternative forage production practices and risk management scenarios. Case study examples based on Mid-Atlantic conditions demonstrate a substantial profit potential for low cost storage systems for hay and for intensively managed stockpiled forages for producers with the requisite management skill, interest and time.

Key Words: forage economics, beef cattle

Growth and Development: Physiology of Growth In Vivo and In Vitro

303 Modeling lifetime growth and feed efficiency in pigs. A. B. Strathe*[1], A. Danfaer[1], and E. Kebreab[2], [1]*University of Copenhagen, Copenhagen, Denmark*, [2]*University of Manitoba, Winnipeg, Manitoba, Canada*.

Animal genetic selection programs have improved growth rates, feed efficiency and produced leaner pigs at time of slaughter. These programs were based on analysis of data collected from 20 to 120 kg pigs with little or no information given on growth patterns beyond this point. Thus, a growth study was setup to obtain information on growth and feed efficiency patterns in Danish meat type pigs from birth to maturity. A total of 40 pigs (Landrace-Yorkshire × Duroc crossings) originating from 17 litters and of 3 genders were fed 7 diets in the period of 0 to 1007 days of age. Weekly BW and feed consumption data was collected. The BW vs. age data was subjected to analysis using 4 different growth functions i.e. Gompertz, Logistic, Bridges and Lopez. The BW vs. cumulative feed intake (CFI) was modeled using the monomolecular function. All mathematical functions were implemented in multilevel nonlinear mixed effect framework where nested random effects were included i.e. pig within litter. The statistical models where further updated to include a first order continuous autoregressive process and variance weights for modeling the error structure. The Lopez function was best suited to modeling the BW vs. age relations and estimated the maximum rate of growth to occur at 151.2 (SE=4.38), 163.6 (SE=3.67) and 133.0 (SE=3.49) days of age which corresponds to 117.0 (SE=4.47), 134.6 (SE=4.06) and 96.1 (SE=3.35) BW for barrows, boars and gilts, respectively. The feed efficiency curve was obtained as the derivative of monomolecular function with respect to CFI. The results showed that gilts had a distinct feed efficiency pattern when compared to the boars and barrows ($P < 0.001$). These data suggests that growth capacity in boars and barrows is not maximized in the standard growth period which may influence decisions on the time of slaughter.

Key Words: nonlinear mixed model, growth curves, pigs

304 Stimulation of skeletal muscle protein synthesis in neonatal pigs by long-term infusion of leucine is amino acid dependent. F. A. Wilson, A. Suryawan, M. C. Gazzaneo, R. A. Orellana, H. V. Nguyen, and T. A. Davis*, *USDA/ARS Children's Nutrition Research Center, Critical Care Med. Div., Dept. Pediatrics, Baylor College of Medicine, Houston, TX*.

Infusing leucine for 1 h increases skeletal muscle protein synthesis in neonatal pigs, but this is not sustained for 2 h unless the leucine-induced fall in amino acids is prevented. We aimed to determine whether continuous leucine infusion can stimulate protein synthesis for a prolonged period when baseline amino acids are maintained and to identify signalling mechanisms involved. Overnight fasted 7-d-old pigs were infused for 24 h with saline, leucine (400 $\mu mol \cdot kg^{-1} \cdot h^{-1}$), or leucine with replacement amino acids (n=6/group). Fractional protein synthesis and translation control mechanisms were examined in skeletal muscle. Amino acid replacement prevented the leucine-induced fall in plasma amino acids. Leucine stimulated muscle protein synthesis ($P<0.05$), but only when replacement amino acids were infused to maintain fasting levels. Leucine had no effect on phosphorylation of protein kinase B, AMP-activated protein kinase, tuberous sclerosis complex 2, signalling proteins upstream of mammalian target of rapamycin (mTOR). Leucine also did not alter phosphorylation of raptor or PRAS40 nor the association of mTOR with raptor, GβL, or rictor, regulators of mTOR. Phosphorylation of mTOR, as well as its downstream targets that regulate translation initiation, eukaryotic initiation factor (eIF) 4E binding protein (4EBP1) and ribosomal protein S6 kinase, as well as eIF4E•eIF4G association were increased, and eIF2α phosphorylation was reduced by leucine, in the absence and presence of replacement amino acids ($P<0.05$). Thus, prolonged infusion of leucine activates mTOR and its downstream targets that regulate translation in skeletal muscle, irrespective of the circulating levels of the other amino acids. However, the ability of leucine to stimulate muscle protein synthesis is dependent upon amino acid availability. *Supported by Ajinomoto Amino Acid Research Program and USDA/ ARS 6250510000-43.*

Key Words: muscle, amino acids, protein synthesis

305 Dietary starch effects on metabolic gene networks in *longissimus lumborum* of early–weaned angus steers. D. E. Graugnard*, L. L. Berger, D. B. Faulkner, and J. J. Loor, *University of Illinois, Urbana*.

Post–weaning evaluation of gene expression networks driving adipogenesis and energy metabolism provides a means to examine long–term effects of nutrition on *longissimus* muscle development. Angus steer calves (155 ± 10 d age, n = 7/diet) were fed high–starch (HiS) or low–starch (LoS) diets for 112 d followed by a common finishing diet

for an additional 112 d. *Longissimus lumborum* was biopsied at 0, 56, 112, and 224 d for transcript profiling via quantitative PCR of 24 genes associated with aspects of adipogenesis and energy metabolism. Expression of *PPARG* and its target genes *FABP4* and *SCD* increased (time $P < 0.05$) through 112 d. Whereas *PPARG* was greater (diet × time $P < 0.05$) on d 112, *FABP4* and *SCD* were greater at 56 d in steers fed HiS vs. LoS. Interactions during the growing phase also were observed for *THRSP*, *SREBF1*, and *DGAT2* such that feeding LoS resulted in greater ($P < 0.05$) expression at d 112. Among genes involved in driving the lipogenic program, carryover effects of HiS-feeding were reflected by greater (diet × time $P < 0.05$) expression at 224 d of *SREBF1*, the lipogenic genes *ACLY*, *ACSM1*, and *LPIN2*, and the insulin/Akt-signaling gene *IRS1*. Similar carryover effects were observed for genes involved in calcium signaling (*ATP2A2)* , control of glucose oxidation (*PDK4*), and transcriptional control of fatty acid oxidation (*PPARD*, *PPARGC1A*). *FASN*, *GPAM*, *G6PD*, and *ADIPOQ* increased regardless of diet through 224 d. However, HiS led to greater (diet × time $P < 0.05$) expression of FASN and ADIPOQ between 112 and 224 d. Steers fed LoS vs. HiS had greater (diet × time $P < 0.05$) serum NEFA throughout the growing phase as well as a marked increase in insulin by day 224 d all of which were suggestive of insulin resistance. Overall, mRNA abundance provided evidence of greater intramuscular adipose tissue differentiation due to high–starch diets during the growing phase.

Key Words: early weaning, adipogenesis, genomics

306 Effect diet composition on precocious puberty and concentrations of IGF–1 in beef heifers. M. Maquivar*[1], L. A. Souto[1], D. E. Grum[1], D. M. Hallford[2], S. C. Loerch[1], A. V. Pires[3], and M. L. Day[1], [1]*The Ohio State University*, *Columbus*, [2]*New Mexico State University*, *Las Cruces, NM*, [3]*University of Sao Paulo*, *Piracicaba, Sao Paulo, Brazil*.

Feeding a high concentrate diet to heifers weaned at 3 months of age induces precocious puberty (before 300 d of age) in a high proportion of animals. The objectives of the present study were to determine if a diet that had similar energy content but lower starch content would induce precocious puberty, and to compare metabolic responses between diets. Heifers (n=33) weaned at 76 ± 11 d of age received 1 of 3 diets beginning at 98 ± 11 d of age. The control diet (C, n=12) was hay-based and formulated for ADG of 0.75 kg/d. Experimental diets, formulated for ADG of 1.5 kg/d but differing in starch (S) content were designated as H-S (46.4% starch, 50% corn, n=10) and L–S (14.48% starch, 47% dried distillers grain and soyhulls, n=12). Jugular blood was collected weekly to be analyzed for progesterone concentrations, at 174, 184, 212, 239, 269, 297 and 323 d of age for quantification of IGF–1 concentrations and at h 0, 1, 2, 3, 4, and 6 after feeding at 239 d of age for insulin concentration determination. The L–S and H–S treatments did not differ for ADG (1.21 ± 0.34 vs. 1.27 ± 0.39 kg/d respectively) and were greater ($P<0.05$) than the C treatment (0.77 ± 0.41 kg/d). Concentrations of insulin did not differ between treatments at h 0 but were greater in the H–S and L–S than the C treatment from h 2 to 6 (trt x h, $P = 0.06$). Concentrations of IGF–1 were greater in the H–S and L–S than in the C treatment from d 174 to 239, were greater ($P<0.05$) in the H–S than L–S on d 212 and 269 and did not differ between treatments on d 297 or 323 (trt x age, $P<0.01$). Precocious puberty was induced in 42% (5/12) and 60% (6/10) of heifers in the L–S and H–S and in no heifers in the C treatment. Age at puberty was greater ($P<0.05$) in the C (377 ± 26 d) than L–S (269 ± 69 d) and H–S (262 ± 56 d) treatments. Across H–S and L–S treatments, heifers that experienced precocious puberty had greater ($P<0.05$) IGF–1 concentrations from d 174 to 239 than those that did not reach precocious puberty. These data suggest a role of IGF–1 in precocious puberty and support the conclusion that high dietary starch is not essential to induce precocious puberty in early weaned heifers.

Key Words: puberty, IGF–1, heifers

307 Effect of nutrition and chronic infusion of leptin on sexual maturation of *Bos indicus* heifers. M. V. Carvalho*, J. D. Magalhães, L. U. Gimenes, and L. F. P. Silva, *Universidade de São Paulo*, *Pirassununga, São Paulo, Brazil*.

In order to test if increase in leptin concentration is capable of inducing puberty in *Bos indicus* heifers, thirty-six prepubertal Nelore heifers, 18 to 20 months-old, 275.8±17.2kg BW and BCS of 5±0.5 (1 to 9 scale) were randomly assigned to each of three treatments (n=12): H (high energy diet), L (low energy diet), and LL (low energy diet + oLeptin). Diets were formulated to promote weight gain of 0.4kg/day (groups L and LL) or 1.2kg/day (H group). Heifers were fed *ad libitum* once a day, they were weighed and had their BCS evaluated twice weekly. After 21 days of adjustment, heifers in LL group received subcutaneous injections of oLeptin at 4.8µg/kg BW twice a day, for 56 days. Groups H and L received similar injections of 2ml saline solution. Age at puberty was considered to be the age on first detection of a *corpus luteum* by twice weekly transrectal ultrasonography, confirmed by plasma concentrations of progesterone of > 1ng/ml. The mean diameter of the greater follicle in each ovary was also measured. Heifers in H group were younger at ovulation ($P<0.05$) than L group, and did not differ from LL group. Groups L and LL were not different. The H group tended ($P=0.09$) to be heavier at ovulation (357.9±11.4kg BW) than the LL group (331.2±10.2kg BW, and did not differ from L group. As expected, group H had higher ADG (1.3kg/d) than the other two (0.53kg/d for L group and 0.57kg/d for LL group). Also, heifers in high energy diet ovulated with higher BCS ($P<0.05$) then the other two groups. Although there was little difference among groups concerning the time of puberty, there were significant differences in follicle diameters ($P<0.05$), mostly at the beginning of hormonal treatment. Group H had the greatest follicles (1.09cm), group LL was intermediate (0.97cm) and group L had the smallest ones (0.92cm). In summary, exogenous infusion of leptin increased follicle diameters of heifers in low energy diet, although it had no effect on the onset of puberty. Higher energy intake increased BCS at ovulation and tended to increase BW.

Key Words: beef heifers, leptin, puberty

308 Physiological drivers of variation in feed efficiency in Red Angus-sired calves. C. M. Welch*[1], J. K. Ahola[1], J. B. Hall[1], J. I. Szasz[1], L. Keenan[2], and R. A. Hill[1], [1]*University of Idaho*, [2]*Red Angus Association of America*.

Residual feed intake (RFI) is becoming a well-accepted approach to determine variation in feed efficiency in beef cattle. Thirty-five to 40 percent of this variation is due to differences in basal metabolism (Richardson and Herd, 2004). To gain a clearer understanding of the mechanisms that drive this relationship between feed efficiency and metabolic rate, a number of molecular and genomics-based approaches have been suggested (Hill and Azain, 2008). In the present study, forty-two progeny (25 steers, 17 heifers) of red angus bulls divergent for maintenance energy (ME) EPD were RFI-tested in an 84 day post-weaning period. For steers and heifers ADG was 1.24 and 1.06 kg/d,

respectively. RFI was determined as the difference between expected and actual feed consumption for a given growth rate and the ranges were -1.17 to 2.43 and -0.86 to 2.30 kg/day for steers and heifers, respectively. Partial correlations were determined as follows: RFI:ADG, 0.00 (P = 1) for both steers and heifers; RFI:DMI, 0.75 and 0.81 (P < 0.0001) and ADG:FCR, - 0.67 and -0.75 (P < 0.001) for steers and heifers, respectively. Although variation in RFI may be partially driven by differences in maintenance requirements, it is a complex trait that is, as yet, poorly understood. As greater numbers of progeny (also representing a greater number of bulls) are characterized for RFI and physiological data are determined for this population, the relationship between RFI and a range of physiological parameters including ME EPD will be characterized. Variation in RFI in red angus cattle is comparable with other breeds determined to date. Hill, R. A., and M. Azain. 2008. Growth and development symposium: The molecular basis for feed efficiency. J. Anim. Sci. (jas.2008-1418v1-20081418) doi: 10.2527/jas.2008-1418 [Epub ahead of print]. Richardson, E. C., and R. M. Herd. 2004. Biological basis for variation in residual feed intake in beef cattle. 2. Synthesis of results following divergent selection. Australian Journal of Experimental Agriculture 44: 431-440.

Key Words: residual feed intake, feed efficiency, beef cattle

309 Effect of the beta-agonist RU-42173 on growth and body composition of bulls. D. P. D. Lanna*[1], P. R. Leme[2], F. G. F. Castro[1], A. C. Vieira[1], V. M. Quecini[1], L. O. Tedeschi[3], and L. L. Coutinho[1], [1]*ESALQ/USP*, *Piracicaba, SP, Brazil*, [2]*FZEA/USP*, *Pirassununga, SP, Brazil*, [3]*Texas A&M University*, *College Station*.

This study was conducted to determine the effects of the beta-agonist RU-42173 (Hoechst-Roussel) on growth and body composition of bulls. The 2x3 factorial included control or β-agonist and three breed groups (purebred Nellore, Nellore × Marchigiana, and Nellore × Holstein). The 72 bulls came from pasture with an average initial BW of 406 kg. Bulls were fed, three per pen, a 60:40 corn silage:concentrate diet with 15.7% CP. After 28 d of adaptation, RU-42173 was added at 6 ppm to the treated group diet for a 47 d experimental period (actual intake 0.16 mg/kg BW). Results are presented in the table below. There was no hormone × breed interaction (P>0.10). The addition of RU-42173 during the last 47 d before slaughter had positive effects on ADG (P<0.01) and feed efficiency (P<0.01). The decrease in DMI as a percentage of BW (P<0.05), was consistent with the decrease in the deposition of internal fat and the lower fat content of the 9-11th rib cut. Carcass quality characteristics were not affected by treatments.

Table 1. Results

Variables (^{ab}P<0.01 ^{AB}P<0.05)	Control	β-agonist	Change, %	SEM
ADG, kg/d	1.79^{b}	2.02^{a}	13	0.06
DMI, %BW/d	2.53^{A}	2.42^{B}	-4	0.03
Feed efficiency, ADG/DMI	0.157^{a}	0.182^{b}	16	0.004
9-11th rib section physical fat, %	25.1^{A}	23.6^{B}	-6	0.42
9-11th rib section lipid, %	23.2^{a}	19.9^{b}	-14	0.56
Hot carcass weight, kg	282^{b}	298^{a}	6	3.86
Dressing, %	57.7^{b}	59.2^{a}	3	0.003
Ribeye area, cm^2	64.5^{b}	73.5^{a}	14	1.38
Fat thickness, mm	3.1	3.2	3	0.14
Warner-Bratlzer *Longissimus*, kg	3.9	4.1	5	0.09
Warner-Bratlzer *Semimem*, kg	5.0	5.1	2	0.07

Key Words: beef cattle, β-agonist, body composition

310 Effects of ractopamine and gender on serum hormones and skeletal muscle gene expression in finishing steers and heifers. D. K. Walker*[1], E. C. Titgemeyer[1], T. J. Baxa[1], K. Y. Chung[1], D. E. Johnson[1], S. B. Laudert[2], and B. J. Johnson[1], [1]*Kansas State University*, *Manhattan*, [2]*Elanco Animal Health*, *Greenfield, IN*.

We compared growth–related responses to ractopamine (RAC) in steers and heifers. Angus steers (n=16; 512 kg, SD=21) and heifers (n=16; 473 kg, SD=18) in individual pens were used in a complete block design. At 90 to 97 d prior to the experiment, steers were implanted with 120 mg trenbolone acetate and 24 mg estradiol–17β, and heifers were implanted with 140 mg trenbolone acetate and 14 mg estradiol–17β. Treatments were arranged as a 2 × 2 factorial (gender × 0 or 200 mg/d ractopamine–HCl). Cattle were fed a diet based on steam–flaked corn once daily. Blood and longissimus (LM) and biceps femoris (BF) biopsy samples were collected on d 0 (before RAC) and after 14 and 28 d of RAC feeding. Serum insulin was not affected by RAC or gender. Serum insulin–like growth factor (IGF)–I was greater in steers than heifers (P<0.001), and steers demonstrated greater IGF–I mRNA expression (measured by real-time qPCR) in BF than heifers (P=0.05). RAC numerically decreased serum IGF–I concentrations in heifers on d 14 and 28 and in steers on d 14, but increased serum IGF–I concentrations in steers on d 28 (gender × RAC × day; P=0.03). RAC did not affect (P≥0.17) mRNA expression of IGF–I, IGFBP–3, or calpastatin in BF or LM. In LM, RAC increased mRNA expression of IGFBP–5 in heifers but decreased it in steers (gender × RAC, P=0.04). In BF, IGFBP–5 mRNA responded similarly to that in LM, but the gender × RAC interaction was not significant (P=0.17). RAC decreased myosin heavy chain IIA mRNA expression in BF (P=0.02) but not in LM (P=0.72). RAC decreased β2–receptor mRNA expression in LM of steers on d 14, but numerically increased it in steers on d 28; in contrast, expression of β2–receptor mRNA in LM of heifers was not affected by RAC (gender × RAC × day interaction; P=0.03). Although RAC led to a few differences in response between steers and heifers, there were no striking disparities to suggest that effectiveness of RAC markedly differs between genders.

Key Words: ractopamine

311 Bovine satellite cells contain three distinct subpopulations in young and adult cattle. D. K. Walker*, J. Li, M. J. Hersom, and S. E. Johnson, *University of Florida*, *Gainesville*.

Satellite cells (SC) are a heterogenous population of cells that lie adjacent to muscle fibers that are identified by their expression of Pax7 and Myf5. In mice, Pax7+/Myf5– SC undergo asymmetric division producing daughter cells that differentially express Myf5. Pax7+/Myf5+ progenitors proliferate and give rise to myoblasts that fuse into muscle fibers. The diverse populations of bovine SC were characterized by Pax7 and MRF expression in vitro. Satellite cells from young calves (<10 d) and adults (30–32 mo.) were isolated and cultured for 4 d. Cultures were pulsed labeled with 10 uM bromodeoxyuridine (BrdU) for two h prior to fixation at 24 h time intervals. The cells were immunostained for Pax7, Myf5, MyoD and BrdU. Results indicate the percentage of Pax7+/Myf5– cells were not different between young (5%) and adult (6%) animals (P = 0.63). Pax7+/Myf5+ adult cell isolates were not different at 24, 48, 72, and 96 h in culture (79, 70, 78, and 75%, respectively), but decreased from 24 to 96 h in young calves (72, 59, 54, and 19%, respectively; age × time in culture interaction, P = 0.008). Adult SC displayed similar numbers of Pax7–/Myf5+ cells from 24 to 96 h in culture (9, 23, 13, and 13%, respectively), but cells isolated from young calves displayed an increase in Pax7–/Myf5+cells (15, 27, 29, and 48%, respectively; age

× time in culture interaction, P = 0.05). MyoD+ cells were present at 48 h in young calf isolates and at 72 h in adult isolates; MyoD+ numbers increased over time in culture (P < 0.0001). Unlike rodents, the time course of activation did not differ between young and adult SC isolates. Both groups entered S-phase within 48 h and the numbers of BrdU+ cells increased over time in culture (P < 0.0001). Our data demonstrate distinct differences in the percentage of progenitors (Pax7+/Myf5+) and myoblasts (Pax7–/Myf5+) between young and adult animals. Importantly, our data demonstrate clear differences in gene expression and activation kinetics between cattle and rodent SC.

Key Words: bovine, Pax7, satellite cells

312 Abundance of growth hormone secretagogue receptor in adipose tissue from beef cattle undergoing compensatory growth. J. S. Jennings*, J. A. Clapper, A. D. Weaver, and A. E. Wertz-Lutz, *South Dakota State University*, *Brookings*.

We hypothesized that growth hormone secretagogue-receptor (GHS-R) abundance in adipose tissue would be decreased in cattle fed to achieve a faster rate of fat deposition. Beef steers (n=72) of similar age, weight (292±1.44 kg), and genetic background were used to determine the effects of growing diet (high forage vs. high concentrate) on GHS-R abundance in subcutaneous adipose tissue. At trial initiation (d 0), 8 steers were harvested for initial adipose tissue collection. The remaining 64 steers were allotted, by weight, to pen and treatment was assigned randomly. Treatments were 1) 60% forage; 40% concentrate diet fed during the growing period (112 d) followed by 10% forage; 90% concentrate diet during the finishing period (113-209 d) (GRW-FNSH) or 2) 10% forage; 90% concentrate diet fed for the duration of the experiment (0-209 d) (FNSH-FNSH). Steers were allowed ad libitum consumption regardless of dietary treatment. Eight steers per treatment were harvested on d 88, 116, 165, and 209. Subcutaneous adipose tissue samples were collected from each steer and immediately immersed in liquid nitrogen. Proteins were separated and quantified using SDS-PAGE and Western blotting techniques. Abundance of GHS-R was detected using the LI-COR ® system and standardized to β-Actin. Protein abundance data were analyzed statistically using the MIXED procedure of SAS to evaluate effects of diet, harvest date, and their interaction. A significant interaction (P≤0.05) resulted between dietary treatment and harvest date. At the final harvest, carcass weight was not different between treatments, but FNSH-FNSH steers had more (P≤0.01) subcutaneous fat and higher (P≤0.001) marbling scores compared with GRW-FNSH steers. Receptor abundance in the GRW-FNSH was greatest (P≤0.05) on d 84 whereas GHS-R abundance for the FNSH-FNSH treatment was greatest (P≤0.05) at the end of the finishing period (d 209). These data are not consistent with the hypothesis that GHS-R abundance decreases in beef cattle with greater fat deposition.

Key Words: adipose tissue, compensatory growth, GHS-R

313 Effect of Sirt1 on lipolysis and gene expression of adipose triglyceride lipase (ATGL) in porcine adipocytes. Y. Wang*, T. Shan, J. Guo, T. Wu, and C. Liu, *The Key Laboratory of Molecular Animal Nutrition, Ministry of Education. Institute of Feed Science, Zhejiang University*, *Hangzhou, Zhejiang, China*.

Sirt1 is a nicotinamide adenine dinucleotide (NAD)-dependent deacetylase that plays an important role in fat metabolism. To investigate whether Sirt1 could affect the lipolysis and adipose triglyceride lipase (ATGL) gene expression, we treated porcine adipocytes with the general Sirt1 inhibitor nicotinamide (NAM), the Sirt1 activator resveratrol (RES), and knockdown of Sirt1 by Sirt1-specific siRNA. The results showed that treatment with NAM decreased glycerol release (P < 0.05) and the levels of Sirt1 mRNA in porcine adipocytes. Compared with the control (0 μM), treatment with 100 or 150 μM NAM decreased the Sirt1 mRNA levels by 10.76% (P < 0.05), 36.05% (P < 0.01) and 28.58% (P < 0.01), respectively. Meanwhile, treatment with 100 or 150 μM NAM also decreased the mRNA levels of ATGL by 24.65% (P < 0.01) and 14.49% (P < 0.05). Furthermore, treatment with 100 μM NAM for 24, 48, or 72 h significantly decreased glycerol release (P < 0.05) and the mRNA expression of Sirt1 and ATGL. Exposure of cultured adipocytes to Sirt1 agonist (RES) increased (P < 0.01) glycerol release and the mRNA levels of Sirt1 and ATGL. Furthermore, knockdown with Sirt1-siRNA significantly inhibited (P < 0.01) Sirt1 mRNA expression, further decreased ATGL mRNA levels and reduced glycerol release. These results revealed that Sirt1 could promote lipolysis and up-regulate the expression of the ATGL gene. The results add to our understanding of the role of Sirt1 in adipose mobilization and as a potential target for regulating fat metabolism and metabolic disorders such as type 2 diabetes.

Key Words: adipose triglyceride lipase, pig, Sirt1

314 Breed difference and regulation of porcine adipose triglyseride lipase (pATGL) and hormone sensitive lipase (HSL) by TNFα and insulin. T. Shan*, Y. Wang, T. Wu, C. Liu, and J. Guo, *The Key Laboratory of Molecular Animal Nutrition, Ministry of Education. College of Animal Science, Zhejiang University*, *Hangzhou, China*.

Adipose triglyceride lipase (ATGL) and hormone sensitive lipase (HSL) are major novel triglyceride lipases in animals. The aim of this study was to determine if there are differences in the porcine ATGL (pATGL) and HSL between Jinhua pigs (a fatty breed) and Landrace pigs (a leaner breed). In addition, the effect of TNFα and insulin on the expression of pATGL and HSL mRNA levels in porcine adipocytes was also examined. The results showed that the body weight (BW) of Jinhua pigs was lower (P < 0.01), while intramuscular fat content (in the longissimus dorsi muscle), as well as the back fat thickness and body fat content were higher (P < 0.01) compared to Landrace pigs. Compared with Landrace pigs, the expression of pATGL and HSL mRNA in Jinhua pigs was lower (P < 0.01) in subcutaneous adipose tissue, and higher (P < 0.01) in longissimus dorsi muscle. In vitro treatment of porcine adipocytes with TNFα and insulin decreased (P < 0.01) the glycerol release and the gene expression of pATGL and HSL in porcine adipocytes. Compared with the control (0 ng/mL), treatment with 1, 12.5, 25, or 50 ng/mL TNFα signficantly decreased (P < 0.01) the mRNA levels of pATGL by 32.06%, 28.27%, 50.54% and 28.54% respectively, and decreased (P < 0.01) the mRNA levels of HSL by 28.02%, 17.40%, 25.22% and 18.34%, respectively. Furthermore, treatment with 25 ng/mL TNFα for 12, 24, 36, 48 h decreased (P < 0.01) the glycerol release and the gene expression of pATGL and HSL. Exposure of cultured adipocytes to 10, 50 and 100 nM insulin decreased (P < 0.01) the glycerol release and the mRNA levels of pATGL and HSL. Treatment with 50 nM insulin for 12, 24, 36, and 48 h, the glycerol release and the mRNA levels of pATGL and HSL were also decreased (P < 0.01). These results provide useful information to further the understanding of the function of pATGL and HSL in porcine lipid metabolism, which should have applicability to regulation of fat deposition and improvement of meat quality.

Key Words: adipose triglyceride lipase (ATGL), hormone sensitive lipase (HSL), pig

315 Effects of plane of nutrition and bioavailable trace minerals on claw growth and wear in transported male dairy calves. J. S. Osorio*[1], J. K. Drackley[1], R. L. Wallace[1], D. Rincker[1], D. J. Tomlinson[2], M. T. Socha[2], and T. J. Earleywine[3], [1]*University of Illinois, Urbana*, [2]*Zinpro Performance Minerals, Eden Prairie, MN*, [3]*Land O'Lakes Animal Milk Products Inc., Madison, WI.*

Data are limited on how claw development early in life will affect the susceptibility to lameness and claw disorders later in life. Adequate nutrition and bioavailable trace minerals might enhance claw development by ameliorating various stressors early in life. Ninety Holstein bull calves <1 wk old were purchased in 3 groups and transported to the Illinois research facility from Wisconsin. Calves were randomly assigned to treatments in a 2x2 factorial arrangement of plane of nutrition (PN) and trace mineral source (TM). Conventional PN received a fixed amount (568 g/d) of milk replacer (22% CP, 20% fat) plus ad libitum starter (18% CP) and were weaned at 6 wk; they received ad libitum starter to wk 12 and 0.5 kg/d of hay wk 10-12. During wk 13-20 calves were fed 3.2 kg/d of grower (16% CP) plus chopped hay ad libitum. Intensified PN received variable amounts (810, 1136, and 568 g/d for wk 1, 2 to 6, and 7, respectively) of milk replacer (28% CP, 20% fat) plus ad libitum starter (22% CP), were weaned at 7 wk, were fed ad libitum starter to wk 12, and fed ad libitum grower plus 0.5kg/d hay wk 13-20. Feeds contained either inorganic sulfates of Fe, Cu, Zn, and Mn or bioavailable sources (Zinpro Performance Minerals, Eden Prairie, MN). Calves were individually housed in hutches bedded with straw through wk 9 and group-housed by diet wk 10-20. Calves had free access to water. Claws were measured at wk 0, 5, 10, 15, and 20. Calves were born with uneven claw length (P<0.001), with rear and medial claws longer than front and lateral claws. Organic TM tended to increase claw length (P=0.105) after wk 15. Net growth increments were established after wk 5 regardless of treatment, which could be associated with complete establishment of corium tissue and physiological changes such as rumination and thermoregulation. Rear medial claws had more growth and wear (P<0.05) regardless of treatment. Intensified PN increases biological value of organic TM reflected by enhanced hoof dynamics and body growth.

Key Words: trace minerals, claw growth, calves

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316 Gene expression profile research of dairy goat mammary gland by Long-SAGE. H. Yan, C. Li, Q. Li*, and X. Gao, *Northeast Agricultural University, Harbin, China*.

Serial analysis of gene expression (SAGE) is a high-throughput, sensitive and efficient method for global expression profiles analysis that allows the quantitative and simultaneous analysis of large-scale transcripts under different conditions or in certain tissues. The Long-SAGE technique, developed from original SAGE, generates longer tags (21bp) than typical 14bp tags, which are more unambiguous in uniquely identifying with corresponding genes. Therefore, Long-SAGE technique was chosen to study gene expression profile of lactating dairy goat mammary gland, to find candidate genes that could control or regulate function of mammary gland.An improved protocol of Long-SAGE, considering characters of mammary gland, was applied to construct Long-SAGE libraries. Briefly, mRNA were isolated and synthesized into double-strand cDNA (ds cDNA), concatemers were formed by linking tags randomly which were extracted from ds cDNA through a series of restriction enzyme cleaving and ligating processes, sequenced the positive clones of concatemers to get information of tags. An extra heating process was necessary to increase cloning efficiency of concatemers.7 Long-SAGE libraries of different lactation stages (initiation, peak, stabilization and involution) of healthy dairy goat lactating mammary gland were successfully constructed. Over 21 thousands Long-SAGE tags were obtained by sequencing 7 thousands positive clones of concatemers. Removing the of duplicated and invalid tags, there're about 10 thousands of 17bp unique Long-SAGE tags, only 12% tags were matched to UniGene data according to limited genome resources. Further gene expression profile research of dairy goat mammary gland is still going on.

Key Words: gene expression profile, mammary gland, Long-SAGE

317 Selection of key gene related to development of mammary gland in dairy goat. C. Li, H. Yan, Q. Li*, and X. Gao, *Northeast Agricultural University, Harbin, China*.

To identify key genes involved in the initiation and development of mammary gland in dairy goat, we analyzed the global gene expression profiles of 7 different developmental stages using long serial analysis of gene expression (LongSAGE). We performed LongSAGE in healthy dairy goat mammary at seven different developmental stages (early puberty, late puberty, early pregnancy, late pregnancy, middle lactation, early involution and late involution). Computational analysis was carried out to identify differentially expressed genes in mammary gland between early puberty and late puberty, early pregnancy and late pregnancy which were further validated by real-time quantitative RT-PCR. Approximately 8,000 clones were sequenced for the seven libraries. Totally, 104,995 valid LongSAGE tags were obtained with 12,574 unique tags. Compared with the gene expression profile of early puberty mammary gland, 404 genes were identified to be differentially expressed in late puberty. 83 genes were high-abundance expressed in late pregnancy and early pregnancy contrast with late puberty. These diversely expressed genes were related to cell proliferation, biosynthesis, signal transduction, and cellular transport. In this study, seven LongSAGE libraries of different developmental stages of dairy goat mammary gland were successfully constructed. The genes expression profiles of these seven developmental stages were depicted on a genome-wide scale. For the restriction of annotation databases, we provided novel candidate genes that might be related to mammary gland development.

Key Words: dairy goat, mammary gland, LongSAGE

318 Epigenetic changes during functional differentiation of the mammary gland. M. Rijnkels*, C. Freeman-Zadrowski, and J. Hernandez, *USDA/ ARS Children's Nutrtion Research Center, Baylor College of Medicine, Houston, TX*.

The packaging of the DNA that surrounds a gene, the conformation of chromatin, is an integral part of gene regulation. Chromatin conformation is determined by DNA methylation, the post-translational modifications of the core histones and the proteins that bind to this. Hypermethylated DNA is usually associated with silent genes, whereas actively transcribed genes are hypomethylated. Different histone modifications are associated with open (active) or closed (inactive) chromatin. DNAseI hypersensitivity (DHS) indicates an open chromatin conformation and is often associated with regulatory elements. To identify a role for chromatin

in functional differentiation in the mammary gland we investigated the epigenetic changes (DNA methylation, Histone modiciations and DHS) in the casein gene cluster. The casein genes encode the major milk protein genes, which are expressed exclusively in the functionally differentiated mammary epithelial cells. We analyzed the presence of DHS, as well as the presence of an active histone modification (histone H3 Acetylation, H3Ac), using Chromatin immuno-precipitation (ChIP), in lactating mammary gland tissue of mice. We showed that chromatin surrounding the casein genes is in an open chromatin conformation in the lactating mammary gland as compared to liver. In addition we show that the promoters and potential distal regulatory elements are hypomentylated in lactating mammary tissue. Analysis at different time points during post-natal mammary gland development showed that DNA methylation is lost (opening up of chromatin) on promoters in concordance with major transcriptional up-regulation in pregnancy, while some potential distal regulatory elements already acquire an open chromatin structure (loss of DNA methylation) during pubertal development. This implies a model where chromatin conformation is changed at regulatory elements at different stages of mammary gland development to prepare the genomic region for further chromatin changes that will allow full transcriptional activity upon lactation.

Key Words: lactation, epigenetics, casein

319 Expression of peptide transporter PEPT2 gene in bovine mammary tissues influenced by oligopeptide and lactogenic hormones. M. M. Zhou*, H. Y. Liu, Y. M. Wu, and J. X. Liu, *Institute of Dairy Science, Ministry of Education Key Laboratory of Molecular Animal Nutrition, Zhejiang University*, *Hangzhou, P.R. China*.

The study was conducted to investigate the effects of oligopeptides (di- or tripeptide) and hormones (insulin or prolactin) on expression of peptide transporter PEPT2 gene in cultured bovine mammary tissues. The explants were obtained from the mid-lactating dairy cows and cultured in DMEM/F12 medium containing 10% fetal bovine serum. Contents of other essential amino acids were similar during the whole experiment. Phenylalanine (Phe) was firstly replaced by different ratios (0, 5, 10, 15 and 20%) of dipeptide, phenylalanylphenylalanine to investigate the oligopeptide level for optimal expression of PEPT2 gene. The mRNA expression was determined by SYBR green method of quantitative real-time PCR, and protein by immunocytochemistry, respectively, after the tissues were cultured for 48 h. The PEPT2 protein was successfully detected in the cultured bovine mammary tissue. The abundance of PEPT2 mRNA was highest (P<0.01) when 10% of phenylalanylphenylalanine was included. And then, this level (10%) of dipeptide (phenylalanylphenylalanine or phenylalanylthreonine) or tripeptide (threonyl-phenylalanyl-phenylalanine) was added to the medium, respectively, to replace free Phe. Both dipeptides and tripeptide enhanced expression of PEPT2 gene. Compared with phenylalanylthreonine, inclusion of phenylalanylphenylalanine or threonyl-phenylalanyl-phenylalanine had a greater effect (P<0.05) on PEPT2 gene expression. The mammary tissues were also incubated with insulin or prolactin for different times to detect the effects of hormones on PEPT2 gene expression. The abundance of PEPT2 mRNA was significantly(P<0.01) increased when the insulin was added into the culture medium for 1 h, but prolactin did not have effect on PEPT2 gene expression. These results indicate that peptide transporter PEPT2 in bovine mammary gland may be influenced through its gene expression by oligopeptides or hormones.

Key Words: bovine mammary gland tissues, oligopeptide, small peptides transporter II

320 Microarray analysis of gene expression profiles in dry period bovine mammary gland. X. Hou and Q. Li*, *Northeast Agricultural University*, *Harbin, Heilongjiang, China*.

Mammary gland undergoes dramatically functional and metabolic changes during the transition from lactation to dry period. To better understand the molecular events underlying these changes, the microarray analysis was performed using Affymetrix GeneChip Bovine Genome Array to analyze the gene expression profiles in bovine mammary tissue. Mammary tissues samples were collected in dry period and lactation from Holstein dairy cows, At the cutoff criteria of the signed fold change ≥2 or ≤2, A total of 143 genes were identified as differentially expressed, including 57 up-regulated and 86 down-regulated genes during dry period compared with lactation, and the results was identified by quantitative real-time PCR. Gene ontology analysis showed that the mainly up-regulated genes in dry period were those associated with metabolic process, regulation of apoptosis and immune system process. the mainly down-regulated genes were those associated with cellular components, binding, transport, biosynthetic process and signal transduction. The microarray data provided insight into the molecular events in the dry period bovine mammary gland and established the groundwork for further studies of the basic genetic control in bovine mammary gland apoptosis and reconstruction.

Key Words: mammary gland, microarray, genomics

321 Palmitate affects larger gene networks in MACT cells compared with *trans*-10,*cis*-12-CLA or PPAR-gamma activation via Rosiglitazone. G. Invernizzi*[1,2], A. K. G. Kadegowda[1], M. Bionaz[1], G. Savoini[2], R. E. Everts[1], H. A. Lewin[1], and J. J. Loor[1], [1]*University of Illinois*, *Urbana*, [2]*University of Milan*, *Milan, Italy*.

Activation of PPARγ in bovine mammary cells increases expression of lipogenic genes. Fatty acids regulate expression of genes controlling networks of lipid metabolism to different extents and potentially through PPARγ and other transcriptional regulators. To investigate the effects of palmitate on mammary gene networks, RNA from MACT cells cultured in triplicate for 12 h with control (CTR), 50 μM rosiglitazone (ROSI), or 100 μM palmitate (16:0) or t10c12-18:2 (CLA) were hybridized to a 13K bovine oligonucleotide microarray in a dye-swap design (24 microarrays). ANOVA (FDR-adjusted P ≤ 0.1) identi_ed 1,107 differentially expressed genes (DEG). Palmitate led to 622 DEG compared with CTR. Analysis of DEG suggested 16:0 increased cell differentiation, calcium flux, immune response (e.g. IκBK/NFκB cascade), and affected apoptosis. Data also suggested 16:0 increased triglycerides (TAG) synthesis and catabolism of amino acids. Large networks controlled by transcription factors (e.g., EGR2, JUND) were uncovered among DEG due to 16:0 vs. CTR. We observed 840 DEG between 16:0 and ROSI involved in proliferation, lipid accumulation (e.g., cholesterol), development and cell adhesion, and immune response. However, few genes with similar patterns were observed between 16:0 and ROSI (26 up and 15 down). There were 144 DEG between CLA and ROSI. Clustering analysis uncovered a larger degree of similarity among DEG between CLA and ROSI. There were few genes similarly affected by all treatments vs. CTR (n = 25; APOA1, VAMP2). Data clearly uncovered a larger effect of 16:0 on transcript profiles compared with ROSI or CLA. Outcomes suggest that 16:0 increases milk fat synthesis by up-regulation of genes implicated in TAG synthesis (i.e., FABP3, SCD, LPIN1). Palmitate might partly act through PPARγ but data strongly indicate its effects on mammary cells are likely through yet unknown transcription factors/ nuclear receptors.

Key Words: transcriptomics, milk fat, mammary gland

322 Energy metabolism in the development of dairy goat mammary gland. N. A. Zhang, Q. Li*, and X. Gao, *Northeast Agricultural University*, *Harbin, Heilongjiang, China*.

It is well known that mammary growth is a major determinant of milk yield capacity and longevity of lactation. Appropriate energy supply is critical to normal growth and development of mammary gland. Mammalian cells have sensory systems that detect energy and metabolic status and adjust flux through metabolic pathways. It shows that AMPK signaling pathways control cellular energy metabolism in non-ruminant cell systems. The aim of this study was to identify functional energy metabolism parameters and mRNA expression of AMPK-signaling genes which are expected to be important for the energy metabolism in different stages of mammary development. Comparing virginity of puberty, pregnancy, lactation and invoution, the importance of the examined parameters was studied regarding their capability to support the energetic needs of each stage of the mammary development. 36 primiparous Guanzhong dairy goats were allotted in twelve groups according to their mammary development stages: day 90, 150 of virgin, day 30, 90, 150 of pregnancy, day 1,10,35,60 of lactation and day 3,7,21 of involution (three animals per group). Mammary tissue samples were taken for measuring isocitrate dehydrogenase (ICDH) and lactate dehydrogenase (LDH) activities and RNA was isolated for quantitative real-time RT-PCR of *PRKAA2, PRKAB1, and STK11* (AMPK-signaling genes). ICDH and LDH had similar activities patterns and increased from in the middle stage of pregnancy, peaked on day 35 of lactation and remained elevated through lactation. AMPK-signaling genes expression (*PRKAA2, PRKAB1, STK11*) increased sharply by day 10 of lactation and remained high level expression through lactation. Results indicate that energy metabolism in dairy goat mammary gland is possibly regulated by AMPK signaling pathways.

Key Words: dairy goat, energy metabolism, mammary gland

323 Lactose synthesis in dairy goat mammary gland. X. Nan, Q. Li*, X. Gao, and B. Qu, *Northeast Agricultural University*, *Harbin, Heilongjiang, China*.

Glucose not only acts as a fuel but also a precursor of lactose in mammary gland. Lactose synthesis is unique in mammary gland. The process of synthesis also acts as a secretory activated signal and an acknowledged secretory rate-limiting step. For the purpose to invest the process of lactose synthesis in dairy goat mammary gland, 39 healthy Guanzhong dairy goat in different stages (V90d, V150d, P30d, P90d, P150d, L1d, L7d, L35d, L60d, L120d, I3d, I7d, I21d) of mammary gland development and lactation were chosen. Serumal glucose level increased at the beginning of pregnancy, and maintain at about 170 mg/dl ($p>0.05$). Marked up-regulation during lactation was observed for genes associate with lactose synthesis. The mRNA level of *Glut1*, *HK1*, *HK2* and *alpha lactalbumin* increased about 8-fold, 4-fold, 5-fold and 32-fold in L1d, respectively. The mRNA level of *beta-1, 4-Galactosyltransferase* (GolgiÃ¢â‚¬â„¢s apparatus) increased 3-fold in L60d. PAS method revealed that, at the beginning of lactation, the carbohydrate located in acinar lumina abundantly. The lactose content of mammary gland and milk was detected by HPLC. The results indicated that, lactose appeared in mammary gland at late pregnancy, later than milk proteins, and peaked in L60. Our research revealed, increased uptake and the more vigorous metabolism of glucose, activate the secretion. The Glut1 locating in the epithelium of both alveoli and Golgi was the major glucose transporter in mammary gland, but some others may act according to current research. The marked up-regulation of *HK1* and *HK2*, were very dramatic, indicated some unclear roles of *HK2* in lactation.

Key Words: lactose synthesis, dairy goat, mammary gland

324 Mammary expression of activating transcription factor 4 (ATF4) and tribbles homolog 3 (TRB3) is up-regulated during CLA-induced inhibition of milk fat synthesis in the dairy cow. K. J. Harvatine*[1], Y. R. Boisclair[2], and D. E. Bauman[2], [1]*Pennsylvania State University*, *University Park*, [2]*Cornell University*, *Ithaca, NY*.

Milk fat depression (MFD) in dairy cows is caused by unique fatty acids originating from ruminal fatty acid biohydrogenation. The best studied of these is trans-10, cis-12 conjugated linoleic acid (CLA) and its mechanism involves a coordinated decrease in mammary expression of lipogenic enzymes. Endoplasmic reticulum (ER) stress is emerging as a causative mechanism of metabolic diseases, with ATF4 and TRB3 providing a link between ER stress and metabolism. TRB3 inhibits AKT1, MAPK, and acetyl-CoA carboxylase. We conducted in vivo and in vitro studies to examine expression of ATF4 and TRB3 in mammary tissue during MFD and in bovine mammary epithelial cell culture (MACT) during CLA treatment. ATF4 and TRB3 expression was increased in mammary tissue during MFD induced by a low forage, high oil diet fed for 11 d but not by 3 d infusion of CLA. Temporal response was subsequently investigated. An initial priming dose of 7.5 g of CLA was given followed by infusion of CLA for 5d. TRB3 and ATF4 expression was increased at 12 h but not at 30 h and 5 d. Although TRB3 and ATF4 are associated with ER stress signaling, we did not observe increased expression of the chaperone protein HSPA5 or alternate splicing of XBP1 indicating a non-classical ER stress response. CLA dose dependently increased expression of TRB3 and ATF4 with maximal response at approximately 10 μM, response diminished with increasing doses and no response was observed at 50 μM. CLA doses that increased expression of TRB3 and ATF4 decreased lipogenesis with no decrease in expression of fatty acid synthase. However, ER stress induced by tunicamycin or thapsigargin increased expression of TRB3 and ATF4 but did not decrease lipogenesis. CLA induces TRB3 and ATF4 expression in some conditions, but the inconsistency of the signaling response and the lack of an effect of chemically induced ER stress on lipogenesis calls into question the functional importance of TRB3 and ATF4 in the lipogenic phenotype of classical MFD. *USDA-NRI 2006-35206-16643.*

Key Words: ER stress, CLA, milk fat depression

325 Lipid transporters and their regulators in the bovine mammary gland in relation to blood serum metabolites during pregnancy, involution, and lactation. O. Mani[1], M. T. Sorensen[2], K. Sejrsen[2], R.M. Bruckmaier*[3], and C. Albrecht[1], [1]*Institute of Biochemistry and Molecular Medicine, University of Bern*, *Bern, Switzerland*, [2]*Department of Animal Health, Welfare and Nutrition, Aarhus University*, *Tjele, Denmark*, [3]*Veterinary Physiology, Vetsuisse Faculty, University of Bern*, *Bern, Switzerland*.

Several ATP-binding cassette (ABC) transporters are known to play a pivotal role in cellular lipid efflux. To determine if they are involved in maintaining lipid homeostasis of mammary tissue, we investigated the expression and localization of candidate ABC transporters and their regulators during different physiological stages of the bovine mammary gland (MG). MG biopsies were repeatedly taken from ten dairy cows during the pregnancy-lactation cycle. mRNA levels were determined by

quantitative RT-PCR. In parallel, blood serum metabolite levels were measured; proteins were localized by immunohistochemistry. Relative mRNA levels of the lipid efflux transporters ABCA1 and ABCA7 were elevated during involution as compared to lactation (P=0.0197, <0.0001, resp.). The intracellular cholesterol transporter NPC1 and the regulatory genes LXRα, PPARγ, SREBP1, SREBP2 were increased post partum as compared to the dry period (P=0.0003, 0.0271, <0.0001, 0.038 resp.). Correlation analysis of ABCA1, ABCA7 and ABCG1 mRNA profiles with blood cholesterol levels revealed significant inverse relationships (r=-0.39, -0.51, -0.29, resp.; P<0.05). ABCA1 and ABCG1 showed differential localization and activity in mammary epithelial cells (MEC) during involution and lactation. This study demonstrates that lipid transporters and their regulatory genes are differentially expressed in the MG during the pregnancy-lactation cycle and correlate with blood serum cholesterol profiles. Our results suggest that ABCA1 and ABCG1 are involved in the removal of cholesterol from MEC. ABCA7 may play a role in phagocytosis of apoptotic MEC during involution. Regulation of lipid transporters in the MG is only partially associated with transcription factors that control lipid homeostasis because the induction of lactation is triggered by lactogenic hormones that may interfere with regulators of lipid homeostasis.

Key Words: ABC transporters, cholesterol, mammary gland

Meat Science and Muscle Biology: Symposium: Effects of By-product Feeding on Meat Quality Traits

326 Effects of feeding distillers grains on fat deposition in feedlot cattle. B. A. Casey*, S. R. Rust, and J. P. Grobbel, *Michigan State University*, *East Lansing*.

The objective of this study was to evaluate the effects of modified wet distillers grains with solubles (MDGS) on partitioning of fat between various depots. Crossbred cattle (n = 168) were used in a randomized complete block design with 7 pens per treatment. Treatments consisted of 0, 20, or 40% (DM basis) MDGS, as a replacement for high-moisture corn in the basal diet. The basal diet consisted of 83% high moisture corn, 12% corn silage, and 5% protein-mineral supplement. Ultrasound scans were taken every 56 d throughout the study to estimate intramuscular fat (IMF) and subcutaneous fat deposition. Cattle were fed for 139 d and harvested when 12th rib fat thickness (SQF) was estimated to be 1.01 cm. Performance and carcass data was evaluated. Final weight was calculated by adjusting carcass weights to a constant dressing percent. The subsequent weight was used to calculate ADG. Shrunk dressing percent was calculated by adjusting live weights to 4% shrink. Inclusion of MDGS had no effect on DMI, however carcass adjusted G:F tended to increase (P = 0.08) with the inclusion of MDGS in the diet. The inclusion rate of 20 and 40% MDGS tended to increase shrunk dressing percent (P = 0.09) and yield grade (P = 0.06) when compared to the control diet. The ratio of IMF:SQF (IMR) was lower (P < 0.01) in cattle fed MDGS when compared to the control diet. The inclusion of MDGS within the diet may affect energy partitioning between IMF and subcutaneous fat deposition. This data suggests that feeding MDGS at inclusion levels of 20 or 40% may result in greater subcutaneous fat deposition with minimal effects on marbling.

Table 1.

Item	0% MDGS	20% MDGS	40% MDGS	SEM	Probability
Number of pens	7	7	7	-	-
Carcass adjusted ADG, kg	1.33	1.46	1.37	0.05	0.22
DMI, kg/d	8.63	8.85	8.75	0.27	0.85
Carcass adjusted G:F	0.154^{a}	0.164^{b}	0.156^{ab}	0.003	0.08
Shrunk dressing %	61.61^{a}	62.63^{b}	61.83^{ab}	0.32	0.09
Calculated yield grade	2.6^{a}	2.9^{b}	2.9^{b}	0.08	0.06
SQF, cm	1.08	1.22	1.22	0.05	0.12
Marbling (400 = slight, 500 = small)	505.4	515.7	492.6	9.7	0.27
$IMF_{Ultrasound}$ (IMF/SQF)	11.69^{a}	9.97^{b}	9.76^{b}	0.40	0.01

^{ab}Means with unlike superscripts differ.

Key Words: beef, distillers grains, fat deposition

327 Dietary inclusion of CLA changes fatty acid profiles of pigs fed 30% DDGS during the growing-finishing phase. D. Pompeu*, R. B. Hinson, Z. P. Zhu, B. R. Wiegand, J. W. Rickard, and G. L. Allee, *University of Missouri*, *Columbia*.

The objective of this study was to evaluate dietary inclusion of DDGS at 30% and CLA at 0.6%. Forty barrows were assigned to a 2×2 factorial arrangement within a completely randomized design with a total of 10 replications. Pigs received ad libitum access to water and feed. Pigs were slaughtered at an average live weight of 129.88 ± 1.21 kg. Data was collected for growth performance, carcass and meat quality and fatty acid profile analysis. The inclusion of CLA in the diet did not significantly affect any of the parameters analyzed for carcass and meat quality. However, the inclusion of DDGS decreased the redness (P<0.05) of the longissimus muscle and increased the flexibility (P<0.05), both vertical and horizontal, of the belly. A significant interaction was observed for jowl and belly samples for total saturated fatty acids (SFA) and total polyunsaturated fatty acids (PUFA) (P<0.05). For both jowl and belly samples, the maximum amount of SFA (41.06 and 39.32%, respectively) were obtained by the DDGS only diet. The maximum amount of PUFA was obtained by the treatment DDGS + CLA for both jowl and belly samples (22.53 and 23.76%, respectively). The interaction of CLA and DDGS did not affect (P>0.13) the amount of monounsaturated fatty acids (MUFA) for both belly and jowl samples. However, the inclusion of CLA and also, the inclusion of DDGS in the diet, affected (P<0.05) the MUFA content in both jowl and belly samples. The maximum amount of MUFA (49.21% for the jowl samples and 50.50% for belly samples) was obtained by the samples of pigs fed the control diet, with no CLA and DDGS. The iodine value of the samples were affected (P<0.05) by the inclusion of CLA, DDGS and the interaction between them for both jowl and belly samples. The highest value was obtained from the samples of pigs fed DDGS with no CLA (71.18 and 72.19 for jowl and belly, respectively). Overall, this experiment indicates that DDGS and CLA and their interaction do not affect in a large proportion the carcass and meat quality when fed to finishing barrows. However, significant changes can be achieved in the fatty acid profile as measured in the belly and jowl.

Key Words: CLA, DDGS, iodine value

328 Effects of distillers grains on beef carcass quality and palatability. C. R. Calkins*, A. S. de Mello Jr., and L. S. Senaratne, *University of Nebraska*, *Lincoln*.

Distillers grains, mostly obtained from ethanol production, can be used in cattle diets. Results of 3 experiments show that feeding wet distillers

grains plus solubles (WDGS) does not negatively influence, and may benefit, marbling score. When cattle are fed WDGS, a higher amount of 18:2 fatty acid is observed at the duodenum, and higher amount of polyunsaturated fatty acids (PUFA) as well as 18:2 and Omega 6 are found in the infraspinatus (top blade), longissimus (ribeye), and psoas major (tenderloin) muscles. Those muscles have higher oxidation when displayed at simulated retail conditions for 7, 14 and 21 days ($P < 0.05$). A series of studies suggest that higher visual discoloration ($P < 0.05$) is observed on strip loin, tenderloin and top blade steaks from cattle fed WDGS. Top blade and tenderloin steaks from cattle fed 30% WDGS were significantly less red (lower a* values) after 3 d of retail display ($P < 0.04$). This effect is originated by higher PUFA and oxidation. Higher discoloration is observed when long aging periods are practiced before the meat goes to retail display. No significant effects on objective tenderness (WBSF - Warner-Bratzler shear force) and sensory attributes (except off-flavor notes) were observed. More livery off flavors have identified when meat from animals fed WDGS is subjected to retail display. In addition, the solubles in WDGS are high in minerals which may lead deviation in flavor. Vitamin E tends to mitigate negative effects caused by feeding WDGS. Therefore, it is clear that feeding WDGS does not compromise marbling or tenderness. Shelf life (color stability and oxidation) and off-flavor issues may be controlled by vitamin E.

Key Words: beef quality, distillers grains, palatability

329 Effects of various coproducts on beef consumer sensory and tenderness traits. G. P. Lardy* and R. J. Maddock, *North Dakota State University*, *Fargo*.

Food processing industries generate significant volumes of processing coproducts typically used in livestock diets. As industrial and bioenergy demands for corn continue to increase, increasing emphasis on coproduct use in beef cattle production will occur in an effort to reduce costs. Traditional research has investigated a variety of coproducts and the effects on ADG, DMI, G:F, and carcass data. However, increasing emphasis must be placed on the effects on consumer sensory traits and tenderness when these coproducts are used in beef cattle finishing diets. The effects of corn coproducts are covered in a companion abstract while this abstract focuses on other coproducts such as potato processing waste, wheat middlings, sugar beet processing byproducts, glycerol, and other vegetable wastes. Unfortunately, data regarding the effects of these byproducts on beef consumer sensory and tenderness traits is limited. Work in several laboratories has investigated the effects of feeding potato processing waste on consumer sensory traits and indicates few differences in palatability, including juiciness, tenderness, or flavor when potato waste is fed at levels which maintain acceptable feedlot performance. Little, if any, data has investigated the effects of wheat middlings, sugar beet processing byproducts, and other vegetable wastes on meat quality traits. In the future, additional research should investigate the effects of these and other coproducts on mechanical shear force, and sensory ratings of tenderness, juiciness, and flavor. Future work should focus on characterizing the composition of coproducts, especially as it relates to compounds or components which may have positive or negative influences on beef flavor, color, and palatability (e.g. fat and fat soluble compounds). In addition, steps should be taken to investigate any possible concerns related to chemical components which may result in off-flavors or reductions in shelf life of fresh meat and further processed meat products. The use of feedstuffs or feedstuff combinations which decrease consumer acceptance of beef should be limited, or not used in beef cattle finishing diets.

Key Words: beef, coproducts, sensory characteristics

330 By-product feeding effects on pork quality and carcass traits. J. D. Wood*, F. M. Whittington, and K. G. Hallett, *University of Bristol*, *Langford, Bristol, UK*.

Many components of pig diets are by-products of industrial processes whose main aim is the production of foods or other materials for human use. Protein meals derived from oil seeds from which most of the oil has been extracted are important examples eg soyabean meal and rapeseed/canola meal. Distillers dried grains and solubles (DDGS), a by-product of ethanol production from maize, is another protein source. Interest in these protein meals from a meat quality perspective centers around their effect on the oiliness and firmness of fat tissues. Soft or oily fat is more difficult to process into ham or bacon and causes fresh cuts to lose their rigidity and become 'floppy'. These effects are due to the residual oil present in the meal. This makes an important contribution to energy value but because the oil is high in polyunsaturated fatty acids (PUFA), it will be incorporated into fat tissue and soften it if excessive amounts are fed. By-products high in saturated fatty acids such as palm kernel meal produce firmer carcass fat. The major PUFA in protein meals including soyabean meal and DDGS is linoleic acid (18:2n-6) whose fat softening effect is explained by a very low melting point. A close association between the amount of 18:2n-6 in the diet, its concentration in carcass fat and the hardness/softness of backfat and pork cuts has been demonstrated in several studies. A summary of work at Bristol showed that unacceptably soft fat occurred at values above 15% of total fatty acids in backfat. This was achieved at a level of about 1.6% 18:2n-6 in the diet and this figure has been used as an upper limit for formulation of finishing diets in Britain. However, this figure is based on pigs having fat thickness values of 12-14mm. The 18:2n-6 concentration can be increased above 1.6% in fatter pigs without adverse effects on fat quality because higher fatness itself depresses the concentration of 18:2n-6 in total fatty acids.

Key Words: by-products, swine, fat quality

Nonruminant Nutrition: Amino Acids and Energy

331 Birth order, birth weigh, sow colostrum IgG, and pig IgG concentration and their effects on neonatal piglet survival. R. Cabrera*[1], X. Lin[1], K. Shim[1], T. Inskeep[1], J. Campbell[2], A. Moeser[1], and J. Odle[1], [1]*North Carolina State University*, *Raleigh*, [2]*American Protein Coporation*, *Ankeny, IA*.

Uptake of colostrum after birth is essential to stimulate intestinal growth and function, and provides systemic immunological protection via absorption of Immunoglobulin G (IgG). The birth order and weight of 745 piglets (from 75 litters) were recorded during a one-week period of farrowing. Only pigs weighing greater than 0.9 kg birth weight were chosen for the trial. Sow colostrum was collected during parturition, and piglets were bled between 48 and 72 hours post-birth. Pig serum IgG and colostral IgG concentrations were determined by radial immunodiffusion. The data were analyzed using the GLM and REG procedures of SAS. Sow colostral IgG concentration explained 6% and piglet birth order accounted for another 4% of the variation observed in pig

IgG concentration (P < 0.05). However birth weight had no detectable effect. Pig IgG concentration had both a linear (P < 0.05) and negative quadratic effect (P < 0.05) on % survival. Pigs with 1,000 mg/dl IgG or less (n=24) had a 67% survival; whereas, 39% of the pigs (n=247) had IgG concentrations between 2250 to 2500 mg/dl with 91% survival. Birth order had no detectable effect on survival, but birth weigh had a linear effect (P < 0.05) on % survival. Pigs weighing 0.9 kg (n = 107) at birth had 68% survival rate, and those weighing 1.6 kg (n = 158; ~average birth weight) had an 89% survival. In conclusion, we found that sow colostrum IgG concentration and birth order can account for 10% of the variation of pig IgG concentration and that piglets with less than 1,000 mg/dl IgG serum concentration and birth weight of 0.9 kg at birth had low survival rate when compared to their siblings.

Key Words: neonatal swine, pig IgG concentration, sow colostrum IgG concentration

332 Efficacy of dietary amino acids to replace fish meal and whey protein on physiological changes in weanling pigs. Y. Zhao*[1], C. M. Ballou[1], A. C. Chaytor[1], R. L. Payne[2], and S. W. Kim[1], [1]*North Carolina State University, Raleigh,*, [2]*Evonik-Degussa Corp, Kennesaw, GA*.

One hundred sixty newly weaned pigs at 21 d of age were used in a randomized block design with 4 treatments, 8 replicates per treatment, and 5 pigs per pen (4 × 8 × 5). All diets contained the same amounts of SBM and plasma protein as common protein sources. Treatments with different protein sources were CON (fish meal and whey protein), FA (supplemental amino acids and fish meal), WA (supplemental amino acids and whey protein), and AA (supplemental amino acids). Pigs were fed the assigned experimental diets for 4 wks based on a 2-phase-feeding (P1: 1 wk; P2: 3 wks). Supplemental amino acids were Lys, Thr, Trp, Met, Val, and Ile, and these AA were used to match amounts of standardized ileal digestible Lys (1.34 and 1.19%), Thr (0.93 and 0.80%), Trp (0.26 and 0.24%), Met+Cys (0.68 and 0.64%), Val (0.99 and 0.91%), and Ile (0.78 and 0.76%) among treatment diets for P1 and P2, respectively. Pigs had access to diets and water ad libitum during the study. Body wt and feed intake were measured weekly. Blood samples were obtained from pigs at the end of P1 and P2 to measure plasma insulin and growth hormone contents as well as blood cell numbers. At the end of P2, pigs were euthanized to collect jejunum to measure villus height. Growth performance was reported previously and did not differ among treatments. Plasma insulin content of pigs fed AA (0.058 μg/L) tended to be greater (P<0.10) than CON (0.026), and WA (0.028) at the end of P1 but did not differ at the end of P2. Growth hormone contents and number of lymphocytes did not differ among treatments. Villus height of pigs did not differ among treatments. Collectively, extensive use of supplemental amino acids replacing fish meal and whey protein concentrate did not adversely affect the general performance of pigs but increased plasma insulin content which may benefit utilization of absorbed nutrients for tissue synthesis and energy storage.

Key Words: amino acid, pig, protein source

333 Maximizing the use of supplemental amino acids in diets for 14-kilogram pigs. V. D. Naranjo*[1], T. D. Bidner[1], R. L. Payne[2], and L. L. Southern[1], [1]*Louisiana State University Agricultural Center, Baton Rouge*, [2]*Evonik-Degussa Corporation, Kennesaw, GA*.

Four experiments were conducted to determine the maximum level of supplemental L-Lys, along with the commercially available AA, that can be added to diets for 14-kg pigs. In Exp 1, based on G:F, peanut meal (PM) was validated as a low Lys source. Weanling pigs (n = 150; initial BW of 14 kg [Exp 2]; n = 80; initial BW of 13 kg [Exp 3]; n = 80; initial BW of 14 kg [Exp 4]) were blocked by initial BW, sex, and ancestry to 6 (Exp 2) or 5 (Exp 3 and 4) treatments with 5 (Exp 2) or 4 (Exp 3 and 4) pens per treatment and 5 or 4 pigs per pen. The experiments were 7 to 14 d in duration. In Exp 2, C-SBM-PM diets contained 0.700, 0.825, 0.950, 1.075, and 1.200% SID Lys. A positive control (PC) diet without PM contained 1.200% SID Lys. Daily gain (452, 479, 465, 551, 567; 588 g/d) and G:F (0.46, 0.46, 0.49, 0.53, 0.54; 0.59) were linearly increased (P < 0.01) as SID Lys increased, but ADFI was not affected. Based on ADG, the SID Lys requirement was estimated at 1.075%. In Exp 3 and 4, C-SBM diets contained 1.075% SID Lys. Methionine, Thr, and Trp were kept in constant ratio to Lys in the diet, and Val and Ile were not added to any diet. The PC diet contained 0.10% supplemental L-Lys. In Exp 3, dietary treatments included 4 levels of supplemental L-Lys: 1) 0.146, 2) 0.192, 3) 0.238, and 4) 0.284%; and 5) PC. There was no linear (P > 0.68) or quadratic (P > 0.67) effect in ADG (580, 569, 624, 597; 598 g/d) or ADFI (1,091, 1,083, 1,109, 1,080; 1,067 g/d), but there was a quadratic effect (P = 0.03) in G:F (0.53, 0.53, 0.55, 0.55; 056). In Exp 4, dietary treatments included 4 levels of supplemental L-Lys: 1) 0.238, 2) 0.284, 3) 0.331, and 4) 0.377%; and 5) PC. There was no linear (P > 0.21) or quadratic (P > 0.22) effect in ADG (561, 545, 580, 539; 539 g/d), ADFI (976, 926, 1005, 964; 900 g/d), or G:F (0.58, 0.60, 0.58, 0.56; 0.60), but plasma urea nitrogen was decreased (linear, P < 0.1) as supplemental L-Lys increased (7.27, 5.66, 4.66, 3.66; 11.88 mg/dL). The results of this research indicate that 0.377% L-Lys can be added to diets for 14-kg pigs with no negative effects on growth performance.

Key Words: pig, nursery, amino acids

334 Optimum isoleucine to lysine ratio in a barley and wheat based diet fed to starter pigs. J. Htoo*[1], C. Zhu[2], and C. de Lange[2], [1]*Evonik Degussa Canada Inc., Gibbons, AB, Canada*, [2]*University of Guelph, Guelph, ON, Canada*.

Reducing dietary CP levels, to reduce N excretion, requires reliable information about the pigs' requirements for potentially limiting AA. Isoleucine may be limiting in low CP pig diets that are supplemented with Lys, Thr, Met and Trp. The objective was to determine the optimum dietary standardized ileal digestible (SID) Ile:Lys ratio for 10 to 22 kg starter pigs. A 3-week dose-response performance study was conducted with 144 Yorkshire pigs (initial BW 10.2 ± 0.8 kg), with 6 pen replicates (2 barrows and 2 gilts per pen) per treatment. A barley and wheat based basal diet was formulated, using analyzed ingredient AA contents and published SID AA values, to meet requirements of AA other than Ile (0.40% SID basis) and Lys (0.90% SID basis). Lys was marginally limiting to avoid underestimation of the Ile:Lys ratio. L-Ile was added to the basal diet to create 5 SID Ile:Lys ratios (44, 51, 57, 63 and 70% in diet 1 to 5). A Lys-adequate diet (diet 6, equivalent to diet 5 with added Lys) was formulated as a control. Pigs had free access to feed and water. Pigs' BW and feed disappearance were recorded weekly. Blood samples were taken on d 7 and 21 (2 pigs per pen) for determining plasma urea nitrogen (PUN). Pigs fed diet 6 had higher ADG, gain:feed and lower PUN than pigs on diet 5 (P < 0.02), indicating that Lys was limiting in diet 1 to 5. Among diets 1 to 5, gain:feed and PUN did not differ (P > 0.10), while ADG and ADFI were influenced by dietary Ile level (P < 0.01). Over the 3-week period, ADG were 436, 578, 542, 576 and 548 g (SEM 19), while ADFI were 740, 1030, 940, 990 and 945 g (SEM 29) for diets 1 to 5, respectively. The SID Ile:Lys ratios to optimize ADG were 50 and 51% based on broken-line and broken quadratic regression

analyses of ADG data, respectively. The optimum SID Ile:Lys ratio was determined to be 50 to 51% for 10 to 22 kg pigs that were fed a barley and wheat based diet.

Key Words: isoleucine, lysine, starter pigs

335 Ileal digestibility of amino acids in low-Kunitz soybeans fed to weanling pigs. K. P. Goebel* and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was conducted to determine the standardized ileal digestibility (SID) of AA in 5 sources of full fat soybeans (FFSB) and soybean meal (SBM) with different concentrations of trypsin inhibitor activity (TIU). A cold-processed FFSB (37.7% CP, 35.4 TIU/mg), a cold-processed low-Kunitz FFSB (36.17% CP, 23.5 TIU/mg), a conventional extruded FFSB (40.45% CP, 4.40 TIU/mg), a low-Kunitz extruded FFSB (38.19% CP, 4.0 TIU/mg), and a conventional SBM (47.47% CP, 3.20 TIU/mg) were used. Twelve weanling barrows (initial BW: 11.1 ± 1.3 kg) were fitted with a T-cannula in the distal ileum. Pigs were allotted to a replicated 6 × 6 Latin square design with 6 diets and 6 periods per square. Five diets were prepared using each of the soybean meals as the only source of AA in the diet. An N-free diet was also included to measure basal endogenous losses of AA. The 2 cold-processed FFSB had lower ($P < 0.05$) SID values for all indispensable AA than the 2 extruded FFSB and SBM. The SID values for all indispensible AA except Trp were greater ($P < 0.05$) in the cold-processed low-Kunitz FFSB than in the cold-processed conventional FFSB. The SID values for AA in the 2 extruded meals and in SBM were not different. These results indicate that trypsin inhibitors reduce AA digestibility in cold-processed FFSB, but a reduction in the concentration of the Kunitz trypsin inhibitor is not sufficient to ameliorate this situation.

Table 1. Digestibility (%) of AA in cold-processed conventional and low-Kunitz soybeans (CP-CV and CP-LK), extruded conventional and low-Kunitz soybeans (E-CV and E-LK), and in SBM

Item	CP-CV	CP-LK	E-CV	E-LK	SBM	SEM
Ile	55.3^{c}	68.4^{b}	89.8^{a}	92.3^{a}	92.4^{a}	2.14
Lys	57.5^{c}	71.0^{b}	90.7^{a}	92.5^{a}	90.6^{a}	2.38
Met	58.7^{c}	71.9^{b}	90.8^{a}	93.8^{a}	94.0^{a}	2.07
Thr	56.4^{c}	66.5^{b}	86.4^{a}	88.0^{a}	88.3^{a}	2.74
Trp	66.9^{b}	71.9^{b}	91.8^{a}	92.8^{a}	91.6^{a}	2.38
Val	54.7^{c}	67.5^{b}	88.1^{a}	90.0^{a}	90.6^{a}	2.52

^{a,b,c}Means within a row lacking a common superscript letter are different ($P < 0.05$).

Key Words: amino acid digestibility, soybeans, trypsin inhibitors

336 Amino acid digestibility and energy concentration in soybean meal produced from high protein, high digestible, or conventional varieties of soybeans and fed to weanling pigs. K. M. Baker* and H. H. Stein, *University of Illinois*, *Urbana*.

Two experiments were conducted using 3 sources of soybean meal (SBM). The SBM were produced from high-protein (SBM-HP), high digestible (SBM-HD), and conventional (SBM-CV) varieties of soybeans. The 3 SBM contained 54.9, 53.6 and 47.5% CP, respectively. The standardized ileal digestibility (SID) of AA in the 3 ingredients was measured using 8 barrows (initial BW: 14.3 ± 1.23 kg BW) that were equipped with a T-cannula in the distal ileum and allotted to a replicated 4 × 4 Latin square design with 4 periods and 4 diets per square. Three diets contained SBM-HP, SBM-LO or SBM-CV as the sole source of AA. The fourth diet was a N-free diet that was used to determine basal ileal endogenous losses of AA. Each period lasted 7 d and ileal digesta were collected on d 6 and 7 of each period. Results showed that the SID for all AA, except Pro, was not different ($P < 0.05$) among the 3 sources of SBM. The DE and ME in the 3 sources of SBM were measured using 24 barrows (initial BW: 11.9 ± 1.24 kg BW) that were placed in metabolism cages and randomly allotted to 4 diets. A corn-based diet and 3 diets containing corn and SBM-HP, corn and SBM-LO, or corn and SBM-CV were formulated. Urine and feces were collected over a 5-d period following a 7-d adaptation period. The DE and ME in each source of SBM were calculated using the difference procedure. The concentration of DE in SBM-HP, SBM-LO and SBM-CV was 4,349, 4,283, and 4,367 kcal/kg DM, respectively. These values were not different from the DE of corn (4,100 kcal/kg DM). The concentration of ME was 4,138, 4,047, and 4,244 kcal/kg DM in SBM-HP, SBM-LO, and SBM-CV, respectively. These values were not different. The ME of corn (4,053 kcal/kg DM) was not different from the ME of any of the SBM. It is concluded that the SID values for SBM-HP and SBM-LO are similar to the SID values for SBM-CV and there is no difference in DE and ME values among the 3 meals.

Key Words: amino acid digestibility, energy concentration, soybean meal

337 Amino acid digestibility in corn and corn co-products fed to growing pigs. G. I. Petersen* and H. H. Stein, *University of Illinois*, *Urbana*.

Many alternative feedstuffs are co-products of corn milling and fermentation. Little is known about the standardized ileal digestibility (SID) of AA in most of these products such as hominy feed, corn gluten meal, corn gluten feed, and corn germ meal in pigs and it is not known how the SID of AA in these ingredients compare to the SID of AA in corn and in distillers dried grains with solubles (DDGS). Eight growing barrows (initial BW: 55 ± 0.85 kg) originating from the matings of line 337 boars to C22 females (Pig Improvement Company, Hendersonville, TN) were randomly allotted to an 8 x 8 Latin square design with 8 diets and 8 periods in each square. Diets contained corn, two different sources of DDGS, hominy feed, corn gluten meal, corn gluten feed, or corn germ meal as the sole source of protein and AA. An N-free diet was used to measure basal endogenous losses of AA and protein. Results showed that the SID of most AA were greater ($P < 0.05$) in hominy feed and in corn gluten meal than in the other ingredients, whereas the SID for most AA in corn gluten feed was lower ($P < 0.05$) than in the other ingredients (Table 1). The SID of Lys in one source of DDGS was lower ($P < 0.05$) than in the other source, but no differences between these 2 ingredients were observed for the other AA. The SID of Ile, Met, and Thr in corn germ meal were lower ($P < 0.05$) than in corn, but for the remaining AA, no differences between corn and corn germ meal were observed. In conclusion, corn gluten feed has a very low SID of Lys and most other indispensable AA, but other corn co-products have SID values for most AA that are comparable to or greater than in corn.

Table 1. Standardized ileal digestibility (%) of AA

Diet	DDGS1	DDGS2	Hominy	Corn Gluten Meal	Corn Germ Meal	Corn Gluten Feed	Corn
Ile	76.27^{c}	79.32^{bc}	87.13^{a}	85.60^{a}	77.11^{c}	64.27^{d}	80.93^{b}
Lys	46.10^{c}	65.39^{b}	79.55^{a}	76.39^{a}	61.01^{b}	28.59^{d}	67.12^{b}
Met	81.12^{b}	83.52^{b}	89.54^{a}	89.03^{a}	81.50^{b}	67.17^{c}	87.29^{a}
Thr	69.77^{c}	74.56^{bc}	79.90^{ab}	82.38^{a}	66.02^{c}	53.90^{d}	76.48^{b}
Trp	86.35^{ab}	86.42^{ab}	90.70^{a}	91.18^{a}	85.50^{bc}	58.31^{d}	80.68^{c}
Val	74.85^{c}	78.54^{bc}	86.03^{a}	84.18^{a}	75.66^{bc}	63.14^{d}	79.12^{b}

$^{a, b, c, d}$ Means lacking common superscript in same row are different ($P < 0.05$).

Key Words: corn co-products, pig, standardized ileal amino acid digestibility

338 Net energy of distillers dried grains with solubles and high protein distillers dried grains fed to growing and finishing pigs. N. A. Gutierres*, D. Y. Kil, and H. H. Stein, *University of Illinois, Urbana*.

An experiment was conducted to measure the NE in distillers dried grains with solubles (DDGS) and in high protein distillers dried grains (HP-DDG) fed to growing and finishing pigs. Conventional DDGS (DDGS-CV), uncooked DDGS (DDGS-BPX), and HP-DDG were used. A total of 52 growing (20 ± 2 kg BW) and 52 finishing pigs (87 ± 10 kg BW) were allotted within each stage of growth to 6 groups based on BW. At each stage of growth, there were 8 replicate pigs in 2 groups and 9 pigs in the remaining 4 groups. The 2 groups with 8 pigs at each stage of growth were used as the initial slaughter group and were harvested at the initiation of the experiment. Pigs in the remaining 4 groups at each stage of growth were housed individually and had free access to feed and water. Treatments included a basal diet containing corn and soybean meal and 3 diets that were formulated by mixing 70% of the basal diet and 30% DDGS-CV, DDGS-BPX, or HP-DDG. Experimental diets were fed to growing pigs for 28 d and to finishing pigs for 35 d. All pigs were harvested at the end of the experiment and blood, carcass, and viscera samples were analyzed for GE, CP, and ether extract. The NE for DDGS-CV, DDGS-BPX, and HP-DDG were calculated by subtracting the contribution from the basal diet to the NE of the treatment diets. In growing pigs, no differences were observed in energy retention and the NE of DDGS-BPX (1,596 kcal/kg), DDGS-CV (1,665 kcal/kg), and HP-DDG (1,783 kcal/kg) were not different. Finishing pigs fed the DDGS-CV diet had greater ($P < 0.05$) lipid gain than pigs fed any of the other diets. The NE of DDGS-CV (2,718 kcal/kg) was also greater ($P < 0.05$) than the NE of DDGS-BPX (2,065 kcal/kg) and HP-DDG (2,291 kcal/kg). The NE of DDGS-CV, DDGS-BPX, and HP-DDG were greater ($P < 0.05$) in finishing pigs than in growing pigs. In conclusion, the NE of DDGS and HP-DDG may vary according to the stage of growth, but the NE of corn-soybean meal diets containing 30% DDGS or HP-DDG, is not different from the NE of corn-soybean meal diets containing no DDGS or HP-DDG.

Key Words: distillers dried grains with solubles, high protein distillers dried grains, net energy

339 Effect of saturated fat in diets with corn distillers dried grains with solubles (DDGS) on growth performance, carcass characteristics and apparent digestibility of nutrients of diets for finishing pigs. L. S. Freitas*[1], M. J. Azain[2], D. C. Lopes[1], C. R. Dove[2], T. D. Pringle[2], P. Cline[2], and T. C. Tsai[2], [1]*Federal University of Viçosa, Vicosa, Brazil*, [2]*University of Georgia, Athens*.

The objective of this study was to determine if the negative effects of DDGS on carcass characteristics could be offset by the addition of saturated fat to the diet. The study was conducted as a 2 × 2 × 2 design with main effects of: DDGS (0 vs 30%), saturated fat (0 vs 4%) and gender (barrow vs gilt). The saturated fat was a dry, animal fat with 70% saturated fat content and an iodine value of 28. There were a total of 80 pigs (IW = 76 kg) randomly assigned to 16 pens (5 pigs/pen) within gender. Experimental diets were fed for 6 wk and the effects on performance, carcass characteristics and nutrient digestibility evaluated. Two pigs/pen were slaughtered to collect samples of leaf and belly fat, backfat and loin for fatty acid profile determination and carcass characteristics. There were no significant effects of the saturated fat addition in either the control or 30% DDGS diets. Overall, ADFI (2.51 vs 3.06 kg/d, $P < 0.01$) and ADG (0.81 vs 1.02 kg/d, $P < 0.01$) were reduced in the pigs fed diets with 30% DDGS, as compared to those fed the control diet. This was largely due to reduced gain and intake in the first 2 wk. Overall, barrows had higher ADFI and ADG than gilts. Changes in carcass characteristics were largely a reflection of the reduced final body weight of pigs fed diets with 30% DDGS and of gilts relative to barrows. The content of linoleic acid was higher in the inner, outer, leaf, and belly fat, and loin muscle of the pigs fed 30% DDGS. As a result of this change, calculated iodine value (IV) of all adipose tissue depots was greater in pigs fed DDGS, with the greatest change in belly fat (Control 69.9 vs. DDGS 79.1, $P < 0.01$). There was no change in the calculated IV of the lipid in loin muscle. The results of this study indicate that the addition of a saturated fat source did not overcome the effects of DDGS on the carcass. This was most likely due to the low digestibility of the saturated fat used in the study.

Key Words: carcass quality, lipid, unsaturated fat

Production, Management and the Environment: Dairy

340 Short dry period: A new reality? Results from a long term field study. D. E. Santschi*[1,2], D. Lefebvre[3], C. L. Girard[1], and D. Pellerin[2], [1]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [2]*Université Laval, Quebec, QC, Canada*, [3]*Valacta, Ste-Anne-de-Bellevue, QC, Canada*.

The purpose of the present project was to verify the effects of two dry period length management practices on production and health of dairy cows in a large field study. Commercial dairy farms (n=13) were involved in this trial for 2 yr. Every two months and within each herd, Holstein cows (n=817) were randomly assigned to a SHORT (SDP; 35d, only pre-calving ration) or CONVENTIONAL (CDP; 60d, dry cow ration until d-21 then pre-calving ration) dry period management, based on parity, predicted 305d milk yield and calving interval. Actual dry period length was 38.2 and 65.8 ± 2.0d ($P<0.001$) for SDP and CDP, respectively. On average, SDP cows produced an extra 350 kg of milk before being dried off, compared to CDP cows. For 2nd lactation cows, incidence of ketosis was lower following the SDP (20 and 32% for SDP and CDP, respectively; $P=0.01$). For cows in their 3rd or greater lactation, incidence of retained placenta was increased (23 and 11% for

SDP and CDP, respectively; *P*=0.002), while udder edema was decreased (*P*=0.02) with SDP. There was no treatment effect on incidence of milk fever and displaced abomasum. Production responses are reported for cows which completed a whole lactation before January 30, 2009. Overall, milk yield for a 305d lactation period was not affected by the dry period management (10,185 ± 415kg; *P*=0.37) but yields varied according to parity (Table). Metabolic and preliminary production responses suggest that a 35d dry period management is suitable for today's dairy cows entering their 3rd or greater lactation.

Table 1. Partial results for milk and component yields

	2nd Lactation				3rd Lactation and greater			
	SDP	CDP	SE	P	SDP	CDP	SE	P
n	62	62			86	83		
305d lactation period (kg)								
Milk	9,412	9,942	433	0.03	10,865	10,762	394	0.64
Fat	360.5	375.8	17.3	0.09	417.6	405.7	19.1	0.18
Protein	316.2	322.3	12.7	0.38	346.7	338.7	12.2	0.20
Total lactation (kg)								
Milk	9,896	10,425	548	0.11	11,507	11,258	445	0.41
Fat	383.4	395.6	21.8	0.35	446.1	428.1	21.4	0.16
Protein	335.7	340.2	17.3	0.69	372.0	358.1	14.4	0.16
Lactation length (d)	321.4	317.8	9.5	0.68	337.5	324.1	7.1	0.07

Key Words: dry period length, dairy cow, production

341 Short dry period management improves peripartum ruminal adaptation in dairy cows. M. S. Jolicoeur*[1,2], A. F. Brito[2], D. Pellerin[1], D. Lefebvre[3], R. Berthiaume[2], and C. L. Girard[2], [1]*Université Laval, Québec, QC, Canada*, [2]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [3]*Valacta, Ste-Anne-de-Bellevue, QC, Canada*.

The objective of this study was to investigate the effects of dry period length management (65 vs. 35 d) on lactational performance and energy balance from 65 d before to 60 d after calving. Holstein cows (n=12) were blocked according to parity, previous milk production and calving date and randomly assigned to either a conventional (CDP: 63.2 ± 2.0 d) or a short dry period (SDP: *35.2* ± 2.0 d). CDP cows were fed a far-off diet up to 28 d before calving, followed by a pre-calving diet, while SDP cows received only the latter diet. After calving, both groups were fed the same lactation diet. Milk yield and DMI were recorded daily and milk composition, weekly. Blood samples were taken twice a week during the first 4 weeks post-calving and weekly otherwise. Ruminal samples were collected 19.6 ± 1.1 d prior and 16.8 ± 1.2 d after calving within a 12 h feeding cycle. Before calving, treatments had no effect on DMI of pre-calving diet, plasma NEFA, BHBA and glucose (*P*>0.05). Plasma urea and ruminal pH were lower (*P*≤0.03) and total VFA concentration was higher for CDP (104.1 vs. 97.0 ± 2.5 mM; *P*=0.04). After calving, there was no treatment effect (*P*>0.05) on plasma glucose and urea, milk component yields and milk production (SDP=38.9; CDP=37.7 ± 1.49 kg/d). Milk fat content was lower (*P*=0.02) in SDP, 3.40 vs. 3.79 ± 0.12%. DMI was higher (*P*≤0.03) for SDP during the first 21 DIM (19.6 vs. 16.9 ± 0.9 kg/d). There was no treatment effect (*P*>0.05) on ruminal pH but total VFA was higher for SDP (114.2 vs. 103.7 ± 3.5 mM; *P*=0.001). Plasma NEFA (228 vs. 304 ± 22 μM) and plasma BHBA (0.71 vs. 0.83 ± 0.05 mM) were both lower (*P*≤0.02) in SDP than CDP cows. The decrease in milk fat content and plasma NEFA and BHBA in SDP cows without effect on milk yield suggest better energy balance likely due to an increased DMI. Results from the present study seem to indicate that reducing the stress associated with dietary changes during the dry period could facilitate ruminal adaptation and improve energy balance.

Key Words: dairy cow, dry period length, transition period

342 Effect of a shortened dry period on the mammary gland physiology. P. Bernier-Dodier*[1], B. G. Talbot[1], and P. Lacasse[2], [1]*Université de Sherbrooke, Sherbrooke, QC, Canada*, [2]*Dairy and Swine R&D Centre, Sherbrooke, QC, Canada*.

The objective of this study was to evaluate the effect of a shortened dry period (35 d vs 65 d) on milk production, on hormone release and on mammary cell proliferation, apoptosis and gene expression during the following lactation. Holstein cows (n=18) were assigned randomly to a conventional (CDP; n=9) or a short dry period (SDP; n=9). Cows were fed the same lactation diet both prior to and after the dry period. During the dry period, CDP cows were fed with a conventional dry period diet until 28 days before calving and then with a pre-calving diet, whereas SDP cows received only pre-calving diets for this period. Milk yield was measured at each milking from 85 d prior to calving to 150 DIM. During this period, serum samples were collected weekly and mammary biopsies were taken at 20 and 150 DIM. The dry period averaged 64.3±1.1 and 31.9±1.0 days for CDP and SDP, respectively. Cows in the SDP group had a lower milk yield than cows on CDP ($P < 0.05$). Interestingly, the mammary gland functional capacity (a measure of mammary gland volume) at 80 DIM was not significantly different ($P > 0.15$) averaging 31.4±1.5 and 28.6±1.5 L for CDP and SDP, respectively. Both groups had similar DMI in the weeks when both were dry and during the following lactation ($P > 0.15$). Serum level of growth hormone level were similar for both groups prior to calving and during the following lactation ($P > 0.15$). Mammary cell apoptosis and proliferation rates were evaluated, respectively, by TUNEL detection and by immunohistological detection of the Ki-67 antigen. Cows from both groups had similar rates of mammary cell apoptosis ($P > 0.15$) which averaged 0.18±0.05 and 0.22±0.04% at 20 DIM and 0.11±0.05 and 0.15±0.04%, at 150 DIM, for SDP and CDP, respectively. Likewise, mammary cell proliferation was unaffected by the dry period length and averaged 0.21±0.09 and 0.31±0.08% at 20 DIM and 0.36±0.09% and 0.38±0.08% at 150 DIM. Consequently, shortening the dry period reduced milk production during the subsequent lactation but did not seem to affect mammary gland functional capacity and the turnover rate of the mammary cells during the following lactation.

Key Words: dry period length, apoptosis

343 Effects of heat stress and monensin on production and metabolism in lactating Holstein cows. J. B. Wheelock*[1], S. R. Sanders[1], M. D. O'Brien[1], C. E. Moore[2], H. B. Green[2], M. R. Waldron[3], R. P. Rhoads[1], and L. H. Baumgard[1], [1]*University of Arizona, Tucson*, [2]*Elanco Animal Health, Indianapolis, IN*, [3]*University of Missouri, Columbia*.

Multiparous cows (n=34, 89 DIM; 537 kg) in environmental chambers were fed a control TMR or a TMR containing monensin (450 mg/cow/d) for 2 experimental periods (P): 1) thermal neutral (TN) conditions (constant 20°C) and ad libitum intake for 9 d, and 2) heat stress

(HS, n=16) or pair-fed (PF; in TN, n=18) for 9 d. HS was cyclical with temperatures ranging from 29.4 to 38.9°C. Rectal temperatures and respiration rates increased in HS vs. PF cows (38.4 to 40.4°C and 40 to 93 bpm). HS reduced DMI (28%), and by design PF cows had similar intakes. Monensin fed cows consumed less DMI (1.59 kg/d) and this was independent of environment. Milk yield decreased 29% (9.1 kg) in HS and 15% (4.5 kg) in PF cows indicating reduced DMI only accounted for 50% of the decreased milk yield during HS. Monensin had no effect on milk yield in either environment. Both HS and PF cows entered into calculated negative energy balance (-2.7 Mcal/d) and had increased feed efficiency (16.5%) during P2. Feeding monensin increased feed efficiency (7%) regardless of environment. Glucose response to an epinephrine (EPI) challenge increased (27%) during P2 for both HS and PF cows while the NEFA response to the EPI was larger (106%) during P2 in the PF compared to the HS cows. Compared to P1, whole-body glucose rate of appearance (Ra) decreased during P2 in both HS and PF cows (646 vs. 514 mmol/h), but increased (15%) on a DMI basis in both HS and PF cows, suggesting an increase in glucose Ra from non-dietary substrates. Although producing similar quantities of glucose, HS cows synthesized ≈225 g less milk lactose, therefore on a milk yield basis, glucose Ra decreased (3.3%) in PF but increased (5.6%) in HS cows. Regardless of environment, monensin fed cows had increased (10%) glucose Ra on a DMI basis. Results suggest the liver remains sensitive but adipose tissue becomes refractory to catabolic signals and that glucose production is preferentially utilized for processes other than milk synthesis during HS.

Key Words: heat stress, monensin

344 Effects of soaking dairy cows at the feed line on dry matter intake and milk production in a tunnel ventilated barn equipped with evaporative pads located in a tropical climate, Thailand. D. V. Armstrong*[1], S. Rungruang[2], V. Wuthiranarith[2], M. J. Brouk[3], and J. F. Smith[3], [1]*University of Arizona*, *Tucson*, [2]*Charoen Pokphand Group Co., Ltd.*, *Bangkok, Thailand*, [3]*Kansas State University*, *Manhattan*.

An experiment was conducted using 86 lactating cows under 150 days in milk and grouped by days in milk and lactation number in two groups. Group 1 was sprayed with water every 5 minutes using approximately 1.65 liters in 30 seconds, for all 24 hours per day. Group 2 was a control group with no water spray. The trial lasted from February to August (26 weeks) and stopped when the first cows were dried off at 55 days before their due to calving date. The free stall barn was a tunnel ventilated barn with a center feed lane and was 16m by 113m with a ceiling height of 2.6m. The barn was equipped with 55.7 sq m of 2.4cm thick evaporative pads on one end and eleven 130cm fans on the opposite end of the barn. Total air exchange for the barn takes place every 42 seconds. Twenty nozzles were located every 1.87m on the feed lane at a height of 1.6m from the floor of the feed line. Outside the barn, temperatures during the trial reached daily highs of 27-34°C, and lows of 22-31°C. Temperatures inside the barn ranged from 23-25°C at 1300 and 17-25°C at 0400. Daily milk weights were collect and averaged by cow and week. Feed and feed refused was weighted daily and samples taken dairy for weekly analysis for D.M.%. Water nozzle performance was observed daily at 0800 and water output measured at the beginning of the trial and every 30 days. Eight of the control cows were removed for foot and leg injury, mastitis or indigestion. Three of the control cows were also removed for the same reasons. The feed intake data was not significantly different, controls averaged 20.60kg per day and spray line group 21.29kg. Milk production was higher for the spray groups in heifers and multiple lactation animals, 0 .85kg heifers and 0.87kg for the multiple lactation cows (P=0.039). Although the numbers are small 90%, of the cows not pregnant before the trial started, were pregnant (17/19) at the end of trial, compared to 55% of the controls (11/20) or non spray animals, which would have an effect on milk production.

Key Words: heat stress, cow cooling, heat abatement

345 Animal welfare in cross-ventilated and naturally ventilated dairy barns in the upper Midwest USA. K. M. Lobeck*, M. I. Endres, E. M. Shane, S. M. Godden, and J. Fetrow, *University of Minnesota*, *St. Paul*.

The objective of this observational study was to describe animal welfare in low profile cross-ventilated freestall barns (CV) compared to conventional naturally ventilated freestall barns (NV) in the Upper Midwest. The study was conducted on 12 commercial dairy farms in Minnesota and eastern South Dakota with herd sizes ranging from 400 to 1600 lactating cows. All herds had stalls bedded with sand. Farms were visited once seasonally between January and November 2008 and approximately ninety percent of the lactating herd was scored on each visit for body condition, hygiene, hock lesion and locomotion. DHIA records were collected monthly. Body condition scores (1=emaciated, 5=severely obese) for winter, spring, summer, and fall, respectively, were (mean±SD): 3.07±0.27, 3.06±0.30, 2.97±0.36, 3.00±0.32 for NV herds; 3.10±0.29, 3.10±0.31, 3.04±0.36, and 3.04±0.37 for CV herds. Hygiene scores (1=clean, 5=dirty) were: 2.6±0.6, 2.5±0.5, 2.8±0.6, and 2.7±0.6 for NV herds; 2.6±0.6, 2.7±0.6, 3.0±0.6, and 2.9±0.5 for CV herds. Hock lesion percent prevalence for winter, spring, summer and fall (mild or severe lesion, respectively) was: 18.9, 6.7; 22.0, 9.3; 25.3, 8.7; 20.2, 6.0 for NV herds; 19.7, 8.9; 19.6, 12.0; 27.9, 11.7; and 18.1, 8.6 for CV herds. Lameness percent prevalence (lame or severely lame, respectively) determined by locomotion scoring (1=normal locomotion, 5=severely lame) was 18.7, 5.4; 19.7, 3.5; 13.2, 2.0, and 13.2, 2.5 for NV herds; 14.1, 3.8; 13.7, 1.3; 9.2, 1.2; and 9.5, 1.9 for CV herds. Somatic cell counts (x 1,000) were: 349±1020, 292±827, 294±827, and 269±713 for NV herds; 323±888, 280±731, 346±918, and 288±813 for CV herds. Cow comfort quotient (%) was 83.4±13.4, 86.5±7.0, 77.3±17.2, and 83.5±15.3 for NV herds; 89.0±10.5, 89.0±7.4, 85.5±14.6, and 88.7±5.2 for CV herds. Stall usage index (%) was 70.1±19.2, 74.7±9.3, 77.3±17.2, and 71.7±15.5 for NV herds; 77.1±11.0, 75.7±9.8, 72.6±16.5, and 77.2±8.4 for CV herds. Based on these results it appears that cross-ventilated and naturally ventilated freestall barns can provide relatively similar animal welfare conditions, but additional investigation and analysis are needed.

Key Words: housing, welfare, lameness

346 Environmental characteristics in cross-ventilated and naturally ventilated dairy barns in the upper Midwest USA. K. M. Lobeck*, M. I. Endres, E. M. Shane, and K. A. Janni, *University of Minnesota*, *St. Paul*.

The objective of this study was to characterize air quality, light intensity, and air velocity in low-profile cross-ventilated freestall barns (CV) compared to conventional naturally ventilated freestall barns (NV). The study was conducted on 12 commercial dairy farms in Minnesota and eastern South Dakota between January and November 2008. Each farm was visited seasonally for a total of four visits for the year. Representative measurements were taken with portable meters along the feed bunk and inside the pen twice daily. Measurements included

ammonia and hydrogen sulfide concentrations, light intensity, and air velocity. Ammonia concentrations (ppm, mean±SD) were 3.5±2.3 in the NV barns and 5.2±2.3 in the CV barns. Ammonia concentrations for winter, spring, summer, and fall, respectively were 1.9±2.19, 3.59±2.1, 5.6±1.3, and 2.9±1.5 for NV barns; 5.4±2.6, 5.0±2.4, 6.2±1.7, and 4.3±2.2 for CV barns. There were housing system and season($P \leq 0.001$), and system-season interaction ($P=0.039$) effects for ammonia concentrations. Hydrogen sulfide concentrations (ppb) were 24±26 for NV barns and 67±240 for CV barns. Seasonal concentrations of hydrogen sulfide were 40±27, 14±14, 30±35, and 13±11 for NV barns; 118±418, 56±179, 69±235, and 42±54 for CV barns. There were system and season effects ($P \leq 0.01$). Light intensity (lux) was 945.6±2200.6 for NV barns and 158.0±129.5 for CV barns. Seasonal light intensity was 827.4±616.6, 871.1±2293.4, 931.7±923.9, and 1130.8±3545.6 for NV barns; 214.4±193.1, 174.4±161.8, 144.6±83.4, and 131.5±80.3 for CV barns. There was a system effect ($P \leq 0.001$) and a trend for season effect ($P=0.057$). Air velocity (m/s) was 43.9±48.6 for NV barns and 56.6±50.5 for CV barns. Seasonal air velocity was 17.7±17.4, 44.1±38.5, 61.5±53.2, and 48.9±58.7 for NV barns; 15.1±10.8, 78.1±55.8, 84.7±48.5, and 39.8±35.0 for CV barns. There was no difference between systems for air velocity. However, there was a season effect ($P \leq 0.001$). These results indicate that there were some environmental differences between cross-ventilated barns and conventional naturally ventilated barns.

Key Words: housing system, air quality, light intensity

347 Changes in body condition scores during the transition period in Holstein cows. J. Moro-Méndez*, H. Monardes, and R. I. Cue, *McGill University, Department of Animal Science, Ste-Anne-de-Bellevue, QC, Canada*.

The objectives were to characterize body condition scores (BCS) on Holstein cows by studying two overlapping stages (before and after drying-off, and during the transition period) and to determine the relative importance of some environmental factors on BCS. Data were provided by Valacta, and consisted of BCS recorded on a 5-point scale (1=thin, 5=obese). The statistical analysis of BCS before and after drying-off included BCS records collected between 60 days before and after drying-off. After edits there were 11784, 10778 and 7840 records of first, second, and third parity cows, respectively. Analysis of BCS during the transition period included records of cows with consecutive pairs of lactations for each transition period (i.e. first to second, second to third, and third to fourth lactations). Only one BCS record per cow per lactation, collected between 90 days before and 21 days after calving, was kept. After edits, there were 8321, 6503, and 4313 records of first to second, second to third, and third to fourth parities, respectively. Two models, using SAS Proc Mixed, were fitted with the following fixed effects: Herd-Year-Season of calving (HYS), calendar month of BCS recording, age (either at drying-off or at calving of the lactation being transitioned into), days (either, dry days, or transition days), and level of milk production. BCS increased after drying-off, decreased just before calving and there was an increase from the nadir at 45 days post calving. Days dry and transition days were highly significant in all parities under study. In contrast with average cows, lower and higher producing cows in the previous lactation showed lower BCS in the subsequent lactation. Level of production and HYS were the main environmental factors affecting BCS during the dry and transition periods. The recording system of body condition score in Quebec provides information suitable for the analysis of BCS throughout the lactations of Holstein cows.

Key Words: body condition score, drying-off, transition period

348 The association of level of milk production with reproductive performance. M. S. Campbell[1], K. Hand[1], D. F. Kelton[1], F. Miglior[2,3], and S. J. LeBlanc*[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Canadian Dairy Network, Guelph, ON, Canada*, [3]*Dairy and Swine Research & Development Centre, Agriculture and Agri-Food Canada*.

There is debate about possible antagonism between high milk production and reproductive performance in dairy cattle. The objectives were to examine the association of the level of production with reproductive performance at the herd and animal levels. Data were extracted from all 6326 herds on milk recording in Ontario and western Canada. There were 3297 herds with complete AI and pregnancy data for the year 2005 to which herd demographics, production, milking frequency and housing type were added. Herd annual mean (SD) 21-d pregnancy rate (PR), insemination rate (IR) and conception risk (CR) were 12.5 (4.7), 33.9 (10.5) and 37.2 (9.9), respectively. Herd PR was modeled with mixed linear regression with random herd effect. Accounting for herd size, parity distribution, breed, and housing, each 1000 kg of herd mean mature equivalent milk was associated with an increase of 0.7 points of PR ($P < .0001$). Individual data (at least the first 3 test days (TD)) were available for 103,060 cows in 2076 herds. Times to first AI and to pregnancy were modeled with survival analysis with a random herd effect. Production was described by kg of milk and 305 d projections at TD 1, 2, and 3, and completed 305 d records, each of which had a significant univariable association with shorter time to pregnancy. Milk yield at TD1 was not associated with time to first AI. In the final model accounting for parity, season of calving, and DIM at TD, there was a small association of increased milk yield at TD1 with longer time to pregnancy (hazard ratio (HR) = 0.997 per kg, P = .02) and in the same model increasing 305 d projection at TD3 was associated with shorter time to pregnancy (HR = 1.07 per 1000 kg, $P < 0.0001$). In summary, herd pregnancy rate was significantly higher in higher producing herds, and for individual cows there were significant but conflicting and practically small effects of level of production on time to pregnancy. These results suggest that managing to provide for high production can be compatible with good reproductive performance.

Key Words: reproduction, fertility, milk yield

349 Management practices associated with conception rate and service rate of lactating Holstein cows in large, commercial dairy herds. J. M. Schefers*[1], K. A. Weigel[1], N. B. Cook[1], C. L. Rawson[2], and N. R. Zwald[2], [1]*University of Wisconsin, Madison*, [2]*Alta Genetics USA Inc., Watertown, WI*.

Data from lactating Holstein cows in herds that participate in the Alta Genetics (Watertown, WI) Advantage® progeny testing program were analyzed to explain management factors associated with herd average conception and service rates on large commercial dairies. Dairy Comp 305 herd management software (Valley Ag Software, Tulare, CA) was used as the source of data related to production, reproduction, culling, and milk quality for 108 herds. Also, a survey regarding management, facilities, nutrition, and labor was completed by Alta Genetics Advantage® consultants on 86 farms. A total of 42 explanatory variables related to management factors and conditions that could affect conception and service rate were considered in this study. Models explaining conception and service rates were developed using a machine learning algorithm for constructing model trees. The most important explanatory variables associated with conception rate were the percentage of repeated inseminations between 4 and 17 d post artificial insemination, stocking density in the breeding pen, length of the voluntary waiting period, and somatic cell score. The most important explanatory variables associated with

service rate were the number of lactating cows per breeding technician, use of a resynchronization program, utilization of soakers in the holding area during the summer, and bunk space per cow in the breeding pen. The aforementioned models explained 35% and 40% of the observed variation in conception rate and service rate, respectively.

Key Words: reproductive performance, management, machine learning

350 Pregnancy rates and herd turnover proportions after using a hormonal synchronization protocol in primiparous dairy cows in a California dairy. K. G. Gohary*[1], S. S. Aly[2], D. C. Wagner[1], B. R. Hoar[2], V. M. Lane[3], and J. D. Rowe[3], [1]*William R. Pritchard Veterinary Medical Teaching Hospital, School of Veterinary Medicine, University of California, Davis*, [2]*Department of Veterinary Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis*, [3]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis*.

The objective of this trial was to evaluate the effect of hormonal synchronization on pregnancy rate (PR) and herd turnover (HT) proportions in primiparous dairy cows. To accomplish this goal a clinical trial was designed to estimate the pregnancy incidence density (PID) rate after up to 3 inseminations, median time to pregnancy and herd turnover proportions in the current and subsequent 2 lactations. A cohort of primiparous Holstein cows (n=333) housed in a freestall dairy in the central valley of California was selected. Cows were systematically enrolled into 2 groups. Cows in the treatment group (n=178) received 100µg of gonadotropin-releasing hormone (GnRH) on day 0, 25mg of prostaglandin $F_{2\propto}$ ($PGF_{2\propto}$) on day 7 and a second GnRH treatment (100µg) on day 9 and were artificially inseminated after 16 hours regardless of heat signs. Cows in the control group (n=155) were inseminated upon heat detection or observation of rubbed tail chalk without receiving hormonal treatments unless warranted for pathological reasons. Veterinarians were unaware of cow group allocation during herd checks. Median time to pregnancy was less for the treatment group than the control group (53 days versus 87 days, *P*=0.023). Although not significant, the PID ratio of the treatment group to the control group was 1.13 (*P*=0.46) indicating a 13% higher PR among synchronized cows than controls. In contrast, PID ratio for cows enrolled with a body condition score (BCS)<2.5 was 1.55 indicating that under-conditioned cows had a 55% higher PR when synchronized compared to control cows of similar BCS (*P*=0.34). However, synchronized cows with 2.5 to 3.5 BCS had only a 4% greater PR than controls of similar BCS (*P*=0.82). Proportion of HT after the first, second and third lactations and overall after 3 lactations did not differ among treatment and control groups (*P*=0.14). In summary, hormonal synchronization in primiparous cows reduced the median time to pregnancy, may be of benefit to under-conditioned cows, and had no significant effect on herd turnover in current and subsequent lactations

Key Words: primiparous dairy cows, hormonal synchronization, pregnancy rates

351 Effect of days open in the previous lactation on the risk of culling or death around calving. P. J. Pinedo* and A. De Vries, *University of Florida, Gainesville*.

The objective was to evaluate the effect of days open (days to conception) on the risk of culling and death in the proximity of a subsequent calving in Holstein cows enrolled in the DHI program. After edits, 6,974,152 observations of cows calving between 2000 and 2006 in herds located in 38 states in the Eastern US were available. The period at risk included the time between 14 d before expected calving and 60 d after calving. Days open were categorized in 6 periods; 0 to 45 d, 46 to 90 d, 91 to 150 d, 151 to 210 d, 211 to 300 d, and 301 to 600 d. Other variables of interest included parity, last test day milk yield prior to dry off, last test day milk yield by 60 d after calving, season of calving, and 305-d milk production. Control variables were calving year, herd size, and herd milk production. All variables were categorized. Generalized mixed models were used and included herd as random effect. Interactions between days open and the variables of interest were included in the final model if P â‰¤ 0.10. Least square means (LSM) for the risk of death were 1.01, 1.00, 1.13, 1.27, 1.58, and 2.00%, for increasing categories of days open. Similarly, for the same categories, LSM for the risk of culling (excluding death) were 2.07, 2.19, 2.31, 2.50, 2.69, and 3.07%. Least square means for the risk of culling and death combined (CD) were 2.78, 3.70, and 5.11% for parity 2, 3 and â‰¥4, respectively. For the risk of CD, LSM were 4.52, 3.54, and 3.29% for low, medium or high test day milk yield prior to dry off, and were 10.2, 2.66 and 1.87% for low, medium or high test day milk yield by 60 d after calving. The effect of days open on the risk of culling was slightly greater for lower parity cows, for cows with greater test milk yield prior to dry off, for lower test milk yield by 60 d after calving, for winter calvings, and for lower 305-d milk production in the previous lactation. Similar trends for these interactions were found for the risk of death. It is concluded that increased days open in the previous lactation were associated with a greater risk of culling and death around calving.

Key Words: culling risk, death risk, days open

Ruminant Nutrition: Fat Supplementation

352 Effective use of safflower seeds in early lactation diets with alfalfa hay and corn silage. A. Alizadeh[1], G. R. Ghorbani[1], M. Alikhani[1], H. R. Rahmani[1], and A. Nikkhah*[2], [1]*Isfahan University of Technology, Isfahan, Iran*, [2]*Zanjan University, Zanjan, Iran*.

Safflower seed (SS), *Carthamus tinctorius* L., has the highest concentration of linoleic acid among 80 oilseeds. We hypothesized that SS can be effectively fed with cottonseeds (CS) in diets with dry hay and ensiled forage to maintain feed intake, energy metabolism and productivity of early lactation cows under negative energy balance. Our objective was to determine the effects of feeding diets containing 1) 10% whole CS with no SS (SS0), 2) 7.5% CS + 2.5% SS (SS2.5), and 3) 5% CS + 5% SS (SS5), on a DM basis, on feed intake, rumen fermentation, blood metabolites and lipids, and milk production. Nine multiparous early lactation Holstein cows (46 ± 7 days in milk) were used in a replicated 3 × 3 Latin square design study with 21-d periods. Each period had 14-d of adaptation followed by 7-d of data collection. Cows were fed isoenergetic and isonitrogenous total mixed rations, based on alfalfa hay, corn silage, and barley and corn grains, twice daily at 0900 h and 1600 h. Data were analyzed using mixed models with the fixed treatment effect and random period and cow effects. Feeding SS0, SS2.5 and SS5 diets did not respectively affect dry matter intake (23.3, 24.1, 22.8 kg/d, P=0.42), rumen pH (6.58, 6.49, 6.55, P=0.86) and ammonia (9.4, 8.5, 8.5 mg/dl, P=0.24) and VFA concentrations, blood levels of

insulin (6.6, 7.0, 7.0 µIU/ml), NEFA (161, 165, 156 µEq/l, P=0.20), urea (19.3, 20, 20.7 mg/dl, P=0.22) and triglycerides (13.0, 14.8, 14.5 mg/dl, P=0.32), as well as milk yield (36.0, 36.8, 35.4 kg/d, P=0.44) and energy-corrected milk yield (36.3, 36.5, 35.3 kg/d, P=0.13). Adding SS to the ration linearly reduced blood glucose (54.8, 52.3, 50.7 mg/dl, P=0.05) and BHBA (5.05, 5.13, 3.95 mg/dl, P=0.03) and increased blood total cholesterol (241, 247, 257 mg/dl, P<0.01) and low-density lipoproteins (193, 194, 203 mg/dl, P=0.02). Results demonstrate that SS as an economical and rich source of essential fatty acids can be included up to 5% of diet DM alongside CS for early lactation cows without affecting feed intake while maintaining rumen fermentation, peripheral energy supply and milk production.

Key Words: safflower seed, early lactation, palatability

353 Effect of flaxseed oil supplementation on *in vitro* ruminal fermentation in the rumen simulating fermenter (RUSITEC). K. J. Hart*, F. Wurlod, D. A. Kenny, and T. M. Boland, *University College Dublin, Lyons Research Farm, Newcastle, Co. Dublin, Ireland*.

Flaxseed oil has a high content of the essential dietary poly unsaturated fatty acids (PUFA) linolenic and linoleic acid. Supplementation of ruminant diets with PUFA may provide an alternative hydrogen sink within the rumen and as a result may reduce enteric methane production. The aim of this experiment was to investigate the effect of increasing flaxseed oil inclusion level on fermentation products and methane production using a rumen simulating fermeter (RUSITEC) system. Sixteen RUSITEC fermentation vessels were used in this study, each with a volume of 0.85 L. Rumen fluid was collected from four fistulated lactating dairy cows grazing grass supplemented with 6 kg/d concentrate. Artificial saliva was infused at a constant rate of 0.7 L /d using a peristaltic pump. Vessels were fed 16 g/d of a 70:30 dried grass:dairy concentrate on a DM basis. Raw flaxseed oil was added directly to the feed bags prior to incubation at 0, 20, 40 or 60 g/kg DM. Treatments were assessed in quadruplicate. Following a 10 d stabilization period daily methane production was recorded and subsamples of outflow liquor were collected for VFA and ammonia analysis for the following 4 d. Data were anlayzed using the MIXED procedure of SAS with terms for oil level and machine included in the statistical model. There was no effect of level of oil inclusion (P > 0.05) on any of the variables measured. Results from this experiment show that the addition of flaxseed oil does not affect *in vitro* rumen production of VFAs, ammonia or methane at least at the forage to concentrate ratio used here.

Key Words: methane, dairy, flaxseed oil

354 Effect of prepartum feed restriction and oilseed supplementation on peripartum cow metabolism. A. Hayirli*[1] and L. Doepel[2], [1]*Atatürk University, Erzurum, Turkey*, [2]*University of Alberta, Edmonton, AB, Canada*.

This experiment was conducted to determine if feed restriction and supplementation of unsaturated fatty acids (UFA) during the close-up dry period would improve metabolic status and alleviate the severity of negative energy balance (EB) and hepatic lipidosis (HL) in early lactation. Holstein cows (n=77) were assigned randomly to 1 of 2 feeding schemes (FS): ad libitum (AL) and 30% feed restriction (FR) and 3 oilseeds (OS): canola (C), linola (L), and flax (F) for 4 wks before expected calving. During the first 63 DIM cows were fed a common lactation diet. Blood samples were collected 19 times between d -34 and d 63 relative to calving and liver samples were obtained on d -34, 1 and 21. Data were subjected to ANCOVA for main effects of FS and OS and their interactions by time. There were no FS by OS interaction effects on the response variables. FR was associated with a lower EB prepartum but a less negative EB in early lactation. FS did not alter plasma glucose (mg/dl), BHBA (mg/dl), IGF-1 (ng/ml), and CCK (pmol/l) concentrations that averaged 67.1, 6.8, 69.9, and 1.2 prepartum and 58.9, 11.5, 35.7, and 1.8 postpartum, respectively. Liver TG was not affected by FS or OS. Overall, OS type did not affect response variables. In conclusion, feed restriction but not UFA provision during the close-up dry period improved EB without altering the severity of HL in early lactation.

Table 1. Energy balance and metabolic profile of peripartum cows

	FS			OS	
Variables	AL	FR	C	L	F
Prepartum					
EB, Mcal/d[a]	4.63	-0.33	1.97	2.52	1.97
Insulin, µIU/ml[a]	6.8	4.4	5.6	5.9	5.3
NEFA, mEq/ml[a]	436	572	541	491	480
Leptin, ng/ml[a]	14.2	10.8	12.8	12.5	12.0
Postpartum					
EB, Mcal/d[a]	-6.99	-4.49	-5.25	-5.87	-6.08
Insulin, µIU/ml	3.5	4.3	3.9	4.8	3.0
NEFA, mEq/ml	810	727	774	759	773
Leptin, ng/ml	8.6	8.9	8.8	9.2	8.3
Liver TG, µg/g DM	13.7	12.4	12.9	14.5	11.9
Liver Gly, µg/g DM[b]	2.9	4.4	3.1	3.3	4.5

[a]FS effect: P<0.01; [b]OS effect: 0.05≤P<0.10

Key Words: feed restriction, fatty acid supplementation, liver metabolism

355 Effects of duodenal infusion of linolenic acid on milk fatty acid composition in dairy cows. D. P. Bu[1], . Khas-Erdene[1], J. Q. Wang*[1], H. Y. Wei[1], L. Y. Zhou[1], and J. K. Drackley[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, P. R. China*, [2]*Department of Animal Sciences, University of Illinois, Urbana*.

Increasing the linolenic acid content of milk fat might be desirable to meet consumer preference. Our objective was to determine the potential to alter the content of C18:3 in milk by duodenal infusion of a high C18:3 free fatty acid mixture. Four multiparous Chinese Holstein cows (BW = 556 ±19 kg, DIM = 93 ± 9 d) fitted with duodenal cannulas were administered 2 treatments in a crossover design. Treatments were homogenized aqueous mixtures of α–linolenic acid (LNA; 82.4% *cis*–9, *cis*–12, *cis*–15 18:3; 14.7% *cis*–9, *cis*–12 18:2; 2.8% *cis*–9 18:1) or control containing only the emulsifying ingredients. The control infusate consisted of 15 g/d of xanthan gum, 5 g/d sodium alginate, and 25 g/d of Tween 80 in 10 L of water. Each period lasted 5 wk, in which 2 cows received each amount (0, 40, 80, 120, and 160 g/d) of LNA for 1 wk each, and the other 2 cows received only the carrier infusate. Measurements were made during the last 3 d of each infusion amount. Data were analyzed statistically by using PROC MIXED of SAS. Polynomial contrasts were constructed of linear, quadratic, and cubic effects of amount by treatment. Significance was decleared at P < 0.05. Increasing the amount of LNA infused into the duodenum linearly increased concentrations of

cis–9, *cis*–12, *cis*–15 C18:3 (0.16, 6.49, 12.42, 18.75, and 25.38% for LNA infused at 0, 40, 80, 120, 160 g/d, respectively) and *cis*–9, *cis*–12 C18:2 (2.38, 2.94, 3.19, 3.77, and 4.16%). Increasing LNA decreased percentages of short-chain fatty acids, C14:0, and C16:0 so that total FA ≤16C (65.2, 60.7, 57.8, 51.4, 46.0%) decreased linearly. Increasing LNA linearly decreased percentages of *cis*–9 C18:1 (17.4, 16.6, 13.7, 11.7, 11.5%) and *cis*-9, *trans*–11 C18:2 (0.37, 0.37, 0.28, 0.26, 0.18%) in milk fat. Milk fat content of *cis*–5, *cis*–8, *cis*–11, *cis*-14, *cis*–17 C20:5 (0.09, 0.18, 0.22, 0.21, 0.22%) was quadratically affected, whereas concentrations of C18:0, *trans*–9 C18:1, *trans*–11 C18:1, and *trans*–10, *cis*–12 C18:2 were not affected. Increasing the supply of linolenic acid to the small intestine linearly increased linolenic acid in milk fat and markedly altered milk fat composition.

Key Words: linolenic acid, milk fatty acids, supplemental fat

356 Milk fatty acid and protein profiles of grazing cows fed high–fat protein supplements. R. Nyoka*, A. R. Hippen, K. F. Kalscheur, and D. J. Schingoethe, *South Dakota State University*, *Brookings*.

To determine the effect of supplementing grazing cows with various protein and fat supplements, 27 multiparous cows (9 Brown Swiss and 18 Holsteins, 144 ± 83 DIM) were allowed to graze alfalfa pasture and fed partial Total Mixed Rations (pTMR) containing: 1) dried distillers grains with solubles (DDGS), 2) soybean meal (SBM), or 3) fishmeal (FM). The pTMR were fed to supply 50% of estimated energy requirements (NRC 2001) and were formulated to have similar crude protein and fat content. Cows had *ad lib* access to alfalfa pasture during the 8-week experimental period. Intakes of pTMR (DM basis) were 23.8, 22.3 and 23.3 kg/day for DDGS, FM and SBM supplemented groups respectively. There were no dietary effects on milk yield with 31.7, 31.4 and 31.5 kg/cow/day for DDG, FM, and SBM. Milk fat percent was greatest for FM followed by DDG and SBM (3.61, 3.53, 3.23%, $P \leq 0.01$). Cows fed DDGS and SBM had lesser ($P \leq 0.05$) concentrations of C12:0, C14:0 and C16:0 in milk fat compared with FM. Dietary treatments did not affect the CLA concentrations in milk (1.10%, 1.14% and 1.04% for DDGS, FM and SBM). Milk from cows fed DDGS and SBM had greater ($P \leq 0.04$) concentrations of long chain fatty acids (58.6% and 58.5%, respectively) and polyunsaturated fatty acids (8.7% and 9.6%) compared with 56.3% and 8.2% from FM. Milk total protein, casein, and casein/protein ratio were not affected by the dietary treatments. A significant breed × diet interaction was observed in both milk total protein and casein ($P \leq 0.01$). Holstein cows produced greater protein and casein concentrations in milk when fed FM (3.0% and 2.7%) followed by DDGS (2.8% and 2.4%) and SBM (2.6% and 2.2%). Brown Swiss cows produced greater protein and casein when fed DDGS (3.2% and 2.7%) and SBM (3.2% and 2.6%) compared with FM (2.6% and 2.2%). Supplementing grazing cows with high–fat protein supplements can increase the levels of the more desirable long chain and polyunsaturated fatty acids in milk without compromising on milk yield and components.

Key Words: high–fat protein, grazing, milk fatty acids

357 Production response to fat supplementation of corn silage based diets in dairy goats. C. Montes de Oca G, L. Olivares R, J. G. Estrada F, and M. Gonzalez-Ronquillo*, *Universidad Autonoma del Estado de Mexico*, *Toluca, Mexico*.

High quality milk and dairy products are nutritious and healthy foods that are frequently consumed by people which desire healthy products. Recently the ruminant fats are the major source of CLA in the human diet, the available evidence suggests that increases in 18: 2n-6 intake on high-forage diets could be used as a nutritional strategy for enhancing the supply of cis-9,trans-11-CLA available for absorption. The objective of the present study was to determine the milk yield and milk composition in dairy goats, supplemented with different fat sources, sunflower seeds oil rich in 18:2n-6, linaza seeds or Megalac R. Six lactating dairy French alpine goats were used, BW 52.5 Kg, The experimental design was a 3x 3 Latin square 3, 9-wk periods. Goats were housed in a metabolism unit in individual stalls, and feeded at 0800 and 1600 h, with free water access and milked in situ at 0800 h. Diets (14% CP, 2.8 Mcal EM) were formulated with rye grass silage and hay and supplemented cereal based concentrated with sorghum grain, canola meal and minerals plus one fat source, T1: Megalac-R, T2: Sunflower seed oil, T3: Linaza seeds oil. . Experimental takes 20 days, the first 14 days were for adaptation period and the last 6 days for taking samples. Individual intake and daily milk production were recorded daily. Milk fat, true protein, SNF, were determined by near-IR spectroscopy (Milko-Scan 133B analyzer; Foss Electric, Hillerød, Denmark). Data from the last 6-day of each period were analyzed using proc glm in SAS; LS means are reported in the table. With the exception of milk fat content, there were not significant effects of diet ($P>0.05$), on all production traits. However, yield of milk and true protein were not different between diets. Results indicated that Megalac-R increase milk fat content.

Table 1.

Item Dietary fat source	Megalac-R	Linaza seed	Sunflower seed	SE	Diet
Milk yield (Kg/d)	0.743	0.772	0.782	0.004	NS
Fat (g/d)	39.9	38.5	40.5	0.27	NS
Fat (%)	5.35a	4.98b	5.14ab	0.10	P<0.05
True Protein (g/d)	33.6	35.2	35.6	0.21	NS
True Protein (%)	4.5	4.6	4.6	0.02	NS
SNF (g/d)	71.8	75.1	76.0	0.44	NS
SNF (%)	9.7	9.7	9.7	0.03	NS

ab in the same row P<0.05

Key Words: goats, milk composition, fat sources

358 Tracer studies in cultures of ruminal microorganisms reveal the formation of conjugated double bonds originating from biohydrogenation of ^{13}C- labeled linolenic acid. Y. J. Lee, C. M. Klein, and T. C. Jenkins*, *Clemson University*, *Clemson, SC*.

Conjugated linoleic acid (CLA) isomers accumulate in ruminal contents of cattle and are believed to arise exclusively from the microbial biohydrogenation of linoleic acid. Yet, the addition of linolenic acid to ruminal cultures causes shifts in CLA production. To test the possibility of direct conversion of linolenic acid to CLA, two separate in vitro experiments were run that each included 24 culture tubes containing ground dairy feed, buffer, and strained rumen fluid from a continuous culture fermenter. Substrate in half of the cultures contained unlabelled linoleic acid and the remaining cultures contained the same quantity of either 1-^{13}C-linolenic acid in Exp. 1 or U-^{13}C-linolenic acid in Expt. 2. Samples were taken from each flask at 0, 3, 24, and 48 hours. Methyl esters of fatty acids were separated on a 100-m CP-Sil 88 column and abundances of the quasimolecular ion (M) and M+1 or M+18 ions were determined by mass spectroscopy in positive chemical ionization mode using methane reagent gas. Geometry and double bond posi-

tion of CLA isomers was verified by acetonitrile chemical ionization tandem mass spectrometry. Enrichment for each peak was calculated as [(M+1(18)/M) * 100] in labeled minus unlabelled cultures and tested for their difference from zero by t-test ($P < 0.05$). From 0 to 48 h of incubation, linolenic acid quantity declined ($P < 0.05$) from 2.19 to 0.06 mg/culture, t11 18:1 increased ($P < 0.05$) from 0.06 to 0.82 mg/culture, and stearic acid increased ($P < 0.05$) from 0.42 to 1.90 mg/culture indicating active biohydrogenation. Enrichment of linolenic acid remained constant over all incubation times ranging from 33.3 to 35.5%. The t11 18:1 was enriched ($P < 0.05$) by 3 h through 48 h incubation, and stearic acid was enriched ($P < 0.05$) by 24 and 48 h incubation. At 48 h of incubation, enrichment was observed in all CLA isomers identified including c9t11, t10c12, and t9t11. The results of this study verified the formation of a multitude of CLA isomers originating from linolenic acid biohydrogenation, including c9t11 and t10c12 CLA.

Key Words: linolenic acid, biohydrogenation, conjugated linoleic acid

359 Effect of linolenic acid, fish oil and dietary vitamin E supplementation on sustained conjugated linoleic acid production in milk fat from dairy cows. A. M. O'Donnell*, K. P. Spatny, J. C. Alishauskas, and D. E. Bauman, *Cornell University, Ithaca, NY.*

Dairy products are increasingly recognized for the beneficial health effects provided by their bioactive components, among which is rumenic acid (*c*-9, *t*-11 CLA; RA). RA is found predominantly in ruminant products and can be enhanced through manipulation of the cow's diet with inclusion of oils rich in polyunsaturated fatty acids. However, the addition of these oils to a ruminant diet often causes a shift in biohydrogenation pathways that results in milk fat depression (MFD). The objective of this study was to examine if vitamin E supplements together with linseed oil and low levels of fish oil would improve sustainability of enhanced RA content in milk fat while minimizing the risk of MFD. Holstein cows (n=48) were assigned to a randomized complete design with repeated measures into four treatments for 28d: 1) control (C), 2) 2.5% linseed oil (L), 3) 2.5% linseed oil plus 0.5% fish oil (LF), and 4) 2.5% linseed oil plus 0.5% fish oil plus 10,000 IU vitamin E/d (LFE). A 2 wk pre-treatment period served as the covariate. Cows were individually fed a corn-based TMR; oil supplementation was incorporated in the mixed diet and vitamin E top-dressed daily. Milk fat percent and yield (wk 4) were reduced incrementally with increased oil supplementation (3.69, 3.21, 2.09 and 2.24% for C, L, LF, and LFE, respectively; $P<0.05$). Vitamin E was ineffective in preventing MFD. Milk fatty acid profiles for LF and LFE treatments were indicative of classical MFD with increased content of *t*-10 18:1 and *t*-10, *c*-12 18:2 CLA, as well as increased *t*-9, *c*-11 18:2 CLA. RA also increased significantly (0.38, 0.94, 2.70, and 2.62 for C, L, LF and LFE), as well as its endogenous precursor, *t*-11 18:1 (0.91, 2.43, 6.71 and 6.46 for C, L, LF and LFE, respectively). In conclusion, dietary supplementation of fish and linseed oil markedly increased milk fat content of RA, but also shifted biohydrogenation pathways to produce fatty acid intermediates known to induce MFD, and this effect was not altered by vitamin E supplementation.

Key Words: conjugated linoleic acid, milk fat

360 Lactation performance of dairy cows supplemented with different oil sources. J. A. Ye[1], C. Wang*[1], H. F. Wang[2], H. W. Ye[3], B. X. Wang[1], H. Y. Liu[1], Y. M. Wang[1], Z. Q. Yang[1], and J. X. Liu[1], [1]*Institute of Dairy Science, Zhejiang University, Hangzhou, P.R. China*, [2]*School of Forestry and Biotechnology, Zhejiang Forestry University, Hangzhou, P.R. China*, [3]*Hangzhou Zhengxing Animal Industries, Hangzhou, P.R. China*.

The objective of the study was to investigate the effects of supplemented oils on milk yield, milk composition and fatty acid profiles in lactating dairy cows. Forty-eight Chinese Holstein dairy cows were used in a completely randomized block design. The animals were allocated to four dietary treatments according to DIM and milk yield, and supplemented with none (control), 2% flaxseed oil (FSO), 2% soybean oil (SBO), or 2% oil from extruded soybeans (ESB). The experiment lasted 9 weeks including the first week for adaptation. Milk yield was recorded daily, and milk compositions and fatty acid profiles were analyzed weekly. Feeding FSO, SBO and ESB resulted in higher milk yield vs. the control (27.0, 27.0, and 26.5 vs. 25.4 kg/d), but decreased milk fat content (3.29, 3.31, 3.20 vs. 3.60%), with little difference in fat-corrected milk yield and content of milk protein and total solids among all the treatments. The fatty acid profile of milk was improved by fat supplementation. Feeding oil reduced the proportion of both short-chain ($C_{8:0}$ to $C_{12:0}$) and medium-chain ($C_{14:0}$ to $C_{16:1}$) fatty acids, and increased the proportion of long-chain fatty acids in milk fat. *Cis*-9, *trans*-11 CLA in milk fat was increased from 0.38% for the control to 0.79, 1.51, and 1.56% for the cows supplemented with FSO, SBO, and ESB, respectively. Feeding oils rich in linoleic acid (SBO and ESB) was more effective in enhancing *cis*-9, *trans*-11 CLA in milk fat than oils containing linolenic (FSO). There was a linear relationship between transvaccenic acid and *cis*-9, *trans*-11 CLA content in milk. Over all, oil supplementation increased milk yield and improved fatty acid profile in milk fat.

Key Words: conjugated linoleic acid, dairy cows, milk performance

361 Milk production and composition from cows with different levels of cashew nut in the diet. P. G. Pimentel[1], L. A. Leite[2], I. R. F. M. Veiga[2], and R. B. Reis*[2], [1]*Animal Science Department, Federal University of Ceará, Brazil*, [2]*Veterinary School, Federal University of Minas Gerais, Brazil*.

The objective of this research was to evaluate the milk production and composition of dairy cows fed diets containing increasing levels of cashew nut. The cashew nut is produced and processed in the Northeast of Brazil and primarly used as human food. It has an average 22.0% of crude protein and 44.10% of ether extract, and it is rich in long chain unsaturated fatty acids ($C_{18:1}$ and $C_{18:2}$) and has a 3.68 unsaturated:saturated ratio. Although, its low cost compared to corn and soybean it is poorly explored as animal feed. Treatments consisted of replacement of corn and soybean meal in the diet by 0, 4, 8 or 12% of cashew nut in dry matter of the diet. Eight multiparous Holstein cows, between 50 and 74 days in milk and 28 ± 4 kg milk/day were allocated in a 4 x 4 double Latin Square Design. Corn silage was used as main forage in a 50:50 forage to concentrate ratio. The PROC GLM of SAS was used for the statistical analysis. Analysis for linear and quadractic contrasts were performed. The milk production varied between 29.9 to 30.7 kg/day and was not affected by increasing levels of cashew nut in th diet. The milk fat yield (1.09 to 0.79 kg/day) and content (3.68 to 2.66%) decrased linearly with greater proportions of cashew nut in the diet. The decrease in milk fat was followed by lower proportions of short chain fatty acids and higher proportions of long chain fatty acids. The diet contained 12% of cashew nut in the dry matter was responsible for a 38.32% reduction in short chain fatty acids and 38.21% of increase in long chain fatty acids in the milk fat. The milk protein percentage and production were not affected by high levels of cashew nut in the diet. The mainteinance of the milk production, protein content and production

and fat reduction content, along with the milk fatty acids profile made the cashew nut utilization a good alternative for obtaining milk with a better nutraceutic value.

Key Words: fatty acids, by-product

362 Effect of dietary n-3 polyunsaturated fatty acids (PUFA) on gene expression of the insulin-like growth factor (IGF) system in the bovine uterus. G. S. Coyne*[1,2], D. A. Kenny[2], and S. M. Waters[1], [1]*Animal Bioscience Centre, Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*, [2]*School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*.

Nutrition plays a key role in reproduction and there is evidence to suggest that dietary long chain n-3 PUFA may improve reproductive performance in cattle. Furthermore, localised IGF signalling in the uterine endometrium may play a role in influencing the initiation and maintenance of pregnancy. The objective of this study was to examine the effects of dietary supplementation of n-3 PUFA on the expression of genes involved in the GH-IGF signalling system in the bovine uterine endometrium. Reproductively normal crossbred beef heifers were fed a straw and barley/beet pulp based concentrate diet supplemented with a rumen protected source of either saturated fat or high n-3 PUFA, for 45 days. Animals were slaughtered on day 18 of the estrous cycle. Endometrial tissue was harvested and total RNA extracted from animals on the high (n=7) and low PUFA (n=7) diets. RNA was reverse transcribed into cDNA. Primers were designed to amplify specific fragments of genes involved in the GH-IGF signalling axis. The relative expression of each gene was analyzed using real time RT-PCR. Animals supplemented with the high PUFA diet showed a 6 fold decrease in IGF-1 ($P<0.05$) and a 1.5 fold increase in IGF-2 gene expression compared with the low PUFA diet ($P<0.05$). Animals offered the high PUFA diet also showed an 11 fold decrease in IGFBP-3 and a 4 fold decrease in IGFBP-6 compared to the low PUFA diet ($P<0.05$). IGF-1 and IGF-2 are both associated with key reproductive events such as preimplantation and placental development. IGFBPs can have an inhibitory effect by competing with IGF-1R for IGF binding; thus down-regulation of IGFBPs could indicate an increase in available IGF-1 for IGF-1R binding. IGFBP-3 is suggested to regulate local IGF bioavailability and transport of IGFs across the endometrium while IGFBP-6 has a higher affinity for IGF-2, inhibiting its effects, including cellular proliferation and differentiation. Differential gene expression of IGF-1, IGF-2 and the IGFBPs in the endometrium may positively influence reproductive efficiency by providing a more suitable environment for embryo survival.

Key Words: PUFA, IGF, uterus

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363 Oats grain as an alternative to corn in beef cattle diets. J. A. Marcenac[1], H. M. Arelovich*[1,2], M. F. Martínez[1], M. I. Amela[1], and R. D. Bravo[1,2], [1]*Dto. Agronomía-Universidad Nacional del Sur*, [2]*Comisión de Investigaciones Científicas de la Provincia de Buenos Aires (CIC); CERZOS, Bahía Blanca, Argentina*.

Although corn is used for beef cattle feeding in Argentina, its availability is limited in semiarid areas. This experiment was designed to evaluate the effect of replacing corn with oats on beef cattle performance. Eight Aberdeen Angus calves (229 kg initial BW) were individually housed and fed a mixed diet. The treatments were: 1) Oats grain diet (OGD): 20% hay plus 80% oats-pellet, and 2) Corn grain diet (CGD): 20% hay plus 80% corn-pellet. The hay was an alfalfa-grass mixture, and the pellet ingredients were 75.0, 14.4, 7.0, and 0.06% in OGD; and 75.0, 11.05, 10.0, and 0.45% in CGD of grain, wheat middlings, sunflower meal and urea respectively. Pellets also included 1.5% NaCl, 1.0% $CaCO_3$, and 1.0% mineral-vitamin mix with monensin.The average chemical composition of both diets was 14.6, 36.9, 17.5, and 9.8% of DM for CP, NDF, ADF, and ash, respectively. The treatments OGD and CGD were randomly allotted to 4 individually fed calves/treatment, fed ad libitum once daily at 0900 h for 62 d. Performance measurements included DMI, ADG, feed-to-gain ratio (FC), and total tract apparent DM digestibility (DIG). Blood samples collected via jugular venipuncture were analyzed for glucose (GLU), total protein (TP), and non-esterified fatty acids (NEFA). Data were analyzed by ANOVA as a completed randomized design. Results are reported in the table. The DMI and ADG were increased by CGD ($P < 0.05$); however, no differences were found for FC, probably because total DDMI was similar for the 2 diets. Blood measurements were not affected by treatments, remaining within standard reference values. As far as FC is concerned, oats seems to effectively replace corn in diets for growing beef cattle.

Table 1.

Item	OGD	CGD	SEM	P =
Performance,				
DMI kg/d	7.1	7.9	0.20	0.03
DIG, %	77.5	74.1	0.37	0.17
DDMI, kg/d[1]	5.5	5.9	0.20	0.22
ADG, g	1225	1412	18	0.0003
FC	5.8	5.6	0.10	0.26
Blood serum,				
GLU, g/L	1.41	1.19	0.17	0.26
TP, g/100 mL	6.79	6.53	0.09	0.14
NEFA, mEq/L	0.40	0.44	0.06	0.66

[1]DDMI: digestible DM intake, computed from DIG x DMI

Key Words: oats, corn, beef cattle

364 The effect of steam-flaked corn storage method on enzymatic starch availability and in situ dry matter disappearance. K. L. Neuhold, J. J. Wagner*, T. E. Engle, S. L. Archibeque, and K. S. Sellins, *Colorado State University*, *Fort Collins*.

The objective of this study was to investigate the effect of steam-flaked corn (SFC) storage method (SM) on in situ DM disappearance and enzymatic starch availability (SA). Steam-flaked corn was sampled immediately off the roller for five consecutive days and immediately prior to feeding on the following day. Two SM for SFC were evaluated: 1. stored overnight in an enclosed metal bin (HOT) or 2) stored overnight on a concrete slab allowing SFC to cool (COOL). Samples of SFC collected pre- and post-storage for each SM were submitted to a commercial laboratory for SA analysis. Additional samples were collected and prepared for in situ work through a 2mm screen. Dacron

bags were filled with ground SFC at 10mg/cm^2 surface area. Bags were placed sequentially into the rumen of 2 steers to allow fermentation times of 0, 2, 4, 8, 12, 24, 48, and 72 hr. After removal from the rumen, bags were washed manually and then dried in a 60°C forced air oven for 48 hr. Polynomial curves, pre- and post-storage, were generated over incubation time for each SM and day. The area under each curve was calculated and used for statistical analysis of the in situ data. Starch availability was higher ($P < 0.01$) for SFC stored under COOL conditions as compared with HOT (44.8 versus 34.2 mls). Post storage samples had lower ($P < 0.0001$) SA as compared with pre-storage samples (29.7 versus 49.3 mls). The interaction between SM and time of sampling (pre- versus post-storage) was not significant. Storage method differences for in situ DM disappearance were not significant averaging 53.95 versus 54.23% for the HOT and COOL treatments, respectively. In situ DM disappearance was reduced ($P < 0.08$) during storage from 57.93% to 51.25%. Interactions between SM and time of sampling were not significant. Reductions in DM disappearance during storage that were observed for each SM varied widely from day to day. Enzymatic SA estimates were reduced for SFC stored HOT. In situ DM disappearance from SFC was not affected by SM.

Key Words: steam-flaked corn, starch, retrogradation

365 Effect of type and length of dietary fiber on growth, efficiency and carcass quality of feedlot cattle. M. J. Baker*, D. E. Hogue, M. L. Thonney, and D. J. Ketchen, *Cornell University, Ithaca, NY.*

High fiber ingredients often are included in diets for feedlot cattle, but the fermentability of the fiber necessary to maintain rumen function is seldom considered. The purpose of this study was to evaluate how level of fermentable fiber and fiber length affect feed intake, growth, and carcass characteristics of feedlot cattle. Crossbred yearling heifers (n = 36, BW = 388 kg) were blocked by weight and randomly assigned to three diets. All cattle were fed diets with 70% whole shelled corn. Two diets included either chopped hay (CH) or ground hay (GH) as 20% of the diet with a premix of protein, minerals, vitamins, and Rumensin in pellet form at 10% of the diet. The third diet included a pellet composed of high NDF grain byproducts (BP) and a premix similar to that for the hay diets at 30% of the diet. Each diet was formulated to contain 21% NDF. The BP diet was expected to contain 17% potentially fermentable NDF (pfNDF) and the hay diets were expected to contain 12% pfNDF. The formula for pfNDF was NDF-[100-TDN-Metabolic fecal loss]. The cattle were fed for 82 d in 9 slatted floor pens (4/pen), with 3 pens per diet. Diet analysis showed that NDF was 23% and 21%, calculated pfNDF was 15% and 14%, and TDN was 80% and 81% for BP and hay diets, respectively. For BP, CH, GH, there were no significant differences due to fiber source or fiber length on the rapid ADG (1.9, 1.8, 1.8 ± 0.04 kg), or on final weight (550, 548, 542 ± 8.9 kg), DMI (11.8, 12.3, 12.0 ± 0.19 kg), or gain:feed (159, 150, 149 ± 5.8 g/kg). Rumen epithelia showed no evidence of degradation related to diet. There were no condemned livers. There were no statistical differences due to diet for carcass measurements with the exception of marbling (MRB). Cattle fed BP had higher ($P < 0.05$) MRB than cattle fed hay diets (4.2 vs 3.8 ± 0.20) and cattle fed CH had lower ($P < 0.03$) MRB than cattle fed GH (3.4 vs. 4.1 ± 0.20). These results suggest that cattle fed a diet with 15% pfNDF, regardless of fiber source or length, are expected to have equal performance.

Key Words: beef, particle size, fermentable fiber

366 Effect of nitrogen supplementation on urea kinetics and microbial use of recycled urea in steers consuming corn-based diets. D. W. Brake*[1], E. C. Titgemeyer[1], M. L. Jone[2], and D. E. Anderson[2], [1]*Department of Animal Sciences and Industry, Kansas State University, Manhattan*, [2]*Department of Clinical Sciences, Kansas State University, Manhattan*.

We analyzed effects of N supplementation as distiller's grains with solubles (DDGS) or urea to steers consuming corn-based diets. Six ruminally and duodenally cannulated steers (244 kg) were used in a replicated 3×3 Latin square and fed 1 of 3 corn-based diets: control (CON; 10.2% CP), UREA (11.4% CP), or DDGS (12.7% CP). Periods were 14 d with 10 d for adaption and 4 d for collection. Steers were in metabolism crates for collection of urine and feces. Venous infusions of $^{15}N^{15}N$-urea with measures of $^{15}N^{15}N$-urea and $^{14}N^{15}N$-urea in urine were used to measure urea kinetics. Dry matter intake (6.0 kg/d) was not affected by treatment, but N intake differed (99, 151, 123 g/d for CON, DDGS, and UREA). Urea-N synthesis tended to be greater for DDGS (118 g/d) than for UREA (86 g/d), which in turn tended to be greater than CON (52 g/d). Urea-N excreted in the urine was greater ($P<0.05$) for DDGS (35.1 g/d) and UREA (28.6 g/d) than for CON (12.6 g/d). Gut entry of urea-N was numerically greatest for DDGS (83 g/d), intermediate for UREA (57 g/d), and least for CON (39 g/d). The amount of urea-N returned to the ornithine cycle tended to be greater for DDGS (47 g/d) than for UREA (27 g/d) or CON (16 g/d). The fraction of recycled urea-N that was apparently used for anabolism tended ($P=0.09$) to be greater for CON (0.60) than for DDGS (0.31) or UREA (0.46), but no differences were observed among treatments in the amount of urea-N utilized for anabolism ($P=0.71$). The fraction of total microbial N derived from recycled urea-N tended ($P=0.11$) to be greater for DDGS (0.28) than for UREA (0.18) or CON (0.15). The fraction of urea production that was captured by ruminal bacteria was greater ($P<0.05$) for CON (0.37) than for DDGS (0.20) or UREA (0.18). Urea kinetics in cattle fed grain-based diets were related to the amount of N consumed. *This project was supported by National Research Initiative Competitive Grant no. 2007-35206-17848 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: cattle, recycling, urea

367 Effects of a slow-release urea product on the N balance of growing cattle fed steam flaked corn. B. M. Bourg*[1], T. A. Wickersham[1], L. O. Tedeschi[1], and J. M. Tricarico[2], [1]*Dept. of Animal Science, Texas A&M University, College Station*, [2]*Alltech Inc., Nicholasville, KY.*

An experiment was conducted to determine the impact of source, urea (U) or Optigen II (O), and level of NPN on N balance of growing cattle fed steam-flaked corn. Five ruminally-cannulated Holstein steers in a 5 × 5 Latin square design were used in the study. Steers were fed a steam-flaked corn based diet with either no supplemental NPN, 0.75% U or N equivalent O, or 1.5% U or N equivalent O. Intake was measured, and feed, orts, urine, and fecal samples were obtained and composited for each steer by period. Data were analyzed using PROC mixed of SAS. Orthogonal contrasts were used to evaluate differences between O and U, and high and low level of NPN. Steers fed O tended ($P = 0.06$) to have lower N intake than those fed U, with high treatments (TRT) having greater N intake than low for both U and O. There were no differences in DMI among any of the TRT. However, steers fed O had lower TDOMI ($P = 0.05$) than steers fed U, but there were no differences in TDOMI between high and low levels of U or O. Steers fed high O tended ($P = 0.08$) to have greater fecal N excretion than low O; 46.8 and 36.3 g/d, respectively. There were no differences in fecal N excretion between

U and O TRT. As expected, for both U and O, high TRT levels had greater urinary N excretion (P < 0.05) than low TRT, while urinary N did not differ between U and O. N absorption differed (P < 0.05) for both source and level of NPN. N retention did not differ between high O and low O (58.0 vs 46.0 g/d), while steers fed high U tended (P = 0.08) to have greater N retention than steers fed low U (78.3 vs 55.9 g/d). There was no difference (P = 0.09) in N retention between U and O TRT. The ratio of N absorbed to N intake differed between high and low U (P = 0.03), but not between high and low O or between U and O. In summary, high levels of either NPN source had greater N intake and urinary N excretion, as well as N absorption and no major differences were observed between O and U, suggesting that O can replace U at different levels of N intake.

Key Words: slow-release urea, N balance

368 Effects of a slow-release urea product on performance and carcass characteristics of growing cattle fed steam-flaked corn. B. M. Bourg*[1], L. O. Tedeschi[1], J. M. Tricarico[2], T. A. Wickersham[1], and W. K. Krueger[1], [1]*Dept. of Animal Science, Texas A&M University, College Station,* [2]*Alltech Inc., Nicholasville, KY.*

The impact of source, urea (U) or Optigen II (O), and level of dietary NPN on performance of growing cattle was examined on 60 Angus crossbred steers (initial BW = 353 ± 13.9 kg), fed 1 of 3 steam-flaked corn based diets: U (T1, 1.2% NPN), O (T2, 1.3% NPN), or O without cottonseed meal (T3, 3.1% NPN). T1 and T2 contained cottonseed meal and NPN as CP sources, while T3 contained only NPN. T1 and T2 were isonitrogenous (CP = 13.2%) and isoenergetic (ME = 2.58 Mcal/kg DM), while T3 had more CP (14.8%). Steers were blocked by post-weaning BW and assigned to treatments (TRT) and pens within block (5 pens/TRT). BW was collected bi-weekly and ultrasound carcass measurements were collected at the start and end of the 105-d trial. Six steers from each TRT were harvested and carcass and organ measurements were obtained. Cumulative animal performance was evaluated in 3 periods (0-35, 0-70, and 0-105 d) using a mixed model with initial BW as a covariate. Orthogonal contrasts were used to evaluate differences between T1 and T2, and T1 plus T2 with T3. There were no differences in initial BW, final BW, ADG, or DMI among TRT for any of the periods. However, for period 1 steers on T3 had lower F:G than T1 (5.71 vs. 7.39; P = 0.03), and steers fed T2 tended to have lower F:G than those fed T1 (6.07 vs. 7.39; P = 0.07). In period 2, T3 had lower F:G than T1 (5.58 vs. 6.56; P = 0.03), but did not differ from T2 (5.97). There were no differences in F:G for the entire trial. Steers fed T3 were leaner (P = 0.04) than T1 and T2 (1.04 vs. 1.21 and 1.16 cm fat thickness, respectively). Steers fed T3 had lighter heart and kidney weights than T1 and T2 combined (P < 0.05; heart: 1.59, 1.57, and 1.42 kg, respectively, and kidney: 0.93, 0.85, and 0.76 kg, respectively). Liver and spleen weights and 9-11 rib chemical composition did not differ among TRT. In summary, no major differences on performance and carcass composition were observed between U and O diets. Steers had better initial F:G when O was used as the only source of feed N (T3), suggesting that O may replace both NPN and true protein feeds in finishing cattle diets.

Key Words: slow-release NPN, urea

369 Dose and release pattern of anabolic implants affects growth of finishing beef steers. S. L. Parr*[1], K. Y. Chung[1], J. P. Hutcheson[2], W. T. Nichols[2], D. A. Yates[2], M. N. Streeter[2], R. S. Swingle[3], M. L. Galyean[1], and B. J. Johnson[1], [1]*Texas Tech University, Lubbock,* [2]*Intervet / Schering-Plough Animal Health, De Soto, KS,* [3]*Cactus Research Ltd., Amarillo, TX.*

Three experiments evaluated the effect of implant dose and release pattern on steer performance and carcass traits. In Exp. 1, steers (n = 2,153; 4 to 7 pens/treatment; BW = 315 kg) were fed an average of 173 d. Treatments were: 1) no implant (NI); 2) Revalor-S (120 mg trenbolone acetate [TBA] and 24 mg estradiol 17β [E_2]; REVS); 3) Revalor-IS followed by REVS (cumulatively 200 mg TBA and 40 mg E_2; reimplanted at 68 to 74 d; REVISS); and 4) Revalor-XS (200 mg TBA and 40 mg E_2; REVX). Carcass-adjusted final BW was greater (P < 0.05) for REVX and REVISS than for REVS (610, 609, and 598 kg respectively). Daily DMI did not differ (P > 0.10) among the 3 implant treatments, but carcass-adjusted G:F was greater (P < 0.05) for REVX and REVISS than for REVS (0.197 and 0.195 vs. 0.188). Both HCW and LM area were greater (P < 0.05) for REVX and REVISS than for REVS. Marbling scores were greatest (P < 0.05) for NI and REVS and least (P < 0.05) for REVISS. In Exp. 2, steers (n = 5,773; 10 pens/treatment; BW = 391 kg) were fed an average of 131 d, with treatments of REVS, REVISS (reimplanted at 44 to 47 d), and REVX. Carcass-adjusted final BW (598 kg), ADG (1.6 kg), DMI (9.4 kg), G:F (0.17), and HCW did not differ (P > 0.10) among treatments. Yield grade was greatest for REVS and least for REVISS (P < 0.05), and quality grade was less (P < 0.05) for REVISS than for REVS and REVX. In Exp. 3, steers (n = 1,833; 10 pens/treatment; BW = 277 kg) were fed an average of 197 d and received either REVISS (reimplanted at 90 to 103 d) or REVX. Carcass-adjusted final BW (625 vs. 633 kg) and ADG (1.81 vs. 1.76 kg) were greater (P < 0.05) for REVX-implanted steers. Daily DMI did not differ between treatments, but G:F tended (P < 0.10) to be increased and HCW was greater (P < 0.05) for REVX than for REVISS. These data indicate that when TBA/E_2 dose is equal, the altered release rate associated with REVX may improve performance and marbling score, but these effects seem to depend on the length of the feeding period.

Key Words: beef steers, estradiol 17β, trenbolone acetate

370 Nutritional and management methods to decrease nitrogen losses from beef feedlots. G. E. Erickson* and T. J. Klopfenstein, *University of Nebraska, Lincoln.*

Nitrogen losses from open lots are a concern. Methods that increase manure N while decreasing losses to the air would be beneficial in open lot beef operations. Twelve or more pens have been dedicated to N research whereby N intake, retention, and excretion are quantified, and a mass balance conducted using manure, runoff, soil balance, and loss quantities. The objective has been to decrease N losses and increase manure N. Dietary CP impacts N excretion and N losses. Four experiments across two years compared industry average CP (13%) to diets that were phase-fed to not exceed protein requirements (12.1 to 10.9%). Phase fed cattle excreted 12 to 21% less (P<0.01) and N losses were reduced 15 to 33% (P<0.01). In 2 other experiments, phase fed diets were formulated to recycle undegradable intake protein. Steer G:F was similar (P=0.18) or improved (P=0.09) while N excretion and N losses were reduced (P<0.11) and N in manure was not affected (P>0.35) compared to cattle fed 13% CP. Feeding less protein did not impact manure N, suggesting manure N from open lots is related to other factors. A series of experiments have evaluated increasing OM on the pen surface to increase N in manure. Feeding less digestible diets using fiber increased manure N (P<0.01) and decreased (P<0.10) N losses in two experiments conducted from November to May, but did not impact (P>0.30) manure N or losses during two summer experiments. Adding bedding (OM) increased manure N in the winter as well. Another method evaluated was increasing pen cleaning frequency, which decreased N losses by 19 to 44% and increased manure N by 26 to 41% across 3

experiments. Other methods such as acidifying manure by manipulating dietary cation anion difference, clinoptilite zeolite clay addition, and feeding different amounts of byproducts have had variable impacts on N losses. No treatments have markedly impacted runoff N, which is <5% of excreted N. Dietary protein impacts N losses but not manure N. Other factors such as OM on the pen surface impact manure N. Cleaning manure frequently, which decreases exposure, decreases losses. Treatments should be evaluated across seasons due to seasonal effects.

Key Words: beef cattle, loss, nitrogn

371 Increasing dietary concentration of coconut oil reduces enteric methane emission from lactating Holstein cows. M. Hollmann*[1], W. J. Powers[1,2], A. Fogiel[1], N. M. Bello[1,3], J. S. Liesman[1], and D. K. Beede[1], [1]*Department of Animal Science, Michigan State University, East Lansing*, [2]*Department of Biosystems Engineering, Michigan State University, East Lansing*, [3]*College of Agriculture and Natural Resources Statistical Consulting Center, Michigan State University, East Lansing*.

To examine the effects of dietary coconut oil (CO; source of medium-chain fatty acids) on enteric methane emission, 24 lactating Holstein cows in two blocks of 12 cows each were allocated randomly in a balanced design to 12 possible dietary treatment sequences in 2 periods of 35 d each. Dietary treatments were 0.0 (Control), 1.3, 2.7, or 3.3% CO, dry basis. Other dietary components included corn and alfalfa silages, ground dry corn, heat-processed soybean meal (SoyPlus™), soy hulls, wheat middlings, minerals, and vitamins. Control diet contained 16.5% crude protein (60% from RDP), 34% NDF (71% from forage), and 31% starch, dry basis. Cows were housed, fed, and milked individually in environmentally-controlled chambers from d 22 through 35. Air flux and respective temperature and relative humidity of each chamber were measured during a 5.5-min cycle every 3 h. Simultaneously, an Innova™ photoacoustic analyzer detected methane concentrations in inlet and outlet air 3 to 6 times, adjusted to standard temperature and pressure. Methane emitted was computed from the difference in concentrations of inlet and outlet air, and flux. Subsequently, data were averaged within cycle and the average was weighted by the number of observations. Statistical analyses were conducted using mixed effects models, including the fixed effects of period, block, dietary treatment, potential carryover effects, day, and time of day, and relevant 2- and 3-way interactions; random effects were fitted to account for appropriate experimental units of each fixed effect factor. Results are presented in the Table as least-squares means. Dietary CO reduced methane emission per unit of FCM yield. (L: linear; Q: quadratic)

Table 1.

	CO, % of DM					Contrast
Item	0.0	1.3	2.7	3.3	SE	(*P* <)
CH_4, L/d[a]	644	622	406	349	0.04906	0.01,Q
DMI, kg/d	23.0	21.5	17.9	17.1	0.69	0.01,L
__CH_4/DMI, L/kg[a]	29.9	30.5	24.4	22.8	0.03407	0.02,Q
MY, kg/d	37.7	37.0	33.7	33.3	1.04	0.01,L
__CH_4/MY, L/kg[a]	18.2	17.6	12.9	11.5	0.04778	0.03,Q
FCMY, kg/d	34.2	35.5	27.3	26.3	1.12	0.01,L
__CH_4/FCMY, L/kg	20.4	19.2	16.5	14.5	0.70	0.01,L
Milk fat, %	3.39	3.67	2.74	2.67	0.109	0.01,Q
Milk fat, kg/d	1.27	1.37	0.92	0.88	0.054	0.01,Q
Milk protein, kg/d	1.07	1.05	0.91	0.93	0.034	0.01,L

[a] SE from natural log transformed data reported.

Key Words: methane, dairy cow, medium-chain fatty acid

372 Effects of two strains of *Saccharomyces cerevisiae* on methane emissions from Holstein dairy cattle. Y.-H. Chung*[1], S. M. McGinn[1], N. Walker[2], and K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [2]*Lallemand Animal Nutrition, Montréal, QC, Canada*.

The objective of this study was to measure the efficacy of supplementing diets with strains of *Saccharomyces cerevisiae* on reducing methane (CH_4) emissions from Holstein dairy cattle. Fifteen ruminally cannulated, nonlactating, and nonpregnant cows were blocked by dry matter intake (DMI) and randomly assigned to: (1) control: no yeast, (2) yeast strain 1 (Levucell SC), and (3) yeast strain 2 (Test A). Both of the yeast strains were provided as active dried products (Lallemand Animal Nutrition, Montréal, QC) to provide 1×10^{10} cfu/head/d. Yeast products were dosed via the rumen cannula daily at the time of feeding (1×feeding/d). Cows were fed a barley-based total mixed ration (50:50 forage to concentrate ratio) formulated to meet the nutrient requirements of a dairy cow producing 30 kg/d of milk. The experiment consisted of a 35-d yeast feeding period and CH_4 gas was collected daily using the sulphur hexafluoride tracer gas technique (halter/PVC yoke) during the last 4 d of the experimental period. Feeding the two yeast strains did not affect ($P > 0.10$) DMI or BW during the entire feeding period. Total CH_4 emissions were not affected ($P > 0.10$) by yeast feeding and averaged 264 g/d. However, there was a tendency ($P = 0.07$) for yeast strain 2 to reduce CH_4 emissions by 6.5 or 5.5% (vs. control) after adjusting CH_4 emissions for DMI or gross energy (GE) intake, respectively. Cows that received yeast strain 2 produced CH_4 at 15.7 g /kg of DMI or 5.2% of GE intake compared with the control at 16.8 g CH_4 /kg of DMI or 5.5% of GE intake and yeast strain 1 at 17.5 g CH_4/kg of DMI or 5.8% of GE intake. The study provides evidence that strains of yeast vary in their ability to mitigate CH_4 emissions from cattle and demonstrates the feasibility of developing commercial yeast strains that could be used to reduce greenhouse gas emissions from livestock production.

Key Words: yeast culture, methane emissions, sulphur hexafluoride tracer gas technique

373 The effect of pre-grazing herbage mass on growth rate and methane emissions of grazing beef cattle. T. M. Boland*, K. J. Hart, K. M. Pierce, B. M. Lynch, R. McDonnell, D. Murphy, A. K. Kelly, and D. A. Kenny, *School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*.

Irish beef production systems are predominantly grass based with over 80% of the animals energy requirements provided by pasture. The Irish beef herd (including dairy replacements) accounts for 60% of enteric CH_4 production and subsequently 8.1% of total national GHG emissions. Therefore, any CH_4 mitigation strategies must focus on pasture management. Pre grazing herbage mass (HM) is one of the main determinants of sward quality. The objective of the current study was to examine the effect of pre-grazing HM on growth rate and CH_4 emissions of grazing beef heifers. Thirty Limousin X heifers were blocked on the basis of bodyweight (346±34kg) and allocated to one of two treatments (n=15). Animals were offered a low (L: 1900kg DM/ha) or high (H: 3800 kg DM/ha) target pre-grazing HM. Methane was determined over a five day period on three occasions using the SF_6 tracer gas technique during a 126 day grazing period. Rumen fluid was sampled on the fifth day of each CH_4 measurement period using an oesophageal sampler and analysed for concentration of volatile fatty acids (VFA). Animals were weighed on a fortnightly basis. Data were analysed using the MIXED procedure in SAS. Actual pre-grazing HM across the grazing period were 2103 and 3841 kg DM/ha for L and H respectively. Average daily

gain was higher (P<0.001) on L as were total concentrations of ruminal VFA (P=0.06). Treatment had no effect (P>0.05) on proportion of individual VFA. Treatment had no effect (P>0.05) on daily CH_4 emissions overall or within any individual period. There was a trend (P=0.10) for lower CH_4 emissions per kg ADG for animals on L (143 v. 166 g CH_4/kg ADG). These results show that reducing pre-grazing HM will lead to increased animal performance, and thus may lead to reduced CH_4 emissions in beef production systems where cattle are slaughtered at a target live-weight. A data modelling approach is required to fully quantify these effects.

Key Words: beef cattle, methane, pasture quality

Small Ruminant: Symposium: Organic and Grass-Fed Small Ruminant Challenges and Opportunities

374 Obstacles to organic and grass fed small ruminant production in the U.S. J. M. Burke*, *USDA, Agricultural Research Service*, *Booneville, AR*.

Certified organic and grass fed production systems must align to standards defined by the USDA Agricultural Marketing Service. There is very little research being conducted on organic livestock systems in the U.S. by land grant colleges or federal research agencies. The demand for organic, grass fed, locally-grown, and natural products is strong and there is a desire to increase the sustainability of farming systems, which is perceived to occur by using organic and grass fed management. Obstacles to becoming certified organic include increased record keeping, increased risks, limited awareness of organic farming system practices, lack of processing facilities, lack of certified organic feeds, and inability to capture market share. In many environments, internal parasite control remains a large barrier. Small ruminants must be managed to minimize internal parasite infection. Also, growing animals must only graze certified organic pastures or feed. The latter is limited by availability and may not be sustainable because of dependency on off-farm inputs. These same obstacles do not necessarily apply to grass fed management. Grass fed ruminants are defined as those provided a diet solely from forage with the exception of milk before weaning. This standard applies to animals destined for slaughter, but not necessarily breeding animals. Both management systems are in need of basic and applied research to optimize production and maximize profitability. Research should follow a systems-oriented approach that applies organic or grass fed principles. Priorities have been identified and include development of effective parasiticides, parasite management strategies, development of emergency and preventative health care strategies, development of improved genetics to fit the system, and environmental impact studies. In addition, research is needed on forage management to optimize growth of weaned animals. A case study will be presented.

Key Words: goat, sheep, systems research

375 Ecology as a model for organic dairy production. F. Thicke*, *Radiance Dairy*, *Fairfield, IA*.

Natural ecosystems are characterized by biodiversity, self sufficiency, and the conservation and recycling of nutrients. The diversity of a natural ecosystem precludes off-site pollution because the waste of each species is recycled as substrate for other species. By contrast, industrial crop and livestock systems are characterized by monocultures and requirements for high external inputs. The inability of monoculture systems to efficiently process waste *in situ*, combined with practices that disrupt ecological integrity, result in leakage of materials (e.g., nutrients, pesticide residues and eroded soil) from these systems to become pollutants to off-farm resources. An organic, grass-based dairy mimics the ecosystem of prairie plants and bison which created the highly productive soils of parts of North America. In that prairie ecosystem, prairie grasses and forbs produced massive growth, both above-ground and below-ground. Migrating bison herds periodically grazed off the above-ground plant growth, resulting in the plants sloughing root mass off into the soil to balance their reduced photosynthetic capacity. Repeated growth-and-grazed cycles pulsed organic matter deep into the soil, creating the productive, high-organic-matter soils of the prairies. Similarly, organic grazing systems that are designed and managed in accord with ecological principles can enhance the farm resource base (soil quality, water quality, air quality, and wildlife habitat) as well as promote good animal health, reduce reliance on fossil-fuel energy and other external inputs, and minimize pollution-causing leakages. A case study will be presented of an Iowa monoculture-crop farm that was converted to an organic, grass-based dairy that processes milk on the farm and markets finished dairy products locally. The farm design and management will be discussed as a model of an ecologically based farming system.

Key Words: dairy, organic, graze

376 Successful organic dairy systems. K. J. Soder*, *USDA-ARS, Pasture Systems & Watershed Mgmt. Research Unit*, *University Park, PA*.

Demand for organic dairy products has continually increased and at times outpaced supply for a number of years, creating favorable milk pricing for certified organic dairy farmers. This stability in organic milk prices has provided organic dairy farmers with a security not found in the conventional milk marketing system. Many organic dairy farmers transitioned organic production to implement philosophies of the organic production system. Others transitioned in an effort to increase profitability. However, even with relatively high premiums paid for organic milk, transitioning to organic production does not guarantee profitability. There are many challenges unique to organic milk production, including accessing markets for milk pickup, sourcing organic feeds and veterinary care. Additionally, the recently volatile input prices have significantly challenged the sustainability of organic dairies. While organic dairy systems are primarily forage-based systems, emphasizing high-quality pasture, supplementation is still an important component for many farms. Organic feed prices have increased at a greater rate than conventional feed prices, in part due to demand outpacing supply as an increasing number of dairies transitioned to organic production in recent years. Some organic farmers have opted to decrease, eliminate, or find alternative supplementation strategies to decrease feed costs. Others produce more of their feeds on-farm. This presentation will provide an overview of the organic dairy industry. Data will be presented showing recent trends in organic dairy production, including recent growth of the

industry, current statistics and economics of organic milk production. A summary of strategies used by organic dairies to adapt to current industry challenges will be discussed including those mentioned above as well as changing herd genetics, putting even more emphasis on cropping and pasture fertility, and exiting the industry. Finally, a brief review of changes to the organic pasture standard currently being proposed and revised by the National Organic Program will be presented.

Key Words: dairy, organic, systems

377 Grass-fed management systems for profitable livestock production. S. K. Duckett* and J. G. Andrae, *Clemson University, Clemson, SC.*

Consumer markets for natural, forage-finished livestock products are expanding in the U.S. As a result of this demand, some livestock producers are electing to finish animals on forages and market products directly to consumers. Agricultural Marketing Service has established a voluntary standard for a grass (forage) fed marketing claim for ruminant livestock. The grass (forage) fed claim standard is that grass (annual and perennial), forbs, browse, forage, or stockpiled forages, and post-harvest crop residue without separated grain shall be at least 99% of the energy source for the lifetime of the ruminant specie, with the exception of milk consumed prior to weaning. Producers can now request a grass fed claim be verified by USDA. Results from our research show that forage-finishing decreases LM lipid content and increases fat-soluble and water-soluble vitamin contents. Forage-finishing also increases concentrations of cis-9 trans-11 CLA, trans-11 vaccenic acid, and all n-3 fatty acids (linolenic acid, EPA, DPA, DHA). One of the greatest challenges facing livestock producers is the consistent supply of high quality forages for finishing. Forage nutritive and fatty acid content are variable among species, variety, harvest time, and growing season. These differences in forage fatty acid content influence meat and milk fatty acids produced in grazing animals. Forage systems that optimize stocking rates and nutritive density and minimize input costs are needed. Evaluation of alternate forages is of considerable interest to fill gaps in perennial forage production and/or promote high rates of gain. Forages we have evaluated for finishing include: alfalfa, chicory, cowpea, pearl millet, non-toxic tall fescue, and bermudagrass. Alternative fertilizers, legumes, and supplements should be evaluated to determine their effects on forage production, animal performance (including parasite load) and product quality.

Key Words: livestock, forage, fatty acid

Animal Behavior and Well-Being: Animal Behavior and Well-Being 1

378 Enriched colony cage for laying hens and the effects on behavioural and physiological parameters. N. J. Cook*[1], J. Feddes[2], D. Korver[2], D. B . Haley[2], and J. S. Church[3], [1]*Alberta Agriculture and Rural Development, Lacombe Research Centre, Lacombe, Alberta, Canada*, [2]*University of Alberta, Edmonton, Alberta, Canada*, [3]*Thompson Rivers University, Kelowna, British Columbia, Canada*.

The benefits to laying hens of colony cages of 40, 20 and 10-birds/cage, and enrichment with perches, nest boxes and scratch pads, were assessed by behavioural and physiological parameters. Non-enriched, "conventional" cages of 5-birds/cage were included for comparison. Laying hens were Brown (n = 360) and White (n = 360) Leghorns over an egg laying period of 65wks. Behavioural and physiological parameters were the % perch use for roosting at 57, 61 and 62 weeks, claw length (n = 288) for use of scratch pads at week 65, and the comparative numbers of eggs laid within nest boxes at 35 and 60 weeks. Feather cover was assessed by infrared thermography of 144 birds at 35 and 60 weeks. Densities and areas of the humerus and femur (n = 60) were assessed by quantitative computer tomography at week 65. Time-integrated adrenocortical activity was assessed by egg yolk and albumin levels of corticosterone in 20% of the eggs from each cage type during weeks 35 and 60. Data were analyzed by mixed models using JMP v6. The majority of eggs (72.6%) were laid in nest boxes. Nest use was highest in Brown hens ($P < 0.03$). Perch use was >80% but was significantly less in the 10-bird cages ($P < 0.0001$) due to a shorter perch length. Claw length was longer in the 5-bird cages compared to enriched cages ($P < 0.0001$). Bone densities and areas were not associated with cage type or enrichment. Densities and areas of the humerus and femur were highest in Brown birds ($P < 0.005$). White birds exhibited better feather cover than Brown ($P < 0.0001$). Feather cover declined from 35 to 60wks for breast and back areas ($P < 0.0001$). Feather losses were highest in 20 and 40-bird cages and lowest in the 5-bird cages. Egg albumin corticosterone was significantly lower at 60wks compared to 35wks ($P < 0.001$). Yolk corticosterone was significantly lower at 60wks in 5-bird cages ($P < 0.05$). The findings indicated a preference for the use of nest boxes, perches and scratch pads. However, the materials and size of the enrichment amenities had implications for feather cover.

Key Words: laying hens, colony cages, environmental enrichment

379 Animal welfare indicators of Holstein bulls ring-castrated at three months of age. S. Marti*[1,2], A. Velarde[2], J. L. de la Torre[1,3], A. Bach[2,4], X. Manteca[1,3], A. Aris[2], A. Serrano[2], and M. Devant[1,3], [1]*Animal Nutrition, Management, and Welfare Group, Barcelona, Spain*, [2]*IRTA, Barcelona, Spain*, [3]*UAB, Barcelona, Spain*, [4]*ICREA, Barcelona, Spain*.

Ring castration at 3 mo of age is an effective and low-time consuming procedure, however it has been questioned from the welfare point of view. Forty-seven bulls (130 ± 3.43 kg BW and 95 ± 1.5 d of age) individually housed were randomly assigned to 2 treatments (control, CTR, n = 23 or castrated, CAS, n = 24) to evaluate the effect of ring castration at 3 mo of age in Holstein bulls on welfare indicators. Castration was performed with local anesthesia (lidocaine 2%, 3 mL in each testis and 2 mL in the scrotum) and analgesia (flunixin meglumine, 3 mg/kg BW) treatment, no local anesthesia and analgesia were used in CTR bulls. Serum cortisol concentration was determined at -120, 0, 30, 60, 90, and 180 min after castration. At days 1, 3, and weekly thereafter during 2 mo serum haptoglobin concentration, rectal temperature, lesions at the castration site, and behavior of 12 CTR and 12 CAS bulls recorded continuously for 24 h, BW and concentrate and straw intake were analyzed. Serum antibody titers against ovoalbumin were determined at 14 and 35 d. At day 49, bulls were i.v. injected with ACTH and serum cortisol concentration at 0, 1, 2, and 4 h thereafter, and serum testosterone concentration were determined. The statistical model included initial BW as a covariate, castration, time, and the interaction between castration and time, as fixed effects, and animal as a random effect. Gain was greater ($P < 0.001$) in CTR than CAS bulls (1.36 vs 1.16 ± 0.038 kg/d, respectively). Area under the curve of serum cortisol at day 0 was smaller ($P <$

0.05) in CAS than in CTR bulls (18 vs 33 ± 5.2 nmol/L/h, respectively) where no local anesthesia and analgesia were used. At 49 d, 100% of CAS bulls had no testes and no serum testosterone was detected. Ring castration performed at 3 mo of age with local anesthesia and analgesia decreases ADG but does not alter other welfare indicators.

Key Words: beef, castration, welfare

380 Pain mitigation at time of castration improves performance and intake in feedlot bull calves. L. A. González*[1], K. S. Schwartzkopf-Genswein[1], E. Fierheller[2], E. Janzen[2], N. A. Caulkett[2], T. A. McAllister[1], D. B. Haley[4], J. M. Stookey[3], and S. Hendrick[3], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [2]*University of Calgary*, *Calgary, AB, Canada*, [3]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [4]*University of Alberta*, *Edmonton, AB, Canada*.

Angus bulls (n = 173; 6 to 8 mo of age; initial BW 301 ± 3 kg) were randomly assigned to 1 of 6 treatments according to a 3 × 2 factorial design to study the effect of castration method and pain medication on performance and feed intake. Castration (Cast) treatments consisted of sham (C), band (B), and surgical (S) castration. Pain medication (Med) treatments consisted of either lactated ringer solutions (NM) or pain mitigation drugs (M). Drugs used were 2% lidocaine with epinephrine injected at 10 mL into each testicle plus 10 mL subcutaneously at the scrotal base, and a subcutaneous injection of flunixin meglumine (2.2 mg/kg BW) in the neck of calves. Bulls NM received the same injections with ringer solutions except no intratesticular injection was given to avoid causing orchitis. All animals were fitted with electronic ear tags to monitor individual feed intake and randomly assigned to 1 of 4 pens within each treatment. Intake and BW were measured weekly from 1 wk before (used as covariates) until 6 wk after castration. Data were analyzed with a mixed-effects regression model considering the fixed effects of covariate, Cast, Med, wk as repeated measure, and all possible interactions. Pen, Pen×Cast×Med, and Pen×Cast×Med×Wk were random effects. Overall ADG was lower in S and B compared to C calves ($P < 0.01$). However, S calves grew slower than both B and C during wk 1 ($P < 0.001$) whereas B calves grew slower than both S and C during wk 3 ($P < 0.05$). Final BW was greater in C than B and S ($P < 0.001$), and in M than NM calves ($P = 0.04$). Calves S ate less DM than C ($P = 0.003$), and NM ate less than M ($P = 0.003$). Pain mitigation using a local anesthetic and a systemic analgesic upon castration improves feed intake and BW compared to non-medicated calves up to 6 wk post castration.

Key Words: beef bulls, castration method, pain medication

381 Feeding behavior and weight gain of dairy calves in the post-weaning period. A. L. Stanton*[1], D. Kelton[1], K. E. Leslie[1], S. J. LeBlanc[1], K, Hester[1], and S. T. Millman[2], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Iowa State University*, *Ames*.

The objectives were to investigate associations between post weaning weight gain and behavior of dairy heifers. Holstein heifers (n=74) were group housed in a naturally ventilated heifer barn in groups of 4-6 and were 56.6 (±7) days old at weaning. Prior to enrollment, calves were housed individually in outdoor hutches or in a nursery barn. Post-weaning diet consisted of component fed grain and hay. Behavioral data was collected from video-recordings for a subset of calves (n=65) immediately post-weaning (Day 0) from 12pm-7pm and on Days 1, 2, 4 and 6 from 7am to 7pm, using 5 minute instantaneous scan sampling. Calves were recorded as eating (head through bunk and lowered), bunk engaged (head through bunk not lowered) or bunk directed (at bunk but head not through bars). The probability of eating and Day 7 body weights were modeled with random effects of group in the weight model and calf and group in the eating model. Day 7 weight increased with weaning weight, such that a 1.0 kg increase in Day 0 weight increased day 7 weight by 1.09 (± 0.03) kg, $P < 0.001$. On Day 7, nursery raised calves weighed 7.9 (± 2.2) kg more than hutch raised calves ($P<0.01$). Total time eating and pre-weaning housing interacted in this model. For nursery raised calves, a 1% increase in eating time during the first week increased day 7 weight by 3.7kg ($P<0.01$). For hutch raised calves, a 1% increase in eating time increased day 7 weight by 0.23(±0.1) kg ($P<0.01$). This indicates that nursery calves are likely either consuming more feed or absorbing increased nutrients while they are eating. Bunk engaged and bunk directed behavior did not influence day 7 weight. The amount of time spent eating increased over time with calves eating 3.8 (±0.4) percent on Day 0 and 12.8 (±0.7) percent on day 6, ($P<0.001$). These findings suggest that calves became more adept at accessing feed with a longer time in the new environment. Low levels of eating on Day 0 may result from low feeding motivation, perhaps due to weaning stress or novelty associated with a new environment, diet and presentation of feed.

Key Words: growth, feeding behavior, heifers

382 Evaluation of the Pedometry Plus system for the detection of pedometric activity and lying behaviour in dairy cattle. J. H. Higginson*[1], K. E. Leslie[1], S. T. Millman[2], and D. F. Kelton[1], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Iowa State University*, *Ames*.

The objective of this study was to validate the Pedometry Plus system (SAE Afikim, Israel), which measures pedometric activity as well as lying and standing behaviour. The device provides information regarding the number of steps taken, the duration of lying time, and the number of lying bouts. Sixteen Holstein cows housed individually in maternity stalls were used for the validation in the fall of 2008. In stage one of the trial, eleven cows had a Pedometry Plus tag on one hind leg and a previously validated IceTag (IceRobotics, UK) on the opposite hind leg. Allocation of devices to right or left legs was random. Digital video recordings were made throughout the validation process, with each cow being observed for three days. The duration of lying time and the number of lying bouts were recorded from video analysis. Pearson product-moment correlation between the two devices for the number of steps taken was r=0.73 ($p<0.0001$). This lower correlation was unexpected; however video analysis revealed that during bouts of lying, there was movement of the upper leg while the lower leg was immobile. This could account for differences in pedometric activity recording between the two legs, and hence the two devices. In stage two, five cows were fitted with Pedometry Plus tags and IceTags, with both tags on each hind leg. Correlation between the two devices for the number of steps taken was r=0.82 ($p<0.0001$). Additionally, the number lying bouts and the duration of lying time were highly correlated for all cows, r=0.98 ($p<0.0001$) and r=0.90 ($p<0.0001$), respectively. The Pedometry Plus device appears to be a useful tool for the measurement of activity, including steps taken, number of lying bouts, and duration of lying time in dairy cows. In addition, differences in activity measurements in the initial experiment may in part be attributable to differences in movement of upper and lower legs during bouts of lying, and should be considered in the interpretation of data from pedometers.

Key Words: pedometry, biotelemetry, activity

383 Behavioral and physiological responses to lipopolysaccharide induced clinical mastitis. J. L. Zimov*, N. A. Botheras, and J. S. Hogan, *The Ohio State University*, *Wooster*.

The behavioral and physiological effects of lipopolysaccharide induced mastitis were examined in lactating Holstein cows. Twenty cows were assigned to five blocks of four cows grouped by parity and stage of lactation. Two cows within a block were randomly selected to receive either intramammary infusion of 25 µg of sterile lipopolysaccharide or intramammary infusion of sterile saline. Uninfected mammary quarters were infused three hours post milking. Experimental cows were under continuous video monitoring during the study. Cows receiving the lipopolysaccharide treatment had higher (P≤ .05) mean (± s.e.) peak quarter milk somatic cell counts (6.75± 0.04 vs. 4.57 ± 0.32 log10/ml), rectal temperatures (41.4± 0.2 vs. 38.4 ± 0.2 C), concentrations of milk amyloid (3.4 ± 0.3 vs. 1.4 ± 0.2 µg/ml) and serum cortisol (63.0 ± 6.0 vs. 28.3± 2.9 µg/dl) the first twenty four hours after infusion compared with saline treated cows. Lipopolysaccharide treated cows spent a reduced percentage of the first twenty four hours after challenge eating (16.9 ±0.8 vs. 21.0 ±1.2%), cud chewing (35.8 ± 2.3 vs. 39.8 ± 1.5%), and laying in their stalls (40.7± 4.0 vs. 47.9± 3.4%) compared with saline infused cows. Rumen contractions were reduced in lipopolysaccharide infused cows compared with saline infused cows at sample times corresponding with peak rectal temperatures. Hock to hock distance following intramammary infusion did not differ between lipopolysaccharide and saline treated cows. Results of the current trial suggest that lipopolysaccharide induced mastitis affects both behavioral and physiological responses in lactating dairy cows.

Key Words: behavior, mastitis, lipopolysaccharide

384 A comparison of the effects of two different Korral Kool® systems on dairy cows in a desert environment. X. Ortiz*[1], J. Smith[1], B. Bradford[1], J. Harner[1], and A. Oddy[2], [1]*Kansas State University*, *Manhattan*, [2]*NADA Al-Othman*, *Saudi Arabia*.

An experiment was conducted to investigate the effects of two different Korral Kool® (KK) systems on core body temperature (CBT) of dairy cows. Two different KK systems were tested; a system with 2m diameter, 3 hp fans and spaced at 6m (SMALL), and a system with 2.2m diameter, 5hp fans spaced at 8m (BIG). Forty eight multiparous Holstein cows were randomly assigned to 8 pens (4 BIG, 4 SMALL) and pens were randomly assigned to sequence of treatments (KK were operated for 21 [21h] or 24 [24h] hours per day) in a switchback design. CBT measurements were obtained at 5-minute intervals using data loggers (HOBO U12®) attached to blank continuous intravaginal drug release (CIDR®) devices. The experiment lasted 6 days, with 3 periods of 2 days each. All treatments started at 0600h and KK were turned off at 0300h for the 21h treatment. The data were analyzed using a repeated measures model, with time, treatment, and time by treatment included as fixed effects and cow within pen, day, and pen as random effects. Average ambient temperature was 35°C and average relative humidity was 45%. Significant treatment effects on mean CBT were observed; cows on the SMALL 24h treatment had a lower average CBT (P<0.01) compared to the SMALL 21h treatment (39.22 vs. 39.36°C), and cows on the BIG 24h treatment had a lower average CBT (P<0.01) compared to the BIG 21h treatment (38.95 vs. 39.09°C). The average CBT of cows on the BIG 24h treatment was significantly lower (P<0.01) than the SMALL 21h treatment (38.95 vs. 39.36°C). There was a significant treatment by time interaction (P<0.001), with greatest treatment effects occurring at 0100h; treatment means at this time were 39.05, 39.01, 39.72, and 39.89°C for BIG 24h, BIG 21h, SMALL 24h, and SMALL 21h, respectively. Results demonstrated that at certain parts of the day the BIG system had a better performance compared to the SMALL system. These results showed that CBT can decrease when KK running time is increased from 21h to 24h, regardless the size of the KK cooling system.

Key Words: heat stress, dairy cow, evaporative cooling

385 Effect of feedline soakers complementing Korral Kool systems on lactating dairy cows in a desert environment. X. Ortiz*[1], J. Smith[1], B. Bradford[1], J. Harner[1], and A. Oddy[2], [1]*Kansas State University*, *Manhattan*, [2]*NADA Al-Othman*, *Al Ahsa, Saudi Arabia*.

An experiment was conducted in a dairy in Saudi Arabia to investigate the effects on core body temperature (CBT) of dairy cows when Korral Kools (KK) were complemented with feedline soakers (FS). Twenty multiparous Holstein cows averaging 44 kg/d of milk and 67 days in milk were randomly assigned to 2 pens, which were randomly assigned to treatment sequence in a switchback design. The experiment lasted 4 days, in which the KK were operated for 24 hours while alternately the FS in one of the pens remained off while the FS in the other pen would stay on for 12 h periods. All treatments started at 0600 h and FS were operated from 1200 h to 0000 h with a soaking frequency of 5 min (36 s on and 264 s off). Core body temperature measurements were obtained at 5-minute intervals using data loggers (HOBO U12®) attached to blank continuous intravaginal drug release (CIDR®) devices. CBT data were analyzed with a repeated measures model including fixed effects of time, treatment, and treatment by time interaction and the random effects of day and cow within pen. Average ambient temperature was 35°C and average relative humidity was 33% during this experiment. A significant treatment effect was observed; FS significantly decreased the mean 24-h CBT from 39.16 to 38.99°C (P < 0.04). Treatment by time interaction was also significant (P = 0.02), with greatest treatment effects at 1500 h, when FS reduced CBT from 39.38 to 38.81°C. These results demonstrate that the use of FS complementing the KK cooling systems decreased the CBT of dairy cows.

Key Words: desert environment, Korral Kool, feedline soakers

386 Revised temperature humidity index (THI) for high producing dairy cows. R. B. Zimbleman*, R. P. Rhoads, L. H. Baumgard, and R. J. Collier, *University of Arizona*, *Tucson*.

Current THI underestimates impact of thermal environment on high producing cattle because studies utilized low producing cows (<15 kg/d) constant temperatures and long intervals (2 wks) before estimating milk yield losses. Therefore, eight studies (100 multiparous Holstein cows) were used to determine minimum, maximum, and average THI threshold for milk yield loss for high producing (> 35 kg/d) multiparous dairy cows. In addition 48 lactating multiparous cows were used to evaluate effects of black globe humidity index (BGHI) on these same parameters to apply solar radiation effects to this index. Studies were carried out in climate controlled rooms at the University of Arizona. Physiological measures of heat strain included respiration rate (RR/min), infrared surface temperature (ST, °C), rectal temperature (RT. °C), heart rate (HR/min), and evaporative heat loss (EVHL, g/m2). Respiration rates, ST, RT, EVHL, and HR were collected 2-4 times per day. Data was analyzed using ANOVA and REGRESSION procedures of SAS (SAS, 1999). Milk yields recorded during acclimation periods and prior to environment initiation were included as a covariate in the analyses. All physiological measures of heat stress were linearly increased between

THI values of 60 and 90. Respiration rates increased by 2.0 breaths per minute per increase in THI unit ($P < 0.001$; $r2 = 0.4343$). Milk yield losses became significant when minimum THI on any given day was 65 or greater. Milk yield losses per day were 2.2 kg between a minimum THI of 65 and 73. Furthermore, milk yield losses became significant after 17 hours of exposure to an average THI of 68 and equated to a 2.2 kg per day loss in milk yield. This suggests that cooling of dairy cows producing more than 35 kg milk/d should be initiated at a minimum THI threshold of 65 or above or when average THI is 68 for more than 17 hours. We did not detect any advantage of BGHI index over THI in predicting milk yield losses or physiological responses. This project was supported by National Research Initiative Competitive Grant no. 2006-01724 from the USDA Cooperative State Research, Education, and Extension Service.

Key Words: heat stress, dairy cattle, index

387 Evaluation of the stress response of heifers during transportation. S. M. Behrends*[1], T. B. Schmidt[1], D. H. Keisler[3], J. W. Daily[2], J. O. Buntyn[1], D. J. Sykes[1], L. E. Hulbert[2], K. M. Cooley[1], D. T. Dawson[1], and J. A. Carroll[2], [1]*Mississippi State University, Mississippi State*, [2]*Livestock Issues Research Unit, USDA-ARS, Lubbock*, [3]*University of Missouri, Columbia*.

To evaluate the stress associated with transportation; 22 heifers (326 ± 47 kg) were randomly assigned to a control (Con) or transport (Tran) group. On d 0, 12 h prior to the transportation, heifers were weighed and fitted with an indwelling rectal temperature (RT) probe, jugular catheters and heart rate (HR) monitors. On d 1, all heifers were haltered and tied for 2 h prior to transportation. At the end of the 2 h period all heifers were weighed, controls were returned to their tie stall and transported heifers were loaded on the trailer for transport. The first transport period (FTP) began when Tran heifers were loaded on a trailer with 12 individual stanchions and Con heifers were returned to tie stalls. Blood samples were obtained throughout the 4 h transport period (Con and Tran heifers) at 30-min intervals. After transport, Tran heifers were taken to a new location unloaded and weighed; blood samples were obtained for 2 h post-transport. Simultaneously, Con heifers were weighed and blood samples obtained. Heifers were allowed a rest period for 14 h. After the rest period on d 2, heifers were subjected to a second transport period (STP; same protocol as in FTP). Serum was analyzed for cortisol (CS), insulin-like growth factor-1 (IGF-1), and growth hormone (GH). The FTP resulted in a 6% loss in BW for the Tran heifers as compared to a 2.5% loss for the Con heifers ($P<0.001$). Overall, BW loss was 2% greater ($P>0.02$; FTP and STP combine) for Tran heifers compared to Con heifers. During FTP ($P < 0.001$) and STP ($P < 0.002$) Tran heifers had an elevated RT compared to Con heifers. Prior to- and post-transport (both FTP and STP), CS concentrations did not differ between the treatment group's. Differences ($P < 0.05$) in CS were observed starting 1 h into the FTP and 30 min into the STP. After three h in transit, no difference ($P\geq0.05$) was observed in CS for both the FTP and STP. Results of this study indicate that transportation can be an acutely stressful event, as seen with increased CS concentrations, increased RT and increased BW losses. However, after 3 h, it appears that heifers are able to acclimate to initial stress induced by transportation.

Key Words: cortisol, stress, transportation

388 Use of an automated sampler to assess bovine adrenal hormone response to transportation. N. C. Burdick*[1,2], J. A. Carroll[2], R. D. Randel[3], S. T. Willard[4], R. C. Vann[5], C. C. Chase, Jr.[6], D. A. Neuendorff[3], A. W. Lewis[3], J. W. Dailey[2], L. E. Hulbert[2], L. C. Caldwell[1,3], J. G. Lyons[1], and T. H. Welsh, Jr.[1], [1]*Texas AgriLife Research, Texas A&M System, College Station*, [2]*USDA ARS Livestock Issues Research Unit, Lubbock, TX*, [3]*Texas AgriLife Research, Texas A&M System, Overton*, [4]*Mississippi State University, Mississippi State*, [5]*MAFES, Mississippi State University, Raymond*, [6]*USDA ARS Subtropical Agricultural Research Station, Brooksville, FL*.

Automated blood sampling would aid characterization of acute endocrine responses to transportation procedures. In this study, the IceSampler™ device was programmed to collect blood samples via jugular catheter from the herd's 7 calmest (C; temperament score=0.84±0.03) and 8 most temperamental (T; temperament score=3.37±0.18) 10-month-old Brahman bull calves at 15- and 30-min time intervals relative to transportation. Bulls were fitted with indwelling jugular catheters, rectal thermometer probes, and heart rate monitors and were then transported. Bulls were loaded onto a trailer that contained individual stalls. The trailer remained stationary for 120 min to allow for acclimation. After initiation of transportation at time 0, bulls were transported (390 Km roundtrip) for 480 min at an average speed of 91 Km/h. Plasma concentrations of cortisol, epinephrine (EPI) and norepinephrine (NE) were determined by RIA and by EIA, respectively. Data were analyzed using ANOVA specific for repeated measures. Rectal temperature increased over time (38.3±0.2 and 39.3±0.2°C pre- and post-transport, respectively; $P<0.01$) but was not affected by temperament ($P>0.10$). Heart rate remained steady in C bulls (μ=100.8±26.2 bpm) but varied over time in T bulls (time*temperament $P<0.01$). Cortisol concentration increased ($P<0.01$) in C bulls (18.6±5.5 at time 0 to 44.6±5.7 ng/mL at 15 min) but not T bulls (μ=36.8±3.2 ng/mL) in response to the initiation of transportation at time 0. Concentrations of EPI remained unchanged in C bulls (μ=43.7±15.4 pg/mL) throughout the sampling period but decreased in T bulls (235.7±32.1 and 78.6±54.2 pre- and post-transport, respectively $P<0.05$) whereas NE concentrations were not affected ($P>0.10$) by transportation or temperament (μ=267.19±48.2 and 261.3±49.8 for C and T bulls, respectively). These data suggest that temperament affects the stress response to transportation. The use of remote samplers allows us to detect specific indices of transportation stress, and to discern that although some changes were attributable to handling stress and temperament, the transportation process was not equally stressful within temperament groups.

Key Words: bovine, stress, transportation

Animal Health: Animal Well Being: Tackling the Issue of Cow Longevity

389 New frontiers in mastitis research. S. C. Nickerson*, *University of Georgia, Athens*.

Mastitis or bacterial infection of the mammary gland is the most costly disease of dairy cattle, with estimated economic losses approaching $2 billion each year in the US. Approximately 40 years ago, the 5-point plan for mastitis control was developed, and although modifications have been added to this plan, it has remained the cornerstone for controlling this disease in dairy cows over the past 4 decades. However, as consumers and milk processors demand higher quality products free of adulterants, dairy farmers continue to strive to lower the prevalence

of intramammary infection and the associated milk somatic cell and bacteria counts, in attempts to improve milk quality and meet higher quality standards. As a result, newer products and enhanced mastitis management practices have been developed to further lower the new infection rate and eliminate existing cases of mastitis. For example, novel antimicrobial formulations for pre- and postmilking teat antisepsis focus on rapid and complete killing of mastitis-causing pathogens, while improving teat skin condition to reduce microbial colonization. Intramammary infusion products being developed are based on natural antimicrobials that minimize withdrawal times and enhance cure rates. More attention is now focused on managing the coagulase-negative staphylococci, which cause minimal increase in somatic cell counts, but are the most prevalent mastitis-causing bacteria on all dairies. And finally, newer attempts to enhance the bovine immune system against mastitis-causing bacteria through dietary supplementation, immunization, and controlling immunosuppression continue to show promise for the control of this disease.

Key Words: dietary supplementation, immunosuppression, vaccination

390 Tackling the issue of cow longevity: Battling lameness. J. K. Shearer*, *University of Florida*, *Gainesville*.

According to a 1996 NAHMS report, 15% of cows are culled from US dairy herds as a direct effect of lameness. Indirect effects of lameness on milk production and reproduction are estimated to account for an additional 49.1% of culling in US herds. These figures suggest that lameness is a significant cause of reduced cow longevity. Research on lameness in cattle has been directed toward improvement in understanding of the pathogenesis of laminitis (subclinical laminitis). Laminitis associated with rumen acidosis results in low rumen pH predisposing to the release of potent vasoactive substances that disrupt blood flow to the corium. Inflammation, intravascular coagulation, ischemia and the activation of metalloproteinase enzymes (MMP) follow with weakening of the suspensory apparatus of the third phalanx (P3). Weakening of the suspensory system leads to rotation and sinking of P3 and is accompanied by compression of the supportive tissue and digital cushion that lie beneath P3. Alternative mechanisms responsible for weakening or laxity of the suspensory apparatus of P3 have been proposed by UK researchers. These include activation of MMP by a gelatinolytic enzyme observed in prepartum heifers termed hoofase and by hormonal changes associated with calving. Researchers observed fewer claw lesions in heifers housed in straw yards during the transition period compared with heifers housed in free stalls indicating that soft flooring surfaces during the peripartum period are important to foot health. This suggests that heifers may be less resistant to compressive loading forces that may cause injury to the digital cushion and adjacent supportive tissues. Downward displacement of P3 results in damage to the digital cushion with subsequent reduction in fat content and replacement with collagenous tissue. This reduces shock absorbing function of the digital cushion and predisposes to sole uclers. Recent work suggests that fat content of the digital cushion may also be affected by body condition (BC). If these observations are correct, lameness may be the result of, rather than the cause of, poor BC as most believe.

Key Words: lameness, laminitis, subclinical laminitis

391 Increasing longevity by increasing reproductive efficiency in dairy cattle. M. C. Wiltbank*, *University of Wisconsin*, *Madison*.

Some of the decrease in longevity of dairy cattle is attributed to decreasing reproductive efficiency. Poor reproduction in dairy cattle is multifactorial with physiology, genetics, management, health, and nutrition underlying the problems and the solutions to poor reproduction. Many dairy managers are using hormonal programs to manage reproduction with increased reproductive efficiency primarily due to increasing service rate with little improvement in pregnancies per AI (fertility). Newer programs have been developed that result in improved fertility, compared to breeding after estrus. These programs involve increasing numbers of targeted hormonal treatments to optimize gamete viability and hormonal environment for pregnancy. Genetic selection for reproduction has also now become a part of the selection indices in many countries potentially leading to dairy cattle genetics with improved reproductive potential. In addition, reproduction is a primary target of other genetic selection strategies including genomics and cross-breeding within the dairy industry. In spite of the focus on reproductive protocols and genetic selection for improved reproduction, it is clear that management and health underlie some of the variability between herds in reproductive efficiency. However, randomized studies showing improvements in reproduction after manipulation of these variables are still scarce. Dairy cattle nutrition has been found to alter dairy cattle reproduction in both positive and negative ways; however, the experimental designs utilized in these studies are frequently not optimal for making firm conclusions about reproduction. In general, the relative contribution of these varied factors to reproductive efficiency or inefficiency in dairy cattle has been surprisingly difficult to define. This has led to inaccuracy and inefficiency in diagnosing reproductive problems on specific dairy herds and in determining the most efficient directions for future reproductive research.

Key Words: fertility, productivity, service rate

392 Improving longevity with new genetic models and marker assisted selection. K. A. Weigel*, *University of Wisconsin*, *Madison*.

Historically, programs for genetic improvement of dairy cattle have been completely dependent on national milk recording systems or breed association type programs for data collection. Due to increases in average herd size, a large percentage of records now come from on-farm herd management software programs. These allow timely measurement of traits such as conception rate, calving ease, and stillbirth rate, because events are recorded when they occur, rather than at monthly intervals. More importantly, they provide data for traits that are ignored in national milk recording systems, such as flow rate, milking duration, and the incidence of infectious diseases and metabolic disorders such as mastitis, ketosis, lameness, metritis, and displaced abomasums. In the future, radio-frequency identification systems may allow routine measurement of new traits, such as activity, body temperature, and hormones associated with female fertility or animal health. Therefore, performance testing may become concentrated in large herds with on-farm software and electronic data capture systems. One breeding company has implemented intensive data recording in 175 large commercial herds, as compared with 1600 to 3800 progeny test herds for its competitors. Consolidation may also occur in sire acquisitions, with breeding companies relying on a few large, extensively phenotyped supplier herds. In the era of whole-genome selection, phenotypes for novel traits from contracted data farms, which may include commercial dairy herds, custom heifer growers, or wet calf ranches, can be combined with dense single nucleotide polymorphism genotypes to develop genomic predictions that can be used in the population at large.

Key Words: health, longevity, genetics

ARPAS Symposium: Feed Management: ARPAS, NRCS, and the National Project

393 Feed management from perspective of national feed management project. J. H. Harrison*[1], R. A. White[1], G. Erickson[2], R. Koelsch[2], A. Sutton[3], T. Applegate[3], R. Burns[4], and G. Carpenter[5], [1]*Washington State University, Puyallup*, [2]*University of Nebraska, Lincoln*, [3]*Purdue University, Lafayette, IN*, [4]*Iowa State University, Ames*, [5]*USDA-NRCS, Washington, D. C.*

In 2006 a Feed Management Education Project was implemented for the species of beef, dairy, poultry and swine. The project is national in scope and funded by the USDA - Natural Resources Conservation Service (NRCS) Conservation Innovation Grant program. The project is designed to encourage adoption of the NRCS Feed Management Conservation Practice Standard 592 and feed management practices that can have a positive impact on soil, water, and air quality. A goal of the project is to assist NRCS staff and agricultural professionals increase their understanding of Feed Management, its impacts on environmental sustainability of livestock and poultry operations, and inclusion of a Feed Management Plan (FMP) as part of a comprehensive nutrient management plan (CNMP). The Feed Management curriculum is organized in a four-hour format for both technical service providers and nutrition consultants. Information is provided that links the FMP to the CNMP and the requirements for certification to write a feed management plan. Real farm case studies are used to provide training in use of on-farm assessment checklists for assessing the opportunity of a Feed Management Plan to impact whole farm nutrient balance; and, develop and implement a FMP. Electronic decision aid tools include: whole farm balance, manure excretion estimator, and the relative economics of a ration change vs. transporting manure. The manure excretion estimator tool and economics tool are both linked to feed nutrient use. Species specific and practice specific fact sheets are provided to assist with evaluating the relative merit of feed management practices listed in the on-farm assessment checklists. Examples of a FMP template are provided, as well as a completed example FMP.

Key Words: dairy, feed management, environment

394 Update on feed management from the perspective of USDA NRCS at the national and state levels. G. Carpenter*, *USDA NRCS, Beltsville, MD.*

The USDA Natural Resources Conservation Service (NRCS) has been interested in feed management as a means of decreasing manure nutrients since the early 2000s. NRCS sees feed management as a major tool in helping the animal industries to control water and air pollution possibilities. In 2001, NRCS assembled a Feed Management Action Plan and brought in a visiting scientist to begin actions to support feed management. A national dialogue on feed management was held in 2002, with over 100 scientists and industry nutritionists. In 2003 a series of focus group sessions was held with industry nutritionists to establish areas in which NRCS could further the role of feed management in manure nutrient control. NRCS adopted a feed management conservation practice standard in 2003 that allows NRCS to supply technical and financial assistance to producers for adopting the practice. NRCS entered into a Memorandum of Understanding with ARPAS in 2004 for ARPAS to train and certify animal nutritionists to work with producers on feed management for manure nutrient reduction. In the NRCS Conservation Innovation Grants program a number of projects have been funded that are feed management related. Feed management is one of the six core elements of the Comprehensive Nutrient Management Plan (CNMP) the NRCS tool for nutrient management planning that has been designated by USEPA as satisfying its permitting requirements for a nutrient management plan, in its Concentrated Animal Feeding Operations (CAFO) rule. Since 2004, NRCS has approved EQIP contracts for CNMPs with feed management that cover over 58 thousand animal units. Not-to-Exceed payment rates for feed management for FY 2009 were set at five dollars per animal unit, and not to exceed six thousand dollars per contract. At the time of this writing, eleven individuals were registered with NRCS as Technical Service Providers (TSPs) certified to write the feed management section of the CNMP. One nutritionist is registered as a TSP to formulate diets for manure nutrient reduction.

Key Words: feed management, nutrient management, CNMP

395 The Virginia feed phosphorus monitoring project. C. C. Stallings*, K. F. Knowlton, R. E. James, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg*.

To reduce the potential for phosphorus (P) runoff into streams, a project was undertaken to use feed management as a tool to reduce P excreted by dairy cows. A survey was sent to all Virginia dairy farms (806) asking for information related to nutrient management practices, and assessing potential interest in an incentive-payment project to reduce overfeeding of P. Interested farms were contacted, visited, and signed to the project. The program provides free feed testing for major nutrients and minerals every two months for three years, ration consultation on request, educational materials and updates via a newsletter, and educational meetings for both producers and nutritionists. In addition a P Report is provided to producers after each set of samples are submitted and analyzed. This report includes calculated amount of P fed and calculated P requirement for cows in that herd. The P requirement and dry matter intake are calculated according to NRC based on producer-reported body weight, milk yield, and fat test. The result is expressed as P consumed as a percent of required. 215 herds signed up for the project. By 2009, 160 herds had completed enough samplings (5) to have a year end summary prepared calculating eligibility for payment. Ten herds fed P within 5% of required and qualified for the highest year-end payment ($12/cow), 37 herds fed P at 105 to 115% of required for a $6/cow pay rate, 38 herds fed P at 115 to 125% for a $3/cow pay rate, and 75 herds fed more than 125% of required P and did not qualify for payment. The remaining herds have not completed their first year or submitted enough samples for a summary. The Virginia P Feeding Incentive Program has engaged producers and their advisors in an ongoing dialogue about herd feeding practices. More than 50% of producers completing sufficient sampling for year 1 evaluation have earned an incentive payment, and average dietary P consumed in all 160 herds declined by 3.3 grams/cow/day with a total calculated reduction of 32.6 tons P per year from 24,522 cows.

Key Words: phosphorus, incentive, feed management

396 Feed management: Northeast perspective on workshops, ARPAS certification and relationship with national feed management project and NRCS. V. Ishler*[1], C. Stallings[2], and R. Kohn[3], [1]*The Pennsylvania State University, University Park*, [2]*Virginia Polytechnic and State University, Blacksburg*, [3]*University of Maryland, College Park*.

Land Grant Universities in Delaware, Maryland, Pennsylvania, Virginia and West Virginia and USDA's Cooperative State Research, Education and Extension System (CSREES), working with EPA Region III, formed a partnership to advance water quality protection and restoration efforts in the Mid-Atlantic Region by providing water quality science support, training and education. In the winter of 2006, University specialists in dairy nutrition were invited to participate in the Mid-Atlantic Regional Water Program that until then was predominately comprised of engineers and agronomists. Penn State, Virginia Tech and the University of Maryland represented the dairy nutrition component. Specialists from these three Universities decided the greatest opportunity to positively affect water quality was to implement the national initiative: Development and Integration of a National Feed Management Education Program and Assessment Tools into a Comprehensive Nutrient Management Plan, which was being lead by Washington State University. The goal of the dairy nutrition group was to cater the national program to issues affecting the Mid-Atlantic Region. Collaboration with the local NRCS specialists was an essential component in getting the certification process initiated. In November 2007, the first training on how to become a certified feed management planner was held in Grantville, Pennsylvania with 105 consultants in attendance. More training followed that included both feed industry and NRCS personnel. The Mid-Atlantic group felt that for nutritionists to buy into the concept of becoming a certified feed management planner through ARPAS, off-setting the cost of the exam would be a positive incentive. As of January 2009, ARPAS lists a total of 65 certified feed management planners and 56 are in the northeast and would have attended trainings provided by the Mid-Atlantic dairy nutrition group.

Key Words: feed management, mid-Atlantic region, certification

Beef Species: Symposium: Population Data Analyses to Evaluate Trends in Animal Production Systems

397 Enhancing management decisions in modern animal agriculture using population data and appropriate analytical methodology. P. D. Matzat*[1], J. Bargen[2], and W. J. Platter[1], [1]*Elanco Animal Health, Greenfield, IN*, [2]*AgSpan, Overland Park, KS*.

Improvements in data capture and analytics in animal protein production industries has reflected the change and opportunity observed in many manufacturing and value creation segments of the global economy. Imagination and cost are the only things that limit the amount and type of individual or unique data captured, analyzed and reported in modern animal protein production systems. As the result of mountains of data being accessible, large production systems struggle with how to best capture, analyze, evaluate, interpret and act on information that emanates from daily downloads of production related measurements. Management decisions based on scientific methodology for analysis of population information is sometimes difficult and misleading based on system bias and the appearance of significant effects simply based on the volume of data or observations involved. Furthermore, the economic impact of small differences in efficiency or production output often times outweigh science based evaluation or analysis. A decision making constraint that the food animal production industry must grapple with is the difference between controlled research results reported in peer reviewed scientific publications compared to commercial production outcomes. Additionally, conclusions with regard to treatment efficacy reported in scientific journals often do not match up with optimal economic outcomes or return on investment when evaluated in commercial production enterprises. Large commercial operations have the capability of replicating treatments across entire systems, allowing replication of treatments by barns or houses in the case of pork, broiler and layer production or pens in the case of feedlot cattle. Individual measurements are also accessible in the case of daily dairy cow output, as well as carcass metrics in pork and beef production. Linking this information to treatments, seasonal changes in environment and the impact of specific management decisions can have a dramatic impact on system profitability, long range planning and financial sustainability of animal agriculture.

Key Words: population data, management, analysis

398 An animal breeding approach to the estimation of genetic and environmental trends from field populations. D. Garrick*, *Iowa State University, Ames*.

Selection of parents from candidate individuals that outperform their contemporaries is the basis for the genetic improvement that leads to long-term trends in the performance attributes of populations. Theoretical formulae to predict the genetic trend or response to selection are well known and are functions of population parameters including heritability, intensity of selection, phenotypic variation and generation interval. Field data produced from successive generations of selected individuals do not always reflect expected gains, in part because phenotypic changes result from both genetic and environmental causes. Estimating realized trends from field data, and partitioning them into various causes, is therefore of critical interest. Prior to the 1980's, control populations were the basis for separating genetic from environmental causes of change. The development of mixed model theory, notably by Dr Henderson and colleagues, led to recognition that in certain circumstances phenotypic observations from a selected population could be decomposed into their underlying genetic and environmental components without recourse to a control population. This controversial suggestion has, over the last 2-3 decades, been accepted throughout the world as the routine approach to predict trends in populations with known parentage. It is now also frequently applied to wild populations, with molecular techniques rather than pedigree used to infer parentage. The philosophical basis that underpins the method involves a model equation that accounts for performance as the sum of various unobservable fixed and random effects. It is widely applicable to the analysis of appropriate field and experimental data.

Key Words: mixed models, BLUP

399 Data collection and determination of factors affecting efficiency and profitability of beef cattle production systems. R. Jones[1] and M. Langemeier*[2], [1]*Oklahoma State University, Enid*, [2]*Kansas State University, Manhattan*.

This paper summarizes a series of research examining the relative efficiency and profitability of various beef cattle production systems. This type of research has historically been very common in the social sciences, particularly economics, where scientists rely on population data and population research tools and techniques rather than controlled experiments. Much of the particular research referenced in this paper has been conducted using a combination of production and financial data from a sample of actual beef producers. A variety of specific techniques are available, and more than one technique may need to be utilized in the same study to provide answers to the questions at hand. For example, it is quite common to use one technique to quantify the magnitude of relative efficiency (inefficiency) exhibited within a given data set, and then use another technique to identify factors that contribute to that relative efficiency and their magnitudes. The study of important economic outcomes (efficiency, profits, costs, etc.) lends itself particularly well to this type of analysis. Given appropriate data, a wide variety of beef industry research questions can be addressed using similar techniques. We discuss specific data required to conduct various types of population analysis, and suggest potential sources and appropriate collection techniques. In addition, we provide examples of previous and ongoing research projects to illustrate the wide variety of issues that can be addressed using alternative techniques. Finally, we address potential shortcomings and other issues that need to be considered when collecting data and performing economic analyses of beef production systems.

Key Words: efficiency, economic analysis, profit

400 Applications of population data analysis in on-farm dairy trials. M. Engstrom*[1], W. Sanchez[2], W. Stone[2], and N. R. St-Pierre[3], [1]*DSM Nutritional Products, Inc., Parsippany, NJ*, [2]*Diamond V Mills, Cedar Rapids, IA*, [3]*The Ohio State University, Columbus*.

With appropriate statistical designs and management controls, research trials done on-farm can generate good data, speed up technology interchange, and in some cases couldn't be done anywhere else. Useful designs include split-herd ("pen vs. pen") trials where pen comprises the experimental unit, and crossover or switchback designs where treatments are imposed on a schedule over one or more experimental groups. We've also used a "paired-herd" design, where two switchback studies are run in tandem, but with the treatments out-of-phase to neutralize environmental variation. A multi-site design utilized 35 dairies to compare milk responses to a protein source, using individual cow records to evaluate differences in milk production. Recently, we have used statistical process control techniques (SPC) to evaluate current management changes, using repeated measures on the dairy. Although a drawback to SPC might be the lack of traditional statistics to test differences, standard rules can be used to demonstrate that a process or variable has changed, or to characterize a seasonal change. Meta-analysis techniques are the most powerful tools to evaluate many similar trials for low-frequency or subtle effects. Meta-analysis can be used to segment a database to validate and compare trial methods or to investigate for publication bias. Additional design concerns for reproduction stuides include the need for adequate numbers of observations and planning for the lag time between an experimental treatment and response measurement (i.e. pregnancy confirmation).

Key Words: trial design, statistical process control, meta-analysis

401 Application of statistical process control techniques to monitor changes in animal production systems. A. De Vries*, *University of Florida, Gainesville*.

Statistical process control (SPC) involves using statistical techniques to measure and analyze the mean and variability in process observations. Emerging trends in animal production systems can be detected with the aid of SPC techniques. The conceptual idea is that variability in process observations comes from 2 basic sources. Common cause variability includes all sources of random variability that can be removed only by changing the process. Special cause variability results from some potentially identifiable source that can be removed if needed. Production processes that are influenced by special cause variability are said to be out of control. The goal of SPC is to detect when a process moves from in control to out of control, and possibly suggest the way it went out of control. A process that is out of control warrants further investigation, at a cost of time and effort, to identify the special cause of the shift or drift. On the other hand, processes that are in control should be left alone, unless the process is intentionally changed. Statistical techniques, primarily control charts, are needed to determine if there is enough evidence that the process has changed. The amount of evidence depends on the relative cost of type I (false positive) and type II (false negative) decision errors. Control charts have their origin in manufacturing in the 1920s but there are now abundant applications in health care and epidemiology. Various types of control charts have been applied in animal production systems, with examples in poultry, swine, dairy, and beef. Examples include monitoring of growth, disease incidence, water intake, and reproductive performance. Common challenges for applications in animal production systems are the identification of the best statistical model for the common cause variability, grouping of data, selection of type of control chart, the cost of type I and II errors, and difficulty identifying the special causes when a change is signaled. Nevertheless, carefully constructed SPC applications are powerful methods to monitor animal production systems.

Key Words: monitoring, statistics, system

Breeding and Genetics: Dairy Breeding III - Parameter Estimation

402 Estimates of heritability of feed intake in Canadian Holsteins. J. Song*, J. F. Hayes, and R. I. Cue, *McGill University, Macdonald Campus, Ste-Anne de Bellevue, Quebec, Canada*.

95,678,311 feed records from January 2000 to May 2007, corresponding to 16,866,117 test-day records were obtained from the Quebec Dairy Herd Improvement agency, Valacta. Each feed record contained information on animal identification, test-day date, feed type, quantity of feed intake for each feed, percentage composition of each feed for dry matter (DM), crude protein (CP), net energy for lactation (NEL), acid detergent fibre (ADF), etc. Weight of each different feed type fed to a cow on a test-day was recorded by the producer except for forage which was measured on a cow group basis according to production. Any test-day feed record with at least one feed variable outside the range of the

feed composition (DM%, CP%, ADF%, etc) stored in the Valacta Feed Reference Library for that particular feed was deleted as well as all other associated records for the same cow on that test-day. There remained 72,290,760 feed records corresponding to 11,798,912 test-day records. Thereafter, records with missing information (e.g. missing information in pedigree files), abnormal total DM intake or lactation length, and records of cows that were sold, died or culled were removed, leaving 2,527,442 test-day records in first parity, 1,801,004 in second parity, and 1,229,436 in third parity, corresponding to 258,759, 187,871 and 128,592 lactation records in first, second and third parity respectively. Further editing to ensure that age at first calving was between 18 and 42 months, that each herd-year-season (hys) had at least 3 records, and that sires had at least 10 progeny in 5 herds reduced the data sets to 119,628 cow records in parity 1, 27,628 in parity 2, and 28,840 in parity 3. Heritabilities of feed intake traits were then estimated using an animal model which included hys at calving, age at calving, male and female phantom groups as fixed effects, and animal and residual as random effects. The model was fitted by Restricted Maximum Likelihood and relationships among animals were taken into account on both the male and female side of the pedigree. Heritability estimates ranged from 0.06 to 0.10 for total DM, from 0.08 to 0.12 for NEL, and from 0.06 to 0.11 for CP intake.

Key Words: feed intake, heritability, Holsteins

403 Heritability of body condition score and relationships with milk production traits in Canadian Ayrshires. S. Loker*[1], C. Bastin[2], F. Miglior[3], A. Sewalem[3], J. Fatehi[1], L. R. Schaeffer[1], and J. Jamrozik[1], [1]*CGIL, University of Guelph, Canada*, [2]*Gembloux Agricultural University, Belgium*, [3]*Agriculture and Agri-Food Canada, Canadian Dairy Network, Guelph, Canada*.

The overall objective of this study is to develop a genetic evaluation for body condition score (BCS) in Canadian dairy cattle breeds using two sources of data: a) BCS collected in Quebec by DHI, and b) BCS collected nationally by type classifiers. The specific objective of this preliminary study were to estimate genetic parameters of BCS from Quebec herds and to estimate relationships between BCS and production traits in Canadian Ayrshires. After preliminary edits, there were 32,317 BCS records on 10,067 cows and 547,450 milk production records (which included milk, fat and protein yield, and somatic cell score) on 34,462 cows. There were 45,817 milk urea nitrogen (MUN) records on 9,490 cows and 47,603 lactose percentage records on 9,890 cows. Body condition scores were not always taken on the same test-day as milk production, MUN, or lactose records. Phenotypic correlations were estimated based on the entire data set (parities 1 to 3) after preliminary edits. They were calculated on an overall basis and also by lactation stage (with about 30 days per stage). Overall, BCS was significantly correlated with all traits. Per lactation stage, BCS was significantly negatively correlated with milk, fat and protein yield, and fat:protein ratio toward the end of lactation (correlations between -0.05 and-0.21). Across lactation, BCS was significantly positively correlated with protein percent (between 0.12 and 0.21). For variance component estimation data was edited further, leaving 4,641 first lactation BCS records on 1,338 cows. Body condition score was analyzed longitudinally with a random regression model with Legendre polynomials of the third order. The analysis was attempted with fourth order Legendre polynomials but resulted in the same residual variance as the third order model, so the model with fewer parameters was chosen. The overall heritability for BCS was 0.30±0.06. Heritability across the lactation ranged between 0.17 at 5 days in milk (DIM) and 0.36 at 275 DIM. Heritability estimates were reasonable considering the literature.

Key Words: body condition score, genetic parameter, random regression model

404 Effect of test-day records beyond 305 days in milk on variance components and 305-d estimated breeding values for production traits and somatic cell score of Canadian Holsteins. J. Bohmanova*[1], F. Miglior[2,3], and J. Jamrozik[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada*, [2]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [3]*Canadian Dairy Network, Guelph, ON, Canada*.

The Canadian Test-Day Model (CTDM) includes test-day (TD) records from 5 to 305 days in milk (DIM). Because 47% of Holstein cows have longer lactation than 305 DIM there is a significant number of TD records beyond 305 DIM that could be included in the genetic evaluation. The additional information could increase accuracy of 305-d estimated breeding values (EBV). On the other hand, extending range of TD records beyond 305 DIM can cause a lack of fit due to inability of regression functions to properly fit the peak or end of the lactation curve when fitting longer lactations. The aim of this study was to investigate the optimal range of TD records for estimation of 305-d EBV for milk, fat and protein yield and somatic cell score (SCS). Three multiple-trait (milk, fat, protein and SCS), multiple-lactation (first three lactations) random regression models fitting TD records up to 305 DIM (M305), 335 DIM (M335) and 365 DIM (M365) were used. The effects common to all models were fixed effects of herd x test-date, DIM class and fixed regression on DIM nested within age × season class, and random regressions for additive genetic (G) and permanent environmental (PE) effects. Legendre polynomials of order 6 and 4 were fitted for fixed and random regressions, respectively. Milk, fat and protein yields were pre-adjusted for the effect of pregnancy. Three data sets were created for variance component estimation by random sampling of 50 herds. Variance components were estimated using Gibbs sampling. Full data sets were used for estimation of breeding values. Overestimation of G and PE variances at extremes of lactations was observed with all three models. The increase of G and PE variances was at earlier DIM with M305, resulting in higher variances at 305 DIM with M305 than M335 and M365. M305 had the best ability to predict TD yield from 5 through 305 DIM. This model had also the smallest Error of Prediction of 305-d EBV and smallest decline of 305-d EBV of bulls. TD records from 5 through 305 DIM only should be used in the CTDM.

Key Words: random regression model

405 Genetic variability of test-day stearoyl coenzyme-A desaturase 9 activity. V. M.-R. Arnould*[1], N. Gengler[1,2], and H. Soyeurt[1], [1]*Gembloux Agricultural University, Animal Science Unit, Gembloux, Belgium*, [2]*National Fund for Scientific Research, Brussels, Belgium*.

Milk fatty acid (FA) profile is far from the optimal fat composition in regards to human health. Different natural sources of variation such as feeding or genetics could be used to modify the contents of unsaturated fatty acids. The impact of feeding is well described; however, genetics effects on the milk FA composition are not well studied. Increasing the unsaturated fatty acids contents of bovine milk could have the potential to raise the nutritive and therapeutic values of dairy products. The stearoyl Coenzyme-A desaturase 9 (delta-9) gene was identified

as a potential functional candidate gene affecting milk fat composition in dairy cattle. The objective of this research was to study the genetic variability on this enzyme activity across lactations. A total of 199,977 test-day records were obtained from 29,603 Holstein cows in first lactation, 154,267 records from 23,453 Holstein cows in second lactation, and 173,244 records from 75,887 Holstein cows in third and later lactations. The used model was a multiple-trait random regressions test-day model. Fixed effects were: herd × date of test, and class of age. Random effects were: herd × year of calving, permanent environmental, additive genetic, and residual effects. The studied traits were milk yield, protein content, percentage of fat, monounsaturated fatty acids estimated by mid-infrared spectrometry, and the ratios reflecting the delta-9 activity. Obtained heritability estimates of delta-9 as well as the genetic and phenotypic correlations varied across lactations. These results suggest potential improvements of milk fat composition based on delta-9 activity using animal selection and appropriate management practices.

Key Words: stearoyl coenzyme A desaturase, genetic variability

406 Influence of non-coagulating milk records on estimates of genetic parameters of milk coagulation properties. A. Cecchinato*, M. De Marchi, L. Gallo, G. Bittante, and P. Carnier, *University of Padova, Legnaro, Padova, Italy*.

Milk coagulation properties (MCP: clotting time, curd firmness) of dairy cows have been studied because of its association with cheese yield. Exploitable additive genetic variation exists for milk clotting time (RCT, min) and curd firmness (a30, mm) and, thereby, enhancement of these traits through breeding is a viable option. A critical feature of MCP data is the presence of non coagulating milk (NCM) records. These records, originating when milk does not coagulate at all in a standard 30-min testing time, are usually discarded from statistical analyses. A possible alternative is to consider NCM as censored records while the value of RCT may occurs outside the range of a measuring instrument (i.e. 30 min). The aim of this study was to evaluate the effect of including or not including NCM records on the estimates of genetic parameters of MCP. A total of 1,290 Brown Swiss cows (progeny of 50 sires) and 1,025 Italian Holstein cows (progeny of 54 sires), reared in 38 and 34 herds, respectively, were milk sampled once. Individual milk samples were collected during the morning milking and analyzed for RCT and a30, The percentage of NCM was 10% and 4% for Holstein and Brown Swiss cows, respectively. A Bayesian standard linear model (LMO) and a censored linear model (LMC) were implemented via Gibbs sampling. For LMC, data were augmented from a truncated normal distribution for samples that did not coagulate within 30 min since rennet addition, corresponding to a censoring of those observations, whereas for LMO those records were excluded from the statistical analysis. For RCT, marginal posterior means (SD) of heritabilities using LMO were 0.26 (0.09) and 0.25 (0.07) for Holstein and Brown Swiss cows, respectively. For LMC, corresponding estimates were slightly lower. Estimates of heritabilities for a30 were close to 0.17 (0.06) for both cattle breeds and both models. Results indicate that inclusion of NCM in the estimation of genetic parameters of MCP has limited effects on the magnitude of the estimated parameters.

Key Words: milk coagulations properties, non-coagulating milk, genetic parameters

407 Estimates of genetic parameters among body condition score and fertility traits in first-parity Canadian cows. C. Bastin*[1], S. Loker[2], N. Gengler[1,3], and F. Miglior[4,5], [1]*Animal Science Unit, Gembloux Agricultural University, Gembloux, Belgium*, [2]*CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*, [3]*National Fund for Scientific Research, Brussels, Belgium*, [4]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [5]*Canadian Dairy Network, Guelph, ON, Canada*.

The objective of this research was to estimate genetic correlations between body condition score (BCS) and female fertility traits using random regression animal models. Fertility traits were a) days between calving and first service (CTFS), b) days between first service and conception (FSTC), and c) days open (DO). The data analyzed included first-parity Ayrshire and Holstein BCS records collected between 2001 and 2008 by field staff in herds from Québec. On average 2.4 BCS observations were available per cow. Fertility records were extracted for herds with at least one BCS record. For Ayrshire, data included 9,739 BCS observations and from 10,613 to 11,942 fertility records depending on the trait. For Holstein, data included 197,583 BCS observations and from 185,464 to 207,553 fertility observations. (Co)variances were estimated by REML on the whole data set for Ayrshire and on a herd-based random sub set for Holstein. For each breed, genetic parameters were estimated with 3 two-trait models. For BCS, regression curve of genetic and permanent environmental effect were modelled using Legendre polynomials of order 3. All genetic correlations were negative: a genetically low BCS increases the number of days when the cow is not pregnant. The shape of the correlation curve between BCS and fertility varied among traits and breeds. Overall, genetic correlations changed significantly across lactation. For CTFS and FSTC in Ayrshire, genetic correlations were the highest (about -0.8) in the middle of the lactation (220 days in milk) and lower at the extreme of the lactation curve. Concerning DO in Ayrshire and all the traits in Holstein, correlations were high at calving (about -0.6) then slightly increased to be the highest around 180 days in milk (-0.8) and were the lowest at the end of the lactation. This suggested that the BCS measured at mid-lactation is the best indicator of fertility. Although analyses need to be extended to other traits and to later parities, these preliminary results indicated the interest of using BCS in indirect selection for better reproductive performances in Canadian dairy cows.

Key Words: body condition score, fertility, random regression

408 The influence of genetic selection and feed system on milk production and fertility performance of spring-calving dairy cows. J. Coleman*[1,2], K. M. Pierce[2], D. P. Berry[1], A. Brennan[1], and B. Horan[1], [1]*Teagasc, Moorepark Dairy Production Research Centre, Fermoy, Co. Cork, Ireland*, [2]*UCD, School of Agriculture Food Science and Veterinary Medicine, Belfield, Dublin 4, Co. Dublin, Ireland*.

The objective of Irish pasture based dairy production systems is to maximise profitability per hectare through excellence in grassland management within low cost feed systems (FS). Reproductive wastage within such systems results in additional financial losses due to a reduction in pasture utilisation and lower milk productivity from extended calving intervals. The objective of this study was to investigate the influence of genetic selection using the Irish total merit index (Economic Breeding Index; EBI) and intensive pasture based FS on milk production and fertility performance. Three genetic groups were compared: 1) LowNA, national average herd genetic potential; 2) HighNA, high genetic potential North American Holstein-Friesian (HF) and 3) HighNZ, high genetic potential New Zealand HF. Animals were randomly allocated to one of two FS: Moorepark (MP) pasture system

(2.64 LU/ha and 500 kg concentrate/cow) and a high output per hectare (HC) pasture system (2.85 LU/ha and 1,200 kg concentrate/cow). A total of 126, 128 and 140 animals were used during the years 2006, 2007 and 2008, respectively. HighNA had the greatest milk and solids corrected milk (SCM) yields, HighNZ had the lowest milk yield but similar SCM yield to LowNA group. Increased stocking rates combined with concentrate supplementation increased milk production per cow and overall farm output. HighNA and HighNZ genotypes had greater odds of being served within the first 24 days of the breeding season, becoming pregnant to first service and being pregnant after 42 days of the breeding season compared to the LowNA group. Both HighNA and HighNZ animals also had a lower hazard of being culled compared to the LowNA animals. Concentrate supplementation at pasture had no effect on fertility performance. There was no genotype by FS interaction for any measures recorded. These results demonstrate the EBI as a total merit index to improve reproductive capacity while maintaining milk production performance.

Key Words: genotype, feed system, fertility performance

409 Consequence on reproduction of two feeding levels with opposite effects on milk yield and body condition loss in Holstein and Normande cows. E. Cutullic*[1], L. Delaby[1], G. Michel[2], and C. Disenhaus[1], [1]*INRA UMR1080 Dairy Production, Rennes, France*, [2]*INRA UE326 Le Pin-au-Haras, Exmes, France*.

The objective of this study was to evaluate the respective effects of milk yield and body condition (BC) loss on cows' postpartum reproductive status taking breed differences into account. 105 Normande (dual-purpose) and 98 Holstein cows were assigned to a low or high feeding level (L-group: 50% grass silage and 50% haylage in winter, no concentrate at grazing; H-group: 55% maize silage, 15% alfalfa hay and 30% concentrate, 4kg concentrate at grazing). Milk progesterone assays led to determine commencement of luteal activity (CLA), postpartum ovarian activity profile, ovulation detection rate and late embryo mortality. Data were analysed by variance-covariance and logistic regression models. In both breeds, L-group cows had a lower 100-day average daily milk yield (MY) than the H-group cows but lost more BC (0-5 scale) (21.5 vs. 30.9 kg/day, -1.38 vs. -0.94 unit, N=102 and 101; P<0.001). Feeding level effect on MY was greater for Holstein than for Normande cows (+10.9 vs. +8.0 kg/day; P<0.05). As expected, Normande cows had shorter CLA, less prolonged luteal phase cycles and higher calving rate than Holstein cows (P<0.01). Feeding level had little effect on CLA and ovarian activity profile. In both breeds, ovulation detection rate was higher in the L-group (77% vs. 60%, N= 254 and 282; P<0.001). At 1st and 2nd inseminations, conception rate was improved in the H-group (74% vs. 57%, N=125 and 138; P<0.01), especially for Holstein cows (73% vs. 48%; P<0.01). As late embryo mortality frequency was very high in the H-Group Holstein cows (30% vs. 9%, N= 64 and 64; P<0.01), difference in calving rate was not significant between feeding groups (P>0.25). Owing to feeding level effects, MY and BC loss could affect reproduction at different stages. Consistent with the literature, a greater BC loss coincides with reduced conception rate. High milk yield coincides with depressed ovulation detection and embryo survival.

Key Words: reproduction, milk yield, body condition loss

Breeding and Genetics: Swine Breeding

410 Performance and carcass composition of pigs selected for residual feed intake on restricted and ad libitum diets. N. Boddicker*, D. Nettleton, N. Gabler, M. Spurlock, and J. C. M. Dekkers, *Iowa State University, Ames*.

Understanding the biology behind genetic differences in feed efficiency is important to develop selection strategies to improve efficiency. To this end, a line of Yorkshire pigs selected for lower residual feed intake (LRFI) was developed. The objective of this study was to evaluate the 5th generation of the LRFI line against a random control line (CTRL) for performance, carcass and chemical composition, and overall efficiency. Forty barrows from each line were paired by age (~132 d) and weight (74.8±9.9 kg), and randomly assigned to 1 of 4 feeding levels in individual pens in 10 replicates: 1) ad libitum (adlib), 2) 75% of adlib (A75%), 3) 55% of adlib (A55%) and 4) weight stasis (WS). Pigs were on test for 6 weeks with feed intake adjusted once or twice per week for each pig. Although initial BW did not differ between lines (p=0.49), all results were adjusted for initial BW. The adlib LRFI consumed 8% less feed (p=0.15) with no difference in growth rate versus the CTRL. However, the A55% LRFI gained 10% more (p<0.01) than the CTRL on the same amount of feed. Despite attempts to hold the WS pigs at constant BW for six weeks, the LRFI gained BW while consuming 11% less feed than the CTRL (p=0.05). The LRFI line also had a higher dressing percentage (p<0.03) and lower visceral weights than the CTRL, but this was significant only for the A75% level (p<0.02). Based on chemical analysis of the empty carcass, the LRFI line had lower fat% and greater water% than the CTRL, but this was significant only for the adlib level (p=0.08). There were no line differences in protein% and ash%. In conclusion, pigs selected for LRFI consumed less feed for the same rate of gain but differed in carcass composition, indicating differences in the partitioning of energy. LRFI pigs also had lower viscera weights and required less energy to maintain BW, indicating possible differences in maintenance requirements. Further analysis will focus on differences between retained and consumed energy. *This research was funded by grants from the National Pork Board and the Iowa Pork Producers Association.*

Key Words: residual feed intake, performance, carcass composition

411 Effect of selection for residual feed intake on feeding behavior and daily feeding patterns in pigs. J. M. Young*, W. Cai, and J. C. M. Dekkers, *Iowa State University, Ames*.

Residual feed intake (RFI) is a measure of feed efficiency defined as the difference between observed and predicted feed intake based on average requirements for growth and maintenance. The objective of this study was to evaluate the effect of selection for lower RFI on feeding behavior traits (FBT) and to estimate the relationship between FBT and RFI. Data were from 3 parities from the 4th and 5th generations of a selection experiment for lower RFI (LRFI) and a random control line (CTRL) were analyzed by parity. Lines were mixed in pens of 16 and evaluated for FBT obtained from a single-space electronic feeder (FIRE©) over a growing period of ~3 months prior to ~115 kg. The following FBT were evaluated as averages over the entire test period (TP) and over the first (TP1) and second half (TP2) of the test period: number of visits per day (NVD) and per hour (NVH), occupation time per day (OTD), per visit (OTV) and per hour (OTH), feed intake per day (DFI), per visit (FIV) and per hour (FIH), and feeding rate per visit

(FRV). Models used included fixed effects of line and feeder, covariates of onage and DFI, and random effects of pen, on-test group, sire, and litter. Repeated measures models were used to analyze feeding patterns during the day. LRFI pigs had a significantly lower DFI than CTRL pigs for all 3 data sets. With adjustment for DFI, line differences in FBT were in the same direction for all 3 data sets but differed in significance and size. FIV, FIH, NVD, and NVH did not differ between lines but the trend was for LRFI pigs to have fewer visits, in particular during peak eating times. LRFI pigs had a higher FRV and lower OTD, OTV, and OTH than CTRL pigs but this was not significant for all datasets. Residuals correlations of RFI were positive with DFI and NVD, although its strength differed between datasets. In conclusion, feed efficiency may be affected by feed intake behavior because selection for RFI has resulted in pigs which spend less time eating and eat faster. *Funding provided by the National Pork Board, the Iowa Pork Producers Association, and National Needs Fellowship grant no. 2007-38420-17767.*

Key Words: swine, feeding behavior, residual feed intake

412 Longitudinal random regression analysis of growth and feed intake in selection lines for residual feed intake in Yorkshire swine. W. Cai*, H. Wu, and J. C. M. Dekkers, *Iowa State University*, *Ames*.

A 5-generation selection experiment in Yorkshire pigs for feed efficiency consists of a line selected for lower residual feed intake (LRFI) and a random control line (CTRL). The objectives of this study were to use random regression models to evaluate the effect of LRFI selection on daily feed intake (DFI), body weight (BW), backfat (BF) and loin muscle area (LMA) along the growth trajectory and to estimate genetic parameters. Data from ~3 to ~8 months of age on 586 boars and 495 gilts were used, along with data on generations -1 and 0, with data on the LRFI line from all generations and on the CTRL line from generation 5. The average number of measurements for DFI, WT, BF, and LMA was 85, 14, 5, and 5. Random regression models were fitted with pen by on-test group as fixed effect and second-order Legendre polynomials of age as fixed curves for each generation by line and also as random curves for additive genetic and permanent environment effects. Different residual variances were used for the first and second half of the test period. 3-trait analyses for DFI, WT, and BF and single-trait analyses for LMA were run by sex. For boars from 90 to 210 d of age, estimated heritability of DFI and WT had S-shaped increasing trends, but for BF and LMA, estimates initially increased until 200 d and then decreased. For gilts, estimated heritability of WT was constant across age but initially increased and then remained constant for DFI, BF, and LMA. In generation 5, compared with CTRL boars, LRFI boars had lower average genetic curves for DFI and WT, especially towards the end of the test period; estimated line differences (CTRL-LRFI) for DFI and WT were -31 g/d and -7 g at 90 d and 209 g/d and 4384 g at 210 d. LRFI boars also tend to have lower BF and LMA at the end of the test period. In conclusion, LRFI selection has resulted in a lower feed intake curve toward maturity and a slightly lower body weight curve.

Key Words: longitudinal analysis, pigs, residual feed intake

413 Impact of genetic social interactions on relationships between average daily gain and feeding pattern in pigs. C. Y. Chen*[1], I. Misztal[1], S. Tsuruta[1], W. O. Herring[2], J. Holl[2], and M. Culbertson[2], [1]*University of Georgia*, *Athens*, [2]*Smithfield Premium Genetics Group*, *Rose Hill, NC*.

The objective was to examine social genetic effects on correlations between average daily gain (ADG, g), daily feed intake (DFI, g), daily feeder occupation time (DOT, min), and daily feeding rate (DFR, g/min). A total of 547 Duroc boars were housed in 41 pens (size=12 to 15 pigs, area=14.3 m^2), each equipped with one FIRE feeder and allowed *ad libitum* feeding. Traits were averaged over the entire test period from about 103 to 158 d of age and weight from 41 to 92 kg. Social genetic effects (including, excluding), pen (random, fixed) and linear covariates (pen sizes and initial age or weight) were fitted differently in single trait animal models for ADG and feeding pattern traits. Fixed effect of year and random effect of litter were also in the model. Variance components were estimated by REML. Initial results for ADG indicated confounding of social genetic effects and other effects (e.g. litter and pen). Therefore, six sets of parameters for ADG (heritability about 0.19) were evaluated based on estimates in literature with variance components scaled appropriately. Positive and negative signs of direct-social genetic covariances were interpreted as heritable cooperation and competition. Egoistic and altruistic pigs were classified as pigs with higher direct and social genetic values, respectively. Estimates of heritability were 0.18, 0.38, and 0.42 for DFI, DOT, and DFR. Correlations of estimated breeding values between ADG and DFI, DOT, and DFR were 0.46, 0.04, and 0.29 for egoistic pigs. With cooperation for altruistic pigs, those correlations were 0.36, 0.02, and 0.25. With competition for altruistic pigs, the slow eating rate (r = -0.31) was considered as a consequence of eating during less busy hour of feeding. The decreased feed intake (r = -0.53) indicated that altruistic pigs fail to compensate for the competition.

Key Words: feeding behavior, genetic correlation, social interactions

414 Genetic relationships of individual pig birth weight with weaning weight, off-test weight, feed intake, backfat and loin depth. J. S. Fix*[1], J. W. Holl[2], W. O. Herring[2], J. P. Cassady[1], C. Maltecca[1], and M. T. See[1], [1]*North Carolina State University*, *Raleigh*, [2]*Smithfield Premium Genetics Group*, *Rose Hill, NC*.

Studies have shown low birth weight pigs are poorer performing and less likely to survive to harvest. The objective was to examine the potential for selection of individual pig birth weight and its genetic relationships with performance traits. Variance components were estimated using Large White (LW) and Landrace (LR) for birth weight (BWT) (127,188; 93,273), weaning weight (WW) (105,760; 78,131), off-test BW (OTW) (45,278; 42,407), ADFI (2,959; 1,914) backfat depth (BF) (26,842; 25,858) and loin depth (LD) (26,789; 25,840) from data provided by Smithfield Premium Genetics. Cross fostering (12.6%) was completed within 24 h of birth. Pigs were weaned at 21.7±0.01 d and removed from test at 171±0.02 d of age. Pigs with ADFI data were fed using FIRE® feeders during the last portion of test period. Breed specific 6 trait models were used for analyses. Models included fixed effects of sex, farm, parity (birth and nurse sow), cross foster status, and contemporary group (BWT and WW: farrowing group (yr-mo); OTW, LD and BF: off-test group (yr-wk); ADFI: contemporary group (sex-yr-wk)); covariates of number of fully formed pigs (linear and quadratic), wean age (linear and quadratic), off-test age, OTW, ADFI; random effects of animal, maternal (birth dam), litter (birth or nurse). Analyses were conducted using GIBBS2F90 and POSTGIBBSF90 with 100,000 cycles, burn-in period of 20,000 and every 20th sample stored thereafter. Direct heritability estimates (LW, LR): BWT (0.06, 0.06), WW (0.11, 0.08), OTW (0.25, 0.29), BF (0.52, 0.45), LD (0.33, 0.25), ADFI (0.30, 0.31). Maternal heritability estimates (LW, LR): BWT (0.12, 0.11), WW (0.10, 0.08), OTW (0.09, 0.09), BF (0.08, 0.08), LD (0.07, 0.07), ADFI (0.17, 0.16). Direct genetic correlations (LW, LR) between BWT and WW,

OTW, BF, LD, ADFI: (0.54, 0.54), (0.48, 0.55), (-0.23, -0.16), (-0.19, -0.01) and (0.11, 0.24), respectively. Estimated direct heritability for BWT was low. Low direct heritability estimates for BWT combined with high favorable genetic correlations with OTW suggest birth weight could be increased through selection for OTW.

Key Words: genetic parameters, birth weight, performance traits

415 Breed differences in swine temperament and its phenotypic relationship with performance. C. L. Yoder*[1], C. Maltecca[1], J. P. Cassady[1], S. Price[2], and M. T. See[1], [1]*North Carolina State University*, *Raleigh*, [2]*Ivey Spring Creek Farms*, *Goldsboro, NC*.

Nucleus populations of Chester White (CW), Duroc (D), Landrace (L), and Yorkshire (Y) boars and gilts (n=2466) were used to estimate breed differences for temperament and its relationship with performance. Backfat (BF), loin depth (LD), off-test weight, estimated percent lean (LEAN), and three temperament scores: loading score (LS), scale score (SS), and vocal score (VS) were recorded. All scores ranged from 1(calm) to 5(highly excited). While loading into the scale LS was recorded, SS and VS were recorded while in the scale. Temperament scores were evaluated as categorical traits with a statistical model including fixed effects of breed, sex, farm, date of scoring, and off-test weight as a covariate. Statistical models for BF, LD, off-test weight, and LEAN included fixed effects of breed, sex, farm, LS, SS, VS, and appropriate interactions. Traits BF, LD, and LEAN were adjusted to the mean off-test weight (116.6 ± 0.54 kg). Breed differences for LS, SS, and VS were estimated as odds ratios. The odds of a higher LS were greater (1.33; $P < 0.05$) for L vs. D. CW were more likely ($P < 0.01$) to have higher SS than D (2.18) and Y (1.85), respectively. Landrace had a greater ($P < 0.01$) probability of a higher SS and VS compared to CW (1.52, 1.95), D (3.31, 4.99) and Y (2.80, 2.15). For VS, CW were 2.56 ($P < 0.01$) times more likely to be higher than D. Pearson′s Correlations ($P < 0.01$) for SS with VS, BF, LD, off-test weight and LEAN were 0.29, -0.18, -0.10, -0.15 and 0.09, respectively. Pearson′s Correlations for VS with off-test weight and BF were -0.07 and -0.11, respectively. An increase of one SS resulted in 0.87 ± 0.09 mm less BF ($P < 0.01$), 0.71 ± 0.13 mm less LD ($P < 0.01$), and 1.57 ± 0.21 kg less off-test weight ($P < 0.01$). Landrace were more excited and vocal in the scale than Chester White, Duroc and Yorkshire. Landrace were more difficult to load than Duroc. Chester White were more excited in the scale than Duroc and Yorkshire, and more vocal than Duroc. Pigs with lower SS were heavier, fatter, and had greater loin depth.

Key Words: pigs, breed, temperament

416 Genetic parameters for litter traits and piglet survival in Norsvin Landrace. B. Zumbach*[1], P. Madsen[2], and B. Holm[3], [1]*Norsvin*, *Hamar, Norway*, [2]*Aarhus University*, *Tjele, Denmark*, [3]*Norsvin USA*, *Rochester, MN*.

The study examined the genetic background of piglet mortality both as a litter trait and as a trait of the individual piglet in the Norsvin Landrace. Data included 20,531 and 7,332 1st and 2nd parity litters, respectively, and 229,651 piglets from 17,822 1st parity sows collected from 2001 to 2008. Litter traits analyzed were # piglets born alive (LB), # stillborn piglets (SB), # piglets dying during the suckling period (DS), total # piglets dying until weaning (TD), # weaned (W), within litter SD at 3 wk (SD_LW3), and litter weight at 3 wk corrected by # piglets weighed at 3 wk (LW3). Individual survival was measured at birth, after birth until the age of 3wk, and at 3 wk. Heritability (h2) estimates for litter traits in 1st and 2nd parities were 0.11±0.01 and 0.10±0.02 for LB, 0.08±0.01 and 0.09±0.02 for SB, 0.07±0.01 and 0.05±0.01 for DS, 0.11±0.01 and 0.11±0.01 for TD. Based on h2 estimates, TD is as well apt as a selection trait as LB. Genetic correlations (rg) between LB and SB in 1st and 2nd parity were -0.04±0.10 and 0.29±0.17, between LB and DS 0.66 ±0.06 and 0.47±0.12; rg between TD and SB in 1st and 2nd parity were 0.75±0.05 and 0.79±0.08, between TD and DS 0.90±0.02 and 0.92±0.03. While selection for LB increases DS, selection for low TD should reduce both, SB and DS. In 1st and 2nd parity rg between LB and W were 0.79±0.04 and 0.80±0.06; rg among TD, W and LW3 were not significantly different from 0 in both parities; rg between SD_LW3 and LW3 were 0.54±0.07 and 0.43±0.12 in 1st and 2nd parity; rg between SD_LW3 and TD was slightly positive. Selection for LB increases efficiently W at the cost of TD. LW3 as a mother ability does not counteract this relationship. Direct h2 for individual piglet survival was about 2% from birth to 3 wk. Maternal h2 decreased from birth (2.1%) to 3 wk (1.4%). Total h2 was about 3% from birth to 3 wk. The rg between direct and maternal genetic effects were not significantly different from 0. Sow and piglet genotype contribute to piglet survival.

Key Words: piglet survival, genetic parameters, sow productivity

417 Marker assisted selection using simulated IGF2 gene in Canadian Landrace. M. Jafarikia*, B. Sullivan, and L. Maignel, *Canadian Centre for Swine Improvement*, *Ottawa, ON, Canada*.

Marker Assisted Selection (MAS) can increase the accuracy of selection in comparison to accuracy from conventional Best Linear Unbiased Prediction (BLUP). One of the major genes in the pig is Insulin-like growth factor 2 (IGF2) which has a large effect on muscle mass. The objective of this study was to investigate the advantage of using IGF2 paternal alleles on the accuracy of selection in MAS using simulated data. A population with almost one million pigs was simulated using the QMSim package (Schenkel and Sargolzaei, 2008). This simulated population was based on the Canadian Landrace population which existed in the national database managed by the Canadian Centre for Swine Improvement (CCSI). Data was simulated using heritability of 25% and with 15% of the phenotypic variance under the effect of the simulated IGF2 gene. Selection was at random because when simulation was performed with a major gene such as IGF2 and selection was by using BLUP, the major gene became fixed after a few generations. The proportion of genotyped animals was approximately 0.05% of the population and mostly chosen from recent generations. A software program was developed for estimation of genotype probabilities of the entire pedigree using the genotype information of relatively few genotyped animals. Estimated paternal allele probabilities of the simulated IGF2 gene were used as a covariate in the model. The observed accuracy of Estimated Breeding Value (EBV) for BLUP and MAS for genotyped animals were 71% and 80%, respectively.

Key Words: IGF2, marker assisted selection, BLUP

418 A DNA based test for evaluating and improving pork colour in Canadian pigs. B. Uttaro*[1], M. Jafarikia[2], W. Van Berkel[3], S. Wyss[2], B. Sullivan[2], and S. Chen[4], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre*, *Lacombe, Alberta, Canada*, [2]*Canadian Centre for Swine Improvement*, *Ottawa, Ontario, Canada*, [3]*Western Swine Testing Association*, *Lacombe, Alberta, Canada*, [4]*University of Guelph, Labora-*

tory Services Division, *Guelph, Ontario, Canada*.

Meat colour is an important characteristic of pork quality but quantitative selection requires sacrifice of animals. Meat colour and single nucleotide polymorphisms (SNPs) of exon 14 and partial codon sequences of SLC44A3 gene of 500 pigs were used to examine the association of this gene with meat colour and change of colour during storage. Significant differences ($p \leq 0.01$) were found among breeds for subjective colour (NPPC; Scale 1-6). Duroc (4.45±0.07) and Lacombe (4.49±0.09) had significantly darker loins than other breeds: Yorkshire (4.16±0.07), Landrace (3.94±0.08) and crossbreds (3.98±0.06). Females (4.25±0.05) were darker on average than castrates (4.16±0.06). Thirteen SNPs were found in the SLC44A3 gene. Four of the 13 SNPs were in the coding region but only one resulted in an amino acid change. Three SNPs at base pair (bp) positions of 234, 381 and 386 were selected for analysis based on the following criteria: minor allele frequency above (5%) and no confounding with other SNPs. Defining the haplotypes of the three SNPs revealed four different haplotype alleles in the sampled pigs. SNP at bp 386 showed significant association with NPPC colour ($p \leq 0.05$), and a significant effect of haplotypes was also found within breeds ($p \leq 0.05$). Loin colour (Minolta CIE L*, a*, b*) was recorded on days one, four and seven post-mortem, and colour differences calculated. The greatest change in L* was observed during dark storage (days 1 to 4) with little change during storage in light (days 4 to 7). A significant difference between L* values as well as change in L* was observed among breeds ($p \leq 0.05$) and gilts tended to remain darker than castrates.

Key Words: meat colour, SLC44A3 gene, pork

419 Estimation of the IGF2 effect on backfat and lean muscle depth in Canadian Landrace. M. Jafarikia*, B. Sullivan, L. Maignel, and S. Wyss, *Canadian Centre for Swine Improvement*, *Ottawa, ON, Canada*.

IGF2 is a paternally expressed gene located at the distal tip of porcine chromosome 2. Allelic variation of this gene is associated with 15-30% of the phenotypic variation in muscle mass and 10-20% of the phenotypic variation in backfat thickness. Canadian Landrace with approximately one million records was used to investigate the proportion of the phenotypic variance in backfat thickness and muscle mass explained by IGF2. The genetic variance was estimated as $\sigma_{IGF2}^2 = 2pq\alpha^2$ where σ_{IGF2}^2, p, q and α represent IGF2 variance, frequency of paternal A, frequency of paternal G and allele substitution effect respectively. The traits under study included backfat and lean muscle depth adjusted to 100 kg live weight. The statistical models included the probability of inheriting the IGF2 allele from sire as a covariate along with contemporary group and sex as fixed effects. The GLM procedure of SAS was used for the analysis. In order to determine the paternal allele origin, a genotyping probability software was developed to estimate the paternal allele probabilities of all the animals in the pedigree using information from a limited number of genotyped animals from recent generations. The numbers of AA, AG and GG genotypes were 456, 304, 38, respectively. Using the homozygote genotypes (AA, GG), the total number of known paternal alleles was 494. The number of animals with known paternal alleles increased to 36,371 after using the genotyping probability estimation software. The estimated paternal A over G allele substitution effects were -1.28 mm and +2.05 mm and the estimated variances were 0.61 mm^2 and 1.55 mm^2 for backfat and lean muscle depth, respectively. The estimated variances were 14% and 11% of the observed phenotypic variance of backfat and lean muscle depth, respectively. The observed variance for backfat corroborated the range reported in previous studies but for lean muscle depth, a lower variance was found than the range reported in previous studies on other swine populations.

Key Words: IGF2, variance, backfat and lean muscle depth

420 Proximal promoter of the pig HMGCR gene: Structural and functional study. A. Cánovas*[1], R. Quintanilla[1], J. M. Reecy[2], M. Marquiés[3], and R. N. Pena[1], [1]*IRTA. Genetica i Millora Animal.*, *Lleida, Spain*, [2]*Iowa State University*, *Ames*, [3]*INDEGA. Universidad de León*, *León, Spain*.

HMGCR is the rate-limiting enzyme in the biosynthesis of cholesterol. We have studied the role of the HMGCR gene in pig lipid metabolism by means of expression and structural analysis. Animals came from a high intramuscular fat commercial Duroc line used in the production of fine quality cured ham. The experiment was based on a half-sib design, generated by mating five parental boars with 385 females and using only one male offspring per litter. We characterized the mRNA expression profile of the porcine HMGCR in six tissues involved in lipid metabolism. HMGCR is expressed at high levels in the duodenum and back fat. In contrast, heart and liver had lower HMGCR mRNA expression levels. In addition, we amplified the proximal promoter (600 bp) of this gene and identified two SNP at positions -239 and -16 bp. In silico analysis of the distal and proximal promoter SNPs revealed that they may potentially affect the binding of myogenic bHLH family members (e.g. myoD, myogenin, myf5 and myf6), and Ets-2 family members, respectively. The pig HMGCR promoter region exhibited a high level of conservation (72 to 86% sequence identity across species) with conserved motifs for several transcription factors. Futhermore, we evaluated the interaction between HMGCR:c.-239G>T promoter SNP and promoter activators and inhibitors in hepatic (HepG2) and muscle (C2C12) cell lines. In C2C12 and HepG2 transfected cells, we observed that insulin (1 μM), increased the transcriptional activity of the HMGCR G allele promoter, whereas 25-hydroxycholesterol (12.5 μM) also inhibited the transcriptional activity of the G allele promoter. Our findings indicate that HMGCR may play an interesting role in the genetic variability of lipid and cholesterol metabolism in pigs.

Key Words: pig, meat quality, lipid metabolism

Dairy Foods: Dairy Foods 1

421 Value-added components derived from whey. W. Modler*, *Agriculture Canada (formerly, Centre for Food & Animal Research, Ottawa, Ontario, Canada)*, *Kemptville, Ontario, Canada*.

Initially, whey products, such as roller dried whey powder, had poor functionality and limited food product application. Technological advances in evaporation and spray drying, along with the development of demineralization and electrodialysis technology, led to further improvements in functionality in whey-based powders. The next generation of products consisted primarily of WPC and WPI prepared primarily through the development of membrane technology, particularly microfiltration. More recently, improvements have provided cleaner separations, improved membrane performance and durability. In addition, nanofiltration and microfiltration have provided additional tools for whey processors for

producing and modifying the functionality of whey-based ingredients. These technological developments have diversified ingredient selection and expanded their use in frozen desserts, snack foods, beverages, processed meats, fermented dairy products, processed cheese foods/spreads, baked goods and confectionary. More recently emphasis has been placed on the isolation of the major proteins in whey for use as gelation agents (beta lactoglobulin) and nutritional supplements (alpha lactalbumin). In addition, good progress has also been made in the isolation, characterization and production of bioactive components from whey, now termed nutraceuticals. The components of interest include both major and minor proteins, enzymes, peptides, lipids/lipoproteins, vitamins and minerals. Selected components of this group have been shown to reduce hypertension, sarcopenia, cancer, osteoporosis and modulate immune function. This paper will highlight the development and application of the value-added products derived from whey, with emphasis on the food and nutraceuticals industry. Future technological challenges could include the isolation, purification and characterization of pharmaceutical components from whey.

Key Words: whey, functional foods, nutraceutical

422 Optimizing the recovery of protein during microfiltration of preconcentrated whey. C. Marella*, L. E. Metzger, and K. Muthukumarappan, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Microfiltration processing is an integral part of filtration based manufacture of WPC and WPI and is utilized to remove lipid material from whey. Generally whey preconcentrated with ultrafiltration is subjected to microfiltration. During microfiltration about 25-30% of the protein is lost in the retentate along with the lipid materials. The objective of this research was to optimize the recovery of protein and determine if mineral chelating processing aids have an impact on protein recovery and fouling of microfiltration membranes. Experiments were conducted using whey preconcentrated by ultrafiltration to a volume reduction (VR) of 4.5. Initially three levels of VR (4, 5 and 6) and three levels of diafiltration (DF) (0, 50 and 100% of feed volume) were used during microfiltration. All the experiments were conducted in triplicate using a lab scale plate and frame membrane separation unit. A Polyvinyledene fluoride membrane of 0.5 μ pore size, transmembrane pressure of 10 kPa, pH of 6.2 and temperature of 25°C were used. Treatment combinations of 5VR x 100 DF and 6VR x 100DF resulted in maximum protein recovery of 84%. Subsequently the treatment combination 6VR x 100DF was used to conduct experiments with the addition of disodium phosphate (2.201 g/L), trisodium citrate (3.04 g/L) and sodium hexameta phosphate (3.1605 g/L). These quantities are sufficient to chelate all the Calcium (15 mM) present in the WPC. Addition of mineral chelating aids did not significantly ($P>0.05$) affect on the recovery of protein but resulted in significant ($p<0.05$) reduction in both overall and irreversible fouling. Addition of sodium hexameta phosphate resulted into the lowest overall and irreversible fouling resistances (0.67×10^{12}/m and 0.07×10^{12}/m respectively). The results from this study indicate that maximum recovery of protein can be obtained with VR of 6 and DF of 100%. Addition of sodium hexameta phosphate leads to reduced fouling during microfiltration.

Key Words: microfiltration, protein recovery, processing aids

423 Nanoparticulation of denatured whey protein by pH–cycling. M. Britten*, J. Houde, and H. J. Giroux, *Agriculture and Agri-Food Canada*, *St-Hyacinthe, QC, Canada*.

Nanoparticles are used for entrapment, protection and delivery of highly sensitive ingredients or bioactive compounds in food systems. Cross–linking of denatured whey protein through pH–cycling is proposed to develop nanoparticles with controlled size and properties. Whey protein soluble polymers were produced by heating at low ionic strength and neutral pH. Acidification was used to induce aggregation. The effect of aggregation conditions on the physicochemical characteristics and stability of nanoparticles was studied. Nanoparticles with a diameter varying from 40 to 300 nm were produced by modifying the aggregation pH, $CaCl_2$ concentration and the holding time at the aggregation pH before readjustment to pH 7.0. Nanoparticle size and dispersion turbidity increased with increasing maturation time while the concentration of accessible thiol groups decreased. Thiol–disulphide exchange reaction is likely responsible for the stabilization of nanoparticles. Size, turbidity and voluminosity of whey protein nanoparticles were controlled by aggregation conditions. The stability of nanoparticles in the presence of different dissociating agents (EDTA, urea, SDS and DDT) was evaluated and the results confirmed that the nanoparticles are mainly stabilized by disulphide bonds. Hydrophobic interactions seem also involved in the formation of nanoparticles. Whey protein nanoparticles obtained by pH–cycling is a promising approach for the protection and delivery of sensitive compounds such as aroma and nutraceuticals.

Key Words: whey protein, nanoparticle, thiol-disulphide

424 Development of an optical backscatter method for determining thermal denaturation of whey proteins during milk processing. A. M. Lamb*, M. Castillo, F. A. Payne, and Y. L. Xiong, *University of Kentucky*, *Lexington*.

The heat denaturation of whey proteins impacts the functional properties of milk. After denaturing, β-LG associates with κ-CN, which significantly impairs milk coagulation by creating a steric obstacle for κ-CN hydrolysis and by increasing the gel moisture retention. Correlations of the degree of β-LG denaturation to gelation time, gel firmness, and gel moisture content have been widely documented. The resulting high moisture and soft gels are undesirable for cheese manufacture but advisable in yogurt processing, as it aids in preventing one of its most frequent defects, wheying-off. Currently no inline technique is available for quantifying β-LG denaturation and aggregation with κ-CN in milk. The goal of this study was the development of an optical sensor method with inline potential for the determination of β-LG denaturation and subsequent association with κ-CN during milk heat treatment. Duration of thermal exposure at 80°C was the factor with 5 levels (3, 5, 7, 12, 25 min). The levels were chosen from preliminary kinetic calculations based on current literature findings. The samples were tested to determine the level of denaturation and protein association by SDS-PAGE, differential scanning calorimetry, and undenatured whey protein analysis before and after heat treatment. Samples also underwent light backscatter analysis for the correlation and validation of optical response to protein denaturation. The physical-chemical analysis performed indicated that denaturation represented a first order reaction, as expected. Light backscatter response was found to be proportional to heat treatment intensity, increasing as much as 4.5% after treatment. This suggests that light scatter could be used to determine the whey protein denaturation degree. Early prediction of the potential gelling strength of milk will allow milk batches to be used for their most suitable purposes. Successful development of this optic sensor technology

will aid in the decision-making process of dairy plants for the assurance of a high quality product.

Key Words: light backscatter, optical sensors, protein denaturation

425 Use of whey protein fractions as a fat substitute for sausage. A. C. B. Ferreira[1], W. L. M. Santos[1], L. M. Fonseca*[1,2], and R. L. Bradley Jr.[3], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis, UFMG*, *Belo Horizonte, MG, Brazil*, [3]*University of Wisconsin, Department of Food Science*, *Madison*.

Special attention has been given to the excess of calories and fat ingestion, mainly for health reasons. As consequence, there is a growing interest for products with low fat content. This work had as objective to evaluate the physico-chemical and sensorial quality of pork sausages, manufactured with whey protein concentrate (WPC) or protein concentrate with high level of β-lactoglobulin (called hereof β-lactoglobulin; US Patent n. 6,900,290), as substitutes of the fat. The sausages were manufactured in the Laboratory of Meat Technology of the DTIPOA/ School of Veterinary Medicine-UFMG. Seven treatments were used, six containing different levels of addition of WPC, or β-lactoglobulin and a group control containing 20% of fat (three treatments containing 10% of fat and three different levels of WPC, that is, 0.2%, 0.5% and 1.0%, and three treatments containing 10% of fat and three different levels of β-lactoglobulin that were, 0.1%, 0.3% and 0.6%). Each level of treatment was repeated in five batches, with two times of evaluation, in the day of production and after a period of seven days of storage at 4°C. The samples were analyzed for protein (g/100g), fat (g/100g), ashes (g/100g), chlorides (g/100g), water content (g/100g), and for the determination of the caloric value (Kcal/g), water activity (Aw), pH, texture (Kgf), and loss after cooking (g/100g). Analyses were done in the first week of production and after seven days of storage. Results for protein, fat, caloric value and moisture content presented statistical difference between the group control and the other treatments ($p \leq 0.05$). The other analyses results were not different among the treatments and between the two weeks of evaluation ($p \geq 0.05$). Additionally, the sensorial analyses results showed that there was no difference among the different treatments with the level of fat substitution used in this experiment ($p \leq 0.05$). The milk proteins were efficient for the fat substitution in pork sausages, in the treatment levels for the present experiment, complying with the Brazilian legal requirements, in addition to maintain the sensorial quality.
Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq; CAPES.

Key Words: whey protein concentrate, β-lactoglobulin, reduced fat

426 Influence of casein on flux and passage of serum proteins (SP) during microfiltration (MF) using polymeric spiral wound (SW) membranes at 50°C. J. Zulewska*[1], M. Newbold[2], and D. M. Barbano[2], [1]*University of Warmia and Mazury*, *Olsztyn, Poland*, [2]*Cornell University*, *Ithaca, NY*.

The objective was to determine the influence of casein on flux and passage of SP during MF using polymeric SW membranes at 50°C. Flux, percentage and rate of SP removal from skim milk and casein-free skim milk using polymeric SW membranes were compared. Skim milk was pasteurized (72°C, 16 s), cooled and split into 2 batches. One batch (620 kg) was MF 3X at 50°C using 0.1 micron ceramic (1.7 m^2) uniform transmembrane pressure (UTP) membranes, to produce casein-free skim milk (UTP MF permeate). Casein-free skim milk (380 kg) was recycled for 65 min using 0.3 micron polymeric (polyvinylidene fluoride, 20.5 m^2) SW membrane, the system was flushed with water, then skim milk (1106 kg) was MF at 3X bleed-and-feed at 50°C. The percentage SP removal was determined by the mass of SP [((TN-NPN)-(TN-NCN))*6.38] in permeate divided by the mass of SP [((TN-NPN)-(TN-NCN))*6.38] in skim milk multiplied by 100 where SP was determined using Kjeldahl. This process was replicated 3 times. Flux, percentage SP removal, and rate of SP removal for casein free skim milk and skim milk were significantly different: 80.2 vs. 17.2, ($kg/m^2/h$), 59.5 vs. 35.2%, and 0.40 vs. 0.06 ($kg/m^2/h$), respectively. The presence of casein in skim reduced flux by 4.7 times and increased the rejection of SP. The rate of SP removal ($kg/m^2/h$) from casein free skim milk is 7 times that of skim milk with the same membrane and processing conditions. The presence of casein in a feed stream decreases the efficiency of polymeric membranes. The membrane performance on casein free skim milk demonstrates the potential that could be achieved with polymeric membranes, if casein fouling could be reduced. Approaches that could be investigated to reduce casein fouling in MF for separation of casein and SP are: membrane configuration (spiral-wound vs. flat-sheet), cross-flow velocity, retentate flow channel volume, and membrane surface characteristics. If casein fouling was reduced, the area of SW membranes and the time required to process a given volume of skim milk and produce a defined composition MF permeate could be decreased.

Key Words: serum protein, casein, microfiltration

427 A non-pasta filata Mozzarella cheese making method using CO_2: Cheese composition and yield. L. Li[1], M. Newbold[2], and D. M. Barbano*[2], [1]*South China University of Technology*, *Guangzhou, China*, [2]*Cornell University*, *Ithaca, NY*.

A new Mozzarella cheese making method was developed using CO_2 to control calcium-protein equilibria during cheese making. Our goal was to develop a lower cost method of producing full-fat Mozzarella with acceptable functionality for pizza baking without using any added starch or phosphates to retain moisture and fat during baking. About 2000 to 2500 ppm of CO_2 was injected into pasteurized skim milk and this was blended with the appropriate amount of cream without added CO_2. Fat content of the cheese was controlled by adjusting the casein to fat ratio in the milk. The pH of the milk plus CO_2 mixture at the beginning of cheese making was between 5.9 and 6.0, which increased coagulation firmness and reduced rennet use by 50 to 70%. Coagulation, cutting, and cooking times and temperatures were very similar to those used for Cheddar cheese manufacture. Final moisture content of the cheese was controlled using the relationship between the temperature of the whey and the pH of the curd in a stirred curd process. When the curd reached the target pH (5.1 to 5.35), the whey was drained and the curd was dry salted. The salted curds were chopped to uniform size (about 5 to 10 mm), sprayed with a hydrophopbic surface coating, and individually quick frozen. The experiment demonstrated the ability to control moisture in the range from 52 to 58%, with a fat on dry basis of >45%. Salt retention in the curd can be controlled by temperature conditions during salting and was between 90 and 99.5%. Fat recovery in the cheese was higher (about 94 to 95%) than a typical pasta-filata manufacturing process (about 85%). Higher fat recovery and higher moisture produced actual yields (12 to 13.5 kg/100 kg of milk) without any fortification with nonfat milk solids. The new process eliminates Cheddaring, stretching, molding, brine salting, block packaging, and shredding equipment when the intended use of the cheese is for food service pizza. The frozen cheese is slow thawed at refrigeration tem-

perature and put directly on a pizza for baking.

Key Words: CO_2, mozzarella, yield

428 A non-pasta filata Mozzarella cheese making method using CO_2: Cheese functionality. L. Li[1], M. Newbold[2], and D. M. Barbano*[2], [1]*South China University of Technology, Guangzhou, China*, [2]*Cornell University, Ithaca, NY*.

A new method of Mozzarella cheese making was developed using CO_2 as a processing aide to control calcium-protein equilibria and deliver a full-fat Mozzarella with acceptable functionality for pizza baking without using any added starch or phosphates to retain moisture and fat during baking. Two versions of the new process produced cheeses containing about 52 and 58% moisture, while they both had a fat on a dry basis of > 45% and a protein on dry basis of about 43 to 44%. Cheeses produced by the new process are in a particulate form directly from the cheese making and do not require stretching, brining, or shredding. The objective was to determine the free oil release, expressible serum, meltability, apparent viscosity, and pizza baking characteristics of cheese produced by this new process. Free-oil release of full-fat Mozzarella during pizza baking can often be excessive. Cheeses produced by the new process released 4 to 7% of their oil, while commercial low-moisture Mozzarellas released 25% of their fat. Cheeses from the new process had lower (almost zero) expressible serum release after 4 days of refrigerated storage while the commercial low-moisture Mozzarellas released more than 20% of their moisture after 4 days of refrigerated storage. The cheeses from the new process held their moisture much better when baked on a pizza. Cheese produced by the new process had a tube meltability that was nearly twice that of the commercial cheese of the same age and this difference was clearly visible when the cheeses were baked on pizza. The melted cheese consistency, measured as apparent viscosity by helical viscometry, was much softer and more stretchable than the commercial products. Addition of CO_2 to milk prior to rennet coagulation changed the calcium-protein equilibria in the cheese and increased partitioning of caseins into the water phase of the cheese. Higher casein solubility in the water phase of the cheese increased water and fat holding capacity and this provided excellent baking properties of the high moisture cheese without any added non-dairy ingredients.

Key Words: Mozzarella, CO_2, functionality

429 Caseins as molecular chaperones: Functional analysis and structural considerations. Y. H. Yong* and E. A. Foegeding, *Department of Food, Bioprocessing and Nutrition Sciences, North Carolina State University, Raleigh*.

Denaturation and aggregation of proteins are reactions that are relevant to functional applications of proteins in foods. Depending on concentration, aggregation can result in turbidity, precipitation or gelation. One of the approaches to improve the thermal stability of globular proteins is through addition of other compounds to alter the aggregation process. Numerous studies have shown the ability of molecular chaperones to assist proper folding/unfolding and assembly/disassembly of proteins, especially during stressed conditions. In 1999, a mixture of α_{s1} - and α_{s2} -casein was reported for the first time to possess molecular chaperone-like properties to prevent a variety of proteins and enzymes from different types of stress-induced aggregation. In the intervening 10 years, around a dozen journal papers have reported the molecular chaperone properties of caseins, including α-, β-, κ-caseins, whole casein and sodium caseinate. We have summarized and compared the results of these studies to see if they could be explained by a common mechanism. Also, as caseins were reported to be acting in a manner similar to the small heat shock proteins (sHSP) family, we evaluated the similarities and differences of caseins and α-crystallin (first sHSP as a molecular chaperone) from the viewpoints of their structural information (primary to quaternary) and their functional assistance on select substrate proteins. Caseins were compared to another natively unfolded protein, namely α-synuclein, that also has been reported to act like a molecular chaperone. Through all these details, we provide an insight of the role of caseins as a distinct group of molecular chaperones.

Key Words: caseins, molecular chaperones

430 Development and functionalities of milk protein-based paper glue. X. Chen[2,1], Y. L. Gao[2,1], L. H. Zhou[1], and M. R. Guo*[1], [1]*University of Vermont, Burlington*, [2]*Inner Mongolia Agriculture University, Huhhot, Inner Mongolia, China*.

Commercial paper glue products on the market may contain toxic compounds harmful to the people and the environment. Prototype of environmentally safe paper glues containing polymerized whey protein (PWP) and sodium caseinate were developed and optimized under a full factorial experiment design with factors of protein content, denature temperature, time and other ingredients. The prototypes were analyzed for physicochemical properties including pH value, ash contents, total solids and viscosity, and functional properties including bonding strength, water resistance, temperature and moisture resistance. When compared with the commercial product, the prototypes had higher pH value (6.6/4.7), higher ash content (0.3%/0.1%), lower total solids (15.8%/31.2%) and higher viscosity (5975/2472 mPa), respectively. Bonding strength is considered as the main index because it is the most important property for glues. The bonding strength of the prototypes was up to 161.4 N while commercial sample was 154.6 N. According to the ASTM standards, the water resistance and temperature-and-moisture resistance of the prototypes were better than those of commercial samples. The statistic analyses indicated that the denaturation time had significant effects ($P<0.05$) on bonding strength, while both WPI/PVA ratio and denaturation temperature had very significant effects ($P<0.01$).

Key Words: milk protein, paper glue, bonding strength

Dairy Foods: Dairy Foods/Cheese

431 ADSA Pioneer: A century of predictive cheese yield formulas. D. B. Emmons*, *Food Research Laboratory, Research Branch, Agriculture and Agri-Food Canada,, Guelph, ON, Canada*.

Predictive cheese yield formulas have evolved over more than 100 years from one based only on casein and fat. A major change in 1910 included moisture and a constant for salt and whey solids. Refinements have included salt and whey solids as separate factors, exclusion of whey solids from moisture associated with cheese protein, and use of paracasein instead of casein. Various parts or all of formulas are used in monitoring or controlling experiments and cheese making. The General formula is based on the sum of cheese components: fat, protein, moisture, salt, whey solids free of fat and protein, as well as milk salts associated

with paracasein (Ca, Mg, inorganic phosphate, citrate). The formula was tested using composition of milk, whey, and cheese from 22 vats of Cheddar cheese. Unexpectedly, mean predicted yield was 99.17% (Nx6.31) as a percentage of actual yield; using Nx6.38 it was 99.61%; both standard deviations were 0.18%. That percentage is useful for comparisons among vats. The mean sum of components in cheese was 99.51% (sd = 0.12; Nx6.31) or 99.77% (sd = 0.12; Nx6.38). The predicted yield percentage correlated positively with the sum of components in cheese (Nx6.31); r = 0.992 (P<0.01). This led to the idea of adjusting for each vat the five measured components in the formula by the observed sum of components, as a fraction. The mean of the predicted yields as percentages of actual yields was 99.99% (sd = 0.031%). Another method of equating predicted and actual yields calculated a yield adjustment factor as the ratio of the mean actual yield to the mean predicted yield. As expected, multiplication of predicted yields by this factor of 1.0083 gave a mean of predicted yields of 100.00% as a percentage of actual yields (sd = 0.18%, same as before adjustment). One concludes that systematic or variable errors somewhere in the measurement system of analysis, sampling or weighing is a problem in the use of predictive cheese yield formulas. Also, participation in interlab comparison programs is useful for laboratories analyzing cheese.

Key Words: cheese, yield, formula

432 Cheesemaking properties of camel chymosin. K. B. Qvist*, M. Harboe, H. van den Brink, M. L. Broe, and M. W. Børsting, *Chr. Hansen, Hørsholm, Denmark*.

In cheesemaking, rennet enzymes play decisive roles by initiating milk coagulation, and by hydrolyzing milk protein during cheese maturation. Bovine chymosin (BC) has traditionally been considered the most suitable rennet for most cheeses. Recently chymosin from *Camelus dromedarius* (CC) has been obtained through heterologous expression in *Aspergillus niger* and is now commercially available as CHY-MAX M® from Chr. Hansen. The objective of this work was to determine its main cheesemaking properties, and compare with those of BC. Milk clotting activity was determined in International Milk Clotting Units (IMCU), gelation was monitored using a Formagraph, and general proteolytic activity was determined using dimethylated casein as substrate. Mozzarella, Cheddar and Gouda cheeses were made and chemically analyzed using standard protocols. Texture profile analysis and sensory profiling were used to determine texture and sensory properties of cheese. Proteolysis in cheese during ripening was monitored by determination of soluble and TCA soluble N. Size exclusion and reversed phase HPLC were used to characterize peptides in whey. Milk clotting activity (C) per mole of CC was 70% higher than that of BC, while general proteolytic activity (P) was 75% lower, resulting in a 7-fold higher C/P-ratio. Surprisingly, this means that CC is much more specific for cleaving the Phe_{105}-Met_{106} bond of bovine κ-casein than is BC. Gel firmness developed faster during renneting when using CC, meaning that dosage in IMCU could be reduced by 25% while maintaining time to cutting. Gel formation was less affected by pH and $[Ca^{++}]$ with CC, thus reducing effects of natural milk variation. Whey produced with CC contained lower levels of N, and less casein derived peptides. A cheese yield increase of 0.1-0.2% was observed with CC, compared to BC. During storage, development of soluble and TCA soluble N was slower with CC than with BC. Tendency for development of bitterness was reduced, as was softening of Mozzarella during storage. Taken together these observations suggest that camel chymosin may become the preferred rennet for many applications.

Key Words: camel chymosin, specificity, cheese yield

433 Aggregation of casein micelles by combined rennet and acidification studied by rheology and diffusing wave spectroscopy: Effect of heat treatment. C. Cooper*, M. Alexander, and M. Corredig, *University of Guelph, Guelph, ON, Canada*.

Skim milk was heated using a HTST-microthermics unit, and the effect of the heat-induced soluble complexes on the properties of milk gels obtained by combined rennet and acidification was investigated, by analyzing the soluble complexes formed, and following the gelation using rheology, diffusing wave spectroscopy and monitoring the release of caseinomacropeptide. Soluble complexes, as previously observed in batch-heated milk, were only found in the most extensively heated HTST conditions studied (85°C/300 s). As severity of heat treatment decreased, the soluble complexes formed were smaller and contained less β-lactoglobulin and α-lactalbumin and more hydrophobically-associated caseins. The sera of heat-treated milk always contained disulphide-linked minor whey proteins and κ-casein. Different heating temperature-time regimes did not affect the amount of caseinomacropeptide released. All acid gels with rennet showed an increased pH of gelation and gel stiffness compared to acid gels without rennet. With low amounts of rennet, the effect of heat treatment on the gelation behaviour of the casein micelles was quite similar to that of acid-induced gels, with heat treatment causing a significant increase in the gelation pH and gel stiffness. In high rennet-acid gels, the aggregation of the enzymatically-destabilized micelles occurred prior to and/or was more predominant than the formation of an intermediate network of denatured whey proteins, and the effect of heat-induced soluble complexes on gelation properties was reduced. This work is the first to compare the effect of HTST-heating and amount of rennet on the destabilization and interaction of casein micelles during aggregation by combined rennet and acidification. Better understanding of these systems may allow for optimal design of combined gels.

Key Words: heat induced soluble complexes, renneting, acidification

434 Improvement in the texture of low-fat Cheddar cheese by altering the manufacturing protocol. N. Bansal*[1], N. Y. Farkye[1], and M. A. Drake[2], [1]*California Polytechnic State University, San Luis Obispo*, [2]*North Carolina State University, Raleigh*.

In recent years, due to increased consumer awareness for healthy foods, there has been an increased demand for low-fat cheeses. However, most low-fat cheeses have a hard body and a poor and rubbery texture. The objective of this study was to evaluate the effect of blending mature full-fat cheese with freshly-made low-/nonfat curd on the composition, proteolysis and texture of the low-fat Cheddar cheese. Full-fat control cheese (FFC) was manufactured from whole milk by a standard stirred-curd Cheddar method using commercial cheese starter. Low-fat control cheese (LFC) was manufactured from pre-acidified milk containing <0.55% fat by the stirred-curd Cheddar method, except that a higher cooking temperature was used and curds salted at a higher pH. Experimental low-fat cheese (ELFC) was made like the LFC, except that shredded mature full-fat cheese (10% of the expected yield of the low-fat curd) was blended with the fresh low-fat curd/whey mixture after healing. Cheesemaking was replicated three times. Cheeses were ripened at 45° F. Instrumental analysis and a trained sensory panel documented texture properties of the cheeses. There were no significant differences (p>0.05) in the composition of LFC and ELFC. The moisture and protein content of the low-fat cheeses was significantly (p<0.05) higher than the FFC. The level of water-soluble nitrogen and the level of primary proteolysis, as detected by urea-PAGE, increased with the age of cheese and were similar in all cheeses. At 6 months of ripening there were no

significant differences ($p>0.05$) between the hardness, cohesiveness, springiness, gumminess and chewiness of ELFC and FFC as measured by texture profile analyzer; whereas the LFC was significantly harder, more cohesive, more springy, more gummy and more chewy than the FFC and ELFC. By sensory analysis, both low-fat cheeses were distinct in texture attributes from the FFC ($p<0.05$), but ELFC were less firm and less springy and more cohesive with a higher degree of breakdown compared to LFC ($p<0.05$). These results suggest that blending mature full-fat cheese during the manufacture of low-fat cheese has potential to improve its texture.

Key Words: low-fat, cheese, texture

435 Impact of grating and reforming on the texture of low fat/ nonfat cheese. C. Akbulut*[1], S. Govindasamy-Lucey[2], J. A. Lucey[1], J. J. Jaeggi[2], and M. E. Johnson[2], [1]*Department of Food Science, University of Wisconsin, Madison*, [2]*Wisconsin Center of Dairy Research, University of Wisconsin, Madison*.

Producing nonfat and low fat cheese with desirable texture and flavor is one of the most challenging areas for the cheese industry. In this preliminary study, we investigated the textural properties of nonfat and low fat cheese produced by a novel technique where nonfat/ low fat cheese was produced after grating the cheese and using pressure to try to reform the shreds into a curd mass that was less firm than the original cheese. Our objective was to determine the effects of processing parameters (operating temperature and particle size of cheese) during the reforming process on cheese texture. The pilot plant system that we used was composed of a shredder (commercial Urschel Shredder) and an extruder (Vemag). In bench-top scale experiments we used a food processor (Robot coupe R2Dice) for shredding and placed the shredded cheeses into plastic syringes and pressed them with a Carver Press. Cheese bases having pH value ~5.6 were obtained from skim milk by direct acidification using citric acid. They were grated into 5 different particle sizes by a food processor using graters of different sizes (1.5, 2, 3, 6 and 9 mm diameter) and pressed for 1 h after filling into syringes. Textural analyses were performed on the nonfat cheese base and reformed cheese that were stored within the syringes for 1 week at 4°C in order to let the cheese fuse together again. The use of smaller particle sized cheese tended to produce softer reformed cheese, probably through the greater disruption of physical interactions in the cheese. This trend may depend on the type of cheese base as we also tried other cheese bases and there appeared to be little impact of particle size. To investigate the impact of temperature cheese bases were shredded at same shred size, brought to three different temperatures (4, 21 and 35°C) by incubating overnight and then run through the Vemag for reformation. At high temperatures, cheese tended to be softer and smoother. We are currently performing pilot-scale trials on these variables.

Key Words: low fat cheese, nonfat cheese, texture

436 Influence of brine concentration and temperature on composition, microstructure and yield of feta cheese. D. J. McMahon*[1], M. M. Motawee[2], and W. R. McManus[1], [1]*Western Dairy Center, Utah State University, Logan*, [2]*National Organization for Drug Control and Research, Cairo, Egypt*.

The protein matrix of cheese undergoes changes immediately following cheesemaking in response to addition of salt and lowering of temperature. Normally such changes are limited by the amount of water entrapped in the cheese at block formation. However, for cheeses such as feta cheese, brine acts as a reservoir of water. Our objective was to determine the extent to which the protein matrix expands or contracts as a function of salt concentration and temperature, and whether such changes can be reversed. Blocks of feta cheese made with overnight fermentation at 20 and 31°C yielded cheese of pH 4.92 and pH 4.83 ($P<0.05$) with 50.8 and 48.9 g/100g moisture ($P<0.05$), respectively. These cheeses were then cut into 100 g pieces and placed in plastic bags containing 100 g of whey brine solutions of 6.5, 8.0 and 9.5% salt, and then stored at 3, 6, 10, and 22°C for 10 d. After brining, cheese and whey were re-weighed, whey volume measured and cheese salt, moisture and pH determined. A second set of cheeses were similarly placed in brine (n=9) and stored for 10 d at 3°C, followed by 10 d at 22°C, followed by 10 d at 3°C, or the complimentary treatments starting at 22°C. Cheese weight and whey volume (n=3) were measured at 10, 20 and 30 d of brining. Cheese structure was examined using confocal microscopy. Temperature had greatest influence on composition, weight and cheese volume. Salt-in-moisture content approached expected levels based on brine concentration and ratio of brine to cheese, i.e., 4.6, 5.7 and 6.7%. Brining at 3°C increased ($P<0.05$) cheese moisture, especially for cheese with initial pH of 4.92, with moisture up to 58 g/100g. Cheese weight increased after brining at 3, 6 or 10°C. Cold storage prevented fermentation and the pH remained constant, while at 22°C the pH dropped as low as pH 4.1. At 3°C the cheese matrix expanded (20 to 30%) while at 22°C there was a contraction and a 13 to 18 g/100g loss in weight ($P<0.05$). Expansion of the protein matrix at 3°C was reversed by changing to 22°C. However, contraction of the protein matrix, was not reversed by changing to 3°C and the cheese volume remained less than what it was initially.

Key Words: protein, cheese, brining

437 Impact of the addition of salts on the textural and rheological properties of nonfat cheese. J. A. Stankey*[1], M. E. Johnson[2], and J. A. Lucey[1], [1]*University of Wisconsin, Department of Food Science, Madison*, [2]*Wisconsin Center for Dairy Research, Madison*.

Several salts ($CaCl_2$, NaCl, and NaSCN) were screened in a small-scale method to observe the textural and rheological impact on a nonfat (NF) cheese. Direct acid NF cheese was made (pH 5.6, 58% moisture), sliced into discs (diameter = 50mm, thickness = 2mm) and frozen (-20°C) until use. A synthetic Cheddar cheese aqueous phase buffer (pH 5.4) was modified to reflect the NF cheese composition. Salts were added to buffer at varying concentrations. Thawed slices were wrapped in cheesecloth and incubated (6 h at 25°C) in glass petri dishes with 50 mL of buffer on a shaker. Post-incubation samples were air dried and equilibrated in airtight bags for 18h at 5°C prior to analysis. Small amplitude oscillatory shear properties were measured while heating from 5 to 85°C at the rate of 1°C/min and parameters measured were dynamic moduli and loss tangent (LT). Hardness was determined by texture profile analysis and uniaxial compression. Acid-base buffering was measured to observe changes in insoluble calcium phosphate (CCP). Moisture content decreased as salt concentration increased. The LT values were higher (indicating higher meltability) and occurred at lower temperatures for cheeses incubated in high concentrations of NaSCN compared to control cheeses. The reverse was observed for cheeses incubated in high concentrations of $CaCl_2$. Hardness decreased in cheeses subjected to buffers with high concentrations of NaSCN. High concentrations of NaCl in buffers solubilized some residual CCP in cheese. NaSCN had little effect on CCP, whereas buffers with high concentrations of $CaCl_2$ increased CCP levels strengthening the protein

matrix thus decreasing meltability. High NaSCN cheeses may weaken the protein matrix at higher temperatures due to the chaotropic effect of SCN^-, which by perturbing water structure may reduce hydrophobic interactions weakening casein interactions. Heating typically strengthens hydrophobic interactions but the addition of SCN^- may have disturbed these interactions. This study shows that the addition of NaSCN and $CaCl_2$ influenced the texture and rheology of NF cheese.

Key Words: nonfat cheese, texture, rheology

438 Comparison of mono- and poly-unsaturated fatty acid compositions between reduced-fat and full-fat goat milk cheeses during three months aging. W. Nouira[1], Z. Guler[2], J. H. Lee[1], T. H. Terrill[1], G. Kannan[1], and Y. W. Park*[1], [1]*Fort Valley State University*, *Fort Valley, GA*, [2]*Mustafa Kemal University*, *Hatay, Turkey*.

Consumers demand for reduced-fat dairy products has remarkably increased in recent years. Research on reduced or low fat cow milk products has been numerous, while such studies on goat milk products have been scarce. Three batches each of skim milk (SM) and whole milk (WM) cheeses were manufactured using a bulk goat milk from the University milking herd consisted of Saanen, Alpine, and Nubian breeds to compare the characteristics of monounsaturated and polyunsaturated fatty acid (MUFA and PUFA) compositions and their ratios between the two types of caprine milk cheeses. Cream was separated from the whole milk by a cream separator (Model 17584, Clair Co., Austria) before manufacture of SM cheeses. Both SM and WM cheeses were aged for three months at 4°C, and fatty acid compositions of the goat cheeses were quantified using a GC-MS (Trace DSQ-GC Ultra, Thermo Electron Corp. Austin, TX) equipped with a GC column (SP 2390; 60m x 0.25mm x 0.2um, Supelco, St. Louis, MO). Mean total fatty acid concentrations (mg/g) of SM and WM cheeses were 7.92 and 24.2. Respective mean (%) of MUFA and PUFA for 0, 1 and 3 months aged WM cheeses were: 16.6, 5.07; 24.1, 4.40; 21.1, 2.29, while corresponding means (%) of SM cheeses were 7.52, 1.68; 8.38, 1.83; 7.03, 2.10, indicating that PUFA contents of both cheeses were significantly lower than MUFA, probably due to the high oleic acid content. MUFA:PUFA ratios for 0, 1, and 3 months aged SM and WM cheeses were 4.47, 3.27; 4.57, 5.47; 3.34, 9.21, suggesting the ratios variably changed with a significant reduction in PUFA in WM cheese after 3 month aging. The respective total unsaturated:saturated fatty acid ratios for SM and WM cheeses of 0, 1 and 3 month periods were 0.11, 0.30; 0.12, 0.40; 0.10, 0.32, showing the WM cheeses had higherpercent unsaturated fatty acid than SM counterparts.

Key Words: goat cheese, reduced-fat, fatty acid ratios

439 Distribution of fat in comminuted cheese at varying fat levels and storage times using laser scanning confocal microscopy and textural analysis. W. R. McManus*, N. Garg, and D. J. McMahon, *Western Dairy Center, Utah State University*, *Logan*.

This study examined the microstructural and textural variations of cheese made from comminuted cheese curd and control (non-comminuted) cheese curd. Cheese was produced at increasing fat concentrations of 3, 8, 13, 18, 23, 28, and 33% using stirred-curd Cheddar cheese methods. A portion of the curd was comminuted in a bowl chopper to particle size of about 2 to 4 mm, and then filled into hoops and pressed. Cheese was stored at 6°C and analyzed at 2, 4, 8, 12, and 24 wk using laser scanning confocal microscopic imaging and texture profile analysis using 60% compression. Cheese was stained with 0.1% Nile Red for fat, and 0.01% fluorscein isothiocyanate for protein. As fat level decreased, the fat droplets dispersed within the curd particles decreased in size. At high fat levels, the curd particle junction were devoid of fat because of fat loss from the curd particles during cheesemaking. When the curd was comminuted prior to pressing, free fat was observed between the curd particles. As fat level in the cheese decreased, there was a decrease in inter-particle fat. Differences in texture were observed based on treatment and fat level. Springiness was influenced by fat level ($P<0.0001$) but not by curd treatment. Cohesiveness was different among fat levels ($P<0.0001$) and curd treatment ($P<0.001$). For control cheeses the cohesiveness increased from 0.305 for the 33% fat cheese to 0.786 for the 3% fat cheese. For cheeses with fat contents of 13 to 33% fat, comminuting the curd caused a decrease in cohesiveness, while for cheeses with 3 and 8% fat it caused a increase in cohesiveness. This change in cohesiveness was related to the quantity of fat observed between the curd particles. In the low fat cheeses the fat was observed primarily as small droplets entrapped in the protein matrix of the curd particles, with only a very small amount of fat being released onto the curd particle surface during the comminuting process. At higher fat levels, the fat was observed as larger pools of fat, which could more easily be released during comminuting.

Key Words: cheese, cohesiveness, low fat

440 Development of various paneer based spreads. H. G. Ramachandra Rao* and H. Arun Kumar, *Dairy Science College, Hebbal*, *Bangalore, Karnataka, India*.

Paneer, heat-acid coagulated Indian soft cheese, used mainly for making culinary dishes. Paneer was made by heating whole milk to 90°C, cooled to 70-75°C and coagulated by addition of 1% citric acid and whey drained out through a stainless steel mesh to obtain paneer curd. Salt (1.5%) and stabilizer (0.5%) are added and mixture was subjected to grinding by using mixer-grinder. The moisture % was 65%, exhibited excellent spreading property at 7°C. Dairy spreads generally are high in fat, saturated fatty acids and cholesterol, but poor in spreadability at low temperatures. An attempt has been made to develop various types of paneer based spreads with low fat and low cholesterol, but exhibits good spreadability. Incorporation of 10% WPC or 5% sodium caseinate or 5% soy flour during product preparation resulted in higher yield, better functional properties and nutritional value compared to control (paneer curd was grinded to obtain spread). Replacement of milk fat with vegetable oils at 25% level was highly acceptable with improved body and texture (as determined by using texture analyzer) and spreadability. Sensory analyses of spreads were determined by using a panel of 5 experienced judges. Incorporation of spices such as pepper, clove, cinnamon and their combinations (pepper and clove, clove and cinnamon and cinnamon and pepper) in the form of powder at 1 per cent level resulted in better flavour scores. Pepper and mixture of pepper and clove-flavored paneer spreads recorded highest overall acceptance scores. Among various keeping quality studies undertaken, mere vacuum treatment of paneer spreads resulted in extension of storage up to 35 days at 7±1°C, as against 14 days in control. Microwave treatment of spreads under similar conditions of temperature resulted in extension of keeping quality up to 63 days. Further, when product was subjected to vacuum treatment followed by microwave heating the product was quite stable upto 77 days at 7±1°C. Cheese spreads are not popular in India, probably due to food habits. Therefore paneer type of product with slight modification, with better functionality to improve their utilization was developed in this study.

Key Words: paneer, spreadability, vegetable oil

441 Dam/grand-dam nutrition during pregnancy affects milk supply in offspring and reproductive performance in grand-offspring. H. T. Blair*, D. S. van der Linden, L. C. Davenport, P. R. Kenyon, C. M. C. Jenkinson, S. W. Peterson, D. D. S. Mackenzie, S. T. Morris, and E. C. Firth, *National Research Centre for Growth & Development, Massey University*, *Palmerston North, New Zealand*.

In temperate climates the cost of providing feed is higher in winter than other seasons, causing ewes to be fed restricted rations during some periods of pregnancy. Epidemiological information suggests that undernutrition of the fetus may affect its health and performance in later life; these effects may be passed between generations (fetal programming). In 2005 510 ewes (G0) carrying either singleton or twin fetuses had either ad lib (H) or restricted (L) access to pasture between d21 and d140 of pregnancy. In 2006 onset of puberty in ewe offspring (G1) was assessed and in 2007 220 G1 ewes were mated and a subset milked. In 2008 growth and puberty of G2 offspring were monitored. At d140 of pregnancy H G0 ewes were heavier than L ewes (78.4 vs 65.0±0.36kg). G1 twin-born lambs from L dams were lighter than contemporaries from H dams (4.52 vs 5.23±0.06kg). Lambs reared by H G0 dams were heavier than L lambs at weaning (32.8 vs 31.0±0.37kg), but by 6 months of age there was no weight difference between H and L G1 ewe lambs. No differences were found in onset of puberty or reproductive traits at 18 months of age between H and L G1 ewes. Weights of H and L G1 ewes throughout their first pregnancy were similar. Birth weights of L G2 offspring were heavier than their H contemporaries (4.74 vs 4.53±0.08kg). L G1 ewes tended to produce more milk ($P<0.10$) with higher predicted lactose yield (6.97 vs 6.60±0.14kg) than did their H contemporaries over a 50-day lactation. This was reflected in higher weights of G2 L lambs at weaning (28.5 vs 25.5±1.36kg) and a greater proportion of L G2 ewe lambs reaching puberty at c.8 months of age. These results indicate that dam nutrition can affect the yield and composition of milk in their offspring and the weight and reproductive capability of their grand-offspring. Molecular and physiological mechanisms for these changes are being sought.

Key Words: fetal programming, milk supply, reproduction

442 Fetal programming of skeletal muscle development in ruminant animals. M. Du* and M. J. Zhu, *University of Wyoming*, *Laramie*.

Enhancing skeletal muscle growth is crucial for the profitability of animal agriculture and meat industry. Effective enhancement of skeletal muscle growth is dependent on our understanding of mechanisms controlling skeletal muscle growth and development. Fetal stage is of particular importance for skeletal muscle development because there is no net increase in the number of muscle fibers after birth. The lower priority in nutrient partitioning renders skeletal muscle development venerable to the fluctuation of maternal nutrition. In ruminant animals, skeletal muscle matures at late gestation, when skeletal muscle possesses well developed muscle fibers, intramuscular adipocytes and connective tissues formed by fibroblasts. All these cells are derived from mesenchymal stem cells. Maternal nutrition during fetal stage, especially the mid to late gestation, directly affects the proliferation and differentiation of mesenchymal stem cells and, thus, alters the muscle fiber number and size, intramuscular adipocyte number and collagen content in offspring muscle — a process called fetal programming. Available studies provide several major mechanisms linking maternal nutrition and fetal muscle development, including Wnt/β-catenin signaling, insulin like growth factor signaling, inflammatory signaling and AMP-activated protein kinase, and epigenetic modifications. Future studies should focus on the identification of underlying mechanisms associated with fetal programming of skeletal muscle development, such as analyzing signaling pathways and the subsequent epigenetic modifications in crucial genes regulating myogenesis, adipogenesis and fibrogenesis from mesenchymal stem cells, and the resulting skeletal muscle growth and development and meat quality.

Key Words: fetal programming, skeletal muscle, growth

443 Programming of fetal fat and muscle: Natural and genetic fetal restriction and exogenous nutritional influences. G. J. Hausman*, *USDA-ARS*, *Athens, GA*.

Naturally restricted growth (runts) and genetically reduced birthweights, as in lean and obese pigs, can have a long lasting or permanent influence on postnatal performance. The degree of restriction or reduction in birth weight dictates the influence on postnatal growth and development. Small birth weights increase fat cell development and muscle fiber size but decrease fiber number. Maternal nutrition can reduce fetal growth depending on species and severity of either protein or energy restriction. However, maternal nutrition can influence progeny development without influencing birth weights. Restricted fetal growth and low birth weight influences growth and development in many species. Maternal under nutrition and even over nutrition may restrict fetal development and subsequent postnatal development. The considerable literature including several recent long term studies warrants a review of these topics in regards to pigs, sheep and cattle.

Key Words: fetal, restriction, progranmming

444 Epigenetic programming of behavior and physiology. M. Meaney*, *McGill University*, *Montreal, Quebec, Canada*.

Maternal care alters adaptive behavioral and endocrine responses to stress in the rat. The mechanisms for these 'maternal effects' involve stable changes in gene expression. Thus, the adult offspring of mothers that exhibit increased pup licking/grooming (LG) show increased hippocampal glucocorticoid receptor (GR) mRNA expression. The differences in GR expression associate with effects at the level of both negative feedback inhibition and HPA responses to stress.. Studies of the mechanisms for maternal effects on GR expression focus on DNA methylation within a brain-specific GR gene promoter. These studies reveal sustained effects of maternal behavior on the cytosine methylation of the consensus binding sequences for specific transcription factors that regulate GR gene expression. Pharmacological manipulations that reverse the maternal effect on cytosine methylation of the GR promoter also eliminate the effect at the level of both GR expression and HPA responses to stress. The maternal effect on DNA methylation involves an active demethylation at specific CpG dinucleotides targeted by intracellular signals driven by pup LG. Such processes reveal experience-dependent plasticity in the chemistry of the DNA and chromatin structure.

445 Large animal models of developmental programming. L. P. Reynolds*, J. S. Caton, K. A. Vonnahme, J. S. Luther, C. J. Hammer, K. R. Maddock Carlin, A. T. Grazul-Bilska, and D. A. Redmer, *Center for Nutrition and Pregnancy, and Animal Sciences Department, North Dakota State University*, *Fargo*.

Developmental programming refers to the long-term effects of various `stressors' (e.g., maternal nutrient excess or limitation) on fetal or neonatal development; that is, `programming' of organ systems during a discrete developmental period resulting in compromised function even in adulthood. This concept was first hypothesized based on the results of epidemiological studies in humans and has been subsequently confirmed with controlled animal studies. In addition to its effects in humans, developmental programming likely has profound implications for the efficiency of livestock production. The various large animal models of developmental programming will be described along with the effects that have been observed in various organ systems. The models to be presented include those using cattle, sheep, and swine, and also will include models of maternal and neonatal nutrition (including energy, protein, and specific nutrients such as selenium), maternal age, maternal and fetal genotype, maternal environmental stress, and multiple fetuses. The critical importance of large animal models of developmental programming in solving socioeconomic and health-related issues also will be discussed. Moreover, the consequences of developmental programming for livestock production will be discussed, along with potential therapeutic approaches to minimize or at least manage these deleterious effects. *Supported by NIH grants HL64141 and HD45784, and USDA-NRI grants 2005-35206-15281 and 2007-012. We thank the many colleagues and students who have contributed to our research efforts over the years.*

Key Words: animal models, developmental program, socioeconomic impliations

Meat Science and Muscle Biology: Pork and Beef Quality

446 Effects of dietary oxidative stress on postmortem events and tenderness of fresh pork. D. D. Boler*, L. W. Kutzler, A. C. Dilger, D. M. Fernandez-Duenas, S. F. Holmer, F. K. McKeith, and J. Killefer, *University of Illinois*, *Urbana*.

Extreme postmortem oxidation treatments have been shown to reduce proteolysis of beef steaks; which led to reduced protein degradation and delayed tenderization. The objective of this experiment was to determine if dietary oxidative stress from feeding finishing barrows highly oxidized oils reduced postmortem tenderization and delayed myofibrillar protein degradation. One hundred twenty barrows were allotted to a 2 × 2 factorial in a complete randomized block design with 3 blocks of 40 barrows each. Factors included oil type (fresh or oxidized) and dietary antioxidant (inclusion or exclusion). Fresh or oxidized corn oil was included in the diet at 5%, with or without 132 ppm antioxidant (ethoxyquin + tertiary butyl hydroquinone). Treatment diets were fed for the last 56 d of finishing prior to harvest. Barrows (n=24) whose live weights were closest to their respective pen means were selected for meat quality analysis and humanely slaughtered. Samples were collected to determine the overall effect of diet on oxidation in the carcass. Longissimus muscle was dissected between the 6th and 11th rib of the right side of the carcass at 24 h postmortem. Four pairs of chops were cut from the longissimus muscle beginning at the 6th rib. Pairs of chops were randomly assigned to aging durations of 1 d, 3 d, 7 d, or 14 d postmortem. Tenderness was analyzed on one chop using Warner-Bratzler shear force. Proteolysis of myofibrillar proteins was determined on the paired chop by Western blotting. No differences ($P > 0.05$) were detected in shear force values at any time points. No differences ($P > 0.05$) were detected in Troponin-T degradation between fresh and oxidized oil treatment groups; however, the presence of antioxidant appeared to accelerate ($P < 0.05$) myofibrillar protein degradation. The addition of highly oxidized oils in finisher pig diets does not appear to affect postmortem tenderization or myofibrillar proteolysis. Lack of differences in tenderness may be due to the level of oxidation in the oxidized oil treatment group being inadequate to illicit a response.

Key Words: pork, proteolysis, myofibrillar proteins

447 Effects of oxidized corn oil and synthetic antioxidant blend on pork quality and shelf-life. D. M. Fernández-Dueñas*[1], L. W. Kutzler[1], D. D. Boler[1], S. F. Holmer[1], J. Zhao[2], R. J. Harrell[2], J. Andrews[2], M. Vazquez-Añon[2], M. Ellis[1], F. K. McKeith[1], and J. Killefer[1], [1]*University of Illinois*, *Urbana*, [2]*Novus International Inc.*, *St. Charles, MO*.

The objective of this experiment was to evaluate the effect of oxidized oil and a blend of synthetic antioxidant (AOX, ethoxyquin and tertiary butyl hydroquinone; Novus International Inc.) on meat quality traits and shelf-life. The trial was a 2×2 factorial arrangement, with fresh vs. oxidized corn oil with or without AOX. A total of 32 barrows were selected for meat quality and shelf-life evaluation. Subjective color, marbling, and firmness, as well as objective color, pH and backfat depth (BD) were collected. Drip loss (loin chops) and percent moisture and fat were determined (loin chops and ground pork). Pigs fed oxidized oil had lower carcass yield (P=0.01) and pigs fed AOX had higher carcass yield (P=0.05) when fed either fresh or oxidized oil. Pigs fed AOX had 39% higher loin fat (P=0.07) and higher loin marbling score when fed fresh oil but not oxidized oil (AOX P=0.08, interaction P=0.08). Pigs fed oxidized oil had 13% lower Boston butt fat and less back fat depth at the 10th and last rib ($P<0.05$). Pork chops from pigs fed AOX were more juicy (P=0.08) and tender (P=0.03) and chops from pigs fed oxidized oil were less tender (P=0.06) after 14 days of storage. Shelf–life was measured as thiobarbituric acid reactive substances (TBARS) and discoloration score after stored in display cases for 0, 7, 14, and 21 days. After 14 and 21 days of storage, loin chops from pigs fed fresh oil with AOX had the lowest TBARS values and those fed oxidized oil without AOX had the highest. Chops from fresh oil without AOX and oxidized oil with AOX were intermediate (treatment effect P=0.02). Loin chops from pigs fed fresh oil with AOX had lower discoloration scores after 21 days of storage compared to those fed fresh oil alone (P=0.008). Results indicated pork quality was improved with dietary AOX supplementation by having lower TBARS and lower discoloration score. Pork chops from pigs fed AOX were more juicy and tender compared to the control.

Key Words: antioxidant, pork quality, TBARS

448 Impact of varying CO_2 and O_2 concentrations during stunning and carcass chilling conditions on pork quality traits. G. Bee*[1], M. Gerritzen[2], M. Mull[2], C. Biolley[1], G. Guex[1], B. Dougoud[1], and C. Vonnez[1], [1]*Agroscope Liebefeld Posieux, Research Station ALP, Posieux, Switzerland*, [2]*Animal Sciences Group of Wageningen, Lelystad, the Netherlands*.

Commonly pigs are stunned using high CO_2 concentrations. Audible gasping in the stunner deliver evidence that, due to the high CO_2 levels, pigs experience a certain degree of discomfort, which might accentuate premortem stress and, thereby, affect pork quality. Aiming to lower the adverse effects of inhaling high CO_2 levels, the addition of O_2/N_2 to lower CO_2 levels were tested (60: 60%CO_2+30%O_2+10%N_2; 70: 70%CO_2+30%O_2; 80: 80%CO_2+20%O_2; C: 87%CO_2+air). At 108 kg BW, 24 castrates from 4 litters were assigned within litter to 1 of the 4 stunning groups. Based on behavioral and electro-physiological measurements it was judged if pigs were properly stunned (data not discussed). Prior to bleeding, all animals were shot with a captive bold. Carcasses were then scalded (7 min; 65°C), eviscerated and split. Both carcass sides were weighed and the left carcasses were conventionally (CC) cooled at 4°C for 24 h, the right carcasses were rapidly chilled (RC) for 120 min at -30°C and then stored at 4°C for 22 h. Regardless of the stunning gas, cold loss was 0.6% lower ($P < 0.01$) in RC- than CC-carcasses. Compared to C, postmortem (pm) pH of the LM (10 rib) was lower ($P \leq 0.05$) in carcasses of the 60- and 70-group (3 h: 6.1 vs. 5.7; 24 h: 5.5 vs. 5.4). Intermediate values were observed in carcasses of the 80-group (3 h: 5.8; 24 h: 5.4). At 3 h pm, but not at 24 h, the LM temperature was lower ($P < 0.01$) in RC- than CC-carcasses (12.1 vs. 19.1°C). LM temperature declined faster ($P < 0.05$) in C- and 70- compared to 80-group with intermediate values in the 60-group (3 h pm: 14.8, 14.5, 17.1, 15.9°C; 24 h pm: 2.9, 3.3, 3.4, 3.4°C). Drip loss percentage after 48 h was lower ($P < 0.10$) in loin chops of C- (4.71%) compared to 60- (7.58%) and 70- (6.66%) and intermediate values in the 80-carcasses (5.88%). Regardless of the stunning procedure, loin chops from RC-carcasses were tougher (5.0 vs. 4.3 kg; $P = 0.03$) than from CC-carcasses. From a quality point of view, the current results revealed that lowering the CO_2 level during stunning negatively affected pork quality and rapid carcass chilling had no alleviating effect.

Key Words: CO_2 stunning, rapid chilling, pork quality

449 Using ultrasound technology to predict intramuscular fat of loin in live pigs and potential use in swine genetic improvement. L. Maignel*[1], J.-P. Daigle[2], and B. Sullivan[1], [1]*Canadian Centre for Swine Improvement, Ottawa, ON, Canada*, [2]*Centre de Développement du Porc du Québec, Québec, QC, Canada*.

The use of ultrasound technology to predict meat quality on live animals would be a quick, non-invasive and affordable method including numerous advantages for swine selection. To test newly available equipment, a group of 1,000 Duroc pigs were scanned using ultrasound technology and image analysis to estimate the intramuscular fat percentage in the Longissimus dorsi muscle using Biosoft Swine Toolbox software developed by Biotronics. Among these animals, 150 were slaughtered for a visual examination of marbling and a chemical analysis of intramuscular fat percentage in the Longissimus dorsi muscle. The correlations between in vivo measures with visual scores and chemical analysis were 0.55 and 0.69, respectively, in this sample. The standard error of prediction of chemical analysis from in vivo measures was 0.71%. The estimated heritability of intramuscular fat predicted in vivo was 0.69 and a moderately positive correlation was observed between this trait and backfat thickness as well as a significant negative correlation with loin depth. These results are very encouraging with respect to the possibilities of using ultrasound on live pigs to efficiently predict the percentage of intramuscular fat and to select for this trait.

Key Words: intramuscular fat, ultrasound technology, pig

450 The effects of restricted feeding and subsequent realimentation on pig carcass composition. C. Chaosap*, T. Parr, and J. Wiseman, *Nottingham University, Loughborough, UK*.

The effects of ad libitum feeding after a period of feed restriction were examined in female pigs which were allocated to 3 slaughter groups (S1, S2, S3 at 114, 116, 156 days of age). In S1 pigs were fed ad libitum (A40) or fed restricted to 0.70 of ad libitum for 40 days prior to slaughter (R40) (n=8). For S2, pigs were fed ad libitum throughout 42 day period (A42) and the other group feed restricted for 40 days followed by ad libitum for 2 days prior to slaughter (R40A2) (n=8). In S3, pigs were fed ad libitum for 82 days (A82) and the other group restricted for 40 days then ad libitum for 42 days before slaughter (R40A42) (n=8). At S1, A40 had a higher live weight and carcass weight than R40 ($P<0.05$) but at S2 there was a trend for A42 carcasses to be heavier than R40A2 ($P<0.1$), whilst in S3 there was no significant difference between A82 and R40A42 for live weight and carcass weight. For the individual muscles, longissimus muscle (LM), psoas, semitendinosus, when examined as a proportion of carcass weight, LM was greater in the groups exposed to restriction at S1 ($p<0.1$) and S2 ($p<0.05$) but not at S3. There was no difference between other muscles at all three slaughter dates. At S1 kidney and liver were smaller ($p<0.05$) whilst there was trend for the heart also to be smaller ($p<0.1$) in R40 compared to A40 when these tissues were examined as a proportion of live weight. However at S2 only the kidney was smaller in the group that had been restricted (R40A2) ($p<0.05$) and at S3 there were no significant differences in any of these internal organs between groups. At S1 the level of IGF1 in the plasma was lower in R40 than A40 ($p<0.01$), but at S2 there was a trend for the level to be lower in the group that had been restricted ($p<0.1$), whilst at S3 there was no difference. The dietary restriction period influenced IGF1 plasma levels, which approached those levels of the ad libitum group when animals were refed, as did live weight and carcass weight. It appears that the internal organs, not muscles, underwent a compensatory response when animals were refed.

Key Words: pigs, compensatory growth, IGF1

451 Carcass traits of tropically adapted cattle when evaluated at different endpoints. S. W. Coleman*[1], D. G. Riley[1], C. C. Chase Jr.[1], M. F. Miller[2], J. C. Brooks[2], D. D. Johnson[3], W. A. Phillips[4], and T. A. Olson[3], [1]*USDA ARS STARS, Brooksville, FL*, [2]*Texas Tech University, Lubbock*, [3]*University of Florida, Gainesville*, [4]*USDA ARS GRL, El Reno, OK*.

Brahman (Bos indicus) derivative cows are well adapted to tropical conditions of Florida and the Gulf Coast, but calves are often discounted because their carcasses are perceived to be inferior. This work is from a 3-yr diallel crossbreeding study including Angus (A), Brahman (B) and Romosinuano (R), a tropically adapted B. taurus breed native to Colombia. Steer calves (n=477) of all possible breed combinations were weaned in Brooksville, FL and transported 2100 km to El Reno, OK for grazing wheat pasture and conventional feedlot finishing. Due to the great diversity on how the breeds mature, they were serially harvested at the IBP plant in Amarillo, TX after ~90, 120 and 150 days on feed.

Our objective was to compare selected carcass traits at different endpoints, constant days on feed (DOF), constant slaughter weight (SLWT), constant backfat (BF), and constant marbling score (MS). Mixed model analysis included fixed effects of year (n=3), breed type (n=9), winter grazing treatment (n=2), and the continuous variable for endpoint. All significant two-way interactions were included. Sire within breed was random. Overall, marbling score averaged 405 and 82% of the steaks were judged tender by both WBS (< 5 kg) and taste panel (> 5.0 OT score). Breed affected ($P < 0.05$) MS regardless of endpoint. At a time constant basis, MS was essentially linear with proportion A (573 for AA; 445 for Ax; and 349 for 100% tropically adapted steers). Longissimus area was influenced ($P < 0.05$) by breed group if DOF, BF, or MS were the endpoint, but not for SLWT. All endpoints significantly influenced Longissimus area. Tenderness (WBS) was different ($P < 0.05$) among breed types when SLWT or BF was the endpoint, and tended ($P < 0.10$) to be different if DOF and MS were the endpoint. Days required to reach the average MS were 115 for AA, 128 for Ax, 133 for RR and BR, 142 for RB, and 153 for BB.

Key Words: tropical adaptation, Brahman, Romosinuano

452 Sarcomere length influences postmortem proteolysis of Troponin-T in bovine muscle. S. J. Wells*, T. M. Nath, D. M. Wulf, and A. D. Weaver, *South Dakota State University*, *Brookings*.

Sarcomere length (SL) and proteolysis independently influence meat tenderness. In theory, the extent of overlap between actin and myosin is dependent on SL, which could affect substrate availability for the calpain protease system. The objective of this study was to evaluate the effect of varying SL on postmortem proteolysis of troponin-T (TnT) in intact bovine muscles. The right side of *Bos taurus* (n=7) and *Bos indicus* (n=7) carcasses were normally suspended (NS) and the left side of each carcass was hip suspended (HS). Samples were removed from the *Longissimus dorsi* (LD), *Semitendinosus* (ST), and *Psoas major* (PM) at 0, 1, 4, 7, and 10 d postmortem. Myofibrils were isolated from samples aged 1, 4, 7 and 10 d and SL was measured using fluorescence microscopy and image processing software. Degradation of intact TnT was evaluated at 0, 1, 4, 7, 10 d using SDS-PAGE and Western blotting analysis. In LD and ST, sarcomeres were longer and degradation of TnT was greater for HS than NS ($P < 0.05$). In the PM, sarcomeres were shorter and degradation of TnT was reduced in HS compared with NS ($P < 0.05$). When data from all muscles were pooled and adjusted for the main effects of muscle and breed, the relationship of TnT degradation with SL was linear on d-1 and d-4 and quadratic on d-7 and d-10 ($P < 0.05$). On d-1 and d-4, degradation increased ($P < 0.05$) with increasing SL. On d-7 and d-10, longer sarcomeres resulted in greater degradation of TnT within the SL range of 1.7 - 2.5 μm, but no effect of SL on degradation was detected within the SL range of 2.5-3.9 μm. The effect of SL on proteolysis was most pronounced during the first 24 h postmortem as demonstrated by a linear relationship between SL and rate of TnT degradation from d-0 to d-1 ($R^2 = 0.26$). However, no relationship existed between SL and rate of TnT degradation from d-1 to d-10 ($R^2 = 0.01$). This study indicates that decreased SL results in decreased TnT degradation, by affecting proteolysis during the first 24 h postmortem.

Key Words: sarcomere length, proteolysis, TnT

453 Water access and the carcass characteristics of Holstein slaughter cows. K. D. Vogel*[1], J. R. Claus[2], T. Grandin[1], G. R. Oetzel[2], and D. M. Schaefer[2], [1]*Colorado State University*, *Fort Collins*, [2]*University of Wisconsin*, *Madison*.

During the marketing process, cattle may be exposed to periods of water deprivation. The impact of water withdrawal on the carcass characteristics and fresh meat properties of Holstein slaughter cows was examined through analysis of dressing percentage, postmortem pH decline, proximate analysis, and fresh meat color. Ninety-one multiparous Holstein cows (609 ± 89 kg mean body weight, 2.89 ± 0.51 mean BCS, varying stage of lactation) were purchased over three weeks in three groups (n = 31, 29, and 31) at a terminal market in central Wisconsin. Each cow was randomly assigned to one of three water withdrawal treatments (control, ad libitum access to water for 36 h; 18 h withdrawal, 18 h of ad libitum access to water followed by 18 h of water withdrawal; 36 h withdrawal, 36 h of water withdrawal). Mean ambient temperatures were 1.87 ± 6.23° C during the trial period. Following the water and feed withdrawal period, all cows were transported to a commercial slaughter facility. Mean muscle protein (%) increased ($P< 0.05$) between 18 h (21.11 ± 0.34%) and 36 h (22.22 ± 0.34%) of water and feed withdrawal. Mean muscle moisture (%) decreased ($P< 0.05$) between 18 h (75.05 ± 0.48%) and 36 h (73.57 ± 0.48%) of water and feed withdrawal. Mean 24 hour pH values were 5.94 (control), 5.99 (18h withdrawal) and 5.94 (36h withdrawal) (S.E. = 0.07) and were not different. Observed pH values indicate a borderline dark-cutter state across all cattle in the study, regardless of water treatment. This study determined some effects of water and feed withdrawal during marketing on meat characteristics of Holstein slaughter cows, particularly, the presence of a borderline dark-cutting state.

Key Words: dehydration, meat quality, dairy cow

454 Growth and carcass characteristics of steers fed an omega-3-fatty acid-fortified supplement from flaxseed while on improved pastures and following feedlot finishing. R. C. Vann*[1], S. T. Willard[2], E. L. Schenck[2], J. M. Martin[2], K. Moulton[2], W. Holmes[2], A. Brown[2], B. Thomas[2], T. E. Lawrence[3], and M. S. Brown[3], [1]*MAFES-Brown Loam Exp. Stat., Mississippi State University*, *Raymond*, [2]*Mississippi State University*, *Starkville*, [3]*West Texas A&M University*, *Canyon*.

The objectives of this study were to determine the potential of omega-3 fatty acid fortified supplements as an energy supplement to facilitate decreased mobilization of intramuscular fat deposition associated with cattle grazing forages and to enhance fatty acid content in meat tissue throughout the feedlot feeding period. Angus crossbred steers (n=42) maintained on ryegrass-bermudagrass pastures were assigned to either a control (CON; natural 15 molasses tub; Animal Feed Supplement, Poteau OK.) or an omega-3 fatty acid fortified tub (FLAX; flaxseed molasses tub; Animal Feed Supplement, Poteau OK). Steers were allowed to graze pastures with ad libitum access to tubs for 168 d and were then shipped to a feedlot with continued access to the tubs during the 121 d feedlot feeding period. Ultrasound body composition measurements and semitendinous muscle biopsies were collected on D0, 91 and 168 of the grazing period and longissimus steaks were collected at harvest. Steaks collected at harvest were analyzed for fatty acid profiles and warner-bratzler shear force measurements. The PROC Mixed procedure of SAS was used for data analysis. There were no differences ($P \geq 0.10$) in BW or ADG for the two treatment groups, except for ADG at the end of the feedlot period tended to be greater in the FLAX group compared to CON group ($P \leq 0.07$). The CON group had greater ultrasound ribeye area ($P \leq 0.05$) than FLAX group from D 91 throughout harvest. There were no differences ($P \geq 0.10$) in ultrasound intramuscular fat or carcass ribeye area, marbling scores, quality grades or yield grades between the

two treatment groups. CON steers tended to have greater % oil in steaks ($P \leq 0.08$) and a tendency for a greater C17:0 ($P \leq 0.09$) steak fatty acid content. In conclusion, FLAX supplementation while on pasture did not enhance growth or ultrasound body composition characteristics, and access to FLAX during feedlot finishing had little influence on steak composition post-harvest.

Key Words: flaxseed, steers, body composition

455 Impact of feeding *Fusarium graminearum*-infested barley on meat quality and fatty acid profiles in beef steers. S. L. Scott*[1], D. L. McLaren[1], H. C. Block[1], M. E. R. Dugan[2], Y. Wang[3], and T. A. McAllister[3], [1]*Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, MB, Canada*, [2]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*.

Little is known about the impact of feeding beef steers barley contaminated with the fungal pathogen *Fusarium graminearum* (FG) on meat quality and fatty acid profiles. Sixty-four steers (422±36 kg BW) housed in 8 pens were allocated to one of 4 experimental diets during a 56-day feeding trial. Basal diets comprised 80% whole barley (WB), 19% hay, 1% salt/vitamin/mineral premix (dry matter [DM] basis). FG-infested WB (24 ppm deoxynivalenol [DON]) made up 0, 26.7%, 53.3%, and 80.0% of the DM, with clean WB (<1ppm DON) comprising the remainder. At slaughter, carcass blue tag data were collected at the abattoir by a certified grader. One ribeye steak from each steer was analysed for percent moisture, crude protein (CP) and lipid by proximate analysis. Cooking loss and Warner Bratzler shear force were determined on a second steak following grilling to an internal temperature of 72°C. Fatty acid (FA) profile of lipid extracted from a third steak was analysed by GC following methylation to FA methyl esters (FAME) using the $NaOCH_3/BF_3$ double derivatization method; C19:0 was the internal standard. Conjugated linoleic acid (CLA) concentrations were confirmed with silver ion HPLC. Results were analysed with Proc Mixed of SAS. Diet had no impact on any carcass, meat quality or FA profile parameters ($P>0.05$), except the n-6/n-3 ratio ($P<0.01$), which varied in a cubic fashion with diet. Therefore, feeding FG-contaminated barley to beef steers does not negatively impact carcass or meat quality.

Table 1.

	Diet				
Parameter	0	26.7	53.3	80.0	SEM
Hot carcass weight (kg)	270.6	270.1	278.4	276.2	3.3
Grade fat (mm)	6.2	5.9	6.3	6.3	0.4
Yield grade	60.8	60.6	60.7	60.8	0.3
Rib-eye area (cm^2)	72.1	71.9	73.0	73.9	1.6
Moisture (%)	74.4	74.2	74.1	74.5	0.2
CP (% of DM)	79.5	79.7	78.8	80.2	0.6
Lipid (% of DM)	10.8	10.4	11.5	11.0	0.6
Cooking loss (%)	27.9	28.5	29.9	27.7	0.8
Shear force (kg)	5.9	6.2	6.0	6.3	0.3
C18:1 (t11) (% of FAME)	0.63	0.56	0.54	0.57	0.03
Total CLA (c9t11) (% of FAME)	0.15	0.14	0.13	0.14	0.01
Trans FA (% of FAME)	2.02	1.90	1.78	1.83	0.07
n-6/n-3 ratio	5.28	5.56	5.17	5.47	0.04

Key Words: *Fusarium graminearum*, beef quality, fatty acid profiles

456 Long-term supplementation with sunflower/fish oil-containing concentrates in a grass-based beef production system: Effects on colour and lipid stability during retail display. P. G. Dunne[1], F. J. Monahan[2], and A. P. Moloney*[1,3], [1]*Teagasc, Ashtown Food Research Centre, Ashtown, Dublin, Ireland*, [2]*University College Dublin, Belfield, Dublin, Ireland*, [3]*Teagasc, Grange Beef Research Centre, Dunsany, County Meath, Ireland*.

Increasing the concentrations of unsaturated fatty acids in beef may decrease its shelf-life. The effect on beef shelf-life of one nutritional strategy to alter fatty acids was examined. Sixty heifers were housed in November and fed either unwilted grass silage and a barley/soyabean meal concentrate (UC) or wilted grass silage and a concentrate containing sunflower oil and fish oil (WSFO). In May, both groups were offered either; pasture for 22 weeks (P); restricted P and sunflower oil and fish oil (SFO) for 22 weeks (PO22) or P for the first 11 weeks and restricted P and SFO for the final 11 weeks (PO11). Post-mortem, 21-day aged longissimus muscle (LM) was packaged in a high oxygen atmosphere and displayed for 10 days. Hunter colour coordinates (′L′ (lightness), ′a′ (redness), ′b′ (yellowness)) were measured and saturation calculated on day 0, 1, 3, 6, 8 and 10. Percent metmyoglobin and the difference between reflectance at 630nm and 580nm (R630-R580) were calculated as indices of discolouration. Lipid oxidation on days 0 and 10 was assessed as 2-thiobarbituric acid reactive substances (TBARS). Data were analysed as a split-plot with effects for winter ration, summer ration, days on display and all interactions included in the model. There was no winter and summer ration interaction and no ration by display interaction. Neither winter ration nor summer ration affected vitamin E concentration in LM. The LM from WSFO heifers was more red (13.23 v. 12.62, P=0.003), yellow (8.48 v. 8.01, P=0.027), saturated (15.82 v. 15.07, P=0.007), had higher R630-R580 (20.31 v. 18.74, P=0.004) and lower metmyoglobin (29.06 v. 30.29, P=0.024) than LM from UC heifers. The LM from PO22 heifers had higher ($P<0.05$) TBARS at day 10 (1.57, 1.82 and 2.11 mg/kg for P, PO11 and PO22, respectively). It is concluded that method of grass conservation affected muscle colour and that long term supplementation of grazing heifers with sunflower oil and fish oil increased lipid oxidation.

Key Words: cattle, color, TBARS

Nonruminant Nutrition: Mineral-Mineral Interactions: Implications for Nutrition

457 Ionomics: Mineral nutrition, physiology, and interactions as a biological system. J. Fleet* and D. Salt, *Purdue University, West Lafayette, IN*.

Inorganic elements (metals, non-metals, transition elements, and electrolytes commonly called "minerals" in nutrition science) are critical to all life processes as enzyme cofactors, stabilizers of proteins, structural components of tissues, second messengers, regulators of acid-base balance, participants in redox reactions, and for the maintenance of cellular electrical potential. For this reason, the required mineral elements are essential for the optimal function of a broad array of physiological systems and dysregulation of their metabolism can influence, or be a marker of, disease processes. While traditional reductionist approaches have revealed many aspects of mineral metabolism and function, significant gaps still exist. For example, we don't know all of the proteins that mediate mineral metabolism or whose function is altered by changes in mineral status. It is also clear that mineral-mineral interactions exist but we don't fully understand how they influence the absorption, excretion, storage, and utilization of chemically similar elements. This presentation will explain how understanding the breadth of biological processes influenced by minerals, identifying the genes that control mineral metabolism, and revealing the importance of interactions between inorganic elements can be accomplished by using a new approach that examines the metabolism of minerals in toto, or as an "ionome".

Key Words: ionome, minerals

458 Trace mineral interactions, known, unknown and not used. G. M. Hill* and J. E. Link, *Michigan State University, East Lansing*.

Potentially, trace mineral interactions can occur anywhere from the feed to the organ of storage to exogenous secretions etc. If and where they take place or if it makes a difference, also depends on your point of view. Excess dietary trace elements provided by feedstuffs are usually assumed to be non-existent and/or not available for the animal's use. However, their role in altering the functional outcome for another trace element may be as critical as meeting the animal's unknown requirement. Using the treatise of Hill and Matrone (1970) we can expect interactions based on the chemical and physical properties of the element. For example in aquatic birds, Miller (1996) found an hepatic Mg-Zn interaction due to the spherically symmetric valence orbitals with similar ion pair formation and both ions involved in catalytic hydrolysis of ATP. Yet, this interaction is seldom studied in livestock. Well known interactions such as Fe and Zn are affected by source, species of the element, dietary concentrations and which element is in excess. However, it is not possible to look at the biochemical markers of these two elements without also considering Cu. In areas where I is deficient, the supplementation of Fe and I is another consideration often forgotten due to the large amounts of Fe found in Ca sources. Since Zn is essential in the conversion of β-carotene to vitamin A, perhaps we need to broaden our interaction model to consider all 5 nutrients. One of the most relevant interactions today due to the varying concentration of S in DDGS is the Co/Mo/S interaction. While this may be of greater interest in ruminant animals, it should be noted that a Cu/Fe/Mn and S amino acid interaction also occurs in non-ruminants. Few interaction studies have utilized molecular techniques, so the tools of today are needed to understand practical application of interactions. Clearly, the potential for interactions can affect the functional outcome we desire in dietary formulation.

Key Words: trace elements, interactions

459 Macromineral interactions. J. S. Radcliffe*, *Purdue University, West Lafayette, IN*.

Our understanding of mineral availability, absorption, and utilization is minimal at best. Historically, minerals have been individually studied and requirements determined. However, research has reported numerous interactions between minerals. One of the most noted interactions is between Ca and P in which it has been reported that excess Ca can cause the formation of insoluble Ca-phosphate salts, resulting in decreased P availability. In human medicine this is exploited as a treatment for hyperphosphatemia, where Ca carbonate is used as a phosphate binding agent. However, it is unclear in animal nutrition what should be done with Ca when varying P levels are investigated or when phytase is included in the diet. In reality there are dozens of mineral interactions occurring at any time making it difficult to study any one mineral individually. Another way of stating this is that the concentrations and proportions of every mineral in the diet may impact the results of the mineral being studied. It is impossible to take account for all mineral interactions experimentally, but a better understanding of mineral interactions is needed for proper interpretation of results and requirement estimates.

Key Words: mineral, interactions

Physiology and Endocrinology: Estrous Synchronization of Beef Cattle

460 ASAS Early Career Achievement Award Presentation: Control of the estrous cycle for fixed-time artificial insemination (TAI) in beef cattle. G. C. Lamb*, *North Florida Research and Education Center, University of Florida, Marianna*.

Early estrus-synchronization protocols focused on regressing the corpus luteum with an injection of prostaglandin $F_{2\alpha}$ (PG) followed by detection of estrus. Later, estrus-synchronization systems involved the use of exogenous progestins, which (when administered) prevented estrus from occurring. Gonadotropin-releasing hormone was utilized to control follicular waves to synchronize ovulation and luteinization of large dominant follicles. Our research aimed to develop: 1) reliable protocols that relied solely on TAI; 2) protocols that required a maximum of 3 animal handlings; and 3) protocols that are successful in estrous cycling and noncycling females. In cows, insertion of a CIDR during the 7-d interval between the initial GnRH injection and PG enhanced pregnancy rates by 9 to 10%. In a multi-location study, a fixed-timed AI (TAI) protocol yielded similar pregnancy rates as a protocol involving detection of estrus plus a clean-up AI (54 vs. 58%, respectively, for cows and 53 vs. 57%, respectively, for heifers). A meta-analysis of data for a TAI protocol containing a progestin resulted in pregnancy rates of 54.7% and 50.3% for cycling for noncycling cows, respectively. A similar analysis for the same TAI protocol without a progestin resulted in pregnancy rates of 47.1% and 34.0% for cycling and noncycling cows, respectively. Recent work has indicated that human chorionic gonadotropin more effectively caused ovulation of follicles in cycling

and noncycling females than GnRH, but when administered in a TAI protocol 9 or 10 d before or at the time of TAI fertility was compromised. Development of TAI protocols that reduce the hassle factors associated with ovulation synchronization and AI provide cattle producers efficient and effective tools for improving genetics in their operations. Location variables, however, that may include differences in pasture and diet, breed composition, body condition, postpartum interval, climate, and geographic location, may affect the success of TAI protocols.
Acknowledgments to CR Dahlen, JE Larson, G Marquezini, and JS Stevenson.

Key Words: estrus synchronization, artificial insemination, beef cattle

461 Comparison of progestin-based protocols to synchronize estrus in prepubertal and estrous cycling beef heifers. N. R. Leitman, D. C. Busch, D. J. Wilson, D. A. Mallory, M. R. Ellersieck, M. F. Smith, and D. J. Patterson*, *University of Missouri*, *Columbia*.

The objective of the experiment was to compare differences between 2 controlled internal drug release (CIDR)-based estrus synchronization protocols on the basis of their ability to facilitate a highly synchronized estrus following treatment in beef heifers. The hypothesis tested was that addition of GnRH in a CIDR-based estrus synchronization protocol is required to facilitate an improvement in synchrony of estrus after $PGF_{2\alpha}$ (PG). Beef heifers (n = 285) were assigned to 1 of 2 treatments within reproductive tract scores (2 or 3 = prepubertal; 4 or 5 = estrous-cycling) by age and BW. Heifers assigned to CIDR Select received a CIDR insert (1.38 g progesterone) from d 0 to 14 followed by GnRH (100 μg, i.m.) on d 23 and PG (25 mg i.m.) on d 30. Heifers assigned to Show-Me-Synch received a CIDR insert from d 0 to 14 and PG on d 30. Heifers were fitted with HeatWatch estrus detection system transmitters at PG for continuous estrus detection during the synchronized period, and AI was performed 12 h after the onset of estrus. Estrous response did not differ (P = 0.43) between treatments (94% CIDR Select, 98% Show-Me-Synch). Mean interval to estrus after PG was 7 h shorter (54.4 ± 1.7 h, Show-Me-Synch; 61.5 ± 1.7 h, CIDR Select; P = 0.01) and variance for interval to estrus was reduced (P < 0.01) among Show-Me-Synch compared to CIDR Select treated heifers. Conception rate to AI tended (P = 0.09) to be greater for Show-Me-Synch (67%) compared to CIDR Select treated heifers (58%), and AI pregnancy rate was greater (P = 0.05) for Show-Me-Synch (66%) compared to CIDR Select treated heifers (55%). Final pregnancy rate at the end of the breeding season was similar between treatments (81%, CIDR Select; 81%, Show-Me-Synch; P = 0.94). These results suggest that administration of GnRH 9 d after CIDR removal in the CIDR Select protocol does not facilitate an improvement in synchrony of estrus or pregnancy rate resulting from AI in beef heifers.
This project was supported by National Research Initiative Competitive Grant no. 2005-55203-15750 from the USDA Cooperative State Research, Education, and Extension Service.

Key Words: beef heifer, progestin, estrus synchronization

462 Comparison of progestin-based protocols to synchronize estrus in beef heifers. D. A. Mallory*, D. J. Wilson, D. C. Busch, N. R. Leitman, M. R. Ellersieck, M. F. Smith, and D. J. Patterson, *University of Missouri*, *Columbia*.

This experiment compared estrous response and synchrony of estrus after administration of two progestin-based protocols to synchronize estrus in beef heifers. Heifers (n = 396) were assigned to 1 of 2 treatments by age, BW and reproductive tract score (RTS). Pretreatment RTS were assigned 14 or 15 d prior to treatment to determine estrous cyclicity status (2 or 3 = prepubertal; 4 or 5 = estrous-cycling). Heifers assigned to the melengestrol acetate (MGA) prostaglandin $F_{2\alpha}$ (PG) protocol (MGA-PG; n = 200) received 0.5 mg•animal^{-1}•d^{-1} MGA in a grain carrier from d 0 to 13. PG (25 mg, i.m.; Lutalyse) was administered 19 d after the end of MGA feeding (d 32). Heifers assigned to the Show-Me-Synch protocol (Show-Me-Synch; n = 196) were equipped with a CIDR insert (1.38 g progesterone) on d 2; CIDRs were removed on d 16; and PG was administered on d 32. Heifers were fitted with HeatWatch (DDx Inc., Denver, CO) transmitters for continuous estrous detection during the synchronized period (0 to 144 h following PG), and AI was performed 12 h after the onset of estrus. Estrous response after PG was greater (P = 0.04) among Show-Me-Synch (92%) compared to MGA-PG treated heifers (85%). Mean interval from PG to estrus did not differ (P = 0.73) between MGA-PG (57.4 ± 2.5 h) and Show-Me-Synch (56.2 ± 2.5 h) treated heifers. Mean interval from PG to estrus differed (P = 0.04) between estrous-cycling (62.4 ± 2.4 h) and prepubertal heifers (52.4 ± 4.4 h) assigned to the MGA-PG protocol, but was similar (P = 0.75) between estrous-cycling and prepubertal Show-Me-Synch treated heifers (55.4 ± 2.4 h and 57.0 ± 4.4 h, respectively). Variance associated with interval from PG to estrus was reduced (P < 0.01) among Show-Me-Synch compared to MGA-PG treated heifers, and was not influenced by estrous cyclicity status (P > 0.50). In summary, the Show-Me-Synch protocol resulted in a greater (P = 0.04) and more synchronous (P < 0.01) estrous response compared to the MGA-PG protocol.
This project was supported by National Research Initiative Competitive Grant no. 2005-55203-15750 from the USDA Cooperative State Research, Education, and Extension Service.

Key Words: beef heifer, estrus synchronization, progestin

463 Comparison of progestin-based protocols to synchronize estrus and facilitate AI in postpartum beef cows. D. J. Wilson*[1], D. A. Mallory[1], D. C. Busch[1], N. R. Leitman[1], J. K. Haden[2], D. J. Schafer[2], M. R. Ellersieck[1], M. F. Smith[1], and D. J. Patterson[1], [1]*University of Missouri*, *Columbia*, [2]*MFA, Inc.*, *Columbia, MO*.

Estrus synchronization and AI are valuable reproductive technologies for beef producers. Experiment 1 was designed to compare the 7-d and 5-d Select Synch + controlled internal drug release (CIDR) protocols on the basis of timing and synchrony of estrus following treatment. Cows assigned to the 7-d protocol (n = 59) received GnRH (100 μg i.m. Cystorelin) and CIDR inserts (1.38 g P4) on day 0 and prostaglandin $F_{2\alpha}$ (PG; 25 mg i.m. Lutalyse) and CIDR removal on day 7. Cows assigned to the 5-d protocol (n = 58) received GnRH and CIDR inserts on day 0, PG and CIDR removal on day 5, and a second injection of PG 12 h after CIDR removal and the first PG injection. Estrus detection and AI were performed for cows assigned to each protocol during the 144 h synchronized period. There was no difference in estrous response (P = 0.85), interval to estrus (P = 0.09), or variance for interval to estrus (P = 0.75) between treatments, nor were there differences in synchronized conception or pregnancy rates resulting from AI (P = 0.85, P =.91). Experiment 2 was designed to compare pregnancy rates resulting from fixed-time AI (FTAI) following administration of the 7-d (n = 209) and 5-d (n = 210) CO-Synch + CIDR protocols. Both treatments were administered the same as in Experiment 1, however cows assigned to the 7-d protocol were inseminated 66 h after PG and CIDR removal and cows assigned to the 5-d protocol were inseminated 72 h after the first PG injection. Cows assigned to both protocols were administered GnRH (100 μg i.m.) at AI. There was no effect of

treatment (P = 0.85), technician (P = 0.20), or sire (P = 0.25) on pregnancy rates resulting from FTAI. Given these observations, the 5-d protocol provides an effective alternative to the 7-d protocol for use in facilitating FTAI, however beef producers must carefully consider the increased labor and treatment costs associated with the 5 d protocol. *This project was supported by National Research Initiative Competitive Grant no. 2005-55203-15750 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: progestin, postpartum beef cow, estrus synchronization

464 Comparison of follicular dynamics and hormone concentrations between the 7 d and 5 d CO-Synch + CIDR program in two-year old beef cows. G. A. Bridges*[1], M. L. Mussard[2], L. A. Helser[3], and M. L. Day[2], [1]*Purdue University*, *West Lafayette, IN*, [2]*The Ohio State University*, *Columbus*, [3]*Select Sires Inc.*, *Plain City, OH*.

The objectives of the present study were to compare follicular dynamics, preovulatory estradiol (E2) concentrations, and progesterone (P4) concentrations between the 7 d (7CO, n = 15) and 5 d (5CO, n = 13) CO-Synch + CIDR program in 2-yr old suckled beef cows. On d -7 (7CO) or d -5 (5CO) GnRH (100 μg, OvaCyst®) was administered (GnRH-1) and a CIDR was inserted. On d 0 at h 0 CIDR were removed and cows received $PGF_{2\infty}$ (25 mg/dose; Lutalyse®) at h 0 and 12. Animals were administered GnRH (100 μg, GnRH-2) at either h 60 (7CO) or h 72 (5CO). Follicular growth and ovulation to both GnRH-1 and GnRH-2 were evaluated via ultrasonography. Concentrations of E2 were determined in blood samples taken at h 0, 36, 60 and 72 (only 5CO treatment). Blood samples were collected on d 5, 8, and 14 for P4 concentrations. Ovulation rate to GnRH-1 did not differ between the 7CO (11/15) and 5CO (8/13) treatments and for all other variables, treatment, ovulation to GnRH-1, and the interaction were included in the statistical model. Diameter (mm) of the ovulatory follicle did not differ between treatments (13.4 ± 0.3) but was greater (P < 0.05) in cows that responded to GnRH-1 (13.8 ± 0.3) than those that did not (12.6 ± 0.6). Maximum E2 (pg/mL) tended (P = 0.06) to be greater in the 5CO (7.3 ± 0.5) than 7CO (6.1 ± 0.7) treatment and tended to be greater (P = 0.08) in cows that responded to GnRH-1 (7.1 ± 0.5) than those that did not (5.6 ± 0.9). Three cows in the 7CO treatment failed to develop a CL following GnRH-2. There was a treatment by response to GnRH-1 interaction (P < 0.05) for P4 concentrations. In cows that responded to GnRH-1, P4 did not differ between treatments. In cows that failed to respond to GnRH-1, P4 was greater (P < 0.05) in the 5CO than 7CO treatment. In conclusion, the 5CO treatment resulted in ovulation of follicles of similar diameter that tended to produce greater peak E2 concentrations, and resulted in greater concentrations of P4 during the subsequent luteal phase in animals that did not respond to GnRH-1.

Key Words: estrous synchronization, follicle, estradiol

465 Fertility and luteal regression with 5-d CIDR synchronization programs in postpartum beef cows using differing luteolytic treatments. L. A. Souto*, M. Maquivar, M. L. Mussard, G. A. Bridges, D. G. Grum, and M. L. Day, *The Ohio State University*, *Columbus*.

Timed AI pregnancy rates in postpartum cows is increased by 11% with the 5 d CO-Synch + CIDR program when compared to the traditional 7 d program. This program was developed using two doses of PGF2α given 12 h apart (25 mg/dose; Lutalyse®; 2XPGF). Reproductive performance and luteal regression with the 5 d program when using a single dose of cloprostenol sodium (500 μg dose; estroPLAN®; 1XCLP) was evaluated in 3 studies. In all experiments, cows received 100 μg GnRH (OvaCyst®) and a CIDR® on d 0. The CIDR was withdrawn on d 5, and cows received either the 2XPGF or 1XCLP treatment. In Expt 1, cows (n=195) received no further treatment and estrous detection with AI was performed for 7 d. In Expt 2, cows (n=254) received a second GnRH (100 μg) and timed AI either 72 (2XPGF-72) or 84 (1XCLP-84) h after CIDR removal. The interval to timed AI with 1XCLP was postponed 12 h relative to 2XPGF based on previous results. In Expt 3, (n = 48) blood for analysis of progesterone concentrations was taken at h 0, 4, 8, 12, 16, 24, 48, 72 and 96 after the first dose in the 2XPGF or the 1XCLP treatment and estrous detection was performed. In Expt 1, estrus was detected in more (P < 0.05) cows from the 2XPGF (94.0%) than the 1XCLP (77.9%) treatment but the interval to estrus (66.4 ± 1.2 h) did not differ between treatments. In Expt 2, timed AI pregnancy rate tended to be greater in the 2XPGF-72 than the 1XCLP-84 (68.8% vs 57.9%, respectively; P = 0.08). In Expt 3, progesterone concentrations did not differ between treatments from h 0 to 12, but were greater in the 1XCLP than 2XPGF from h 24 to 96 (trt x h, P<0.05). When the 1XCLP treatment was used, fewer cows were detected in estrus with the 5 d Select Synch + CIDR program, timed AI pregnancy rate tended to be lower, even when timed AI was delayed by 12 h in the 5 d CO-Synch + CIDR program, and the incidence of a delay, or failure of luteal regression was increased. In conclusion, two doses of PGF are necessary to maximize timed AI pregnancy rate with the 5 d CO-Synch + CIDR program.

Key Words: cattle, PGF2α, progesterone

466 Efficacy of the 5 day CO-Synch estrous synchronization protocol with or without the inclusion of a CIDR in beef cows. K. C. Culp*[1], R. P. Lemenager[1], M.C. Claeys[1], P. J. Gunn[1], M. Van Emon[1], R. P. Arias[1], S. L. Lake[2], and G. A. Bridges[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*University of Wyoming*, *Laramie*.

The objective of this experiment was to compare timed-AI (TAI) pregnancy rates in suckled beef cows synchronized with the 5 d CO-Synch protocol with (5CIDR) or without (5NoCIDR) the inclusion of an EAZI-BREED™ CIDR® insert (CIDR). Cows managed at Feldun Purdue Agricultural Center (FPAC; n = 130), Animal Sciences Research and Education Center (ASREC; n = 169) and Voyles Farms (n = 89) were assigned to either the 5CIDR (n = 195) or 5NoCIDR (n = 193) program by breed, age, and calving date. On d 0 all cows received GnRH (100 μg; Cystorelin®) and cows in the 5CIDR treatment received a CIDR. On d 5 CIDR were removed (5CIDR) and all cows received $PGF_{2\alpha}$ (25 mg/dose; Lutalyse®) with another dose of $PGF_{2\alpha}$ given approximately 10 h later. Cows were TAI on d 8, 72 h after CIDR removal, concurrent with GnRH (100 μg). At ASREC and FPAC, but not Voyles Farm, blood samples were collected on d -7 and 0 to determine estrous cyclicity (progesterone ≥ 1.0 ng/mL). Timed-AI and breeding season pregnancy rates were determined via ultrasonography approximately 35 d after TAI and 35 d after the end of the breeding season, respectively. There were no significant treatment by location interactions for any of the variables measured; therefore data were pooled across locations. There was a treatment by age classification (2-yr old versus ≥3 yr) interaction (P < 0.05) for TAI pregnancy rates. In mature cows (≥3 yr of age), TAI pregnancy rates were similar between the 5CIDR (73.6%, n = 159) and 5NoCIDR (74.5%, n = 157) treatments. In 2-yr old cows (n = 36/treatment), TAI pregnancy rates were greater (P < 0.05) in the 5CIDR (77.8%) than the 5NoCIDR (58.3%) treatment. Estrous cyclicity status at treatment initiation did not influence TAI pregnancy rates. Overall breeding season pregnancy rates were similar between treatments (94.6%). In conclu-

sion, the 5 d CO-Synch program without the inclusion of a CIDR was effective in mature cows, but TAI pregnancy rates were decreased in 2-yr old cows that did not receive a CIDR.

Key Words: CO-Synch, timed-AI, beef cows

467 Presynchronization with hCG 7 d prior to estrous synchronization and replacement of GnRH with hCG at fixed-time AI (TAI) in suckled beef cows. G. Marquezini*[1], C. R. Dahlen[2], S. L. Bird[3], B. J. Funnell[3], and G. C. Lamb[1], [1]*North Florida Research and Education Center, University of Florida, Marianna*, [2]*Northwest Research and Outreach Center, University of Minnesota, Crookston*, [3]*North Central Research and Outreach Center, University of Minnesota, Grand Rapids*.

We evaluated whether hCG administered 7 d prior to initiation of estrous synchronization and replacement of GnRH with hCG at TAI would alter pregnancy rates to TAI, concentrations of progesterone, and follicle diameter. Suckled beef cows were stratified by days postpartum and parity and randomly assigned in a 2 × 2 factorial arrangement of treatments: 1) cows received 100 μg GnRH and a CIDR insert (d -7), followed in 7 d by 25 mg $PGF_{2\alpha}$ and CIDR removal (d 0), followed in 67 h by GnRH and TAI (d 3; CG; n = 29); 2) CG but the second injection of GnRH was replaced by 1,000 IU of hCG (CH; n = 28); 3) CG, plus cows received 1,000 IU of hCG administered on d -14 (HG; n = 29); and, 4) HG, but the second injection of GnRH was replaced by 1,000 IU of hCG (HH; n = 29). Use of transrectal ultrasonography determined pregnancy status on d 30 and to evaluate ovaries of cows on d -14, -7, 0, and 3. Blood samples were collected on d -24, -14, -7, 0, 3, 10, 17, and 30 to determine concentrations of progesterone. Pregnancy rate of cows presynchronizated with hCG did not differ from controls; however, treatment of cows with GnRH (54.6%) at TAI tended ($P = 0.07$) to be greater than those receiving hCG (37.6%). On d -7 and 0, concentrations of progesterone differed ($P < 0.05$) between cows receiving hCG on d -14 (2.89 ± 0.4 and 3.14 ± 0.3 ng/mL for d -7 and 0, respectively) and controls (1.91 ± 0.4 and 2.51 ± 0.3 ng/mL for d -7 and 0, respectively). Concentrations of progesterone were similar for cows receiving either GnRH or hCG at TAI on d 10, 17, and 30. Diameter of dominant follicles on d 0 and 3 were smaller ($P < 0.05$) for cows receiving hCG (12.1 ± 0.5 and 13.0 ± 0.7 mm for d 0 and 3, respectively) than controls (14.1 ± 0.5 and 14.5 ± 0.7 mm for d 0 and 3, respectively). We concluded that presynchronization with hCG increased concentrations of progesterone and decreased follicle size prior to TAI, but failed to alter pregnancy rates. Replacement of GnRH with hCG at TAI appeared to reduce pregnancy rates, but failed to increase concentrations of progesterone after TAI.

Key Words: human chorionic gonadotropin, beef cows, progesterone

468 Administration of human chorionic gonadotropin (hCG) 7 days after insemination of suckled beef cows. C. R. Dahlen*[1], S. L. Bird[2], C. A. Martel[3], K. C. Olson[3], J. S. Stevenson[3], and G. C. Lamb[4], [1]*Northwest Research and Outreach Center, University of Minnesota, Crookston*, [2]*North Central Research and Outreach Center, Grand Rapids, MN*, [3]*Department of Animal Sciences and Industry, Kansas State University, Manhattan*, [4]*North Florida Research and Education Center, University of Florida, Marianna*.

We determined the effects of administering hCG 7 d after a fixed-time insemination (TAI) on ovarian response, concentrations of progesterone, and pregnancy rates in postpartum suckled beef cows. Cows at 6 locations (n = 512) received 100 μg GnRH and a CIDR insert, followed in 7 d by 25 mg $PGF_{2\alpha}$ and CIDR removal, followed in 64 h by GnRH and AI, then stratified by days postpartum and parity and assigned randomly to 2 treatments administered 7 d after TAI: 1) 1 mL saline (n = 252); or 2) 1,000 IU hCG (n = 254). Blood samples were collected on d -21, -10 and +33 relative to TAI (d 0) at all locations, on d 7 and d 68 at 5 locations and on d 14 at one location to determine concentrations of progesterone. Use of transrectal ultrasonography determined pregnancy status on d 33 and 68 and to evaluate ovaries of cows at one location (n = 106) on d 7 and 14 and at d 33 in another location (n = 32). Pregnant cows had greater ($P < 0.05$) concentrations of progesterone at the time of treatment (d 7) compared with nonpregnant cows (3.7 ± 0.1 vs 2.6 ± 0.2 ng/mL). On d 14, hCG-treated cows had a greater ($P < 0.05$) volume of luteal tissue (12.1 ± 0.5 vs 7.3 ± 0.5 cm^3) and greater concentrations of progesterone (6.8 ± 0.4 vs 5.4 ± 0.5 ng/mL) compared with saline-treated cows. Percentage of cows having multiple corpora lutea on d 14 was greater ($P < 0.01$) for hCG-treated (90.6%) than saline-treated cows (0.0%) and persisted (75.4 vs. 0%) when diagnosed pregnant at d 33. Pregnancy rates of hCG-treated cows (56.3%) tended ($P = 0.09$) to differ from saline-treated cows (50.0%). Concentrations of progesterone in pregnant hCG-treated cows were greater ($P < 0.05$; 7.7 ± 0.3 vs 5.8 ± 0.3 ng/mL) on d 33 than for saline-treated cows, but similar on d 68 (7.2 ± 0.3 vs 6.7 ± 0.4 ng/mL). We conclude that treatment with hCG increased volume of luteal tissue on d 14 and concentrations of progesterone on d 14 and 33 after TAI. Treatment with hCG tended to increase pregnancy rates at 5 of 6 locations from 1.1 to 27 percentage points compared with saline.

Key Words: human chorionic gonadotropin, estrous synchronization, beef cows

469 Effect of used CIDR and FSH on estrus expression and pregnancy rate during low breeding season in Nili-Ravi buffaloes. N. Ahmad*[1], Z. Naseer[1], E. Ahmad[1], M. Mushtaq[2], and J. Singh[3], [1]*Department of Theriogenology, University of Veterinary & Animal Sciences, Lahore, Pakistan*, [2]*Buffalo Research Institute, Pattoki, Pakistan*, [3]*Department of Veterinary Biomedical Sciences, WCVM, Saskatoon, Canada*.

The objective of the present study was to determine the effect of once used CIDR and FSH on estrus expression and pregnancy rate (PR) during low breeding season (March-August) in Nili-Ravi buffaloes. Two experiments were conducted during June-August, 2008. In experiment 1, buffaloes received either a used CIDR (UCIDR, n=26) or a new CIDR (NCIDR, n=22) for 7 d and PGF2α on d 6. Estrus detection was done twice daily. Buffaloes were inseminated, 12 and 24 hr after the onset of estrus. Pregnancy diagnosis was performed 30 d post insemination using ultrasonography. Estrus expression was similar (P>0.05) between UCIDR (84.0%) and NCIDR (95.0%) buffaloes. The mean interval to estrus after removal of CIDRs in UCIDR was 34±5.2 h compared to 38±12.2 h in NCIDR (P>0.05). The PR did not differ (P>0.05) due to treatment (9/26 in UCIDR vs 8/22 in NCIDR). In experiment 2, buffaloes at unknown stages of estrous cycle received CIDRs on d 0 and PGF2α on d 6. Animals were either treated with two injections of FSH (5mg i/m at 12 hr interval; n=10) starting at CIDR removal on d 7 or remain untreated (Control, n=9). Estrus detection, insemination and pregnancy diagnosis was similar as in experiment 1. FSH treatment did not affect the proportion of buffaloes expressing estrus, mean interval from CIDR removal to estrus and ovulation, size of ovulatory follicle or PR (P>0.05; overall estrus expression rate

(16/19), interval to estrus (52.8±2.77 h) and ovulation (78.51±3.09 h), ovulatory follicle size (10.55±0.55 mm), PR (5/19). In conclusion, a) compared to NCIDR devices, previously UCIDR devices are equally effective to induce estrus and ovulation synchronization with comparable PR in buffaloes during low breeding season and b) low dose FSH treatment at CIDR removal did not improve estrus expression or PR. *Acknowledgements: ALP, PARC.*

Key Words: Used CIDR, Pregnancy rates, FSH

Ruminant Nutrition: Feed Additives

470 Distillers grains-based diets with monensin supplemented with plant extracts: Effects on steer performance, carcass characteristics, and ruminal VFA concentrations. A. L. Shreck*[1], N. A. Pyatt[2], L. L. Berger[1], J. M. Dahlqust[1], T. G. Nash[1], and D. Bravo[3], [1]*University of Illinois, Urbana*, [2]*ADM Research, Decatur, IL*, [3]*Pancosma, Geneva, Switzerland*.

Performance data from early weaned (approximately 90 d of age) Simmental x Angus cross steers (n=140) were used to evaluate the effects of plant extracts in a distiller's grains-based feedlot diet with monensin. Steers were early weaned and backgrounded on a high-energy diet until allotment to a finishing trial. The basal diet consisted of 40% modified wet distiller's grains with solubles, 35% dry rolled corn, 15% corn silage, and 10% supplement. Treatments were: 1) monensin control (CON), 2) monensin + 133 mg•steer^{-1}•d^{-1} capsicum oleoresin (CAP; XT 6933 Pancosma), and 3) monensin + a blend of plant extracts (XT;133 mg•steer^{-1}•d^{-1} eugenol+ cinnamaldehyde, and 67 mg•steer^{-1}•d^{-1}capsicum, XT 7065, Pancosma). Steers were individually fed using the GrowSafe automated feeding system (GrowSafe Systems Ltd, Airdrie, Alberta, Canada). Steers (initial BW 304±44 kg) were fed for 138 d and harvested at one time. There were no differences (P>0.05) in HCW, LM area, G:F, or DMI. Steers consuming CAP tended (P=0.06) to have higher ADG than CON or XT steers (1.93, 1.88 and 1.85 kg/d, respectively). CON or XT steers exhibited higher marbling scores (500=small) (P=0.01) than CAP steers (577, 601, and 545, respectively). Steers fed XT or CAP had lower yield grades (P=0.01) than CON steers (3.60, 3.58, and 3.90, respectively). Steers fed XT and CAP also had less 12th rib fat thickness (P<0.01) than CON steers (14.9, 16.5, 17.5 mm, respectively). VFA concentrations or acetate:propionate ratio (C2:C3) did not differ even though steers consuming CAP had numerically higher C2:C3 ratio (3.2) than CON (2.3) or RMB (2.6). Five animals per treatment limited our ability to detect differences. Including capsicum or a blend of eugenol, cinnamaldehyde, and capsicum in distiller's grains-based diets in conjunction with monensin did not impact finishing performance but may result in leaner carcasses with lower yield grades.

Key Words: beef, plant extracts, performance

471 Meta analysis of growing ruminants fed a mixture of eugenol, cinnamaldehyde and capsicum oleoresin. D. Bravo*[1], N. A. Pyatt[2], P. H. Doane[2], and M. J. Cecava[2], [1]*Pancosma, Geneva, Switzerland*, [2]*ADM Research, Decatur, IL*.

The objective of this study was to use meta analysis to evaluate whether a plant extract mixture consistently affected the productive performance of growing ruminants. Research was conducted by Pancosma and ADM on XTract 7065 (XT) containing 17% eugenol, 11% cinnamaldehyde, and 7% capsaicin oleoresin. Systematic search identified 13 studies organized in 18 trials (884 growing ruminants) with trials on growing sheep (n = 3) and beef cattle (n = 15). Effects of XT were investigated using mixed model analysis and effect size calculation (ES). Treatment means, ES values and 95% confidence intervals (CI) were determined for DMI, ADG and feed efficiency (G:F). Homogeneity was addressed using the I^2 statistic, and publication bias examined with the test of Begg. XT tended to improve ADG for beef (+2.9%, ES = 0.131, CI =-0.004 to 0.266, P = 0.06) and lambs (+16.8%, ES = 0.489, CI = -0.066 to 1.044, P = 0.08). XT did not alter DMI for lambs (P = 0.24) or beef cattle (P = 0.81). Thus, there was a trend for improved feed efficiency with XT in beef (+2.6%, ES = 0.455, CI = -0.072 to 0.982, P = 0.09) and lambs (+11.9%, ES = 0.110, CI = -0.044 to 0.264, P = 0.16). Studies identified did not exhibit publication bias for ADG, DMI or G:F (P > 0.10). DMI for cattle was heterogeneous (I^2 = 40.2%, P = 0.10), indicating response to XT was dependent on an environmental factor. Among moderating variables, dietary ionophore explained the heterogeneity of DMI (P = 0.19). Ionophore did not alter ADG response to XT (P = 0.83), but DMI was lower with addition of XT when ionophore was present, with ES for DMI of -0.061 and 0.213 in presence or absence of ionophore respectively. The interaction of ionophore and XT was not significant for G:F although the ES increased with ionophore. Correlation analysis of diet composition among trials suggested improved efficacy of XT in high-energy (NEg, starch, or concentrate) and/or low NDF diets. This analysis showed consistent improvements in growth and efficiency for growing ruminants fed a blend of eugenol, cinnamaldehyde and capsaicin.

Key Words: beef cattle, plant extracts, meta analysis

472 Synergy of cinnamaldehyde, eugenol and garlic for reduction of methane production in vitro. S. Cavini[1], D. Bravo*[2], S. Calsamiglia[1], M. Rodriguez[1], A. Ferret[1], and G. Schroeder[3], [1]*Universitat Autonoma de Barcelona, Barcelona, Spain*, [2]*Pancosma, Geneva, Switzerland*, [3]*Cargill, Elk River, MN*.

The effect of combination of eugenol (E), cinnamaldehyde (C) and a garlic botanical standardized for propyl propyl thiosulfonate (G) on in vitro microbial fermentation was determined using a simplex centroid experimental design of degree 3 with 3 components. Treatments were mixtures between the 3 extracts totalling 250 mg/L and composed of (doses in mg/L) 1) 125G + 125C + 0E; 2) 0G + 250C + 0E; 3) 250G + 0C + 0E; 4) 41.7G + 41.7C + 166.7E; 5) 41.7G + 166.7C + 41.7E; 6) 0G + 0C + 250E; 7) 0G + 125C + 125E; 8) 166.7G + 41.7C + 41.7E; 9) 125G + 0C + 125E; and 10) 83.3G + 83.3C + 83.3E. Two controls were also used: negative control (CTR) and 500 mg/L of monensin (MON). Each treatment was tested in duplicate and in two periods. Fifty millilitres of a 1:1 ruminal fluid-to-buffer solution were introduced into polypropylene tubes supplied with 0.5 g of DM of a 60:40 forage:concentrate diet and incubated for 24h at 39C. Samples were collected for VFA and methane concentrations (CH_4). Results were analysed with SAS using a special cubic model. Total VFA were unaffected by the 3 extract combinations. The molar proportion of acetate was decreased by C×G (P = 0.015) and by C×G×E (P = 0.023) whereas the molar proportion of butyrate was increased by C×G (P = 0.004) and by E×C×G (P = 0.024). The molar proportion of valerate was decreased by E×C (P = 0.042), by E×G (P = 0.116) and increased by C×G (P = 0.081) and E×C×G (P = 0.021). Concentration of CH_4 for treatments 10, 5 and 4 were lower than CTR (17.96, 18.46, 18.49 and 22.2, respectively; P < 0.001) and higher than MON (5.81, P < 0.001). Concentration of CH_4 was affected by the

combination E×C (P = 0.033) and decreased by E×C×G (P = 0.012). The regression predicting CH_4 concentration with the 3 compounds is: CH_4 = 0.078 E + 0.077 C + 0.096 G + 0.000356 E×C -0.000012 E×C×G (P = 0.012, RSD = 1.61, R^2 = 0.79). Results demonstrate that there is a synergy between the 3 extracts for the reduction of methane in vitro.

Key Words: essential oils, rumen fermentation, methane

473 Essential oils may reduce the risk of ketosis in dairy goats carrying twins. S. Calsamiglia[1], S. Cavini[1], A. Bouattour[1], A. Ferret[1], and D. Bravo*[2], [1]*Universitat Autonoma de Barcelona, Bellaterra, Spain*, [2]*Pancosma, Switzerland*.

Dairy goats carrying twins are highly susceptible to gestational ketosis as the result of an unbalance between energy supply and requirements. The hypothesis was that by increasing intake and glucose precursors (propionate), the indicators of ketosis will be reduced. Pregnant Murciano-Granadina goats (n = 24) carrying twins were used to study the effects of feeding capsicum (to stimulate intake) and eugenol plus cinnemaldehyde (to promote propionate production in the rumen) on intake, milk production and composition, and blood profile. Goats were controlled from 2 wk prior to 6 wk after kidding. Goats received the same 60:40 forage:concentrate diet during the pre and postpartum periods. Treatments were a control (CTR; no additive) and essential oil supplementation (XT; 75 mg of eugenol, 45 mg of cinnamaldehyde and 27 mg of capsicum). Intake and milk production were recorded daily, milk composition determined weekly, and blood samples taken days -15, -7, -3, -2, -1, 0, 1, 2, 3, 5, 7 and 15 around kidding to measure insulin, glucose, non-esterified fatty acids (NEFA), triglycerides and beta-hydroxy-butyrate (BOHB). Results were analyzed using the PROC MIXED procedure of SAS and differences declared at P < 0.05. Intake tended (P < 0.07) to increase in the XT treatment with no effects on milk production (1.93 L/d). However, milk fat (6.48 vs 5.84%) and protein (3.86 vs 3.69%) were higher in XT compared with CTR. Prepartum, plasma glucose concentration tended (P < 0.09) to be higher (58.2 vs 54.5 mg/dL), insulin was lower (0.45 vs 0.62 Î¼g/L), and NEFA tended (P < 0.09) to be lower (0.22 vs 0.33 mmol/L) in the XT treatment compared with CTR, with no treatment effects on blood BOHB (0.30 mmol/L) and triglycerides (0.31 mg/mL). In the postpartum, only BOHB was affected by treatment, being lower in XT compared with CTR (0.52 vs 0.63 mmol/L). Results suggest that the XT reduce body fat mobilization.

Key Words: goats, ketosis, essential oils

474 Effects of feeding an essential oil complex on whole tract nutrient digestion and productive performance of lactating dairy cows. M. B. Santos*[1,2], P. H. Robinson[1], and P. Williams[3], [1]*University of California, Davis*, [2]*CECAV-UTAD, Vila Real, Portugal*, [3]*Advantec Associates, Davis, CA*.

Essential oils (EO) have been shown to positively impact *in vitro* ruminal fermentation, but there are few *in vivo* studies that have examined animal responses. Our objective was to evaluate the efficacy of an EO complex (Agolin Ruminant from AGOLIN SA, Bière, Switzerland), which contained eugenol, geranylacetate and coriander oil as major components, on production of lactating dairy cows (DC), measures of efficiency of use of dietary N as well as whole tract digestion of nutrients. Two pens of approximately 310 early lactation multiparous cows were used in a 2x2 factorial experiment with treatment reversed 28 day periods. Cows were fed a totally mixed ration (TMR) twice daily for *ad libitum* intake based on wheat silage (13.6% TMR (DM)), maize grain (12.9%), alfalfa hay and fresh chop 5.5%) and corn silage (6.3%). The basal TMR was the same for both treatment groups, and differed only in that the EO complex was added to the TMR of the EO assigned pen. Feed premixes, TMR and ingredients were sampled on days 21 and 26 of each experimental period. Cows were milked 3 times daily with milk yield and components measured at the end of each period. Urine samples were collected from 24 cows/pen that voluntarily urinated at the end of each period, with fecal collections from these same cows 24 h later. Actual refusals corrected EO feeding level was 0.85 g/cow/day. The TMR contained 54.7% DM, 16.4% CP, 6.2% EE, 32.2% NDF and 12.0% starch. DM intake was numerically (i.e., P=0.13) lower with EO feeding (i.e., 26.0 vs. 27.4 kg/d) but milk yield was not impacted (mean 49.2 kg/d). However milk fat (MF) production (1.63 vs.1.66 kg/d; P=0.02) and MF proportion (33.2 vs.33.9 g/kg; P<0.0.01) were higher for cows fed EO. There was also a numerically 6.9% higher (i.e., 0.698 vs. 0.746; P=0.17) efficiency of use of dietary net energy for milk energy output. There were no differences in urine parameters or whole tract digestion of OM, CP and NDF. Feeding this EO complex positively impacted performance of high producing DC, primarily by enhancing MF synthesis, suggesting that it may have enhanced acetate and/or propionate production

Key Words: essential oils, dairy

475 Effects of an encapsulated combination of cinnamaldehyde and garlic oil on early and late lactating Red Simmental dairy cows. C. Kamel*[1], H. M. R. Greathead[1], and P. W. Cardozo[2], [1]*School of Biology, University of Leeds, Leeds, United Kingdom*, [2]*Carotenoid Technologies, IQF Group, Tarragona, Spain*.

Two feeding trials were carried out in lactating Red Simmental dairy cows to determine the effects of an encapsulated combination (NE 300) of cinnamaldehyde (129 mg/day as fed) and garlic oil (standardized in diallyl disulfide, 15 mg/day as fed). It was hypothesized that NE 300 effects would depend on microbial populations, and thus remain unaffected by the lactation status of the animal. In Trial 1, 24 Red Simmental (Red Holstein x Simmental) diary cows were fed a forage-based diet over a 12 week period in late lactation (DIM > 200 days) with 2 kg/day of a high protein (40g/g CP) in a ration based on grass silage and hay ad libitum. After a 1-week covariant pre-trial period, cows were assigned randomly to control (CON) or treatment (NE 300) diet. Concentrate intake and milk production were recorded at morning and evening feedings, and milk composition taken as well for analysis of milk protein, fat and lactose percentage, milk urea nitrogen (MUN) and somatic cell counts (SCC). Highly significant (P < 0.001) differences for MUN were recorded over the study for NE 300 versus CON. NE 300 also showed significant (P > 0.05) decreases in SCC versus CON over the trial period. All other parameters were unaffected, except in the final month when milk production was higher (P < 0.05) for NE 300 versus CON. In Trial 2, 67 Red Simmental (Red Holstein x Simmental) dairy cows including some of the same animals carried over from Trial 1 were fed the same forage-based diet over an 8 week period in early lactation (DIM < 100 days) using the same trial as in Trial 1. Feeding of NE 300 showed a tendency to decrease MUN (P < 0.07) versus CON over the entire trial period, decreasing by 13% in the final month (P > 0.05). In addition, protein percentage (P < 0.08) tended to increase over the course of the study. All other parameters were unaffected. The results of this study show that feeding of NE 300 in early and late lactation diets consistently reduces MUN levels in the milk, and in early lactation may tend to have an effect on increasing milk protein level.

Key Words: cinnamaldehyde, garlic oil, dairy cows

476 Yeast culture supplementation interacts with voluntary feed intake to affect ruminal starch digestion. Y. Ying* and M. S. Allen, *Michigan State University*, *East Lansing*.

This experiment was conducted to evaluate responses of ruminal digestion of starch to yeast culture supplementation and if responses are influenced by voluntary feed intake. Fifteen ruminally and duodenally cannulated Holstein cows with a wide range in preliminary voluntary DMI (pVDMI; 20.1 to 31.0 kg/d) measured during a 14-d preliminary period were utilized in a crossover design experiment. Treatments were Diamond V XP™ Yeast Culture (YC) and control (a mix of dry ground corn and soybean meal), top-dressed at the rate of 56 g/d per head. The base diet contained 28% NDF, 30% starch, and 16.5% CP and included corn silage, alfalfa silage, high moisture corn, protein supplement, and a mineral and vitamin supplement. Treatment periods were 28 d with the final 8 d used for sample and data collection. Voluntary DMI was determined during the last 4 d of the preliminary period. Ruminal digestion kinetics were determined using the pool-and-flux method and visual observations of feeding behavior were recorded every 5 min for 24 h per period. Main effects of YC treatment and their interaction with pVDMI were tested by ANOVA. An interaction ($P < 0.01$) was detected between YC treatment and pVDMI for ruminal digestion rate of starch (mean = 37.0%/h); YC increased rate of starch digestion compared to control for cows with pVDMI below 26 kg/d and decreased it for cows with higher pVDMI. This resulted in an interaction between treatment and pVDMI for turnover rate of starch in the rumen ($P = 0.03$) and true and apparent ruminal starch digestibility (tendency, $P < 0.13$) because passage rate of starch from the rumen was not affected by treatment (mean = 16.5%/h). Ruminal pH (mean = 6.0), DMI, milk yield and component percentages were not affected by treatment or its interaction with pVDMI. Yeast culture supplementation reduced the rate of ruminal starch digestion for cows with higher feed intake which could help stabilize the rumen environment when large amounts of starch are consumed to support higher milk production.

Key Words: digestion kinetics, site of digestion, rate of digestion

477 Effect of yeast culture on ruminal fermentation and nutrient utilization in dairy cows. A. N. Hristov*[1], G. Varga[1], T. Cassidy[1], M. Long[1], K. Heyler[1], C. J. Hovde[2], and I. Yoon[3], [1]*Pennsylvania State University*, *University Park*, [2]*University of Idaho*, *Moscow*, [3]*Diamond V Mills*, *Cedar Rapids, IA*.

The goal of this experiment was to investigate the effect of yeast culture (*Saccharomyces cerevisiae*) on rumen fermentation and nutrient utilization in high-producing dairy cows. Eight ruminally cannulated Holstein cows were allocated to two dietary treatments in a crossover design. Treatments were Control (no yeast culture) and YC (yeast culture: XP™, Diamond V Mills, Inc. fed at 56 g/head/d). The basal diet had 16% CP, 32% NDF, and estimated 1.71 Mcal NE_L/kg. Within each period, cows were adapted to the treatment for 21 d before sample collections. Dry matter intake (27.4 and 27.6 kg/d, Control and YC, respectively), milk yield (46.5 vs. 46.4 kg/d), BW, and milk composition were similar ($P = 0.13$ to 0.95) between treatments. Milk urea nitrogen concentration was also not affected ($P = 0.73$) by treatment. Rumen pH was similar ($P = 0.18$) between the Control (6.03) and YC (5.96), but rumen ammonia concentration tended ($P = 0.08$) to be lower with YC (3.03) than with the Control (3.61 mM). Treatment had no effect ($P = 0.15$ to 0.90) on concentrations of total or individual VFA. Urinary N losses did not differ ($P = 0.12$) between treatments, but allantoin and total purine derivative excretions and the estimated microbial N outflow from the rumen (513 *vs.* 471 g/d, respectively) tended to be increased ($P = 0.08$ to 0.10) by YC compared with the Control. Cumulative ammonia and methane emissions from manure were decreased by YC ($P < 0.001$ and 0.002). Total tract apparent digestibility of DM, OM, N, and NDF were not affected ($P = 0.46$ to 0.65) by YC. Concentration of C16:0 in milk fat was decreased ($P = 0.03$) and that of C18:0 was increased ($P = 0.008$) by YC compared with the Control. The yeast culture tested had little effect on ruminal fermentation, digestibility, and N losses, but tended to reduce rumen ammonia concentration and increase microbial protein synthesis and decreased ammonia and methane emissions from manure.

Key Words: yeast culture, rumen fermentation, dairy cow

478 Production response to soybean meal and methionine supplementation of corn silage-based diets in dairy cows. M. Gonzalez Ronquillo*[1], H. Nursoy[2], G. A. Broderick[3], and A. P. Faciola[4], [1]*Universidad Autonoma del Estado de Mexico*, *Toluca, Mexico*, [2]*Yuzuncu Yıl University*, *Van, Turkey*, [3]*U.S. Dairy Forage Research Center*, *Madison, WI*, [4]*University of Wisconsin*, *Madison*.

Corn silage, a major forage fed to dairy cows throughout the world, is energy rich but protein poor. Our objective was to identify the optimal level with which to supplement CP, as soybean meal (SBM), in corn silage-based diets to support of production of milk and milk components. A constant supplement of rumen-protected Met (RPM; Mepron®) was added to SBM to improve its AA balance. Thirty-six cows were blocked by parity and DIM into 9 blocks and randomly assigned to 9 balanced 4 x 4 Latin squares with 4, 16-wk periods. All diets were formulated to contain (DM basis) 50% corn silage, 10% alfalfa silage, 4% soyhulls, 2.4% mineral-vitamin supplement, 42% NFC and 30% NDF. Ground high moisture and dry corn was reduced and SBM plus RPM increased to give diets containing: 12% CP (28% corn, 6% SBM; 4.5 g RPM/d), 14% CP (23% corn, 10% SBM, 9 g RPM/d), 16% CP (19% corn, 15% SBM, 13.5 g RPM/d), and 18% CP (14% corn, 19% SBM, 18 g RPM/d). Data from the last 14-day of each period were analyzed using proc mixed in SAS; LS means are reported in the table. With the exception of milk fat content, there were significant effects of diet ($P \leq 0.02$), and linear effects of dietary CP ($P \leq 0.03$), on all production traits. Mean separation indicated that there was no improvement above 14% CP in most cases. However, yield of milk and true protein were both lower on 12 and 14% than on 16 and 18% dietary CP. Results indicated that 16% CP was required to optimize production in dairy cows fed corn silage-based diets supplemented with SBM plus RPM.

Table 1.

	Dietary CP				Probability	
Item	12%	14%	16%	18%	Diet	Linear
DMI, kg/d	23.8[b]	25.4[a]	25.2[a]	25.8[a]	<0.01	<0.01
Milk, kg/d	35.3[c]	38.7[b]	39.2[ab]	40.5[a]	<0.01	<0.01
Milk/DMI	1.49[b]	1.53[ab]	1.56[a]	1.58[a]	<0.01	<0.01
Fat, %	3.81	4.08	3.91	3.97	0.40	0.55
Fat, kg/d	1.30[b]	1.55[a]	1.52[a]	1.59[a]	<0.01	<0.01
Protein, %	3.13[b]	3.24[a]	3.22[a]	3.27[a]	<0.01	<0.01
Protein, kg/d	1.08[c]	1.22[b]	1.24[ab]	1.30[a]	<0.01	<0.01
SNF, %	8.71[b]	8.95[a]	8.84[ab]	8.96[a]	0.02	0.03
SNF, kg/d	3.04[c]	3.39[b]	3.42[ab]	3.59[a]	<0.01	<0.01
MUN, mg/dl	5.7[d]	8.0[c]	10.6[b]	14.9[a]	<0.01	<0.01

[a-d]Means with different superscripts differ ($P < 0.05$)

Key Words: corn silage, soybean meal, rumen-protected methionine

479 Effects of dietary antioxidants, trace minerals and calcium salt of 2-hydroxy-4-methylthio butanoic acid (Ca-HMTBa) supplementation on lactation performance. G. R. Bowman*[1], M. Vázquez-Añón[1], D. E. Diaz[1], and J. Nocek[2], [1]*Novus International, Inc.*, *St. Charles, MO*, [2]*Spruce Haven Research*, *Union Springs, NY*.

Forty–five lactating Holstein dairy cows housed in tie stalls were used to evaluate the effects of providing combinations of a dietary antioxidant blend, Ca–HMTBa and chelated trace minerals (AGRADO® Plus, MFP™, and MINTREX® Zn, Cu, and Mn; respectively, Novus International) on lactation performance. All cows received a control diet from calving until 14 DIM. Cows were randomly assigned by milk volume at 7 DIM to one of three treatments; control (CON), 5.5 g of antioxidant blend with 2 g of zinc, 1.5 g of Mn, and 0.5 g of Cu chelated minerals (MA), and MA with 22 g of Ca–HMTBa (MAM). All treatments were formulated to contain the same concentration of total Zn, Mn, and Cu. Data was segmented into three separate phases that were characterized by DIM; phase 1 = 29 to 56 DIM, phase 2 = 57 to 84 DIM, and phase 3 = 85 to 112 DIM. Data was analyzed using the MIXED procedure in SAS; weekly averages were used for repeated measures with subject being cow within treatment. There were no differences observed for any of the production parameters measured for phases 1 and 2. In phase 3, cows receiving treatment MAM increased milk production, 3.5% fat corrected milk, efficiency (kg milk/kg DMI), and protein yield when compared to CON (Table 1). Cows supplemented with MA had numerically increased milk volume and decreased DMI which led to an improvement in efficiency when compared to CON for phase 3 (Table 1). No changes in body condition score or weight were observed between the beginning and end of the experiment. With treatment differences occurring in phase 3 the combinations chosen in this study improve persistency of lactation and efficiency.

Table 1. Lactation performance during phase 3.

	CON	MA	MAM	SE
DMI, kg	25.63	24.50	25.35	0.652
Milk, kg	37.96^{a}	40.22^{ab}	41.72^{b}	1.302
3.5% FCM, kg	36.26^{a}	37.84^{ab}	40.63^{b}	1.488
Efficiency	1.51^{a}	1.65^{b}	1.66^{b}	0.049
Fat, %	3.21	3.14	3.34	0.137
Protein, %	2.82	2.92	2.94	0.052
Fat, kg	1.22	1.26	1.39	0.068
Protein, kg	1.07^{a}	1.17^{ab}	1.23^{b}	0.041

^{a,b} $P < 0.05$

Key Words: antioxidant, minerals, milk production

480 High-fat or low-fat distillers grains with dry or high-moisture corn in diets containing monensin for dairy cows. T. M. Owens*[1], A. R. Hippen[1], K. F. Kalscheur[1], D. J. Schingoethe[1], D. L. Prentice[2], and H. B. Green[2], [1]*South Dakota State University*, *Brookings*, [2]*Elanco Animal Health*, *Greenfield, IN*.

Forty-eight lactating Holstein cows were used in a 6-wk study to determine the effects of dietary unsaturated fat from corn distillers grains (DG) and starch fermentability in a 2 × 2 factorial arrangement. Effects of unsaturated fat were evaluated by replacing DG with a low-fat DG (Dakota Gold HP; HP). Effects of fermentability of starch were evaluated by replacing dry ground corn (DC) with high-moisture (wet) corn (**WC**). The DG diets contained 2% fat from DG (DM basis). Energy Booster 100 was added to the HP diets to balance fat across diets. All diets contained 15 g/ton monensin and 15.2% starch from DC or WC. Though BW tended to increase for cows fed DC compared with WC ($P = 0.06$), BCS and DMI were not affected. Feeding DC tended to increase ($P = 0.09$) ammonia and proportions of acetate and isovalerate ($P = 0.03$) in ruminal fluid compared with WC. Feeding DG compared with HP decreased the proportion of acetate ($P < 0.02$) as well as acetate:propionate ratio ($P = 0.01$) and increased the concentration and proportion of propionate ($P < 0.04$). Feeding DC increased milk yield (35.7 vs. 33.6 kg/d for WC, $P = 0.05$). Yield and percentage of milk fat were decreased for cows fed DG compared with HP (1.02 vs. 1.20 kg/d and 2.95 vs. 3.42%, $P < 0.01$) and yield was decreased for WC compared with DC (1.17 vs. 1.05 kg/d, $P = 0.01$). The decrease in milk fat yield and percentage were greatest for cows fed DGWC (0.90 kg/d and 2.76%, $P = 0.01$). Cows fed WC had increased milk protein percentage (3.14 vs. 3.03% for DC, $P = 0.05$). Yield of FCM was greater for HP compared with DG (32.0 vs. 29.3 kg/d, $P = 0.01$) and for DC compared with WC (31.9 vs. 29.3 kg/d, $P = 0.02$). The HP diets increased efficiency of FCM (1.50 vs. 1.33 kg milk/kg DMI for DG, $P = -0.02$). Feeding DG with WC decreased yield of FCM (26.8 kg/d, $P < 0.04$) and tended to decrease efficiency ($P = 0.10$). In summary, feeding DG in combination with WC decreased milk fat and FCM compared with feeding WC in a diet containing saturated fat.

Key Words: fat saturation, starch fermentability, distillers grains

481 Effect of marine algae (ALG) on milk production characteristics and fatty acid (FA) composition in early lactating dairy cows. B. Vlaeminck*[1], M. Hostens[2], G. Opsomer[2], and V. Fievez[1], [1]*Laboratory for Animal Nutrition and Animal Product Quality*, *Ghent University, Melle, Belgium*, [2]*Department of Reproduction, Obstetrics and Herd Health*, *Ghent University, Merelbeke, Belgium*.

Sixteen Holstein cows were randomly assigned to 2 groups according to expected calving date, estimated milk and fat production and genetic origin to evaluate the effect of feeding ALG during early lactation on milk production characteristics and FA profiles. All cows were housed in a loose stable as a single group and received a TMR (corn and grass silage, soybean meal, sugar beet pulp, corn cob mix, hay and minerals; 53.2, 24.2, 10.0, 4.5, 5.7, 2.0% on DM basis). Control cows received 2kg of protein rich concentrate and between 6 and 8kg of a balanced dairy concentrate, according to their requirements. In the ALG group, 2kg of the latter was replaced by an iso-energetic concentrate containing ALG (11% on product basis), starting 3 weeks prior to the expected calving date. Concentrates were provided by means of an automatic concentrate feeder. Milk parameters were monitored weekly during the first 12 weeks of lactation in 24h milk samples. ALG increased milk yield (41.2 vs 38.2 kg/d, P=0.057), whereas milk fat yield (1.18 vs. 1.49 kg/d, P=0.005) and content (30.6 vs. 41.4 g/kg, P=0.011) decreased. Protein yield (P=0.465) was not affected whereas a tendency for reduced protein content (32.9 vs. 34.7 g/kg, P=0.094) was observed. Dietary effects on milk production characteristics were independent (P>0.05) of week after parturition. Proportions of short-chain FA (g/100 g milk FA) (6:0 to 12:0) decreased (P<0.05) in milk fat of ALG cows whereas 4:0, 14:0 and 16:0 were not affected (P>0.05). ALG resulted in marked alterations in milk C18-FA, changes that were characterized as a reduction (P<0.05) in 18:0 (5.92 vs. 11.7) and cis-9-18:1 (18.4 vs. 23.6) and an increase in trans-10-18:1 (5.00 vs. 0.42), trans-11-18:1 (4.70 vs. 1.23), trans-11, cis-15-18:2 (0.28 vs. 0.08), cis-9, trans-11-18:2 (1.37 vs. 0.44) and trans-9, cis-11-18:2 (0.07 vs. 0.01). Milk from cows receiving ALG had greater concentrations of 22:6n-3 (0.20 vs. 0.01, P<0.001). In conclusion, supplementation of ALG to early lactating dairy cows resulted in a decreased milk fat production possibly related to an altered rumen biohydrogenation.

Key Words: dairy cow, marine algae, early lactation

Ruminant Nutrition: Using Molecular Techniques to Advance Research in Ruminant Nutrition

482 Introduction to molecular techniques currently used in ruminant nutrition research. J. R. Knapp*, *Fox Hollow Consulting, LLC, Columbus, OH*.

Molecular techniques have evolved rapidly over the past 20 years, and in conjunction with the expansion of knowledge provided by genome sequencing projects and improvements in computing resources, have provided new research tools and approaches for ruminant nutritionists, physiologists, and microbiologists. Polymerase chain reaction (PCR) and gel electrophoresis are the basis of many molecular techniques; the principles of these techniques will be presented. From these principles, extension of the applications to quantitative and real-time PCR, restriction-fragment length polymorphisms, denaturing gradient gel electrophoresis (DGGE), and ribosomal profiling of rumen microorganisms will be discussed, including advantages, disadvantages, and limitations. Also, an overview of information management and computing resources used in ribosomal profiling and the development of gene networks will be given.

Key Words: molecular biology, microbial genomics, gene expression

483 Integration of microbial profiling techniques to improve the efficiency of nutrient usage in ruminant production. J. L. Firkins* and Z. Yu, *The Ohio State University*, *Columbus*.

Further improvement in the efficiency of conversion of nutrients into ruminant products requires a better ability to explain dietary interactions and reduce unknown variability among studies. Although molecular approaches have expanded the boundaries of microbial diversity in the rumen, key aspects of the microbiome (e.g., community structure and population dynamics) have not been well linked to efficiency of nutrient usage. Emerging technology is expanding our ability to analyze archived samples from nutrition experiments that have important metabolic changes in order to profile important microbial populations over time, among animals, among particulate versus fluid fractions, or their interactions. Profiling techniques such as denaturing gradient gel electrophoresis (DGGE) using universal primers in PCR can be combined with banding analyses and sequencing of DNA recovered from specific bands to identify likely population shifts among treatments. Species- or group-specific PCR-DGGE can provide more detailed information, and dynamics of the population(s) identified can be examined by real-time PCR. Such approaches revealed the importance of previously unrecognized groups of bacteria and archaea, greatly expanded (and sometimes disagreed with) observations made from pure and mixed cultures, shown how protozoal abundance can influence prokaryotic populations, and demonstrated that a change in population need not be requisite for a change in function. In the latter regard, stable isotope profiling can help identify the populations that directly metabolize an isotopically labeled dietary component of interest and for which their RNA or DNA can be fractionated prior to microbial profiling. Thus, the combination of community profiling (diversity and functionality) and quantification of populations identified during the profiling will provide an interface to improve our ability to predict accumulation of trans fatty acids responsible for depression of milk fat secretion, lessen the negative associative effects of feeding mixed diets, and decrease intraruminal nitrogen recycling.

Key Words: rumen microbial profiling, microbiome, efficiency of nutrient usage

484 Metagenomics of the rumen microbial ecosystem. D. Krause*, *University of Manitoba*, *Winnipeg, Canada*.

Rumen microbiology has a rich history of innovation, beginning with the pioneering work of Robert Hungate and Marvin Bryant in the 1940's and 1950's. The questions for rumen microbiologists have always been the same: what species are present; how many of each species are present; and what are each of the species doing? In the 1940's it was possible to look at rumen fluid under a microscope and morphologically identify microorganisms that could be cultured, but the many bacteria that could not be cultured was troubling. The work of Hungate and Bryant gave us anaerobic techniques so that we could now culture important anaerobic species like *Ruminococcus albus* and *Fibrobacter succinogenes* which were important fiber digesting species. In the late 1970's and early 1980's Carl Woes demonstrated that ribosomal genes, present in all life forms, could be used to classify microorganisms. In the late 1980's David Stahl published a manuscript illustrating how ribosomal genes could be used to monitor rumen populations when supplemented with monensin. This was a breakthrough because it was not possible to evaluate microbial population changes without having to culture them. In the late 1990's and early 2000 sequencing technology had advanced to the point where it was possible to obtain a catalogue of all the genes in a single species of bacteria. Sequencing technology has since advanced even further, and new platforms based on pyrosequencing are not available. It is now possible to sequence all the genes of all the species of the rumen ecosystem to produce a metagenome. This presentation will discuss the development of this technology and its application to practical problems in ruminant production.

485 Basal expression of 27 nucleoside and amino acid transporter mRNA by small intestinal epithelia of forage-fed growing beef steers is differentially affected by increased luminal substrate or energy supply. J. C. Matthews*, S. F. Liao, and J. A. Boling, *Department of Animal and Food Sciences, University of Kentucky*, *Lexington*.

In many cool-season forage systems, microbial-derived nucleosides and amino acids typically supply adequate or surplus sources of N, whereas energy supply is typically low enough to limit growth. This talk summarizes a series of relative quantitative real-time RT-PCR experiments that collectively tested the hypotheses that (a) expression of mRNA (normalized to 18S rRNA) for 5 nucleoside (NT), 21 amino acid (AAT), and 1 dipeptide (PepT1) transport proteins differs among duodenal (D), jejunal (J), and ileal (I) epithelia of beef cattle, and (b) expression of these transporter mRNA is affected by increased supply of microbial-derived substrate, starch-derived energy, or both. Total RNA was extracted from a single set of epithelial tissues collected at slaughter from 18 ruminally and abomasally catheterized Angus steers (BW ~ 260 kg) consuming an alfalfa-cube based diet at 1.3× NE_m. Cattle were infused with either (n = 6) water (basal) or ruminal (substrate) or abomasal (energy) corn starch hydrolysate (SH; at 20% ME intake). All 27 mRNA were expressed. Of these, 23 were differentially ($P \leq 0.07$; 1.0- to 49-fold) expressed among D, J, or I epithelia. Substrate and energy treatments affected ($P \leq 0.08$; -0.27- to +2.10-fold) basal mRNA expression. More specifically, increased substrate supply increased D expression of 3 NT mRNA and decreased J content of 4 cationic AAT mRNA, whereas expression of 18 AAT and PepT1 mRNA were not affected. In contrast, increased luminal energy increased 2 D NT mRNA, decreased 2 J cationic AAT,

and increased 6 I neutral AAT and PepT1 mRNA. For a given class of transporter, mRNA expression was altered such that potential capacities of apical and basolateral membranes were changed in a parallel manner. These findings provide an initial understanding of the basal expression of bovine NT and AAT genes and their responsiveness to increased substrate or energy supply.

Key Words: amino acid transport, nucleoside transport, nutrient-gene interaction

486 Molecular adaptations in transition dairy cows. J. J. Loor*, *University of Illinois*, *Urbana*.

The periparturient period is characterized by dramatic alterations in metabolism and function of immune cells and key tissues such as liver, adipose, and mammary. Understanding the molecular adaptations of tissues during this physiological state remains a great challenge. Development of transcriptomic technologies has dramatically accelerated the rate at which biological information can be collected from agricultural animals. Use of oligonucleotide bovine microarrays on liver, adipose, and mammary tissue from transition dairy cows has demonstrated the potential of high-throughput technologies for identifying genes involved in regulating and coordinating function and crosstalk among tissues. Work examining the role of prepartum level of dietary energy has revealed unique clusters encompassing functional categories including signal transduction, cell-to-cell signaling, molecular transport, insulin signaling, lipid metabolism (synthesis and beta-oxidation), immune or inflammatory processes, and cell death in adipose as well as liver. High-throughput technologies and associated bioinformatics tools are especially well-suited for studying the complex regulation of transcriptional networks in tissues from transition cows. Major advances in understanding biology of the transition cow may come from coupling existing knowledge of enzyme kinetics, biochemistry, and hormone action with transcriptomics, proteomics, and metabolomics approaches. Using a systems biology approach to integrate data generated at the mRNA, protein, metabolite, and tissue level can allow the assembly of the important components needed to model the transition cow. Such models will prove useful in determining how we can manipulate complex processes that could have significant long-term economic impact, e.g., lactation persistency, fertility, and efficiency of conversion of feed to milk. An important goal of the future will be to apply additional experimental tools (e.g., gene silencing, chromatin immunoprecipitation) and bioinformatics (e.g., transcription factor binding site identification) to studies focused on periparturient cows.

Key Words: transcriptomics, energy balance, systems biology

Small Ruminant: Production, Management, Lactation

487 Effects of kid genotype on carcass traits of meat goats from a three-breed diallel. R. Browning, Jr.*[1], W. Getz[2], O. Phelps[3], and C. Chisley[4], [1]*Tennessee State University*, *Nashville*, [2]*Fort Valley State University*, *Fort Valley, GA*, [3]*USDA-AMS*, *Lakewood, CO*, [4]*Southern University*, *Baton Rouge, LA*.

Purebred and reciprocal crossbred buck kids (n = 275) from a complete diallel mating of Boer (B), Kiko (K), and Spanish (S) breeds were harvested at about 33 wk of age over three yr to assess breed of kid effects on carcass traits in meat goats. Kids were raised post-weaning on summer pasture supplemented with 0.4 kg/d of 16% CP pelleted feed. Each kid and carcass was graded using USDA meat goat standards. Live kid and chilled carcass grades differed ($P < 0.01$) among genotypes. Purebred BB had better ($P < 0.01$) live grades than KK and SS kids; whereas BB and KK had better ($P < 0.01$) carcass grades than SS. Among the crosses, BK and SB graded better ($P < 0.01$) live than KB, SK, and KS; carcass grades were better ($P < 0.01$) for BK than for KB, SB, and SK. Live weight, chilled carcass weight (without kidney-pelvic fat), and chilled dressing percent varied ($P < 0.01$) by genotype. Live and carcass weights among purebreds were heavier ($P < 0.01$) for KK (26.8 ± 0.8 kg; 11.2 ± 0.4 kg) than for BB (23.3; 9.3) and SS (23.2; 9.6). Crossbred live and carcass weights differed ($P < 0.01$) only between SK (27.0 ± 0.7 kg; 11.5 ± 0.4 kg) and SB (24.2; 9.9). Chilled dressing percent was higher ($P < 0.01$) for KK (41.6 ± 0.5%) than for BB (39.9). Among crosses, dressing percent was higher ($P < 0.01$) for SK (42.4 ± 0.4%) and KS (42.2) than for BK (40.9), KB (40.9), BS (40.2) and SB (40.5). Foreleg, hindleg, and combined boneless fore- and hindleg weights were affected ($P < 0.01$) by genotype. Purebred KK were heavier ($P < 0.01$) than SS and BB for each leg trait. Among the crosses, SK had heavier ($P < 0.01$) forelegs than BS and SB and heavier ($P < 0.01$) hindlegs and boneless leg than SB. Kid genotype did not affect lean content (69%) of leg cuts. Genotype affected ($P < 0.01$) loin weights. Loins were heavier ($P < 0.01$) for KK than for BB and heavier ($P < 0.01$) for SK than for SB. Kidney-pelvic fat differed ($P < 0.01$) by genotype. Among purebreds, internal fat was greater ($P < 0.01$) for KK (177 ± 16 g) than for BB (74) and SS (119). Crossbred genotypes did not differ for kidney-pelvic fat. In conclusion, kid genotype has significant effects on carcass yield traits for meat goats.

Key Words: meat goats, breed, carcass

488 Advantages of using electronic identification for automated lambing data and body weight recording in sheep. A. Ait-Saidi, G. Caja*, S. Carné, and A. A. K. Salama, *G2R, Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

Manual (M), semi- (SA) and fully-automated (A) systems for sheep performance recording were compared in 2 on-farm experiments. System M used visual identification (plastic ear tags), on-paper data recording and manual typing for data uploading. Systems SA and A used electronic identification (20 g mini-boluses, 56 × 11 mm, containing 32 mm half-duplex transponders); performance data were recorded using a reader with keyboard in SA (i.e. lambing data) or automatically in A (i.e. BW), and data uploading was done automatically for SA and A. Each ewe wore an ear tag and a mini-bolus. Exp. 1 compared M and SA lambing recording (1.57 lambs/ewe) in dairy (n = 73) and meat ewes (n = 80) processed in groups of 10. Time for lambing data recording was greater in dairy than meat ewes ($P < 0.05$), due to the lower operator experience and because half of the dairy ewes needed ear tag cleaning, but when systems were compared, M was greater than SA ($P < 0.05$) for both dairy (1.11 vs. 0.80 min/ewe) and meat (0.78 vs. 0.68 min/ewe) ewes. Average time for data uploading was greater in M vs. SA (0.54 vs. 0.06 min/ewe; $P < 0.001$). Consequently, overall time for lambing recording was greater in M than SA in dairy (1.67 vs. 0.87 min/ewe; $P < 0.001$) and meat ewes (1.30 vs. 0.73 min/ewe; $P < 0.001$). Data uploading errors were 4.9% in M, but no errors were detected in SA. In Exp. 2, ewes' BW was recorded by M and A systems in dairy (n = 120) and meat ewes (n = 120). Ewes were processed in groups of 20 using an electronic scale which was interfaced to a computer for A. Weighing

time varied according to breed behavior and recording system, with M being greater than A (0.45 vs. 0.23 min/ewe; P < 0.05). Average time for data uploading (0.18 vs. 0.02 min/ewe; P < 0.05) and errors (8.8 vs. 0%) were greater in M than A. Overall time for BW recording in M and A was 0.63 and 0.25 min/ewe, respectively. In conclusion, the semiautomatic and automatic performance recording systems done through electronic identification increased the throughput and reliability of sheep recording data, which resulted in significant savings in farm labor time.

Key Words: sheep recording, electronic identification, transponder

489 Using retinal image recognition for auditing identity of live and harvested lambs. M. A. Rojas-Olivares, G. Caja*, S. Carné, and A. A. K. Salama, *G2R, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

With the aim of auditing the traceability of sheep, retinal image recognition (RIR) was used in a total of 152 lambs of 2 breeds (Lacaune, n = 70; Manchega, n = 82). The RIR is based on the uniqueness and invariability of the retinal vascular pattern of the eye. Lambs wore ear tags and electronic boluses as controls. Retinal image and capturing time (CT) were recorded twice from the 2 eyes of each lamb using an OptiReader device (Optibrand, Fort Collins, CO), at: 3 (live, n = 152; slaughtered, n = 50), 6 (n = 58) and 12 mo of age (n = 58). The first 2 wk (264 images) were used for operator training. Digitalized images (1,272 images) were treated by using the Optibrand Data Management Software (v. 4.1.3) and 3 mo enrolment images used as the reference for further analysis. Intra- and inter-age comparison of pairs of images were done using the Optibrand's matching score (MS, range 0 to 100) with MS < 80 as exclusion criterion. Values of MS and CT in 3-mo images during the training period averaged 92.1 ± 0.8 and 144 ± 15 s, and improved to 96.4 ± 0.5 and 63 ± 5 s when the operator was trained. Intra-age breed effects were detected in MS at 3 mo (P < 0.10), but no effects were observed at 6 (96.2 ± 0.6) and 12 mo (96.3 ± 0.6); moreover, breed affected CT (P < 0.001) being longer in Lacaune than Manchega lambs, and decreased by age to 34 ± 4 s and 21 ± 2 s, for 6 and 12 mo respectively. Values in the slaughtered lambs were 67.4 ± 2.0% and 45 ± 7 s, both varying by breed (P < 0.05). Live vs. slaughtered image comparisons were unsatisfactory (MS = 58.4 ± 1.8). Inter-age image analysis, used as traceability indicator, showed no effects (P > 0.05) by age (6 mo, 90.9 ± 1.2; 12 mo, 90.6 ± 1.1) and breed (Manchega, 91.7 ± 1.7; Lacaune, 89.9 ± 1.4). On average, MS and CT values were 90.8 ± 1.1 and 27 ± 2 s. Percentage of images showing an inter-age MS higher than 70, 80 or 90 were 97.5, 83.6 and 68.1%, respectively, indicating the convenience of using a MS = 80 as breaking value. In conclusion, RIR was a useful technology for auditing the identity of live lambs, but its use was not adequate in harvested lambs.

Key Words: retinal scannig, traceability, sheep

490 Comparison of body composition measurements in sheep using dual energy X-ray absorptiometry (DXA) *in vivo* and *post mortem*. A. M. Scholz*[1], C. Mendel[2], P. V. Kremer[1], E. Gruber[1], A. Steiner[2], K.-U. Goetz[2], and M. Foerster[1], [1]*Ludwig Maximilians University Munich, Livestock Center, Oberschleissheim, Bavaria, Germany*, [2]*Bavarian State Research Center for Agriculture, Institute for Animal Breeding, Poing, Bavaria, Germany*.

Sheep breeders need to improve the performance of their herds steadily for economic reasons --especially in order to meet consumer demands. Therefore in this study, 39 male lambs were studied by dual energy X-ray absorptiometry (DXA) at an average live body weight of 42.5 ±2.6 kg and an average age of 111 ±11.6 d. The male Merino (land type or 'Wuerttemberger') lambs originating from seven different Bavarian breeders and from two Bavarian research herds were fattened at the central Bavarian performance test station. The performance test started at an age between 6 and 10 wk and at a body weight between 20 and 24 kg. They received a concentrate diet with 18% crude protein and 10.5 MJ ME *ad libitum* and daily 300 g hay. At the end of the fattening period, a whole body scan was performed by DXA with a GE Lunar DPX IQ pencil beam scanner in order to measure the amount and percentage of fat tissue, lean tissue, and bone mineral *in vivo*. Four d later, the lambs were slaughtered. The whole, empty carcass without head (20.2 ±1.9 kg) was X-rayed again with the GE Lunar DPX IQ scanner. *In vivo*, the 'pediatric large' whole body software mode was applied. The 'pediatric small' whole body software mode served for the scan of the carcasses. A regression model procedure using SAS 9.2 was used to analyze the data. There was a medium to high agreement between the *in vivo* and carcass measurements for all traits (table). The lower relationship between the DXA lean mass recordings is most likely affected by the varying filling state of the rumen *in vivo*. Unexpectedly, the highest coefficient of determination showed the DXA bone mineral (g) followed by DXA lean (%), and DXA fat (%). DXA measurements *in vivo* can predict the DXA carcass body composition of male Merino lambs with a high accuracy and may be used for performance testing in meat type sheep.

Table 1. Relationship between *in vivo* and carcass DXA measurements

Trait	Adjusted R^2	√MSE	*F* value*
DXA fat mass (g)	.73	466	105.1
DXA fat (%)	.74	1.92	111.5
DXA lean mass (g)	.43	1092	30.0
DXA lean (%)	.75	1.88	116.6
DXA bone mineral (g)	.84	41	195.8
DXA bone mineral (%)	.46	.18	33.1

Carcass DXA traits as predictors; *p<.0001 for all traits

Key Words: lambs, body composition, dual energy X-ray absorptiometry

491 Cost-benefit evaluation of implementing the electronic identification for performance recording in sheep farms. G. Caja*, M. J. Milán, A. Ait-Saidi, A. A. K. Salama, and S. Carné, *G2R, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

Automated performance recording based on electronic identification (e-ID) proved to be a useful tool for increasing reliability of data collection and for saving labor/time in sheep farms. Despite this, there are few data available on cost-benefit analysis of implementing e-ID in practice. With this aim, previous results comparing manual, semiautomatic and automatic performance recording in dairy and meat sheep farms were integrated in a cost-benefit analysis under Spanish conditions. The analysis scenarios considered: production aim (dairy, meat), intensification level (semi-intensive, extensive), flock size (400, 700), lambing rhythm (1, 1.5), milking or milk recording frequency (once-, twice-daily), and included weighing (2, 3) and 1 annual flock inventory as stated in the current EU regulations. Annual extra costs (Euro 1 = $1.3) necessary to buy the ID devices and the required reading equipment for e-ID ranged between 0.43 and 0.66 Euros/ewe according to scenarios. On the other hand, annual savings achieved by implementing

e-ID ranged between 0.36 and 0.79 Euros/ewe according to scenarios. As a result, benefits of using e-ID fully covered the annual extra costs in the case of dairy farms with 2X (or A4 milk recording) and in intensive meat farms having 1.5 lambing/yr. For dairy farms performing 1X (or AT method) or in extensive meat production, the savings only covered 93 and 86% of the extra costs for e-ID, respectively. Benefits of using automatic recording reached break-even points at: dairy sheep farms (477 ewes milked 1X, or 279 ewes milked 2X) and meat sheep farms (1,110 ewes under extensive, and 565 ewes under intensive management conditions). In conclusion, the implementation of electronic identification for performance recording showed to be cost-effective, especially for large flocks. Ongoing innovations and new software management will also make the use of e-ID more profitable in the future.

Key Words: cost-benefit, identification, sheep

492 Use of sodium dodecyl sulfate (SDS) as a microbicide in goat colostrum. A. Morales-delaNuez[1], J. Capote[2], M. C. Juste[1], D. Sanchez-Macias[1], N. Castro[1], and A. Argüello*[1], [1]*Las Palmas de Gran Canaria University*, *Arucas, Las Palmas, Spain*, [2]*Instituto Canario de Investigaciones Agrarias*, *La Laguna, Tenerife, Spain*.

The present study aim was to evaluate the use of SDS as a microbicide in goat colostrum and the effects on passive immune transfer. Twenty goat colostrum samples from Majorera goat breed were treated with SDS at two concentrations, 0.1 and 1% during 1 h at 36°C, recording the colony forming unit (CFU) and IgG concentration at the beginning and at the end of the process. Twenty male goat kids were fed during 2 d with a colostrum pool that was previously divided in 2 aliquots, one untreated (n = 10) and other one treated with SDS at 1% (n = 10). After 2 d of age, goat kids were fed with milk replacer. IgG, creatinin, glucose, cholesterol, BUN, bilirubin, AST and ALT evolution was recorded on plasma during the first 5 d of age. Differences between IgG and CFU on colostrum for treatments were evaluated using a two Sample t test for means, while differences on goat kid blood parameters during the first 5 d of age were evaluated using a Proc Mixed model of SAS (V9.0). Treatment colostrum with SDS at 1% reduced the CFU from 6.5 to 4.6 log CFU/mL while colostrum treated with SDS at 0.1% did not show CFU reduction. IgG after SDS treatments (1 and 0.1%) was 10% lower than before treatments. No differences were observed for IgG, creatinin, glucose, cholesterol, BUN, bilirubin, AST and ALT during experimental period between goat kids that received untreated or SDS 1% treated colostrum. Previous results support the use of SDS as a new method for colostrums sanitation, although the effects of SDS on caprine arthritis encephalitis virus must be investigated.

Key Words: SDS, goat colostrum, immune pasive transfer

493 Testing the performance of a mechanistic mathematical model of the mammary gland in dairy sheep. C. Dimauro*, A. S. Atzori, A. Cannas, N. P. P. Macciotta, and G. Pulina, *Dipartimento di Scienze Zootecniche, Università di Sassari*, *Sassari, Italy*.

A mechanistic mathematical model of the mammary gland, which simulates the milk production process in dairy sheep, was constructed by using a computer-aided simulation with Stella software (Dimauro et al., 2007. Livestock Science 106, 200-209). The main inputs of the model were energy available for milk production coming from diet and energetic reserves at lambing. The outputs of the model were number of active alveoli throughout lactation, milk production, energy balance and potential milk production. The objective of the present work was to test the model performance in dairy sheep fed a balanced diet. With this aim, the lactation curve of a mature Sarda dairy sheep was fixed assuming a milk production of 0.98 L/d at lambing, 1.50 L/d at peak and 0.50 L/d at the end of lactation. Body reserves were estimated assuming a BCS of 3.0 at lambing, 2.5 after 60 DIM, 2.8 after 150 DIM and 3.0 at the end of lactation. The SRNS model (http://nutritionmodels.tamu.edu/srns.htm) was used to design a balanced daily diet for that animal. The estimated daily energy from diet, minus the energy of maintenance, was used as external energy input of the model. In the first run of the model, the estimated lactation curve did not follow the expected one. Therefore, some model parameters were recalibrated to obtain the desired lactation curve. In particular, the optimal combination of active and progenitor alveoli at lambing was 9×10^9 and 4.2×10^9, respectively. The model predicted the dynamics of the active alveoli throughout lactation, the energy balance and the potential milk production. Milk production over the entire lactation was 234 L, whereas total potential milk production was 256 L. The largest difference between estimated and potential milk production occurred from lambing to 60 DIM. In conclusion, the difference between daily milk production and potential daily milk production could be used to estimate the deficit of dietary energy which would have to be supplied in order to produce the maximum quantity of milk allowed by the mammary gland.

Key Words: mechanistic model, lactation curve

494 Effect of lamb age on response to immunization. M. E. Gailor, J. Gavalchin, and M. L. Thonney*, *Cornell University*, *Ithaca, NY*.

Lamb response to early immunization is not clear. The objective of this experiment was to determine whether the immune response would be different for lambs first vaccinated at 3 d (3D), 5 wk (5W), and 10 mo (10M) old. There were 5 lambs in control (C), adjuvant (A, 0.5 mL of 10% aluminum hydroxide) and vaccinated (V, 0.5 mL adjuvant + 0.25 mg of keyhole limpet hemocyanin (KLH)) treatments within each age group (45 lambs). At 2 and 4 wk after the initial vaccination, blood samples were taken in order to measure KLH-specific lymphocyte proliferation and antibody (Ab) production, and the animals were revaccinated. Samples were also taken 6 wk after the initial vaccination. The statistical model for log-transformed data included the effect of vaccine treatment, lamb age, lamb as a random variable within vaccine treatment and lamb age, sampling time and all interactions (repeated measures model). In vitro lymphocyte proliferation responses to KLH relative to no stimulation or to stimulation by concanavalin-A (ConA) or pokeweed mitogen (PWM) were positive but unrelated to vaccination. Lymphocytes from the 10M lambs and those from the earliest sampling times had the highest proliferative response to KLH, but lamb age x sampling time interactions ($P < 0.01$) complicated the interpretations of proliferation responses to ConA and PWM. Serum KLH Ab was affected by a vaccine treatment x lamb age interaction ($P < 0.001$). V lambs had higher Ab levels than C or A lambs at all 3 ages but the response was greatest for 5W lambs. There was a lamb age x sampling time interaction ($P = 0.001$) for log2 values of KLH Ab titers measured in serum of V lambs (Table 1). At 2 wk after initial vaccination and prior to the first booster, titers were very low for 3D lambs, much higher in 5W lambs and dramatically higher in 10M lambs. Surprisingly, titers declined in 10M lambs after both boosters while they increased in both 5W and 3D lambs. Perhaps this was the result of clonal exhaustion (functional state of non-responsiveness) due to chronic exposure to KLH in the 10M lambs. These results indicate that lambs less than 1 wk old are unlikely to respond to an initial vaccination, but that subsequent boosters are effective.

Table 1. Geometric means of antibody titers against KLH in serum of lambs vaccinated at 3 initial ages and sampled at 3 times after initial vaccination.

Wk after initial vaccination	3 d age	5 wk age	10 mo age
2	38	132	606
4	210	264	400
6	1213	765	264

Key Words: sheep, vaccine, age

495 Control of *Haemonchus contortus* using three chemical classes of anthelmintics and copper oxide wire particles in meat goat kids. M. Rothaug[2], K. Andries*[1], E. Sherrow[1], and J. Burke[3], [1]*Kentucky State University*, *Frankfort*, [2]*Midway College*, *Midway, KY*, [3]*USDA, ARS*, *Booneville, AR*.

Resistance to chemical anthelmintics is becoming a very common problem in many small ruminant herds throughout the US, with an increasing number of herds experiencing total anthelmintic failure. Research has shown copper oxide wire particles (COWP) to be a potential alternative to current chemical control products for H. contortus in sheep and goats. To determine the effectiveness of COWP, a research project was conducted to compare COWP to each of the three classes of chemical dewormers in young meat goat does. Forty meat goat doe kids were available for this project and represented two age groups (fall and spring born). The does were randomly assigned within age group to one of five treatments: control, albendazole (20 mg/kg), COWP (2 g/hd), levamisole (12 mg/kg), or moxidectin (0.4 mg/kg). Fecal samples were collected and egg counts performed, using modified McMaster procedure on d 0, 7, 14, 21, and 28 for each animal. Anemia levels were monitored using the FAMACHA system. Animals were treated on d 0 according to their assigned treatment group and all animals were placed in dry lot on fescue hay and a pelleted feed for 14 d. After 14 d all animals were turned out on a highly infected pasture. Data were analyzed using Proc Mixed in SAS with age and treatment as fixed effects. Correlations between FAMACHA scores and FEC were all positive and significant. The correlation decreased at d 7 ($r = 0.37$, $P = .019$) but recovered by d 28 ($r = 0.50$, $P = .0013$). Treatment had an effect ($P < 0.01$) on egg counts on all days post treatment. Levamisole was the most effective treatment in both age classes on all days. There were no differences between other treatments except albendazole had lower egg counts than the others on d 7 of the experiment. In this study, COWP showed no reduction in fecal egg counts in young does. Over the whole study, COWP and moxidectin did not differ from the control treatment in reducing egg counts. All chemical classes reduced ($P < 0.05$) egg counts by d 7 when compared to the control but only levamisole was still lower by d 14.

Key Words: meat goat, parasite, COWP

Teaching/Undergraduate and Graduate Education: Teaching Issues

496 Comparative development of critical thinking skills in animal science undergraduates who enroll in evaluation courses. L. M. White* and K. D. Layfield, *Clemson University*, *Clemson, SC*.

Challenges faced by American colleges and universities are numerous, including preparing an individual that is capable of higher order thinking. This stipulates that a person is proficient at making independent decisions and thinking critically. Producing a person that is capable of these essentials is no easy task and has been the topic of much discussion and deliberation. Evaluation courses have remained an integral part of animal science programs throughout the country. An evaluation course teaches general accepted criteria for evaluating a particular animal, industry standards and rules to compare multiple animals, and emphasizes defense of judgments both written and orally. Popular opinion believes that students in an evaluation class gain needed and useful experience in judgment, analytical and critical thinking. These attributes of evaluation courses are believed to contribute to higher order thinking. Therefore, this study sought to quantify the change in critical thinking ability of students enrolled in an evaluation course. The Watson-Glaser Critical Thinking Appraisal (WGCTA) exam provided means to objectively analyze critical thinking ability by examining five constructs: inference, recognition of assumptions, deduction, interpretation, and evaluation of arguments. The sample population consisted of students enrolled in evaluation courses (E) and a non-evaluation course (N) at Clemson University: Equine Evaluation (n=17), Livestock Evaluation (n=20), and Animal Reproduction (n=45). Students were issued the WGCTA during the first (pre-test) and last week (post-test) of class. The N group scored 19% of a standard deviation lower than the mean for both groups, while the E group scored 25% of a standard deviation higher than the mean. The mean change in score from pre-test to post-test for the N and the E group was -3.16 and 0.12, respectively and showed a trend toward significance ($P<0.06$). Students enrolled in an evaluation course tended to have increased their critical thinking ability score from pre to post test.

Key Words: critical thinking, Watson-Glaser, evaluation

497 Enhancing underrepresented, minority student learning through agricultural and natural resources based research. R. L. Stanko*[1,2], S. D. Nelson[1], J. C. Laurenz[3], and M. R. Garcia[1], [1]*Texas A&M University*, *Kingsville*, [2]*Texas AgriLife Research*, *Beeville*, [3]*Eastern New Mexico State University*, *Portales*.

A multi-disciplinary, multi-institutional project was initiated to increase the experiential learning of minority agriculture students. A focal point of this program was to provide first-hand experience to scientific research as an opportunity to increase skills in an ever-increasingly, competitive, and science-oriented job market. Two upper-level courses were established to teach experimental techniques and research methodology. One course was developed for teaching Experimental Techniques in Plant, Soil, and Environmental Science and the other for techniques in Animal Science. Courses combine experimental techniques and hands-on laboratory exercises. Students completing either course and interested in pursuing agricultural research in their own area of interest were encouraged to seek faculty mentors. USDA-Hispanic Serving Institution grant monies were made available and selected students were supported to serve as research aides, conduct research projects, and present research findings at annual symposia and professional society conferences. The program has expanded to include support for graduate students who receive short-term research experience external to the university. During the course of the project, 31 undergraduate and 11 graduate students were supported under the guidance of faculty mentors or senior scientists at collaborating institutions. Over 50% of participants were Hispanic, and 90.5% considered to be minorities in the agricultural sciences. Retention rate has been 100% with all students in the program either graduating or planning to graduate. Eight of the 11 (72.7%) M.S. students went on to Ph.D. or DVM and 14 of 31 (45.2%) B.S. graduates have continued onto M.S. thus far. All other graduating seniors have obtained career positions in their field of study within 3 mo. of graduation. Participation and completion of this program has given students experiential learning and skills necessary to make sound decisions concerning future employment

or continued collegiate education. Moreover, these participants have a competitive edge in career preparation for professional agriculture.

Key Words: experiential learning, minority, student

498 Teaching livestock production for niche markets. P. J. Lammers* and M. S. Honeyman, *Iowa State University*, *Ames*.

Niche markets for livestock products are growing nationally. Broadly, niche markets address consumer demand for product differentiation and enable producers to take a more active role in price determination. Commodity livestock production usually requires large-scale production to be economically viable. Commodity livestock operations are out of reach for beginning farmers without extensive financial support. Many young people would like to engage in livestock production as owner-operators, but lack the assets and capital necessary to make commodity production a feasible career choice. Other individuals may not want to engage in commodity livestock production due to personal choice and ethics. Successfully producing livestock for niche markets requires a similar but different skill set than commodity livestock production. Existing courses in livestock management offered by most universities do not extensively address the unique aspects of production for niche markets. Students familiar with conventional animal production typically understand growth in the context of grain-based diets usually supported by growth enhancers. Niche markets often operate under a different set of performance expectations that are not fully understood by students. For example, grass-based dairy and beef production is a major niche market with a production context that is novel to most undergraduates. Therefore, we developed a course focused on livestock production for niche markets. Producer experience guided the establishment of realistic production benchmarks for the major species of livestock under niche market conditions. Producers were also instrumental in discussion of processing and marketing logistics as well as costs and returns for niche markets. Class lectures on production focused on managing livestock to improve performance coupled with financial evaluation of management choices. Students interested in raising livestock as owner-operators may find that niche markets can help them achieve their goals. Understanding livestock production under niche market conditions as well as how niches change over time will better prepare students to engage in entrepreneurial livestock production for niche markets.

Key Words: entrepreneur, niche markets

499 The effectiveness of a distance education laboratory in 'Anatomy of Domestic Animals'. J. Bing*, S. Pratt, L.-A. Gillen, and C. Farin, *North Carolina State University*, *Raleigh*.

The objective of this study was to determine if a laboratory course in 'Anatomy of Domestic Animals' offered in a distance education (DE) format was as effective in helping students learn as a live face-to-face laboratory. It was hypothesized that student learning of material presented in DE format would be as effective as material presented in live format. At the beginning of the semester, 83 students were asked for consent and completed both a pre-test on anatomy material and a pre-survey to determine their experience with, and attitude towards DE. Alternating each week, the laboratory topic was presented either as a traditional face-to-face laboratory (wet-labs and dissection) or as a virtual DE laboratory (videos, animations and dissection software). Two laboratory practical exams were given, one at mid-semester and one at the end of the semester. The practical exams had two sections; a timed identification station section and a short answer section, with material from all labs (both DE and live) split approximately equally. Questions from the pre-test were included in the exams. At the end of the semester, students completed a post-survey regarding if they thought DE was a viable alternative to a live laboratory. Student grades from the DE and live material on each of the lab exams were compared using ANOVA. Learning was evaluated based on the students' performance on pre-test and post-test questions from material presented as DE or live format, using paired t-tests. Results are presented as mean±SEM. Significant learning was achieved in the class, as shown by a significant ($P<0.0001$) increase in pre-test (42±1.8%) vs post-test (88±1.2%) scores, though there was no difference in the change of score between live and DE material ($P=0.94$). There was a significant effect of the type of learning on exam scores, such that students scored higher ($P<0.0001$) on material from DE (77±1.4%) vs. live (71±1.4%) laboratories. The post-survey indicated that 79.3% of students thought DE laboratories were a viable alternative to live laboratories. The results of this study indicate that anatomy material can be effectively taught by distance education.

Key Words: distance education, anatomy

500 Teaching a 'dog lab' in a traditional animal science department. G. M. Hill*, B. B. Snedegar, J. A. Snedegar, and J. E. Link, *Michigan State University*, *East Lansing*.

Animal science (ANS) departments do not maintain a dog kennel for teaching purposes. However, as the need for trained individuals in the companion animal industries increases and more students without agricultural backgrounds enroll in ANS courses, ANS educators have added curriculum to meet the educational needs of students interested in these career opportunities. This year in our entering freshmen class, 19% of the students had a dog or a cat as their primary experience with animals and 22% owned horses. In the Michigan State University introductory ANS course, we designed a 'dog lab' to accompany companion animal lectures. Students enrolled in the class, faculty and several local breeders were invited 'to bring their dogs to class'. Requirements were: up-to-date vaccinations, a hard-sided kennel and a friendly personality. A breeder presented the American Kennel Club's dog group classifications and their functions. Legislative concerns and actions were discussed by a veterinarian; grooming needs and basics were demonstrated by a professional groomer, and dog activities such as rally, obedience and agility were demonstrated in a 2 h lab period. Each guest dog was presented to the class with comments relative to its breed and purpose. As a lab exercise, pre-formed student groups were asked to select a dog and utilizing its size and breed classification, to integrate information gained from the lab and available resources to suggest a nutritional product that would meet the needs of their selected dog. Reports were to be 200 words or less and creativity, accuracy and group cooperation were considered in the grade. During the end of semester course evaluations, students have rated this laboratory as either their first or second favorite lab in each of the past 6 semesters. Thus, it is possible to expand laboratory experiences into the companion animal curriculum by using knowledgeable dog breeders and enthusiasts to provide a 'dog lab' in a traditional ANS department.

Key Words: curriculum, teaching laboratory, companion animal

501 Using companion animal classes to teach biology, nutrition, critical thinking and media literacy to animal sciences majors and

across the University community. S. Rocco and J. P. McNamara*, *Washington State University, Pullman*.

Many Animal Science Departments have taught classes on topics related to pet animals, often the goals relate solely to meeting student interests or to increase enrollment. However, such courses proved a serious opportunity to improve critical analysis, media and information literacy, quantitative reasoning, and integration of social, economic and biological sciences. An example would be in-depth analysis of the human animal bond and all its economic, social and technical implications. There are also concerns from some faculty that we should only teach classes directly related to getting students prepared for a job. In order to increase the depth and breadth of reach of animal sciences courses, two courses at WSU, AS 205, Companion Animal Nutrition (General University Biology Course) taught to all classes and majors; and AS 464, Companion Animal Management, a primarily major course for seniors, have been used to help increase not only scientific knowledge, but media and information literacy, critical thinking across a wide spectrum of endeavors, quantitative reasoning and working with groups to solve complex, real, problems. Lessons in the biology class investigate connections between nutritional chemistry, animal diversity, and practical decision making (use of pet food labels); or the biology behind the interaction of nutritional states and potential disease and its impacts on society. In the advanced class, students work together to research topics from mechanisms of genetic diseases; to discussion of the human animal bond and how it affects economic and political decisions; and they develop teaching modules used by the students in the introductory class. Students self-reported using Likert scale and in text responses that 80 to 90% of students reported improvement in critical thinking and media literacy skills. They also reported a high degree (more than 60% of students reported improvement) of application of basic biology to everyday life decisions.

Key Words: companion animals, undergraduate education, critical thinking

502 Innovative dairy teaching through a broad-based Dairy Consortium. G. R. Hagevoort*[1], M. A. Tomaszewski[2], and R. Collier[3], [1]*New Mexico State University, Clovis*, [2]*Texas A&M University, College Station*, [3]*University of Arizona, Tuscon*.

Over the last two decades, Land Grant Universities have decreased their investment in dairy education while allied industry has increasingly become involved with dairy producers in problem areas that affect dairy management. The Land Grant Universities of the Southwest established a multiple university, multi disciplinary and interagency Southern Great Plains Dairy Consortium (SGPDC). There are three legs to the consortium of which two (research and extension) move in unison, while the third leg (teaching), has progressed on its own. While the research and extension part of the consortium is trying to obtain federal funding for its efforts, the teaching program in the meantime has found financial support from producers, producer trade organizations and allied industry. Its inaugural program was launched in the summer of 2008 in Clovis, New Mexico, an area chosen for its close proximity to dairies with a wide variety of management levels, housing styles and parlor designs. This location provided a unique opportunity to teach students advanced dairy science with a large dose of hands-on, real-world dairy management training in the large herds of the Southwest. The program is coordinated by faculty from the participating universities. The different modules were taught by nationally recognized and experienced faculty in dairy management. Eighteen students from six different universities attended the inaugural program for which they obtained credit with their home universities. In addition to classroom instruction, a large portion of each day was spent on local dairies applying the science and evaluating management practices. Exit evaluations resulted in unanimous high approval ratings for the program. This class is well on its way to become an industry wide training program for graduating dairy and ag-business majors in line to become herd managers, technical representatives, extension agents, etc. While 8 universities had joined the original program in 2008, three additional universities have since joined the consortium while planning the 2009 program.

Key Words: innovative dairy teaching, large dairy herd management, Southern Great Plains Dairy Consortium

503 The Dairy Cattle Breeding Simulation Program (DCBSP 4.9), an interactive software to teach animal breeding principles and practices. J. Casellas[1,2], A. Ahmadi[2], R. A. Verdugo[2], G. A. E. Gall[2], and J. F. Medrano*[2], [1]*Genètica i Millora Animal, IRTA-Lleida, Lleida, Spain*, [2]*Department of Animal Science, University of California, Davis*.

We have developed the Dairy Cattle Breeding Simulation Program (DCBSP) to teach undergraduate and graduate students animal breeding principles associated with selection for multiple traits in dairy cattle. The structure of this program was originally developed at Virginia Tech by M. McGilliard and R. Pearson using a contemporary comparison genetic evaluations procedure. The program was modified throughout the years at the University of California-Davis and a web-based interphase was developed to interact in the teaching environment. The new version of the program (DCBSP 4.9) has been completely rewritten in Fortran90 and focuses on the genetic evaluation of dairy traits by a multivariate animal mixed model, also allowing for marker assisted selection. This software simulates a population of dairy cattle herds and AI bulls through several generations by integrating students' decisions about mating, culling, and selection of new heifers and AI bulls. All simulation parameters (e.g. number of herds and cows, variance components, effect of genetic markers) can be defined by the administrator of the program in relation to the animal breeding course. During each running period, the program simulates the composition of each herd during a virtual year, generating new calves and new productive records and performing a genetic evaluation for all phenotypic traits. A herd-specific extensive summary of all demographic, productive and genetic data is provided to the students at the end of each running period. Students make mating and culling decisions on the basis of the predicted transmitting abilities for phenotypic traits, β-lactoglobulin and κ-casein genotypes, and inbreeding, and upload this information to a server. After several running periods, the genetic trend can be evaluated, providing a realistic experience for the development of animal breeding skills that will be relevant to students with a basic knowledge of animal breeding.

Key Words: animal breeding, dairy cattle, teaching

Wednesday, July 15, 2009
POSTER PRESENTATIONS

Animal Health

W1 The economic impact of five dairy cattle clinical diseases as measured by the correlation between Lactational incidence risk and the income over feed cost in Wisconsin dairy herds. M. C. Ruiz* and V. E. Cabrera, *University of Wisconsin, Madison*.

The objective of the study is to show the reduction in profit associated with herd level disease. The association between the lactational incidence risk (LIR) of five production diseases and the income over feed cost (IOFC) is being established in 30 Wisconsin dairy herds. The studied diseases are: (1) milk fever, (2) retained placenta, (3) displaced abomasum, (4) clinical ketosis, and (5) ovarian cyst. The incidences of these diseases is monthly calculated using standardized definitions to report cases. The IOFC is calculated for each herd according to DHI production records, milk check prices and feed costs reported by the producers. The IOFC is regressed against the LIR of the diseases to obtain the economical losses associated to each of the studied diseases. Preliminary results are showing that the LIR of the diseases found in this study are inside the LIR ranges previously reported in the literature, with exception of displaced abomasum, which seems to be higher than previously reported. Results are suggesting that the 2 most economically important diseases impacting the IOFC are clinical ketosis and displaced abomasum. Inferences from our regression models are indicating that 1% of LIR increase is associated with $0.15/cow/day and $0.08/cow/day of IOFC losses for clinical ketosis and displaced abomasum, respectively.

Key Words: disease economic impact, production disease, profitability measurement

W2 Cows response to glucose tolerance test (GTT) and periparturient diseases: Preliminary study. G. Matteo*, C. Chiara, C. Mauro, and M. Massimo, *Department of Veterinary Clinical Sciences. University of Padua, Legnaro, Padova (PD), Italy*.

Most of the metabolic diseases occur within the first 2 weeks of lactation and most periparturient abnormalities have some metabolic element as a component of the sufficient cause of clinical disease. In pregnancy and lactation the glucose requirements are considerably high than and many studies on ewes demonstrated that as pregnancy advances, circulating maternal insulin concentrations decline and the insulin response to glucose is reduced. Insulinemia decreases during the last third of gestation and early lactation: this have been postulated to be the result of a decreased response of the pancreas to insulinotropic agents. Additionally, the sensitivity of peripheral tissues to insulin is reduced. The objective of this study was to evaluate cows response to glucose load in order to identify potential differences in insulin sensitivity/glucose resistance by circulating concentrations of glucose. Eighteen dairy cows in late dry period (10±5 days from predicted calving) have been submitted to glucose load that consisted in i.v. injection of 0.5g/kg bw (using 50% glucose solution). Glycaemia was measured before the glucose infusion (T0) and at 10 minutes (T10), T20, T40, T80 after the infusion. The basal glycaemia of cows (T0) was 59.60±5.39mg/dl; the mean glycaemia at T10 was 155.40±21.83 at T20 was 128.80±20.05 and decreased progressively until T80. A difference was observed at T80 when some cows reached again the initial glycaemia but others did not. According to this difference we divided cows into two classes: 1 (normal cows) with ratio T80/T0≤1.05, 2 (glucose resistant cows) with T80/T0≥1.05. This classification is justified by the statistically significant difference present between T80 in group 1 and group 2 (P≤0.001). We think that these results are important to start a research about glucose metabolism of dairy cows in the transition period and to understand their susceptibility to periparturient diseases related to their ability to metabolize glucose in peripheral tissues. We could suppose that cows with different response to glucose load will probably present different clinical situation after parturition.

Key Words: dairy cows, pregnancy, glucose metabolism

W3 Effect of modified yeast extract and HSCAS containing mycotoxin adsorbent on blood metabolites of dairy cows challenged with aflatoxin B1. M. R. Akkaya[1], M. A. Bal[1], F. Inanc Tolun[1], F. Bilge[1], Y. Atli[1], and V. Akay*[2], [1]*Kahramanmaras Sutcu Imam University, Turkey*, [2]*Global Nutritech Ltd., Kocaeli, Turkey*.

Mycotoxins are secondary metabolites of fungus and cause economical losses in livestock production. An experiment was conducted to test the efficacy of modified yeast extract and HSCAS containing mycotoxin adsorbent (MP; MYCOPURGE®) on blood metabolites of dairy cows fed an aflatoxin B1 (AFB1) containing diet. Eighteen lactating Holstein cows were used in a 3×2 factorial arrangement of randomized block design. Cows were assigned to one of the six treatments of a 14 d period. Treatments (T) were: 1) control (no MP and no AFB1); 2) no MP + 0.6 mg AFB1; 3) 10 g/d/cow MP + no AFB1; 4) 10 g/d/cow MP + 0.6 mg AFB1; 5) 20 g/d/cow MP + no AFB1; and 6) 20 g/d/cow MP + 0.6 mg AFB1. Blood samples were taken from d 1 through d 8 and again on d 14 before feeding. Blood urea nitrogen concentration was lower (P<0.05) for T6 (12.3 mg/dL) than T2 (14.3 mg/dL). Creatinine concentration was higher in MP supplemented cows fed with AFB1 than cows fed no AFB1 (MP*AFB1 interaction; P<0.01). Although total cholesterol level was reduced by AFB1 feeding (193.6 vs. 240.9 mg/dL for T2 and T1; P<0.01), MP supplementation effect was not observed across treatments. The total triglyceride level was lower for cows that received T4 (16.5 mg/dL) and T6 (17.7 mg/dL) compared to T1 (25.6 mg/dL; MP*AFB1 interaction; P<0.01). Although serum alanine aminotransferase level was reduced by AFB1 challenge (57.5 vs. 77.4 U/L for T2 and T1), MP supplementation increased the level of this enzyme in both T4 (65.1 U/L) and T6 (70.5 U/L; P<0.01). However, alkaline phosphatase level was reduced by MP supplementation in both T4 (34.9 U/L) and T6 (30.9 U/L) compared to the AFB1 challenged cows in T2 (70.5 U/L; P<0.01). Although serum albumin concentration was reduced by AFB1 feeding (1.49 vs. 1.63 g/dL for T2 and T1; P<0.01), MP supplemented cows resulted in a higher serum albumin regardless of AFB1 challenge, averaging 1.67 g/dL (MP effect; P<0.01). Results indicate that impaired blood profiles in AFB1 challenged cows may be controlled by supplementing modified yeast extract and HSCAS containing mycotoxin adsorbent.

Key Words: modified yeast extract, aflatoxin, dairy cows

W4 Comparison of rectal and vaginal body temperatures in lactating dairy cows. L. A. Vickers*[1], M. A. G. von Keyserlingk[1], D. M. Veira[3], D. M. Weary[1], and W. Heuwieser[2], [1]*Animal Welfare Program, Faculty of Land and Food Systems, University of British Columbia, Vancouver, British Columbia, Canada*, [2]*Clinic for Animal Reproduction, Faculty of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany*, [3]*Agriculture and Agri-Food Canada, Pacific Agriculture Research Station, Agassiz, British Columbia, Canada*.

The most commonly used method to identify illness in dairy cows is measuring body temperatures with a rectal thermometer. Although a circadian body temperature rhythm has been described for healthy dairy cows little is known of how illness affects the circadian body temperature rhythm. The objectives of this study were: 1) to validate measures by comparing rectal and vaginal temperatures in fresh cows and, 2) to investigate whether cows at high risk for illness (i.e. retained placenta) have a different diurnal temperature pattern than healthy cows. A total of 27 Holstein cows were enrolled 2 (±0) days after calving (20 healthy, 7 RP). Rectal temperatures were taken at 6:30, 9:30, 12:30, 15:30, 18:30, and 21:30 (±30 min) with a digital thermometer (GLA M750, GLA Agricultural Electronics, San Luis Obispo) for 8 consecutive days. During the same 8 d period vaginal temperatures were measured every 10 min with a modified vaginal controlled internal drug release (CIDR) insert fitted with a microprocessor controlled data logger (Minilog 8, Vemco Ltd., Halifax, Canada). The temperature loggers were inserted into the cows' vaginal cavity 2 d after calving. Approximately 2.4% of vaginal recordings could be objectively identified as extreme outliers. With these points removed there was a strong correlation between rectal and vaginal temperatures (n=1282; R^2= 0.64). The RP cows had consistently higher body temperatures for the majority of the day; however both groups had a similar pattern of diurnal temperature rhythms. Highest temperatures were observed at night, while the lowest values were observed between 8:00-10:00 for cows who shed their placenta and 11:00-13:00 for cows with retained placenta.

Key Words: rectal temperature, vaginal temperature, temperature rhythm

W5 Effects of prepartum dietary carbohydrate source on reproductive performance and metabolic disorders in Holstein cows during the periparturient period. H. R. Mirzaei Alamouti*[1], H. Amanlou[2], K. Rezayazdi[1], and A. Towhidi[1], [1]*University of Tehran, Karaj, Tehran, Iran*, [2]*Zanjan University, Zanjan, Zanjan, Iran*.

Eighty Holstein cows, 46 primiparous and 34 multiparous cows, were used in a randomized complete block design and assigned at random to 1 of 2 treatments to evaluate the effects of 2 diets varying ruminal fermentable carbohydrate sources, ground corn (GC) and rolled wheat (RW), on health problems and reproductive performance of primiparous and multiparous cows after calving. The cows were fed diets as total mixed ration (TMR) with similar energy and crude protein content including 1) 18.57% GC, or 2) 18.57% RW from -23.1 ± 9 d relative to expected calving until calving. At parturition, animals were switched from a close-up dry cow diet to a lactation cow diet and, all animals received the same lactation diet until 28 d. Animal were blood sampled every week and days of -1, 0,+1 relative to parturition. The cows were monitored for all disorders and problems. Reproductive data were analyzed by using PROC MIXED of SAS software. The effects of treatments on incidence of health disorders were analyzed by Fisher Exact Test using the FREQ procedure of SAS. The results showed that, the RW diet in prepartum decreased number of artificial insemination, days open, days to first insemination and gestation length (P<0.05). There was no diet effect on udder edema, calving difficulty, and calf birth weight. The incidence of health problems for each treatment cannot be accurately assessed in trial of this size. However, the RW diet decreased overall incidence rates for health problems. In conclusion, feeding prepartum diets with rapidly fermentable source of starch (rolled wheat) can improve reproductive performance and ease metabolic adaptation from gestation to lactation in Holstein cows.

Key Words: periparturient period, carbohydrate source, metabolic disorders and reproductive performance

W7 Factors affecting milk ELISA scores of cows tested for Johne's disease. H. D. Norman[1], J. R. Wright*[1], and T. M. Byrem[2], [1]*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*, [2]*Antel BioSystems, Lansing, MI*.

Infection with *Mycobacterium avium* ssp. *paratuberculosis* (Johne's disease) has been estimated to cost dairy producers over $1.5 billion per year. Effects of environmental and genetic factors on ELISA milk scores for Johne's disease were examined using scores collected through Dairy Herd Improvement testing. Mean and standard deviation for ELISA scores were 0.04 and 0.18. Effects examined were test year, parity, days from calving until test (test stage), and birth and test seasons. Scores (n = 29,389) with information for all effects designated in the model were from 25 herds and 139 herd-years. Distribution of tested animals was 49% for parity 1, 25% for parity 2, 13% for parity 3, and 13% for parities ≥4. Test stages were seven 60-d increments from calving through ≥361 d and represented 10, 7, 6, 9, 23, 22, and 23%, of the data. Birth and test seasons were four 3-mo seasons beginning with January; scores were distributed uniformly among season. Distribution of scores by test year from 2002 to 2008 (incomplete year) was 3, 6, 12, 16, 19, 26, and 17%. Least square differences ($P < 0.001$) were –0.04, –0.03, –0.01, 0.00, 0.01, 0.00, and 0.00 between test years; –0.03, –0.01, 0.01, and 0.00 between parities; and –0.02, –0.03, –0.02, –0.02, –0.02, –0.02, and 0.00 between test stages. Interaction between parity and test stage showed that ELISA scores were higher near peak yield (61 to 120 d in milk) relative to later test stages for parities 1 and 2 than for parity 3 or 4. Effects of birth ($P = 0.72$) and test ($P = 0.38$) seasons were nonsignificant. Variance components were estimated with AIREMLF90 software using the same model but with random effects for sire and cow added. Heritability was low (1%), but repeatability was moderate (21%). The repeatability of milk ELISA scores suggests that the incidence of Johne's disease can be reduced, but the possibility of improving genetic resistance to Johne's is uncertain.

Key Words: paratuberculosis, milk ELISA, DHI

W8 Characteristics of milk ELISA results for Johne's disease in US dairy cows. T. M. Byrem*[1], H. D. Norman[2], and J. R. Wright[2], [1]*Antel BioSystems, Inc., Lansing, MI*, [2]*Animal Improvement Programs Laboratory, Beltsville, MD*.

The expanding practice of using antibody-capture ELISA on Dairy Herd Improvement (DHI) milk samples to test cows for infection with *Mycobacterium avium* subsp. paratuberculosis (Johne's disease) produced data for further study. Milk ELISA results (196,412) from 696 herds in 16 states between 2002 and 2008 had a mean score of 0.04, a standard deviation (SD) of 0.18, and revealed 3.2 and 6.1% positives based on cutoffs of 0.40 and 0.10, respectively. A subset of data (42,778) from more comprehensive testing in 25 herds from Michigan and Wisconsin had a mean score of 0.04, a SD of 0.18, and 3.0 and 5.6% positives based

on cutoffs of 0.40 and 0.10, respectively. For cows with multiple tests within parity (12%), those with negative scores (<0.10) on the first test were negative on the last test 94.6% of the time. Cows with positive scores on the first test were positive on the last test 51.7% of the time. For cows with multiple tests across parities (36%), equivalent frequencies were 90.9 and 47.0%. Within herd and year, differences in milk yield (kg) between cows with negative and positive ELISA results based on cutoffs of 0.40, 0.10, 0.06, 0.04, 0.02, and 0.00 were 528, 479, 404, 315, 295, and 305, respectively. Differences in milk yield were similar until the cutoff for ELISA score exceeded 0.05, suggesting a point where a notable percentage of infected cows were included in the positive group, thereby revealing their lower productivity through mean milk yield. Untested cows had lower mean milk yield than tested cows, even those whose test was positive. Examining the termination code for positive, negative, and untested cows revealed an unusually high percentage (44%) of the untested cows were removed from the herd by the end of the current lactation. This was in contrast to 15% of the positive cows and 12% of the negative cows being removed from the herd. Further analysis of the data will demonstrate the utility of DHI records in the evaluation of milk testing programs for Johne's disease.

Key Words: paratuberculosis, milk ELISA, DHI

W9 Johne's outreach survey. K. E. Olson*, *KEO Consulting, Schaumburg, IL*.

The Voluntary Bovine Johne's Disease Control Program (VBJDCP), operational since 2002, is available to producers in all states. The program includes `test negative' or `Status Herds' who have found no Johne's positive animals in one or more years of testing, as well as `management' herds who have conducted a risk assessment and implemented a Johne's management plan, but who may not have tested for the disease. Federal funding for the program has decreased from $21m in 2003 to $10.05m in FY08. Metrics used to evaluate effectiveness of the program have included herds enrolled as well as `official' samples tested. In FY07 8,818 herds were enrolled in the program, including approximately 10% of the dairy herds and roughly 0.3% of the beef cow-calf operations. In contrast, 94.1% of participants in the NAHMS Dairy 2007 study indicated they were fairly knowledgeable or knew some basics about Johne's and 30% reported participation in a Johne's program. In addition, responding to producer interest, many DHIA organizations now offer Johne's milk ELISA testing. It is important to document indicators of program impact, beyond herd enrollment, in order to maintain Congressional program funding and effectively implement the new Johne's Strategic Plan based on public private partnership. To document outreach activities not captured in current metrics, surveys were developed and distributed to Designated Johne's Coordinator in each state as well as select extension, DHIA and industry representatives. Preliminary responses found: – A cadre of over 2,000 trained Johne's certified veterinarians available across the nation available to work with producer Johne's programs – Meetings held with industry groups are reaching substantial numbers of producers. – Nearly 200,000 milk ELISA samples are being run annually by DHIA with producers paying the cost – DHIA is seeking new ways to provide milk ELISA results with management information to producers. Final results from the survey will demonstrate the scope of outreach activities that have occurred. They will be used to help set directions for implementation of the new strategic plan and provide information useful in maintaining financial support for the program.

Key Words: Johne's, strategic plan, outreach

W10 Perceptions of and participation in a Johne's control program. E. Hovingh*[1], K. E. Olson[2], and J. McDonald[3], [1]*Pennsylvania State University*, *University Park*, [2]*KEO Consulting*, *Schaumburg, IL*, [3]*University of Wisconsin*, *Madison*.

Recently, the United States Department of Agriculture has promoted a voluntary Bovine Johne's Disease control program in the United States (US). Funds were available to states to support the implementation of this program. Enrollment of herds showed evidence of reaching a plateau and information was desired about the reason that herds did or did not participate in the program, and the value of the program to producers. A team of Johne's Disease (JD) experts developed a survey which was mailed to a systematic random sample drawn from a list of 48,078 US dairy herds. The initial mailing (N=8,013) was followed up with a reminder postcard, and a 3rd mailing of the survey to non-responders. 2601 surveys were returned. Of the 555 blank returns, 302 included a notation that the recipient was no longer dairy farming. 28 surveys (1%) were returned stating that the recipient refused to participate. The respondents reported an average of 160 lactating and dry cows in their herd (min=10, max=7200). 48% of the respondents "agreed" or "strongly agreed" that JD was currently a concern in their herd whereas 55% indicated they expected it to be a concern in the future. 27% of 1363 respondents were participating in their State's JD program at some level, a number slightly higher than the participation rate in the USDA's aggregated state-level data. This indicates that participating herds were slightly over-represented in the dataset. 24% of responders not participating in the state program felt that they were already doing everything they could to manage JD, and that participation in the program would provide no additional benefit. Questions intended to gauge the respondents knowledge of JD indicated that there appears to be a reasonable grasp of how new infections occur, but some misunderstanding about the interpretation and use of diagnostic test results. A number of questions were asked to determine the economic importance of JD. 74% of 1677 respondents indicated that they would be willing to pay a premium for replacement animals that had at least a 95% probability of being free of JD. 18% indicated a willingness to spend an additional $200 per head.

Key Words: Johne's disease, survey

W11 Relationship between lying patterns, feeding management, and udder health in lactating dairy cows. B. L. Kitts*[1], S. Dufour[2], D. T. Scholl[2], and T. J. DeVries[1], [1]*Department of Animal and Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, ON, Canada*, [2]*Facultè de Medicine Vètèrinaire, Universitè de Montrèal*, *Saint-Hyacinthe, QC, Canada*.

Fresh feed is often provided to dairy cows either right before or during milking to encourage cows to stand and feed rather than lay down. It is believed that keeping cows standing after milking provides time for the teat canal to close, reducing the chance of penetration by environmental pathogens and, thus, the risk of intramammary infection (IMI). The objective of this study was to investigate whether feeding management influences the latency in time to lay down following milking, and to determine if this time relates to incidence of IMI. Fifteen lactating dairy cows (5 most recently fresh, 10 randomly chosen) from each of 6 tie-stall dairy farms, were enrolled for a total of 90 cows. Mammary quarter samples of milk were taken (for bacterial culture of environmental pathogens: coagulase-negative streptococci, *Corynebacterium bovis*, *Escherichia coli*, *Streptococcus* spp, *Streptococcus uberis*, *Streptococcus dysgalactiae*, and *Klebsiella* spp) from each cow once every 3 wks, for a total of 3 samplings. A new IMI was defined as a positive culture

sample following a negative culture sample. Data on lying behaviour patterns were collected using data loggers for every cow for 7 d prior to each milk sampling. For these 7 d, individual milking and feeding times of the cows was also recorded. Delivery of fresh feed and/or concentrate ± 45 minutes from the onset of milking resulted in cows having a longer latency to lie down following both the AM (80.1 ± 5.0 vs. 71.5 ± 5.3 min; P=0.048) and PM milkings (98.4 ± 5.5 vs. 73.5 ± 5.4 min; P<0.001). Interestingly, the odds of a new IMI caused by any one of the environmental bacteria increased by 1.09 for every 10-min increase in latency to lie down following milking (P_{Wald}=0.01; 95% confidence interval = 1.02, 1.17). Given that this logistic model only accounted for 2% of the variation in risk of a new IMI (R^2=0.02, $P_{Likelihood\ Ratio}$=0.01) and that the increase in odds was very small, it appears that the amount of time cows spend standing following milking, in the range of that observed, has little effect on the incidence of new IMI caused by environmental pathogens.

Key Words: dairy cow, lying behavior, intramammary infection

W12 Using gait score and resting behavior to detect hoof lesions in cows. N. Chapinal[2], A. M. de Passillé[1], D. W. Weary[2], M. A. G. von Keyserlingk[2], and J. Rushen*[1], [1]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada*, [2]*University of British Columbia, Vancouver, BC, Canada*.

Improved gait scoring to detect lameness requires knowing which changes in gait best indicate hoof lesions. We examined whether changes in gait or resting time predict the development of hoof lesions. Forty-seven Holstein cows housed in a free-stall barn were gait scored every 4 wks from 4 wks before to 24 wks after calving. We assessed overall gait (scored 1 to 5) and 7 gait attributes (abduction/adduction of the back legs, back arch, head bob, tracking-up, joint flexion, asymmetric gait, and reluctance to bear weight) (scored 0 to 100). Activity loggers attached to the cows' legs measured resting time over 24h. Cows' hooves were inspected every 4wks and the occurrence of sole ulcers or sole hemorrhages was noted. Six cows developed sole ulcers after calving and showed no hoof lesions or signs of lameness before calving. These were matched with 6 cows that developed only sole hemorrhages and 6 cows that did not develop any sole lesions and that were of the same parity and DIM. Before calving, there were no differences (PROC GLM P>0.10) between these three groups of cows in any measure of gait. After calving, cows that developed sole ulcers scored higher than cows that did not develop sole ulcers for overall gait score (cows with no lesions vs cows with ulcers; mean ± SE; 2.3 ± 0.1 vs 3.1 ± 0.1), back arch (24.9 ± 2.8 vs 45.0 ± 2.8), joint flexion (41.2 ± 2.9 vs 55.4 ± 2.9), asymmetric gait (40.3 ± 2.8 vs 62.2 ± 2.8) (PROC MIXED P<0.05) and reluctance to bear weight (1.3 ± 0.8 vs 11.7 ± 4.2, P<0.05; Wilcoxon). There were no differences between cows that did not develop any lesion and those that only developed hemorrhages. Overall gait score, back arch and asymmetric stepping were higher (P<0.05) among cows that developed an ulcer 4 wks before the ulcer was diagnosed. An interaction between hoof health and time was found for lying time (P = 0.02). Daily lying time decreased more quickly before calving and increased more quickly after calving in cows that developed an ulcer. Regular gait scoring can detect cows lame from a sole ulcer before the ulcer is apparent on the hoof. An arched back and asymmetric stepping are the gait attributes that best indicate sole ulcers.

Key Words: lameness, gait, welfare

W13 Effect of metritis on health, fertility and milk production in two subsequent lactations in dairy cows. J. R. Lima*[1], J. E. P. Santos[2], and R. G. S. Bruno[1], [1]*University of California - Davis, Tulare*, [2]*University of Florida, Gainesville*.

Lactating Holstein cows (n=953) in their first lactation were monitored daily during 28 d after calving for postpartum diseases. Animals with watery, fetid, reddish/brownish uterine discharge with or without fever were defined with metritis and received intrauterine infusion (IU infusion) with 6 g of oxytetracycline. IU infusions were performed every other day until signs of metritis recede. Cows were monitored in two subsequent lactations. Cows were presynchronized with two injections of PGF at 37 and 51 d in milk (DIM), and those cows not observed in estrus after the second PGF were enrolled in a timed AI program starting at 62 DIM. Milk yield was recorded once a month during the first two lactations. Data were analyzed by ANOVA and logistic regression using SAS. A total of 379 cows (49.6%) and 166 cows (21.7%) were identified with metritis in the first and second lactations, respectively. Out of 166 cows with metritis in the second lactation, 99 cows (59.6%) were also diagnosed with metritis in the first lactation. Dystocia was the main risk factor for metritis in both lactations (odds ratio, OR=4.8; 95% confidence interval, CI=3.15-7.45; and OR=6.0, CI=3.38-10.62 for 1st and 2nd lactations, respectively). Metritis affected (P>0.01) the proportion of pregnant cows at first AI at the 1st lactation (35.3 vs 44.0%) but not (P=0.67) in the 2nd lactation (34.0 vs 38.4%). In the 1st lactation, cows without metritis had increased (P=0.008) pregnancy at first AI than cows receiving 1 or 2 IU infusions, but it was not different (P=0.61) than cows receiving more than 2 IU infusions (44.0, 30.3 and 42.6% respectively). Incidence of metritis affected (P>0.01) milk production on the first month postpartum in both lactations (25.6±0.30 vs. 27.6±0.31 Kg/d in the 1st lactation, and 33.3±0.62 vs. 37.9±0.36 Kg/d in the 2nd lactation for metritis and no metritis cows, respectively). An increased proportion (P=0.007) of cows with metritis was eliminated from the herd before the 2nd lactation compared with cows without metritis (20.1 vs 13.5%). Metritis negatively impacted performance in the first and subsequent lactation.

Key Words: dairy cow, intrauterine therapy, metritis

W14 Effects of feeding menhaden fish meal or Ca salts of fish oil fatty acids on some cytokine genes expression and endometrial cytology in early lactating cows. A. Heravi Moussavi*[1], H. B. Roman[2], T. R. Overton[2], D. E. Bauman[2], W. R. Butler[2], and R. O. Gilbert[2], [1]*Department of Animal Science and Excellence Center for Animal Science, Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran*, [2]*Cornell University, Ithaca, NY*.

The study was designed to test the effects of dietary fatty acid supplementation on IFN-γ, IL2, and IL10 genes expression, and also endometrial cytology in early lactating cows. From d 5-50 postpartum (PP), cows (n = 30; 6/treatment) were fed diets that were isonitrogenous, isoenergetic and isolipid containing 0 (Control), 1.25, 2.5 or 5% menhaden fish meal or 2.3% Ca salts of fish oil fatty acids. Samples for endometrial cytology (low-volume uterine lavage) were obtained on days 25 and 50 PP. A subjective score of 0-3 was assigned with 0 representing the absence of inflammation and 3 as a severe inflammation. On day 50 postpartum, uterine endometrial biopsies were collected for gene expression analysis. Expressions of IFN-γ, IL2, and IL10 were tested by real-time PCR using TaqMan primers/probes. Results were analyzed using comparative critical threshold (ΔΔCT) method in which the amount of target RNA was adjusted to a reference, glyceraldehyde-

3-phosphate dehydrogenase. The initial cytology data were transformed and then were analyzed using mixed models for a completely randomized design with repeated measures. The gene expression data were analyzed using general linear models for a completely randomized design. The cytology data showed that the dietary groups had no effect on uterine inflammation (P=0.07). The effect of time and the interaction of time and treatment were not significant (P>0.16). Compared with the Control, gene expression of IFN-γ (P=0.65; 0.75, 0.58, 0.65 and 0.37 ± 0.22, respectively), IL2 (P=0.079; 0.81, 0.26, 0.36 and 0.35 ± 0.14, respectively) and IL10 (P=0.087; 2.76, 0.83, 1.75 and 0.39 ± 0.63, respectively) were all similar among the supplemented groups. The results demonstrated that the dietary treatments had no apparent effect on the cytokines gene expression and uterine inflammation.

Key Words: dairy cows, endometrial cytology, gene expression

W15 Feeding dairy cows barley grain treated with lactic acid and heat modulated diurnal patterns of selected plasma metabolites. S. Iqbal, Q. Zebeli, A. Mazzolari, S. M. Dunn, and B. N. Ametaj*, *University of Alberta*, *Edmonton, Alberta, Canada*.

The aim of this study was to evaluate the effects of feeding barley grain treated with lactic acid (LA) and heat on diurnal patterns of plasma metabolites in dairy cows. Eight ruminally cannulated Holstein cows (170 DIM) were fed once daily a TMR based on rolled barley grain (32.8% on DM basis) steeped for 48h in equal quantity of water (CTR) or with 1.0% LA (v/v) and heated in an oven at 55°C (TRT). Cows were assigned to the treatments according to a replicated 2 × 2 Latin square design with two 21-d periods, where the first 11d were used for diet adaptation. Blood samples were collected from the tail vein on d 10 of each period shortly before (i.e., at 0h) and at 2, 4, 6, 8, 10, and 12h post-feeding, and analyzed for glucose, lactate, beta-hydroxybutyric acid (BHBA), non-esterified fatty acids (NEFA), and cholesterol. Results showed that feeding the TRT diet decreased concentration of glucose in the plasma (52.7 vs. 49.7 mg/dL; P=0.04), and increased that of BHBA (1,111 vs. 1,502 μmol/L; P<0.01). The time after feeding also affected concentration of metabolites (P<0.01) in the plasma. For example, the effect of TRT diet was more pronounced at 8 and 10h post-feeding for glucose and at 6h for BHBA. Further, feeding the TRT diet tended to increase the overall concentration of circulating NEFA (109 vs. 117 μEq/L; P=0.08). Additionally, cows fed the TRT diet had greater plasma NEFA (110 vs.78 μEq/L; P=0.01) at 12h post-feeding indicating an influence of time after feeding on this variable. However, no effect of diet was obtained for diurnal patterns of plasma lactate (629 vs. 648 μmol/L; P=0.61) or cholesterol (121 vs. 120 mmol/L; P=0.89). In conclusion, feeding 32.8% of diet DM barley grain treated with lactic acid and heat modulated diurnal patterns of selected plasma metabolites. Further research is warranted to establish the influence of these metabolic changes on the health and productivity of early lactating dairy cows.

Key Words: barley grain, diurnal response, dairy cows

W16 Treating barley grain with lactic acid and heat modulates selected plasma metabolites in dairy cows. D. Mansmann, Q. Zebeli, A. Mazzolari, S. M. Dunn, and B. N. Ametaj*, *University of Alberta*, *Edmonton, Alberta, Canada*.

Barley grain contains high amounts of degradable starch and is a potential alternative to corn as a digestible energy source in western Canada. However, feeding dairy cows diets high in readily degradable starch increases the incidence of metabolic diseases. Chemical and thermal processing of barley grain might modify ruminal starch degradation modulating blood metabolic profile. The objective of this study was to investigate the effects of feeding barley grain treated with lactic acid (LA) and heat on variations of plasma metabolites. Eight ruminally cannulated Holstein cows (170 DIM) were offered once daily at 0800 a TMR containing rolled barley grain (32.8% on DM basis) steeped in equal quantity of water (CTR-diet) or with 1.0% LA (v/v) and heated in an oven at 55°C (TRT-diet). The cows were assigned to the treatments according to a replicated 2 × 2 Latin square design with two 21-d periods where the first 11-d were used for diet adaptation. Blood samples were collected from the tail vein at 0730 on days 1, 3, 5, 7, and 10. Cows fed the TRT-diet had similar DMI with controls (19.8 vs. 20.0 kg/d; P=0.28). Results showed that TRT-diet tended to decrease the overall plasma cholesterol (122.1 vs.118.0 mmol/L; P=0.10). In contrast, cows fed the TRT-diet showed higher circulating plasma lactate (663 vs. 537 μmol/L; P=0.02). Other plasma metabolites including beta-hydroxy butyric acid (575 vs. 535 μmol/L; P=0.76), glucose (54.8 vs. 52.4 mg/dL; P=0.36), and non-esterified fatty acids (0.134 vs. 0.128 μEq/L; P=0.34) were not affected by TRT- and CTR-diets, respectively. Additionally, all plasma metabolites measured, except for cholesterol (P=0.73), changed with the day of sampling (P<0.05). This suggests that it is important to take into consideration the day of sampling when interpreting the effect of diets on the blood metabolites measured. In conclusion, the results suggest that feeding dairy cows barley grain treated with lactic acid and heat modulated selected plasma metabolites.

Key Words: barley grain, lactic acid, dairy cows

W17 Effects of *Bacillus subtilis* on antioxidant capacity and immunity of broilers. Y. Dongyou, M. Xiangfei, Q. Yan, and L. Weifen*, *College of Animal Science, Feed Science Institute, Zhejiang University*, *Hangzhou, Zhejiang, China*.

This study was conducted to examine the effects of *Bacillus subtilis* on antioxidant capacity and immunity of broilers. A total of 216 one day-old Ross 308 broilers were divided into 2 groups, the control group (basal diet) and the treatment group (basal diet supplemented with 105 CFU/g *B. subtilis*). Each group had three replicates and each replicate included 36 broilers (half male and half female). The experiment was carried out for 6 weeks. Results showed that T-AOC and the activity of GSH-Px of the treatment group was increased significantly (P<0.05), while level of serum MDA, NO and liver MDA were decreased significantly (P<0.05). *B. subtilis* did improve thymus index, bursa index and the level of serum IgG, but did not significantly affect Spleen index, serum lysozyme, IL-2, TNF-α (P<0.05). These results indicate that antioxidant capacity and immunity of Ross 308 broilers were improved by basal diet supplemented with *B. subtilis*.

Key Words: *Bacillus subtilis*, broiler, immunity

W18 Melamine residues in tissues of ducks fed diets containing graded levels of melamine. M. Lü*, L. Yan, J. Guo, Z. Sun, and S. Zhu, *Research and Development Center, Liuhe Feed Co., Ltd.*, *Qingdao, Shandong, China*.

An experiment was conducted to determine melamine residual levels in the tissues of ducks fed diets containing graded levels of melamine. 300 day-old ducks (Cherry Valley duck SM3) were assigned to 10

dietary treatments. Ten experimental diets were developed to contain 0, 2, 5, 10, 20, 50, 100, 200, 500, and 1000 mg of melamine per kg of diet. Each diet was offered three replicate pens (10 ducks per pen) from d 1 to 42, followed by a 7-d feeding of a withdrawal diet that contained no melamine. On d 14, 28, 42, and 49, one duck was randomly selected from each replicate pen and euthanized by cervical dislocation, then samples of the breast meat, liver and kidney were obtained. The melamine concentrations were determined using high-performance liquid chromatography. The data was analyzed by the Kruskal-Wallis one-way ANOVA. There were no visible signs of ill health or changes in the behaviour of ducks, and no difference ($P > 0.05$) in weight gain among different treatment groups during the 49-d experimental period. The residual levels of melamine in duck tissues were below the detection limit when diets contained less than 50 mg/kg melamine. On d 42, melamine levels in breast meat, liver and kidney increased linearly ($P < 0.05$) with the increasing levels of melamine in diets containing more than 50 mg/kg melamine ($R^2 = 0.95$; $R^2 = 0.96$; $R^2 = 0.94$, respectively). The distribution of melamine differed varied in different tissues, kidney was found to accumulate the highest concentration of melamine. On d 42, when diets contained 1000 mg/kg melamine, the residual levels of melamine in the kidney (18.33 mg/kg) was higher than in the breast meat and liver (9.20 and 8.27 mg/kg) ($P = 0.05$). After a 7-d withdrawal period, melamine was not detected in the duck tissues, it showed that ducks had the ability to quickly deplete the melamine that accumulated in tissues.

Key Words: melamine, duck, residual

W19 Metabolic and histological evaluation of quails fed with or without genetically modified Bt-maize. N. Scholtz*[1], G. Flachowsky[2], I. Halle[2], and H. Sauerwein[1], [1]*University of Bonn, Bonn, Germany*, [2]*Friedrich-Loeffler-Institute, Braunschweig, Germany*.

Feeding *Bacillus thuringiensis* transgenic (Bt)-maize is suspected for potential adverse effects on animal health by some groups. Using quail as a model for up to 20 generations, no consistent and analogous alterations in serum biochemistry and liver histomorphology in the 17th to 20th generation of Bt-feeding occurred. In multigenerational experiments, genetic drift might be an issue and therefore we extended the examinations to animals fed ad libitum with diets containing 50% Bt maize or isogenic maize of the same cultivar (REF1) in first generation. To elucidate the naturally occurring variance of all variables tested, two further controls with isogenic hybrid reference maize (REF2, REF3) were included. The quails were kept in breeding pairs and comprised 30 male and 30 female animals per feeding group. At 16 weeks of age, all animals were slaughtered; blood samples were collected and analysed for serum biochemical parameters. In addition, liver samples from these animals were histomorphometrically evaluated. Statistical analyses were done by ANOVA. Significant ($P < 0.05$) findings (means ± SD) are presented in the following table. The statistical differences observed herein were not limited to Bt × REF comparisons and thus give no indication for targeted pathophysiological alterations induced by Bt feeding. The lack of obvious adverse effects in our quail studies is of general importance to animal science.

Table 1.

Variable	Bt	REF1	REF2	REF3
male				
Hepatocyte nuclear size (μm^2)	18.1±1.2^a	17.1±1.3^b	17.7±1.1^{ab}	17.4±1.4^{ab}
AST (U/l)	493±134^a	419±105^{ab}	377±83.8^b	407±85.3^b
ALT (U/l)	14.8±6.3^a	13.6±6.6^a	9.9±2.7^b	10.5±1.7^b
Glu (mM)	106±92.1^a	97.7±98.8^a	190±22.9^b	183±20.5^b
female				
Hepatocyte nuclear size (μm^2)	20.6±2.1^a	19.2±2.0^b	19.7±1.8^{ab}	19.7±1.5^{ab}
γ-GT (U/l)	2.0±1.7^a	1.2±0.5^b	1.3±1.3^{ab}	1.0±0.0^b
Glu (mM)	101±76.0^a	41.1±69.4^b	173±19.6^c	164±15.1^c

Means within rows with different superscript letters differ significantly

Key Words: genetically modified, Bt-maize, Japanese quail

W20 Immune response in quail fed with or without genetically modified Bt-maize. N. Scholtz*[1], G. Flachowsky[2], and H. Sauerwein[1], [1]*University of Bonn, Bonn, Germany*, [2]*Friedrich-Loeffler-Institute, Braunschweig, Germany*.

Potentially adverse effects of diets containing transgenic plants are a concern for many consumers, particularly in Europe. For Bacillus thuringiensis transgenic (Bt) maize, a number of studies in livestock and poultry is available, showing that both zootechnical as well as blood chemistry data give no indication for such adverse effects. These studies were all done in homeostatic situations; it remained open whether a deflection of the regulatory physiological systems might yield divergent dynamic responses in Bt-maize fed animals. We therefore tested the effect of an active immunisation against BSA in feeding regimen with or without Bt-maize using quail as a model organism. Japanese quail were randomly allocated after hatching to two feeding groups (n=120 per group): group Bt received diets containing Bt-transgenic maize (40% in starter and 50% in grower diets), whereas the control group was fed with analogous rations but with isogenic maize of the same cultivar. After 16 weeks on the experimental diets, one half of each group was immunized intramuscularly with 1 mg BSA in 100 µl Freund's complete adjuvant. The remaining animals were sham-immunized with NaCl. Egg yolk samples were obtained biweekly from 0 to 6 wk following the injection and were analyzed for egg yolk total IgY concentration and BSA-specific IgY titers. Statistical analyses were done by the mixed model; fixed effects included time of sampling, feeding group, immunization mode, and their respective interactions. Expectedly, total IgY as well as BSA-specific IgY titers increased ($p < 0.05$) with time in the BSA-immunized quail. In contrast to sampling time, the response of both variables to the BSA injections was not different between the feeding groups. Our results indicate that feeding of transgenic Bt-maize does not impair the immune system of Japanese quail and thus gives no indication for respective concerns. The lack of obvious adverse effects is something of general importance to animal science.

Key Words: genetically modified Bt-maize, Japanese quail, immune response

W21 Ameliorating effect of ascorbic acid on subacute endosulfan toxicity in male New Zealand White rabbits. F. S. Hatipoglu[1], O. Ozmen[2], A. Ata[3], T. Ileri-Buyukoglu[4], S. Sahinduran[5], F. Mor[6], O. Yildiz-Gulay[1], and M. S. Gulay*[1], [1]*Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Department of Physiology, Burdur, Turkey*, [2]*Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Department of Pathology, Burdur, Turkey*, [3]*Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Department of Reproduction and Artificial Insemination, Burdur, Turkey*, [4]*Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Department of Biochemistry, Burdur, Turkey*, [5]*Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Department of Internal Medicine, Burdur, Turkey*, [6]*Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Department of Pharmacology, Burdur, Turkey*.

The present study was conducted to evaluate the protective role of oral ascorbic acid (AA) against some hematological parameters and histopathological changes in male New Zealand White rabbits (NZW) treated with endosulfan. Rabbits (6 to 8 months old) were divided into 4 groups of 6 animals each. Rabbits in T-I served as control and received corn oil for 6 weeks. Rabbits in T-II received endosulfan (1 mg/kg bw per day) in corn oil. T-III group received corn oil daily and AA (20 mg/kg bw) every other day for 6 weeks. T-IV received the same amounts of endosulfan and AA. All treatments were given by oral gavages. Total erythrocyte, leukocyte, trombocyte and percent hemoglobin, hematoctrit, lymphocyte, granulocyte and monocyte for rabbits in T-I, II, III, and IV were 6.99, 6.91, 6.6 and 6.63×10^6 /μL; 9.13, 8.41, 7.91, and 6.27 $\times10^3$ /μL ($P<0.04$); 480.8, 471.5, 438.5 and 407.3×10^3 /μL; 13.45, 12.76, 13.07 and 13.56 g%; 40.7, 38.0, 37.4 and 39.0% ($P<0.05$); 40.0, 37.8, 35.8 and 41.2%; 52.5, 49.3, 52.6 and 45.9%; and 11.5, 12.9, 11.6 and 12.7%, respectively. The plasma glucose, AA, malondialdehyde, glucose 6 phosphatedehydrogenase, glutathion peroxidase and erythrocyte catalase for same treatment groups were 139.9, 148.6, 121.8 and 128.2 g/dL ($P<0.09$); 1.60, 1.43, 1.72, and 1.44 mg/dL ($P<0.01$); 1.73, 1.51, 1.77 and 1.44 nmol /mL; 3.78, 3.61, 3.90 and 4.88 U/gHb; 11.2, 12.2, 12.1 and 13.0 U/gHb ; and 23.2, 24.1, 26.0 and 23.0 U/gHb , respectively. Gross post-mortem and histopathological changes in liver, kidney, and testes of rabbits in T-II were observed with typical organochlorine dose-dependent signs of toxicity. Degenerative regions in liver, testis and kidney, hyperplasic tissue in gall bladder, and decreased number of spermatozoon in seminiferous tubules were apparent. High numbers of caspase positive cells were visible in the liver. However, AA treatments in T-IV were able to decrease the negative effect of endosulfan in tested organs and numbers of caspase positive cells were lower than T-II. Thus, results suggested beneficial influences of AA in neutralizing some toxic effects of endosulfan in male NZW.

Key Words: blood parameters, histopathology, antioxidant enzymes

W22 Effect of autolysed yeast on macrophage activation in vitro and performance of weaning piglets. A. Ganner*[1], S. Nitsch[2], and G. Schatzmayr[1], [1]*BIOMIN Research Center, Technopark 1, Tulln, Austria*, [2]*BIOMIN Holding GmbH, Industriestr. 12, Herzogenburg, Austria*.

The target of the present study was to investigate the ability of yeast autolysate to activate macrophages in vitro and additionally to evaluate the performance and health status of weaning piglets. As an in vitro model a chicken bone marrow-derived macrophage cell line (HD_11) transformed by a retrovirus (MC29, v-myc oncogene) was used. The nitric oxygen production was determined as an indicator for immune stimulation. It was determined after 48 h of incubation with or without yeast product in the supernatant of the cultures using a Griess reagent which provides a colorimetric reaction. Results were compared with the positive control (LPS *E. coli* 0127; 20ng/mL ±10 μMol NO) and calculated as a % of the positive control. Nitric oxygen production was enhanced up to 60% compared to the positive control. In contrast to yeast autolysate beta-glucans and nucleotides enhanced the macrophages up to 100%. Subsequently, a feeding trial with weaning piglets was conducted to evaluate the efficacy of yeast autolysate on performance and health status of weaning piglets in a 56 days study. 60 mixed sexed 4 weeks old (average weight approx. 7.47 kg) piglets were divided into 2 experimental groups (30 pigs per group) with 3 replicates: control group A and trial group B with 4kg/T yeast autolysate. Results of the feeding trial indicate a positive influence of yeast autolysate on performance of weaning piglets. Body weight (32.84 kg, P-value >0.05) and daily weight gain (449 g, P-value >0.05) were clearly improved as well as FCR (1.62) in comparison to the control (31.92 kg live weight; 432 g daily weight gain; FCR 1.73). In the yeast autolysate supplemented group no mortality was recorded, whereas mortality was 6% in the control group. In vitro and in vivo results indicate that this particular yeast autolysate product is a health and performance improving agent.

Key Words: yeast, macrophages, animal performance

W23 Monitoring of the efficacy of SOP GOLD PIG on the reduction of the microbial load in an Italian commercial fattening piglet farm. G. Tacconi[1], A. Covarelli[1], and A. Zanierato*[2], [1]*Veterinary Medicine Faculty, Department of Biopathological Science and Hygiene of Food and Animal Productions, Perugia, Italy*, [2]*SOP Srl, Busto Arsizio, Italy*.

This study was conducted in order to evaluate in field, over the period 2006-2008, the efficacy of a new technological additive SOP® GOLD PIG. This product is a natural silicate of magnesium, aluminium and iron, modulated by the technology SIRIO OPERATING PROCESS® to control the growth of some bacteria in pig manure. Two units on a pig farm, treated (T) and control (C), were selected for their similarity in size, pig age and number and farm management. In the treated unit, the product was added to the dry feed, using 80 g of SOP GOLD PIG per 1 ton of dry feed. Manure samples were taken monthly both in the unit with pigs receiving the treated food (T) and in the unit with pigs receiving untreated food (C), for a period of 23 months. These samples were analyzed for the presence of the Total Aerobic Bacterial Count (TABC), *Enterobacteriaceae*, *Micrococcaceae* and *Streptococcaceae*, using selective media. The results (Table 1) show significant reductions in the manure of the TABC (-73.1%; $P<0.01$), *Enterobacteriaceae* (-67.6%; $P<0.001$), *Micrococcaceae* (-62.8%; $P<0.01$) and *Streptococcaceae* (-66.9%; $P<0.01$) in unit T. The control of the microbial load in commercial pig farms is essential in order to improve the health and welfare of the animals, and consequently their production performance.

Table 1. Mean values, as log10 (CFU/ml) in pig manure of unit C and T, and statistical evaluations.

Parameters	TABC		Micrococcaceae		Streptococcaceae		Enterobacteriaceae	
	C	T	C	T	C	T	C	T
Geometric mean	8.00	7.30	7.75	7.54	5.03	4.53	4.51	4.18
Mean	7,89	7,32	7.96	7.53	5.02	4.54	4.65	4.16
Std error	0.16	0.14	0.09	0.10	0.09	0.11	0.08	0.08
Std deviation	0.68	0.57	0.43	0.45	0.41	0.47	0.37	0.34
Variance	0.47	0.32	0.18	0.20	0.17	0.22	0.14	0.12
N. samples	19	17	21	19	21	19	21	19
LOC(95%)	0.33	0.29	0.20	0.22	0.19	0.23	0.17	0.17
%reduction		73.1		62.8		66.9		67.6
P=		0.002		0.01		0.00005		0.00003

Key Words: pig health, environment, microbial load

W24 Effect of timing of *Mannheimia haemolytica* challenge following short-term exposure to bovine viral diarrhea virus type 1b on serum cytokine concentrations and muscle and fat gene expression changes in growing beef steers. L. Carlos-Valdez*[1], L. Burciaga-Robles[1], D. L. Step[2], R. W. Fulton[3], A. W. Confer[3], U. DeSilva[1], and C. R. Krehbiel[1], [1]*Oklahoma State University, Department of Animal Science*, *Stillwater*, [2]*Oklahoma State University, Department of Veterinary Clinical Sciences*, *Stillwater*, [3]*Oklahoma State University, Department of Veterinary Pathobiology*, *Stillwater*.

The objective of this study was to determine the effects of an intratracheal Mannheimia haemolytica biotype 1A (MH) challenge following short-term exposure (72 h) to Bovine Viral Diarrhea Virus (BVDV) type 1b persistently infected calves (PI) on serum concentrations of IL-6, TNFα and IFNγ and gene expression changes of TLR4, NFkB, TNFα, and IL6 in subcutaneous fat (SCF) and longissimus dorsi muscle (LDM) of growing beef steers. Eighteen crossbred steers (initial BW = 314 ± 31 kg) were randomly allocated to one of the following treatments: 1) steers not exposed to steers PI with BVDV or challenged with MH (CON); 2) steers exposed to steers PI with BVDV for 72 h followed by an intratracheal challenge with MH 12 h post BVDV exposure (EarlyCh); and 3) steers exposed to steers PI with BVDV for 72 h followed by an intratracheal challenge with MH 72 h after BVDV exposure (LateCh). Blood samples were collected during the first 336 h for serum cytokine analysis and biopsies were performed for the collection of LDM and SCF at -156, 12, 24, 48 and 72 h relative to MH challenge. Serum concentrations of IL6 ($P = 0.001$), TNFα ($P = 0.04$), and IFNγ were increased ($P<0.001$) in EarlyCh and LateCh steers compared with CON steers. Expression of TLR4, NFkB, TNFα and IL6 in LDM were up-regulated ($P<0.02$) for EarlyCh steers compared with LateCh and CON steers. Similarly, TLR4 ($P<0.03$), NFkB ($P=0.07$), and IL6 ($P<0.03$) were up-regulated in SCF for EarlyCh and LateCh steers compared with CON steers. We conclude that muscle and adipose tissue alter expression of cytokines in response to pathogens related to bovine respiratory disease.

Key Words: beef cattle, bovine respiratory disease, cytokines, gene expression

Beef Species: Growth, Concentrate Level, Meat Quality, and Production Traits

W25 Effect of time of ractopamine feeding on growth, carcass characteristics, and muscle biology of steers. M. Hill*[1], K. Chapalamadugu[1], C Schneider[1], R. A. Hill[1], G. Gaylord[2], J. K. Ahola[1], C. W. Hunt[1], J. Szasz[1], and G. K. Murdoch[1], [1]*University of Idaho*, *Moscow*, [2]*USDA/ARS/PWA/SGPGRU*, *Hagerman, ID*.

The labeled use of the β adrenergic agonist; OptaflexxTM in cattle during the last 28-42 days prior to harvest has some practical limitations such as the need to sort cattle. Studies have shown that β-agonists can increase protein accretion and feed efficiency, while potentially decreasing tenderness, marbling, and palatability. An earlier administration of β-agonist (RAC) may enhance the ease of use while maintaining beneficial aspects of late stage RAC supplementation in steers. Eighteen Angus × Hereford steers were evaluated for the effects of a 35 d early (BW = 306 kg) administration of RAC versus 35 d late (BW =508 kg) administration of RAC. Treatments were; no RAC (CON), early RAC (ER), and late RAC (LR) with 6 steer per treatment. Dosage of RAC was based on metabolic body weight (1.15mg RAC kg-1 BW0.75hd-1d-1). Samples of the biceps femoris of each steer were collected before the trial, during the last 2 d of ER, and post-mortem and were evaluated for fiber type. Urine was collected at the end of each administration period for 1-methylhistidine (1METH) analyses, which serves as an indicator of myofibrillar protein turnover. From the first urine collection, ER showed a decrease in 1METH ($P < 0.01$) as compared to all other steers, from the second collection both ER and LR showed decreases in 1METH ($P = 0.03$) from CON. Carcass characteristics and sensory panel analyses were collected and compared among treatments. No significant differences in fiber-types were found between ER and LR. The ER increased ADG during the administration period ($P < 0.01$) when compared to CON and LR. Over the entire trial ADG was not different among the 3 treatments ($P = 0.98$). Values from carcass evaluations (HCW, REA, YG, KPH, fat thickness) were not significantly different between ER and LR. Our study suggests that ER performance is not statistically different from LR; therefore it may be more cost effective and practical to administer ractopamine at an earlier growth stage than the final 35 days pre-slaughter.

Key Words: muscle, beef, beta-agonist

W26 Residual feed intake in progeny of Nellore bulls. Y. B. Farjalla[1], C. U. Magnabosco[2], F. Manicardi[3], F. R. C. Araújo[4], D. P. D. Lanna*[1], and R. D. Sainz[5], [1]*Universidade de São Paulo*, *Piracicaba, São Paulo, Brazil*, [2]*Embrapa Cerrados*, *Planaltina, Distrito Federal, Brazil*, [3]*Guaporé Pecuária*, *Pontes e Lacerda, Mato Grosso, Brazil*, [4]*Aval Serviços Tecnológicos*, *Uberaba, Minas Gerais, Brazil*, [5]*University of California*, *Davis*.

Residual feed intake (RFI), defined as the difference between observed intake and that predicted from average weight and daily gain, has been proposed as a criterion for genetic selection. There has been very little work with this trait in *Bos indicus* breeds. The objective of this study was to assess the genetic variability in RFI in Nellore cattle and to determine the relationship between RFI and carcass and performance characteristics. Seventy-five Nellore steers, progeny of eight bulls (minimum five progeny/bull), were fed individually for 85 days. The diet contained 25% sorghum silage and 75% concentrate on a dry matter basis, and was supplied *ad libitum*. The prediction equation was DMI = 0.0766×Average $BW^{0.75}$ + 1.94×ADG (RSD = 0.725). Animals were classed as low or high RFI if their RFI fell 0.5 SD or more below or above the mean (zero). Individual values of RFI ranged from -1.306 to 2.169 kg/d. Mean RFI for the low and high RFI groups were -0.875 and 0.756 kg/d, respectively; by definition, weights and ADG were similar between RFI groups. There was no difference among RFI groups for hip height and carcass traits. However, intakes and feed:gain were greater ($P < 0.05$) in high as compared to low RFI steers. There was no difference among progeny groups for height, initial and final weight, RFI, carcass weight or marbling score. Progeny groups differed ($P < 0.01$) in dressing percentage (range 53.6 to 55.8%), backfat (range 4.1 to 6.3 mm), 24-hour pH (range 5.57 to 5.84) and shear force (range 3.92 to 6.42). There were tendencies ($P < 0.10$) for differences among progeny groups for DMI, ADG, gain:feed, and ribeye area. None of the carcass traits were clearly related to RFI. These results show the genetic variability in RFI and other traits among progeny of Nellore bulls.

Key Words: beef cattle, carcass, genetic seletion

W27 Effects of breed biotype and concentrate feeding on carcass traits of beef steers. I. M. Oliveira, P. V. R. Paulino*, M. I. Marcondes, S. C. Valadares Filho, J. Cavali, L. F. Prados, A. M. Ribeiro, and N. K. P. Souza, *Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

The objective of this trial was to evaluate the influence of breed biotype (Nellore, NE; 1/2 Nellore × 1/2 Angus, NA; or 1/2 Nellore × 1/2 Simmental; NS) and concentrate feeding (1 or 2% of BW as DM) on carcass traits of beef steers. Steers were assigned to one of six treatments in a completely randomized design resulting from the factorial arrangement of breed biotype and concentrate level. Steers were slaughtered at 22 months of age, averaging 413, 496 and 496 kg for NE, NA and NS, respectively. After slaughter, carcasses were sectioned longitudinally and chilled at 4°C for 24 h. After chilling, carcasses were weighed, and had their subcutaneous fat thickness (BFT), ribeye area (REA; at the 12-13th ribs) measured and dressing percentage calculated. The interaction between concentrate allowance level and biotype was not significant ($P > 0.05$) for any variable evaluated. Crossbred steers (NA and NS) had heavier ($P < 0.05$) carcasses with larger ($P < 0.05$) REA (271 kg and 76.4 cm2,respectively) than Nellore carcasses (222 kg and 61.6 cm2, respectively). Biotype did not ($P > 0.05$) affect dressing percentage (avg. 57.90%). There were differences among biotypes ($P < 0.05$) for BFT. Steers of NA had greater SFT (6.37 mm) than NS (4.62 mm), which was greater than that observed on NE (3.81 mm). Feeding 2% of BW as concentrate led to heavier carcasses and larger dressing percentage (264 kg and 57.6% vs 281 kg and 58.9%, respectively, steers fed 2% vs 1% concentrate as proportion of BW). Concentrate level had no significant ($P > 0.05$) impact on SFT or REA (average 6.56 mm and 75.6 cm2, respectively). Under Brazilian feedlot conditions, feeding crossbred cattle or more concentrate in the diet resulted in heavier carcasses with greater yield per carcass.

Key Words: carcass, *Bos indicus*, biotype

W28 Carcass traits of beef heifers of different genetic groups finished with different concentrate allowance levels. S. F. Reis[1], P. V. R. Paulino*[1], E. J. Souza[3], J. F. Lage[1], R. A. A. Torres Júnior[2], S. C. Valadares Filho[1], L. F. Costa e Silva[1], L. F. Prados[1], and P. B. Benedeti[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*EMBRAPA Beef Cattle Research Center*, *Campo Grande, MS, Brazil*, [3]*Universidade Federal Rural de Pernambuco*, *Recife, PE, Brazil*.

This trial aimed to evaluate carcass traits of heifers of various genetic groups (Nellore n=12, 1/2 Nellore 1/2 Red Angus n=12 and 1/2 Nellore 1/2 Simmental n=12) finished on one of two concentrate levels (0.8% and 1.2% of body weight). The experiment was a completely randomized design with a factorial arrangement of treatments (two concentrate levels × three genetic groups). Diets were isonitrogenous and formulated to meet requirements for maintenance and gain according to Brazilian recommendations. After 84 days on feed, heifers were slaughtered and carcasses cooled for 24 hours at 0°C. Backfat thickness, ribeye area (REA) and cold carcass weight (CCW) were measured. Measurements of carcass temperature and pH were taken immediately after slaughter, and 24 h after cooling. Data were analyzed using the GLM procedure of SAS; effects of treatments were considered significant at $P<0.05$. Concentrate levels had no effect on carcass traits ($P>0.05$). The interaction between genetic group and concentrate level was not significant ($P>0.05$) for any trait evaluated. Differences were detected ($P<0.05$) in carcass traits among genetic groups: 1/2 Nellore 1/2 Angus heifers had higher mean values for backfat thickness (6.71 mm), REA (68.85cm2), HCW (251.8 kg) and CCW (247.0 kg), than the 1/2 Nellore 1/2 Simmental, (4.49 mm; 62.86 cm^2; 212.2 kg; 207.5 kg) and Nellore heifers (4.83 mm; 56.82 cm^2; 205.8 kg; 201.8 kg). The REA/HCW ratio was higher ($P<0.05$) for the 1/2 Nellore 1/2 Simmental heifers (0.60±0.02) than that observed in the Nellore (0.57±0.02) and 1/2 Nellore 1/2 Angus (0.54±0.01) heifers. No differences were detected ($P>0.05$) for carcass pH and temperature, after 24 h of cooling, with mean values of 5.69 and 2.24°C, respectively. As carcass traits were not altered by the concentrate levels assessed (0.8% and 1.2% of BW), costs of feeding concentrate in Brazilian feedlots can be reduced, without compromising carcass quality of beef heifers.

Key Words: Nellore, crossbred, concentrate

W29 Feedlot performance of cull cows fed using three systems. C. L. Wright*[1] and R. J. Maddock[2], [1]*South Dakota State University*, *Brookings, SD, USA*, [2]*North Dakota State University*, *Fargo*.

An experiment was conducted to determine the effect of 3 feeding systems on the performance of cull cows. Seventy-two cull cows (initial BW = 551.3 ± 35.9 kg; initial BCS = 5.1) were randomly allotted to 12 pens. Pens were then randomly assigned to 1 of 3 treatments: 1) traditional, dry rolled corn (DRC)-based finishing diet (TRAD; 81.5% DRC, 11.3% grass hay, and 7.2% supplement), 2) DRC and dried distillers grains (DDGS)-based diet (LOCAL; 54.4% DRC, 29.9% DDGS; 14.3% grass hay, and 1.5% supplement), or 3) a commercial, self-fed product (SELF). Cows on the TRAD and LOCAL treatments were fed a single finishing diet; however, DMI was limited during the first 5 wk of the experiment. Feed was delivered once daily as a totally mixed ration. Cows on the SELF treatment were provided with 3 different blends of the commercial product. On d 0, cows were provided with 75.7 kg/head of a blend containing 60% supplement and 40% DRC in a self feeder. On d 13, 111.4 kg/head of a blend containing 30% supplement and 70% DRC was added to the self feeders. While consuming the first 2 blends, cows were provided grass hay daily at approximately *ad libitum* intake. On d 38, the final blend containing 10% supplement and 90% DRC was added to the self feeder. Grass hay was provided for an additional 7 d once the final blend was added to the self feeder. After 7 d, no forage was provided to cows on the SELF treatment. Treatments were fed for 95 d. Final BW was greater ($P < 0.02$) in cows fed TRAD or LOCAL treatments than those fed the SELF treatment (701.2, 702.6, and 667.8 kg, respectively; SEM = 8.3). Cows fed the TRAD or LOCAL treatments gained faster ($P < 0.04$) than those fed the SELF treatment (1.60, 1.55, 1.28 kg/d, respectively; SEM = 0.08). Dry matter intake (13.1, 13.1, 12.9 kg/d for TRAD, LOCAL, and SELF, respectively; SEM = 0.36) and gain:feed (0.12, 0.12, 0.10 for TRAD, LOCAL, and SELF, respectively; SEM = 0.08) were not affected by treatment. Cull cows fed using traditional feeding systems gain faster than those fed using a commercial self-fed system.

Key Words: cull cows, self-fed, distillers

W30 Impact of castration and weaning age on yearling carcass and meat quality. R. Berthiaume*[1], L. Faucitano[1], I. Mandell[2], S. Miller[2], and C. Lafrenière[3], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*, [2]*University of Guelph*, *Guelph, Ontario, Canada*, [3]*Agriculture and Agri-Food Canada*, *Kapuskasing, Ontario, Canada*.

Our objective was to determine the effect of castration and weaning age on carcass and meat quality of forage-fed yearlings. Spring calving crossbred cows (48 in 2004; 48 in 2005) with male calves were blocked based on parity, breed and calving date. Cow-calf pairs were randomly

assigned to one of six weaning [early (100 d), normal (200 d), late (300 d)] by castration (bull, steer) groups. Weaned calves were fed a grass silage (GS), oats and treated soybean meal (50: 40: 10) diet in confinement. Nursing calves went on pasture with their dams. From d 200 to 300 lactating cows and nursing calves were fed GS ad libitum. All calves were slaughtered at 300 d of age with carcass and meat quality evaluated. Data were analyzed as a randomized complete block design experiment using the MIXED procedure of SAS. Castration decreased carcass weights (197 vs. 213 ± 4.4 kg; $P < 0.01$) whereas carcass weights and carcass yields increased linearly with weaning age (188 vs. 204 vs. 225 ± 5.1 kg and 52.6 vs. 53.2 vs. 54.6 ± 0.38%, respectively; $P < 0.01$). Castration increased subcutaneous (3.7 vs. 2.7 ± 0.36 mm; $P < 0.01$) and renal fat (3.54 vs. 2.68 ± 0.304 kg; $P < 0.01$), and decreased saleable meat yield (61.5 vs. 62.1 ± 2.0%; $P < 0.01$). Weaning age had no effect on carcass fatness. Conversely, castration decreased loin eye area (LEA; 64.4 vs. 69.2 ± 2.50 cm^2; $P = 0.01$) whereas LEA increased linearly with weaning age (63.7 vs. 65.5 vs. 71.2 ± 2.50 cm^2; $P < 0.01$). A castration by weaning age interaction was present for ultimate pH ($P < 0.01$) of the *Longissimus* muscle (LM). Ultimate pH of LM decreased with weaning age in bulls (6.06 vs. 5.62 vs. 5.61 ± 0.045) resulting in a lower incidence of dark cutters in late versus early weaned bulls (0 vs. 25%). Ultimate pH did not vary in steers (5.69 vs. 5.65 vs. 5.71 ± 0.045). Our results suggest that, in a forage based production system, late weaning may enhance carcass yield and may reduce the incidence of dark cutters in bulls.

Key Words: weaning, castration, beef

W31 Fatty acid profile of back fat and intramuscular fat from yak and Chinese Yellow Cattle. Y. S. Peng*[1], M. A. Brown[2], and J. P. Wu[1], [1]*Gansu Agricultural University, Lanzhou, Gansu, PRC*, [2]*USDA-ARS, Grazinglands Research Laboratory, El Reno, OK*.

Meat from yak (Bos grunniens) and Chinese Yellow Cattle (*Bos taurus*) are important human dietary components in Northwest China and throughout the world. Fatty acid (FA) composition is an important factor in the definition of meat quality due to its association with meat odor, flavor, and nutritional value of fat for human consumption. Qinghai yak bulls (3-yr-old; n=6) and Chinese Yellow Cattle bulls (3-yr-old; n=5) were used to evaluate the effects of species on FA profile of longissimus dorsi intramuscular fat (LD) and back fat over the longissimus dorsi (BF). Animals were randomly picked from herds grazing summer pasture in alpine meadow regions of the Qilian mountains in Qinghai Province in China. Fatty acid analyses were done using a GC-MS; which resulted in profiles of 50 FA. Statistical analyses were conducted using mixed model procedures using a linear model that included the fixed effects of species, tissue (LD,BF) and species × tissue and random effects of animal in species and tissue × animal in species. Yak BF, but not LD fat, contained less ($P < 0.05$) palmitic and oleic acid. Yak BF and LD fat contained more vaccenic acid ($P < 0.01$), and tended ($P < 0.10$) to contain more conjugated linoleic acid (CLAc9,t11). Yak LD fat contained greater ($P < 0.05$) concentrations of polyunsaturated FA (PUFA) and ratio of PUFA to saturated FA ratio. Yak BF and LD contained a smaller ($P < 0.05$) ratio of n6 to n3 FA, and more ($P < 0.05$) linolenic acid. Results suggest that the FA profile in yak BF and LD is more consistent FA profile thought to be beneficial to human health; yet, it is dependent on adipose tissue depot.

Key Words: yak, beef cattle, fatty acids

W32 Differences in hair coat shedding, calf weaning weight and BCS among Angus dams. K. A. Gray*, J. P. Cassady, and C. Maltecca, *North Carolina State University, Raleigh*.

The objective of the study was to assess possible variation in coat shedding of Angus cows, and its effect on kg of calf weaned (KGW) and cow's body condition score (BCS). Data were available from 304 registered Angus cows sired by 41 bulls, from NC State University. Cows were grazed on pastures which were predominantly endophyte infected fescue, known to cause increased heat stress in cattle. Over 2 years, beginning at March and for 5 months at 30 day intervals, trained technicians scored cows on a scale from 1 to 5, with 1 representing slick coats and 5 winter coats. For each cow the first month with a score of 3 or less (MS, 5 levels) was considered the beginning of winter coat shedding and used in the analyses. Association between MS and KGW or BCS, was investigated using the mixed procedure of SAS. Each year was at first analyzed separately. Models for KGW and BCS included fixed effects of age of cow and MS, covariate of age of calf at weaning d and random effect of cow's sire. No significant association was found between MS and KGW or BCS. Data were further analyzed by dividing cows into two groups, cows that began shedding by May and those that began after May (MS1, 2 levels). In this analysis different years were pooled and a fixed effect of year was added to the model. Calves from dams that began shedding by May were 8.2 ± 3.9 kg heavier at weaning ($P < 0.04$) than calves from later shedding cows. No significant differences were found among different levels of MS1 and BCS. This data was also analyzed to determine if there were differences in MS among cow's sires using the GLM procedure in SAS adjusting for age of cow. Differences in sire were significant ($P < 0.01$). In this study evidence of increased calf weaning weights amongst cows that shed earlier in the year was found. Differences among sires suggest that Angus cattle may differ genetically in their ability to shed their winter coat. Further collection of hair shedding data will be needed to confirm these results.

Key Words: beef cattle, hair coat shedding, calf performance

W33 Age at first calving and longevity of Charolais cows. F. Szabó* and Z. Zsuppán, *University of Pannonia, Keszhely, Hungary*.

The length of productive life of beef cows is a trait of great importance with a significant impact on the profitability of beef cattle farming. The objective of the study was to evaluate the age at first calving (AFC), age at culling (ACU) and the longevity (LONG) of Charolais beef cows in Hungary. Longevity was defined, as a length of productive life; the period between first calving and culling. A database of 2766 cows, born between 1982 and 1993 was evaluated using multivariate analysis considering breeding region, birth year, birth season, genotype and sire of cows. Excel (MS 2002) and SPSS for Windows (1998) were used for data processing. The overall mean value and standard error of AFC, ACU and LONG were: 2.76±0.02 years, 8.41±0.18 years and 5.65±0.18 years, respectively. Breeding region, birth year, season, and cow sire had significant influence ($P<0.05$) on each of the three evaluated traits, while genotype influenced only the AFC. Age at culling and LONG showed a decreasing trend for the birth years of cows from 1982 to 1993. Longer lifespan (ACU) and productive life (LONG) were reached by crossbred than purebred cows. Heritability values of AFC, ACU and LONG were 0.46; 0.21; 0.25, respectively.

Key Words: length of productive life, environmental and genetic effects, heritability

W34 Weaning performance of Charolais calves. F. Szabó*[1], A. Fördös[1], Z. Domokos[2], and S. Bene[1], [1]*University of Pannonia, Keszthely, Hungary*, [2]*National Association of Hungarian Charolais Breeders, Miskolc, Hungary*.

Weaning weight (WW), preweaning daily gain (PWDG) and 205-day weight (205DW) of 23010 Charolais calves (10696 male and 12314 female) born between 1990 and 2005 from 10098 cows mated with 149 sires were analyzed. Breeding region, year and season of birth, age of dam, and sex of calves were fixed effects, and sire was random effect. Data were analyzed with Harvey (1990) Least Square Maximum Likelihood Computer Program, and two animal models were used for breeding value estimation. Variance, covariance components, heritability, correlation coefficients and the effect of the maternal environment on genetic parameters and breeding values were examined. The overall mean value and standard error of WW, PWD and 205DW were 219±7.60 kg, 939±40.63 g/day and 227±8.58 kg, respectively. Significant (P<0.005) region, year, season, sire and dam age effects, and sire × herd interaction were found. Weaning performance increased with increasing dam age up to six years of age. The direct heritability (h2d) of the evaluated traits was between 0.54 and 0.59. The maternal heritability (h2m) of these traits was 0.32 and 0.38. The direct-maternal correlations (rdm) were strong and negative (-0.84). Contribution of maternal heritability and maternal environment to phenotype was smaller than that of direct heritability (h2m + c2 < h2d). The proportion of the variance of maternal permanent environment in the phenotypic variance (c2) changed from 0.02 to 0.03. The rank of animals based on breeding value for weaning traits was not changed whether the maternal environmental effect was modeled. The genetic value for weaning results of Charolais population has increased since 1993.

Key Words: weaning weight, environmental effects, heritability

W35 Improving the profitability of beef from pastures: A case study of Tasmania's Circular Head Beef Business Group. A. E. O. Malau-Aduli*[1], I. D. Bruce[1], B. Doonan[2], and P. A. Lane[1], [1]*School of Agricultural Science, University of Tasmania, Hobart, Tasmania 7001, Australia*, [2]*Davey & Maynard Consultants, Davenport, Tasmania 7310, Australia*.

This case study on improving grazing management skills was conducted over a 12-month period in 2007 utilizing 1200 beef cattle on two properties of 60 hectares each, subdivided into 24 paddocks. The objectives were to evaluate pasture utilisation, liveweight gains and profitability using a multi-faceted economic model. Leaf emergence rate, average pasture cover, pasture growth rate, pre-grazing pasture mass, post-grazing residual and cattle liveweight gain data were collected monthly. Data were analysed using mixed (PROC MIXED) and general linear (PROG GLM) models in SAS to test for the fixed effects of property, date of sampling, cattle type and their second order interactions, while age of cattle and paddocks were fitted as random effects. Relationships between livestock and pasture variables were tested in correlation analyses using PROC CORR and significance established using Bonferroni probabilities. Results demonstrated that significant improvement in grazing management led to an increase in total pasture utilisation per hectare of over 40%, significantly greater than the set target of 7000kgDM/Ha on both properties. Pasture utilised directly for liveweight gain was positively correlated with total pasture utilised (r = 0.8686, p<0.0001). Energy partitioning for animal maintenance was found to be negatively correlated with total pasture utilised (r = -0.5927, p<0.05), and pasture utilised for liveweight gain (r = -0.8112, p<0.0001) and related to the nutritive value and species composition of the pastures. Average daily liveweight gain was found to be positively correlated with total pasture utilisation (r = 0.7302, p<0.0001) and pasture utilised for liveweight gain (r = 0.9181, p<0.0001) and negatively correlated with energy partitioned for animal maintenance (r = -0.9263, p<0.0001). It was concluded that increased pasture utilisation per hectare allowed for stocking rate increases across each property resulting in significant increases of approximately 73% in beef produced per hectare, thus increasing profitability by an overwhelming average of 250% across both properties.

Key Words: beef, pasture grazing, profitability

Breeding and Genetics: Genomic Evaluation, Molecular Genetics, Statistical Methods, Sheep Breeding, and Swine Breeding

W36 Value of genome-wide selection in Japanese dairy population. H. Ohmiya* and M. Suzuki, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Hokkaido, Japan*.

Little research has been done on the genomic breeding program for the Japanese dairy cattle population. Therefore, we examined the rate of genetic gain, the rate of inbreeding increase, and the reduction of economic costs associated with the implementation of genome-wide selection in the Japanese dairy cattle population. The simulation data, which mimics the Japanese dairy population, were used to evaluate progeny testing by BLUP with an animal model and genome-wide selection scheme by improved BayesB (Meuwissen et al. 2001). These simulations were replicated 20 times with 30 chromosomes and having 100 QTLs and 101 biallelic SNP markers per chromosome. The candidate bulls in the progeny testing scheme were raised for 5 years until their semen could be used, however in the genome selection scheme candidate bulls were selected at birth and put into service in one year. All records and pedigree information were used for calculating breeding values by BLUP, whereas only records and genotyping information of each generation were used in the BayesB scheme because of recombinant locus. The results showed that the accuracy of estimated breeding value for bulls by BayesB was a little lower than BLUP (0.82 vs 0.89), however, the reduction of generation interval and larger selection differential per generation in the genome-wide selection led to more genetic gain than BLUP. The rate of inbreeding increased 0.44 during the 10-year period in the progeny testing scheme, but the genome-wide selection scheme was 0.28. Furthermore, the economic costs in genome-wide selection scheme were reduced by 63% compared with the traditional progeny testing strategy. This suggests that genome-wide selection is effective genetically and economically.

Key Words: genome-wide selection, BayesB

W37 Genomic heritability of beef cattle growth. W. M. Snelling*, L. A. Kuehn, R. M. Thallman, J. W. Keele, and G. L. Bennett, *USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*.

Calf weights were examined to determine association between high-density SNP genotypes and growth, in order to estimate additive genetic variation explained by SNP. Data taken from Cycle VII of the US Meat Animal Research Center Germplasm Evaluation Project included birth weight (BWT), 205-d preweaning gain (WG), and 160-d postweaning gain (PWG) records of over 2,500 animals genotyped with the BovineSNP50 BeadChip. Polygenic and genomic direct and maternal variances were estimated in single-trait analyses. Fixed effects included sex, age of dam, year-season-location contemporary group, and covariates for calf and dam breed composition and heterosis. Direct and maternal additive polygenic and genomic effects, and maternal permanent environment effects were considered random. Polygenic effects were correlated according to a pedigree-based relationship matrix (**A**). Genomic effects were correlated with genotype-based relationship matrices ($\mathbf{A_g}$) constructed from sets of SNP meeting single-SNP association criteria. The 4,242 animals represented in both **A** and $\mathbf{A_g}$ included 2,918 genotyped individuals. Genotypes of the remainder (mostly dams) were predicted by a single-locus BLUP procedure. SNP with minor allele frequencies < 0.05 were excluded. Tests to choose SNP sets were Bonferroni-corrected P (P_b) < 0.05 (~35 SNP), false discovery rate (FDR) < 0.05 (~280 SNP), nominal P (P_n) < 0.01 (~1,760 SNP) and < 0.05 (~5,030 SNP), FDR > 0.90 (~15,760 SNP unlikely to affect phenotype), and all SNP (44,163). Unweighted $\mathbf{A_g}$, with each SNP making equal contribution to relationships, and weighted $\mathbf{A_g}$, with contributions weighted according to estimated effects, were evaluated. Additive variance was split between polygenic and genomic components with P_b < 0.05 and FDR < 0.05, and shifted almost wholly to genomic components using P_n < 0.01, P_n < 0.05, and all SNP. Estimates of genomic variance were negligible for FDR > 0.90. Analyses with weighted $\mathbf{A_g}$ were more likely than with the corresponding unweighted $\mathbf{A_g}$. The most likely model for each trait was with weighted $\mathbf{A_g}$ using P_n < 0.05, which yielded genomic direct heritability estimates of 0.46, 0.27 and 0.44 for BWT, WG and PWG, and genomic maternal heritability estimates of 0.29, 0.41 and 0.21.

W38 Genomic evaluation of Holstein cattle in Canada utilizing MACE proofs. F. S. Schenkel*[1], M. Sargolzaei[1], G. Kistemaker[2], G. B. Jansen[3], P. Sullivan[2], B. J. Van Doormaal[2], P. M. VanRaden[4], and G. R. Wiggans[4], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*, [3]*Dekoppel Consulting*, *Chiaverano, TO, Italy*, [4]*Agricultural Research Service-USDA*, *Beltsville, MD*.

Researchers in Canada and the United States are collaborating to develop and integrate genomic evaluations into their national genetic evaluations for dairy cattle in 2009. There are substantially more genotyped Holstein bulls with MACE proofs than with domestic Canadian proofs in Canada. The use of MACE proofs in addition to domestic proofs for estimating marker effects might, therefore, increase the reliability of genomic prediction in Canada. A validation study was carried out to assess the usefulness of MACE proofs for genomic prediction of 34 traits, including production, SCS and type traits. De-regressed proofs (DD) of genotyped bulls born between 1952 and 2000 (predictor bulls) with February 2005 domestic proofs (*n=1,097*) or alternatively with February 2005 domestic proofs or November 2004 MACE proofs (*n=4,127*) were used to estimated the effect of 38,416 SNP that were selected from the Illumina BovineSNP50™ chip used for genotyping. Then 2005 genomic enhanced parent average (GPA) of younger proven bulls born between 2000 and 2004 (*n=524*) with domestic proofs in November 2008, but only a parent average available in 2005, were predicted using the estimated SNP effects. The squared correlation (r^2) between GPA and the 2008 domestic DD was calculated. The average reliability of the DD of predictor bulls was 0.93, 0.88 and 0.89 for production, SCS, and type traits using domestic proofs only, and 0.82, 0.68 and 0.67 when MACE proofs were included. Despite the lower average accuracy of DD, the use of MACE proofs on average increased the r^2 by 0.12, 0.10 and 0.06 points compared to the use domestic proofs only for production, SCS and type traits, respectively. Thus, the use of MACE proofs increased the prediction ability of GPA and, therefore, should be considered in the genomic evaluation of Holstein cattle in Canada.

Key Words: genomic evaluation, MACE proofs, Holstein cattle

W39 Integrated software tools for genome-wide association analysis and genomic prediction in livestock. J. R. O'Connell*, *University of Maryland School of Medicine*, *Baltimore*.

With the availability of dense SNP chips in many livestock species such as bovine, porcine and ovine, software tools designed to efficiently analyze large numbers of single nucleotide polymorphisms (SNPs) for association to quantitative traits and calculate genomic breeding values are needed. The program MMAP (mixed model analysis in pedigrees) integrates both established and novel algorithms to efficiently analyze SNP data in pedigrees. MMAP allows genome-wide association analysis using single or multi-SNP and/or haplotype fixed effect models accounting for residual variation through a relationship matrix derived from pedigree or genomic data. Genomic selection is implemented using both fixed and random effect models. Genotype error detection is implemented using a penetrance model to compute posterior probability distributions for each animal with genotype calls. The 2008 QTL-MAS workshop data set was used validate the algorithms and performance. The data comprises 6000 SNP genotypes simulated in a seven-generation swine pedigree and a quantitative trait with 30% heritability controlled by major and random QTLs. Genomic regions harboring simulated QTLs were accurately identified in the single SNP analysis. Regression model building identified multi-SNP models that contained location specific signals with effect size estimates similar to simulated values. Genomic breeding values derived from multi-SNP effect estimates had correlation of 0.8 with the true breeding values, similar to values reported using Bayesian methods on this data set. In summary, MMAP has user-friendly command line options to choose analysis option. The program is written in C and will be distributed under the GNU Open Source license.

Key Words: genomic selection, genomewide association, quantitative trait

W40 Effect of CSN2 gene polymorphism on somatic cell count in Czech Fleckvieh. J. Riha*, I. Manga, J. Bezdicek, and J. Subrt, *Agroresearch, Ltd.*, *Rapotin, Czech Republic*.

The goal of this study was to assess the genetic variability of *CSN2* gene polymorphism and its effect on somatic cell count (SCC) in the milk of Czech Fleckvieh. SCC is a key milk quality parameter and status indicator of mammary gland health with high economic impact. Currently, the *CSN2* gene is being used as a major tool in a number of marker assisted selection breeding schemes in dairy cows. The reason for its use is the known positive influence of allele *A2* on human health. The DNA

samples required for molecular analysis were isolated from cattle blood using a columned method (Jet quick DNA spin kit, Genomed^{SM}, USA). Amplification of the PCR product and PCR-RFLP test was performed according to standard method. The dataset consisted of the genotypes of 230 unrelated Czech Fleckvieh cows. The effect of the genotypes was calculated using the GLM procedure with the effects of lactation number and genotype of the *CSN2* gene. The milk SCC was represented as a decadic logarithm. The estimated genotype frequencies consisted of *A1A1* (7.44%), *A1A2* (41.36%) and *A2A2* (51.2%). The basic statistical parameters of the whole model were: r = 0.502, p = 0.000. Likewise, the effect of the lactation stage on SCC reached statistical significance as well as the effect of the *CSN2* genotype ($P \leq 0.05$). Using the Post-hoc Tukey HSD test, significant differences between *CSN2* polymorphisms and SCC were revealed. Individuals with *A1A1* genotype had higher SCC than the *A2A2* ($P \leq 0.001$) and *A1A2* genotypes ($P \leq 0.05$). The SCC decreased according to genotypes in the order: *A1A1* > *A1A2* > *A2A2*. The existence of possible positive phenotypic effects between milk yield and SCC failed to explain this observation as the cows with the *A2A2* genotype had the highest milk production in our dataset. The positive finding is that the valuable *A2A2* genotype is associated with the lowest number of somatic cells and this may indicate new possibilities for applying the *CSN2* marker in the process of Czech Fleckvieh selection. However, the general biological mechanism of this association remains unknown.

Key Words: CSN2 gene, somatic cell count, Czech Fleckvieh

W41 Molecular genetic characterization of Nigerian goats. M. Okpeku*[1], M. Ozoje[2], M. J. O'Neill[3], and I. Imumorin[4], [1]*Niger Delta University, Amassoma, Bayelsa State, Nigeria*, [2]*University of Agriculture, Abeokuta, Ogun State Nigeria*, [3]*University of Connecticut, Storrs, CT*, [4]*Cornell University, Ithaca, NY*.

The domestic goat is one of the important livestock species in Nigeria. They are adapted to the varied climatic conditions and representative of an uninvestigated source of genetic diversity. In this study, we assess genetic diversity in Nigerian goats using 10 microsatellite markers in 295 goats. Breeds were sampled from farms, market places and rural homesteads in the South-western region of the country. The mean number of alleles per locus (NA) ranged from 6.8 in Sahel goats to 10.8 in West African Dwarf (WAD) goats. The mean expected heterozygosity (He) ranged from 0.732 in Sahel to 0.834 in WAD goats. Deviations from Hardy-Weinberg Equilibrium (HWE) were statistically significant ($P < 0.05$). The DA measure of genetic distance between pairs of breeds indicated that the lowest distance was between WAD and Sahel (0.293) and the highest distance was between Red Sokoto and Sahel (0.585). An analysis of molecular variance (Fst) of 0.078 indicated that 89.6% of variance exists among Nigerian goat breeds. Our dendogram clustered Nigerian goats into two major breeds. Our study concludes that Nigerian goat populations can be classified into distinct two genetic groups or breeds and not three current breeds based on these microsatellites. Further studies using more molecular makers in a much larger population would be worth exploring.

Key Words: microsatellite DNA, genetic diversity, Nigerian goats

W42 Analysis of distributions of estimated QTL effects for dairy cattle. G. Gaspa, M. A. Pintus, R. Steri, S. Sorbolini, and N. P. P. Macciotta*, *Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italia*.

The infinitesimal model used to explain the inheritance of quantitative traits has been the paradigm of selection so far. However, results of QTL studies seems to support a model with a small number of loci with large effect and several ones with small effect. In this study three theoretical distributions (Lognormal, Weibull and Gamma distribution) were used to model QTL effect distributions for milk yield (MY), protein yield (PY), protein percent (PP), fat yield (FY), fat percent (FP), type traits (TT) and all milk production traits scaled by genetic standard deviation (AT). All data were retrieved from published QTL mapping experiment in the period 1995-2008. Inclusion of records in the analysis was based on the significance level of the test (p-value<0.05). The goodness of fit of the three distributions was assessed using Kolmogorov-Smirnov, Cramer-von Mises and Anderson-Darling test. Table 1 reports gamma function parameters. The gamma function fitted all QTL effects data but MY and PP. The lognormal distribution fitted FY, FP, PY and AT data. Weibull distribution showed a goodness of fit only for FY, FP and PP (data not shown). These figures partially agree with previous results, that indicated the gamma distribution as the most suitable one for modelling QTL effects. Even if the effect of the genes are affected by bias due to the specific conditions if each study, these results seems to confirm the general hypothesis of the existence of a large number of QTLs with small effects and of a few ones with large effects.

Table 1. Parameters of Gamma distribution used to fit QTL effects

Trait	n	Mean±sd	Scale (α)	Shape (β)
AT (σA)	148	0.764 ± 0.410	0.243	2.879
MY (Kg)	115	189.9 ± 134.2	94.574	2.004
FY (Kg)	79	9.335 ± 4.575	2.244	4.159
PY (Kg)	80	7.018 ± 3.489	1.735	4.045
FP (%)	87	0.0013 ± 0.0008	0.00059	2.205
PP (%)	48	0.0005 ± 0.0003	0.00015	3.226
TT (σA)	91	0.811 ± 0.328	0.13285	6.111

Key Words: QTL, gamma distribution

W43 Investigation for increase reproduction rate with used of identification QTL associated with twining in Shall sheep. N. Hedayat-Evrigh*, S. R. Miraei-Ashtiani, and A Nejati-Javaremi, *University of Tehran, Karaj, Tehran, Iran*.

reproduction is one of the most important economical traits in sheep breeding and recent discoveries shows that it is influenced by a number of major genes. The high prolificacy in Inverdal sheep is the result of a mutation in the BMP15 oocyte-derived growth factor gene. this study was carried out to detect the possible polymorphisms in FecXI gene. the Inverdale prolificacy gene could markedly improve reproductive efficiency in commercial flocks, but as homozygous carrier Inverdale ewes are infertile, it is imperative that these animals are identified at an early age and excluded from breeding stock. Also because native sheep of Iran have low fertility and that substituted with foreign sheep, Therefore for conserved biodiversity in native sheep This study carried out to detect the possible polymorphism in FecxI gene until used of results for increas fertility in this sheep. PCR-RFLP method used to be developed fecXI mutant allele. This study was performed using a

Blood samples were collected from 239 ewes of Shall sheep. Genomic DNA was extracted using modified salting-out method. The polymerase chain reaction (PCR) was carried out for amplification of a fragment with 204 bp at the mentioned locus. For genotyping the individuals at Inverdal locus, the resulted amplified fragments were digested using XbaI restriction enzyme. Shall breed sheep was tested for the presence of the FecXI mutation of BMP15. There was no evidence of FecXI in shall breed sheep sampled. All individuals in the sample showed wild genotype (++). Considering the phonotypic records, the obtained result indicates that in this breed, the relationship of genetic factor responsible for twining or multiple lambing rates with reported mutated alleles at Inverdal major gene is very unlikely. For suppression of elimination native breed we must increase fertility and multiple lambing rates in this sheep and others native sheep. Therefore can with identify and detected major genes affective on this trait increase twinning in native breed. We offer investigate for other major genes effect that identified.

Key Words: Shall sheep, FecXI, PCR-RFLP

W44 Diversity of *ureC* genes from rumen microflora metagenomic library. S. G. Zhao, J. Q. Wang*, K. L. Liu, D. Li, P. Yu, and D. P. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Due the fact that the majority of rumen bacteria were still uncultured, information about ruminal urease gene sequence and phylogenetic diversity were scare. To resolve this problem, a functional screen for urease-active clones was conducted for a rumen bacterial artificial chromosome library from dairy cow rumen microflora. Polymerase chain reaction degenerate primers based on the *ureC* gene which was conserved in ureolytic bacteria were designed and used to amplify the *ureC* genes from positive clones. The universal 16s bacterial primers were used to amplify the 16s rRNA gene of positive clones. Sequences were blasted against GenBank database, and phylogenetic tree were built by Mega 4.0 software. Sixteen clones (U1-U16) were identified as ureolytic positive using urease segregation agar. Four clones (U1, U5, U13 and U15) containing *ureC* genes were identified. The phylogenetic tree based on *ureC* revealed that U1, U5, U13 and U15 clustered to Firmicutes, ε-Proteobacteria, β-Proteobacteria and Actinobacteria, respectively. U1 clone contained a partial 16s rRNA sequence had the most identity to Staphylococcus, which was in agreement with *ureC* phylogenetic analysis. Taking together, this study provided first evidence for the phylogenetic diversity of ureolytic bacteria from cow rumen.

Key Words: metagenome, *ureC* diversity, rumen microflora

W45 Analysis in silico and in vitro of caseinophosphopetides from different genetic variants. A. M. Caroli*[1], O. Bulgari[1], S. Chessa[2], D. Rignanese[1], D. Cocchi[1], and G. Tulipano[1], [1]*Dept. SBB*, *Brescia, Italy*, [2]*Dept. VSA*, *Milano, Italy*.

Milk proteins are the main source of bioactive peptides with different functions. These milk activities are hidden in the native proteins and require the proteolitic cleavage to become extrinsic. Among biopeptides, caseinophosphopeptides (CPPs) possess the ability to bind and solubilise minerals, such as Ca++. The studies on the biological effect of different CPPs were carried out mainly in the bovine species, without taking genetic polymorphism into account. The biological activity of peptides released from milk protein digestion may be affected by amino acid exchanges or deletions resulting from gene mutations, as well as by prost-translational changes. The aim of this work was, first, to carry out an in silico analysis of the CPPs in order to detect differences in the amino acid sequence linked to species (bovine, caprine, and ovine) and genetic variants within each species. We analysed 3, 2, and 3 CPPs respectively carried by αs1-casein, β-casein, and αs2-casein. A total of 29 differences were detected among and within the considered species. Breeding could exploit such differences for improving dairy food biological value. Secondly, an in vitro test was developed to compare the effect on bone mineralization of four selected casein peptides which differ in the number of phosphorylated serines. The chosen peptides, related to different casein genetic variants, were obtained by chemical synthesis and tested on murine osteoblast cell line (MC3T3-E1). The main difference between peptide 1 and 2 was the occurrence of one phosphorylated serine at position 35 of the mature β-casein in the latter peptide. Moreover, Glu at position 37 of peptide 3 was substituted with Lys in peptide 4, carried by bovine αs2-casein C variant. Our results suggest that the distinct peptides in protein hydrolysates may differentially affect calcium deposition in the extracellular matrix. The higher content of phosphorylated serines might compete with calcium deposition, probably subtracting Ca++ from the culture medium. In addition, the genetic variation within peptides may influence their differential effect on osteoblast in vitro mineralization.

Key Words: caseinophosphopeptide, milk protein, genetic variant

W46 Differential gene expression in the testis of adult male mice after treatment with Aflatoxin B1. K. J. Austin*, R. R. Cockrum, A. M. Kaiser, and K. M. Cammack, *University of Wyoming*, *Laramie*.

The dietary mycotoxin, aflatoxin B1 (AFB1), adversely affects the reproductive health of humans and domesticated livestock through variable effects on oocytes in females and spermatogenesis and steroidogenesis in males. The genetic mechanisms by which fertility is disrupted by AFB1 are not known. The objective of this study was to determine changes in gene expression due to exposure to AFB1 in male mice. Male mice 4 wk of age were administered a placebo (control) or 50 μg/ kg BW AFB1 (AFB1 treated) daily for 45 d. Following the treatment period, males were mated to females for 10 d and then euthanized for testis tissue collection. Pregnant females were euthanized on gestational d 17. Fetuses were counted and examined for gross abnormalities. Among treated males, AFB1 tolerant and intolerant males were identified based on average number of fetuses produced per female and number TUNEL positive epididymal cells. Tolerant males produced a similar average number of fetuses (12.5 fetuses) as control males (13.4 fetuses), but a higher (P = 0.01) number than intolerant males (7.6 fetuses). The number of TUNEL positive cells in intolerant males was numerically greater (136.5 cells) than in tolerant (55.0) and control (54.3) males. Microarray analyses were performed on selected control (n = 3), AFB1 tolerant (n = 3) and AFB1 intolerant (n = 3) males. Functional analyses revealed differential expression ($P < 0.05$) of 193 extra cellular space regulation genes, 45 immune response genes, 230 cell differentiation genes, and 49 signal transduction genes. Real-time RT-PCR confirmed numerical upregulation of IBSP and CCK genes and numerical downregulation of PGA, Crisp, and AR genes in AFB1 treated males compared to control males. Similar changes in expression of these genes were observed between AFB1 tolerant and intolerant males, with IBSP and CCK genes upregulated and Crisp and AR genes downregulated in intolerant males. Results from this study demonstrate that testicular gene expression is altered by administration of AFB1, and these genomic changes may contribute to variation in fertility observed among AFB1 exposed males.

Key Words: gene expression, aflatoxin, testis

W47 Development of a two-species cDNA microarray for transcriptional profiling of sow and dairy cow reproductive traits. M. F. Palin*[1], D. Beaudry[1], M. Vallée[2], N. Bissonnette[1], B. D. Murphy[3], and H. V. Petit[1], [1]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [2]*Université Laval, Québec, QC, Canada*, [3]*Université de Montréal, St-Hyacinthe, QC, Canada*.

Limited genetic progress has been reported for livestock reproductive traits in recent years. This is mainly due to the low heritability of these traits and because they are sex-limited and not measurable until sexual maturity is reached. Moreover, most economically important reproductive traits are polygenic. The development of transcript profiling techniques, such as microarray technology, offers the possibility to study polygenic traits more easily and provides the capacity to uncover molecular mechanisms and pathways that regulate reproductive functions. A two-species cDNA microarray was developed for profiling sow and dairy cow transcripts believed to associate with embryo survival during the peri-implantation period. This microarray comprises 1128 unique genes. Among them, are genes expressed in endometrial and embryonic tissues (day 15) and displaying differential expression between prolific Meishan X Landrace and Landrace breeds. This microarray also includes differently expressed genes from embryonic and endometrial tissues that were previously identified in day 17 pregnant dairy cows fed a diet containing flaxseed. Additional cDNAs have been included based on available literature on candidate genes or transcriptional profiling studies related to bovine and pig reproductive traits. This microarray was first used to identify transcripts differently expressed during the peri-implantation period (day 17) in dairy cows fed a control diet or a diet with 10% flaxseed. A list of up- and down- regulated genes was obtained for both embryonic and endometrial tissues. Among those, several prostaglandins-, immune- and development-related genes were identified. These genes illustrate the broad range of biological processes influenced by a diet rich in n-3 fatty acids. It also helps further the comprehension of different molecular pathways which modulate reproductive traits.

Key Words: microarray, reproduction, flaxseed

W48 Genome-wide analysis of QTL effects in Canadian Holstein cattle using empirical Bayes method. H. Li*[1], Z. Wang[1], P. Stothard[1], M. Sargolzaei[2], F. S. Schenkel[2], and S. Xu[3], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*University of Guelph, Guelph, ON, Canada*, [3]*University of California, Riverside*.

A whole-genome analysis to identify QTL affecting milk production traits was conducted on Canadian Holstein bulls using an empirical Bayes method. This method estimates prior variance components using marginal maximum-likelihood and then estimates QTL effects using the Bayesian shrinkage method given the estimated prior variance components as if they were the true prior variances. This method allows simultaneous estimation of all marker effects in a single model. An evenly spaced 316 SNP marker set covering the autosomal bovine genome with an average inter-maker distance of 8.80 Mb was selected from the Illumina BovineSNP50 BeadChip using the deferential evolutionary algorithm. De-regressed EBV of the traits from 646 proven bulls born in North America between 1985 and 2002 were used in this study. Genome-wise critical values for significant QTL effects at 5% level (α=0.05) were determined by permutation tests. The numbers of significant QTL detected were 35, 27, 9, and 19 for fat yield, protein yield, fat percentage and protein percentage, respectively. On average, the sum of all the significant QTL effects contributed 18.6% of the total variance among the de-regressed trait EBVs, with fat percentage having the highest (28.0%) and protein yield the lowest (11.8%). The highest single marker effect explained 10.8% of the de-regressed EBV variance (fat percentage). The significant putative QTLs identified in this study will be further investigated to potentially identify the causal mutations within the nearby candidate genes.

Key Words: QTL effect, bovine genome, Canadian Holstein cattle

W49 Associations of single nucleotide polymorphisms in bovine fatty acid synthase gene with fat deposition and carcass merit traits in Hybrid, Angus and Charolais beef cattle. K. Islam*[1], M. Vinsky[2], R. Crews[3], E. Okine[1], S. S. Moore[1], D. H. Crews Jr.[1,4], and C. Li[1,2], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [2]*Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403-1st Avenue South, Lethbridge, Alberta, Canada*, [4]*Colorado State University, Fort Collins*.

The gene-specific polymorphisms of fatty acid synthase (FASN) were studied for their associations with fat deposition and carcass merit traits in beef cattle. FASN has functional importance in lipogenesis and its location is under the quantitative trait loci (QTL) region for subcutaneous fat on bovine chromosome 19, making it an attractive positional candidate gene. Genotyping of 3 non-synonymous, 1 synonymous and 1 intronic single nucleotide polymorphisms (SNP) between exon 20 and exon 36 of FASN were conducted in populations of 206 Angus, 187 Charolais and 464 Hybrid beef steers. Association analyses were carried out using an animal model as implemented in ASREML with a pedigree depth of 9, 6 and 1 generations for Angus, Charolais and Hybrid cattle populations, respectively. Fat deposition and carcass merit traits analysed in this study included ultrasound backfat thickness, ultrasound rib-eye area, average daily gain of ultrasound backfat thickness during feedlot test, average daily gain of ultrasound rib-eye area, carcass average backfat thickness, lean meat yield, carcass marbling score, carcass rib-eye area, slaughter weight, and hot carcass weight. A non-synonymous SNP was found to be significantly associated with carcass marbling ($P<0.05$), carcass average backfat thickness and lean meat yield in the Angus steers ($P<0.10$). An intronic SNP was also significantly associated with carcass marbling in the Angus steers ($P<0.05$). In the Charolais population, an intronic SNP had associations with slaughter weight ($P<0.05$) and ultrasound rib-eye area ($P=0.055$). In the Hybrid cattle population, a non-synonymous SNP was found to be significantly associated with carcass rib-eye area ($P<0.05$). These findings may provide insight into the role of FASN in regulating fat deposition in beef cattle.

Key Words: fatty acid synthase (FASN), single nucleotide polymorphisms (SNP), fat deposition and carcass merit in beef cattle

W50 Association analyses of single nucleotide polymorphisms in bovine stearoyl-CoA desaturase and fatty acid synthase genes with fatty acid composition in commercial crossbred beef steers. C. Li*[1,2], M. Vinsky[1], M. E. R Dugan[1], N. Aldai[1], and T.A. McAllister[3], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403-1st Avenue South, Lethbridge, Alberta, Canada*.

Single nucleotide polymorphisms (SNP) of bovine stearoyl-CoA desaturase (SCD) and fatty acid synthase (FASN) genes have been reported to have significant associations with fatty acid composition in Japanese

Black cattle and in purebred American Angus cattle, respectively. This study was conducted to evaluate associations of SNPs in SCD and FASN genes with fatty acid composition in commercial crossbred beef steers that originated from Desert Ranches near Lethbridge, Alberta. Fatty acid contents of 84 individual and groups of fatty acids in brisket adipose tissues from 235 steers were analyzed using a combination of GLC and silver-ion HPLC methods. The steers were genotyped on two previously reported SNPs of the SCD and FASN genes, the [C/T] SNP in the exon 5 of SCD that causes an amino acid change from alanine (type A) to valine (type V) and the g:17924A>G SNP in FASN that causes an amino change from threonine to alanine. Association analyses found that the ′C′ allele or type A of the SCD SNP was significantly associated with lower saturated fatty acids including 10:0, 14:0 and 20:0, higher monounsaturated fatty acids including 9c-14:1, 12c-16:1, 13c-18:1, 9c-20:1, higher polyunsaturated fatty acids including 10c12c-18:2, 11c13t-18:2, 12c14t-18:2, 9c15c-18:2, but lower polyunsaturated fatty acids of 9c13t-18:2 and 20:2n-6 ($P<0.05$). The `A' allele of the FASN SNP was significantly associated with higher saturated fatty acids of 13:0, 14:0. 15:0 and 17:0, lower unsaturated fatty acids of 9c11t-18:2, 9c-18:1, 9c-20:1, 20:3n-6, 22:4n-6, and higher unsaturated fatty acids of 9t11c-18:2, 10t12c-18:2, 9c-14:1, 12c-16:1, 10t-18:1, 6-8t-18:1 ($P<0.05$). These results provide further evidence that SCD and FASN are strong candidate genes influencing fatty acid composition in beef cattle.

Key Words: stearoyl-CoA desaturase (SCD), fatty acid synthase (FASN), fatty acid composition in beef cattle

W51 Validation and characterization of 1536 fat-related gene-specific SNPs in beef cattle. M. Vinsky*[1], K. Islam[2], P. Stothard[2], and C. Li[1,2], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*.

Gene-specific single nucleotide polymorphisms (SNP) are of particular importance in dissecting the genetic basis of quantitative traits as they can the direct genetic causes of phenotypic variation. In order to facilitate a whole genome candidate gene association study for fat deposition and carcass merit in beef cattle, a fat related gene-specific SNP panel consisting of 1536 SNPs was developed through searching public databases, mining the bovine SNP databases and through in-house SNP discovery. The 1536 SNPs were located in 418 candidate genes spanning 25 bovine autosomes. The fat related candidate genes were chosen based on their chromosomal location within or in close proximity to reported quantitative traits loci (QTL) for fat deposition in cattle and(or) their possible function and involvement in fat metabolism. Genotyping of the 1536 gene-specific SNPs was performed using the Illumina® Golden Gate Assay across Angus (N=313), Charolais (N=258) and Hybrid (N=456) cattle populations. In total, 1309 SNPs were successfully amplified in all 1027 animals with a successful call rate of 99.3% across all three populations. Of the 1309 SNPs amplified, 357 SNPs were found monomorphic across all the three beef cattle populations. In the Angus population, 827 SNPs were polymorphic and 69 SNPs of those had a minor allele frequency (MAF) less than 0.05. In the Charolais population, 918 SNPs were polymorphic and 82 of those had a MAF smaller than 0.05. In the Hybrid population, 64 of the 918 polymorphic SNPs had MAF smaller then 0.05. This gene-specific SNP panel will provide a useful tool for whole genome candidate gene association studies for fat deposition and carcass merit traits in different breeds of beef cattle.

Key Words: single nucleotide polymorphisms (SNP) validation, candidate genes, beef cattle

W52 Use of low density SNP chip for parental verification in US Holsteins. S. Tsuruta*[1], I. Misztal[1], and T. J. Lawlor[2], [1]*University of Georgia, Athens*, [2]*Holstein Association USA Inc., Brattleboro, VT*.

A subset of SNPs from the Illumina BovineSNP50 genotyping Beadchip, consisting of 73 loci on 28 chromosomes, was evaluated for their effectiveness to verify parentage in Holsteins. These 73 SNPs are part of the parentage panel, being recommended by Heaton et al. (2002), which could be included in a low density SNP chip. Genotypes on 10,442 Holsteins were available, including 9128 animals with only their sire genotyped, 1331 animals with both sire and dam genotyped and 61 animals with only the dam genotyped. The average minor allele frequency (MAF) was 40%, with a minimum and maximum of 19%, and 49%, respectively. Number of exclusions (incompatible alleles: AA/BB or BB/AA) was used to test parentage. The probability of zero exclusions among random pairs of animals can be calculated as $[1-2q^2(1-q)^2]n$ and the average number of exclusions as $2nq^2(1-q)^2$, for n loci and MAF of q, assuming no genotyping errors, no mutation, and unlinked loci. For n=73 and q=0.4, the probability is 0.00013 and the average number of exclusions is 8.4. In our putatively known animal-sire combinations, 9120 pairs had zero exclusion, 5 pairs had a single exclusion, and 3 pairs each with 2, 4 or 6 exclusions. In our putatively known animal-dam combinations, 1390 pairs had zero exclusion and 2 pairs had a single exclusion. Using a threshold of less than 2 exclusions, the rate of false negatives was 0.00099. For 9069 random animal-bull and 1373 animal-cow combinations, excluding our putatively known animal-parent pairs, the average numbers of exclusions were 12±7 and 11±6 with a minimum of 1 and a maximum of 51 and 46, respectively. The modes were 8 and 9, respectively, reflecting a skewed distribution. A single exclusion occurred in 23 animal-bull and 1 animal-dam combinations. Using a threshold of less than 2 exclusions, the rate of false positives was 0.0025. A low density chip may be quite useful for parentage testing.

Key Words: SNP, parental verification, Holsteins

W53 Characteristics of the bovine PL10 gene and its evolution in mammals. T.-C. Chang and W.-S. Liu*, *The Pennsylvania State University, University Park*.

PL10 exists in a wide range of eukaryotes, from yeast, plants to animals. This gene has been evidenced to play an important role in male fertility in mouse. In order to investigate the biological roles and evolution of PL10, we first characterized PL10 in bovine (bPL10) and conducted a phylogenetic analysis for PL10 related genes. PL10 contains a DEAD motif and belongs to the DEAD box polypeptide 3 (DDX3) subfamily. DDX3 is a highly conserved helicase family with essential function in RNA metabolism. The other two major members of DDX3 are DDX3X and DDX3Y, located on the sex chromosome, while mammalian PL10 is autosomal. The human PL10 is a pseudogene, whereas the mouse PL10 (mPL10) is a major gene involved in spermatogenesis and believed to replace the role of mDDX3Y in male fertility. The bovine PL10, like mPL10, is intronless and expressed not only in testis but also in other tissues based on our RT-PCR expression analyses. The nucleotide similarity between bPL10 and mPL10 is 72.7%. Besides, the similarity between bPL10 and bDDX3X is 81.5%, while it's lower, ~74.6%, between bPL10 and bDDX3Y. The further sequence comparisons revealed that the PL10 homologous sequences are present in genomes of many other mammalian species, but most likely in a pseudogene format, which could be the relics of PL10 during evolution. The phylogenetic tree built from these homologous sequences among different species indicated that mammalian PL10 is closer to DDX3X. Therefore, we

proposed that mammalian PL10 could evolve from the DDX3X through the retroposition mechanism.

Key Words: PL10, DDX3 subfamily, bovine

W54 Using a repeated measurements mixed model to analyse some environmental factors affecting weight at different ages of Arabi sheep breed of Iran. H. Farhangfar*[1], B. Zinvand[2], M. B. Sayyadnezhad[3], and I. Mirzaee[4], [1]*Birjand University, Birjand*, [2]*Azad University of Shooshtar, Shooshtar, Iran*, [3]*Animal Breeding Centre, Karaj, Iran*, [4]*Agricultural Jihad Organisation, Khuzistan, Iran*.

A total of 2265 weight records at different ages belonging to 755 Arabi sheep breed of Iran were used to study some environmental factors applying a repeated measurements mixed model. Determining environmental factors affecting body weights is of great importance as genetic evaluation of candidate animals has to be practiced. The lambs in the data set were born between 1994 and 2004 in 16 herds of Khuzestan province. The traits studied were weight at ages 0 (birth), 3 (weaning) and 6 months. In the model, fixed environmental effects of herd, year of birth, sex, litter size, order of ewe lambing, lamb age at weighing, and two way interactions between sex and litter size, between lamb age and sex, between lamb age and litter size, between lamb age and year of birth, and between lamb age and herd were included. Lambs were also included in the model as subjects having repeated measurements over three categories of weighing. Unstructured variance-covariance option was assumed for fitting the model. Analysis was undertaken by using SAS software through mixed model procedure applying repeated measurements. The results obtained in the present research showed that except the order of ewe lambing, all other environmental factors significantly statistically ($P<0.05$) affected weight records of Arabi sheep. Least squares means of female lambs at ages 0, 3 and 6 were 3.54, 20.53 and 29.45 kg respectively and the corresponding figures for male lambs were found to be 4.42, 23 and 33.16 kg respectively. The results also indicated that the least squares means of weight at ages 0, 3 and 6 for single birth lambs were 3.97, 22.04 and 32.52 kg respectively and for twin birth lambs were 3.99, 21.48 and 30.09 kg respectively.

Key Words: Arabi sheep, weight, environmental effects

W55 Improve reproduction with identification of polymorphism in FecXH gene in Shall sheep. N. Hedayat-Evrigh*, S. R. Miraei-Eshtiani, and A. Nejati-Javaremi, *University of Tehran, Karaj, Tehran, Iran*.

Twinning is one of the most important traits in production of sheep breeding and also native breed sheep in Iran have low fertility and twining. Studies of the inheritance pattern of ovulation and litter size in prolific flocks have shown that major genes for prolificacy are segregated example Hanna gene (FecxH) in Hanna sheep. FecXH is a dominant located on the X chromosome. Knowledge of this mutation has prompted researchers to screen other prolific sheep breeds to determine whether this mutation is responsible for their high prolificacy. We considered an Iranian fat tail sheep known as Shall for this study. The ability to adapt to different environmental circumstance is a desirable characteristic of this breed. Therefore with increase twining this breed, used consistently for production by farmer. Shall ewes were sampled from commercial flock in Qazvin provinces. Blood sample were collected from 239 Shall ewes. PCR-RFLP method used to be developed FecXH mutant allele. This study was performed using a Blood samples were collected from 239 ewes of Shall sheep. Genomic DNA was extracted using modified salting-out method. For genotyping the individuals Hanna locus, the resulted amplified fragments were digested using SpeI restriction enzyme. SpeI restrictions enzyme were used to detect possible mutation. In this study we show that none of the sheep sampled carried the Hanna FecXH mutation in the BMP15 gene. And all samples showed wiled allele and fecX+/FecX+ genotype. Although Shall sheep breed has relatively high fecundity. But there are big differences in husbandry systems in which it evolved, and this could affect whether a spontaneous mutation leading to large litter size is retained or lost. Considering the phenotype records in this breed, the obtained result indicates that the genetic factor responsible for twining or multiple lambing rates is not related to reported mutant allele at Hanna major gene.

Key Words: native breed, FecXH, prolificacy

W56 Comparison of genetic diversity between US and Kazak sheep breeds. H. D. Blackburn*[1], Y. Toishibekov[2], C. Welsh[1], S. Spiller[1], and M. Brown[3], [1]*ARS-National Animal Germplasm Program, Ft. Collins, CO*, [2]*Institute of Experimental Biology, Almaty, Kazakhstan*, [3]*ARS-Grassinglands Research Laboratory, El Reno, OK*.

To secure US genetic diversity it is beneficial to compare US and non-US breeds. Such information may also be used to identify areas of sampling for diverse genetic resources. Kazakhstan (KZ) provides an interesting comparison due to its history of sheep production and proximity to the Silk Route, which likely facilitated genetic migration from the Fertile Crescent to China. With microsatellite markers it is possible to quantify genetic differences between US and KZ sheep breeds. Five KZ breeds were sampled: Arkharo-Merino (AM), Chyisskaya (CHY), Degresskaya (DEG), Edil-baevskaya (EDI), and Sary-Arkinsskaya (SA). The AM is a hybrid between wild Arkhar rams (Ovis ammon) and Merino, Precoce and Rambouillet ewes (Ovis aries), the other four breeds are coarse wooled and fat rumped. The 13 US breeds included: fine wool, meat types, long wool, hair, prolific, and fat rumped. Blood and semen samples were collected from both countries (n = 24.5/breed). DNA was extracted and genotyped using 29 FAO/ISAG panel microsatellites. Genotype data were analyzed using GENALEX and PHYLIP. The KZ breeds had greater allelic richness when compared to US breeds (7.8 vs 4.8, respectively). However, Rambouillet and Dorper were similar to KZ breeds with average allele numbers of 8.2 and 7.5, respectively. The KZ breeds had higher levels of heterozygosity when compared to US breeds. Among the four fat-rumped KZ breeds the genetic distances (GD) were relatively small (< 0.14), despite large geographic differences in sample derivation. Dorper and Karakul were the US breeds most closely associated with the CHY, DEG, EDI, and SA with GD ranging from 0.22 to 0.35. The GD between AM and Rambouillet (0.13) was unexpected given the Ovis ammon component of the AM, and suggests that during the formation of the AM that many of the genes associated with the Arkhar were selected against resulting in a population that is primary comprised of Merino/Rambouillet. Concluding, these results indicate substantial GD and variability between the US and KZ breeds evaluated, except for the AM and Rambouillet. The results also illustrate that genetic diversity is greater near the center of domestication.

Key Words: sheep, genetic diversity, conservation

W57 Effect of vitamin E on chromatin integrity of ram epididymal sperm. B. L. Sartini*, K. H. Petersson, and M. Procopio, *University of Rhode Island*, *Kingston*.

Oxidative stress can impair sperm function by peroxidation of the lipid bilayer and fragmentation of sperm chromatin impacting fertilization and subsequent embryonic development. If sperm are not adequately protected against oxidative damage, cyropreservation can enhance the effects of oxidative stress reducing post-thaw fertility. In livestock, addition of antioxidant vitamin E (VE) during sperm cyropreservation improves post-thaw ejaculated sperm quality although the impact of VE supplementation on epididymal sperm has not been investigated. In this study, the effect of VE (d-alpha tocopherol in emulsified base) supplementation on ram epididymal sperm chromatin integrity was examined. Starting at birth, rams (n= 12) were assigned to one of three treatment groups: 1.) 30 IU VE /kg body weight (BW) + 0.1 mg selenium (Se)/kg BW (VE 30, n = 3), 2.) 15 IU VE/kg BW + 0.1 mg Se/kg BW (VE 15, n= 3), or 3.) Emulsified base + 0.1 mg Se/kg BW (placebo, n=3). VE was administered parenterally every two weeks from birth to seven months of age. Selenium was given once within two days of birth. At seven months of age, epididymal sperm was collected at slaughter, cryopreserved, then analyzed for DNA fragmentation using the sperm chromatin structure assay (SCSA Diagnostics, Brookings, ID). Sperm motility was subjectively assessed microscopically before freezing. The DNA fragmentation index (% DFI) of the epididymal sperm from VE treated rams was not significantly different from placebo (VE 30 = 0.887% ± 0.3; VE 15 = 1.4% ± 0.7; placebo = 1.1% ± 0.2). In addition, sperm motility before cryopreservation was not significantly correlated with % DFI. In conclusion, VE treatment did not improve the integrity of ram epididymal sperm chromatin. Further study on the effects of vitamin E during the establishment of spermatogenesis in prepubertal animals will help elucidate the role of vitamin E in sperm production.

Key Words: sperm, ram, vitamin E

W58 Association of beta-lactoglobulin and prolactin genes with milk production in East Friesian sheep. E. A. Staiger*[1], M. L. Thonney[2], B. W. Buchanan[1], and R. G. Mateescu[1], [1]*Oklahoma State University*, *Stillwater*, [2]*Cornell University*, *Ithaca, NY*.

Milk production is an economically important trait for the sheep industry, however the trait is moderately heritable, expressed relatively late in life, and sex limited. The efficiency of selection for milk production in sheep would be improved by the identification of informative genetic markers. A single nucleotide polymorphism in β-lactoglobulin gene (BLG) and prolactin gene (PRL) were investigated with respect to the genetic merit (EBV) for milk production in East Friesian sheep. The EBV was estimated as the phenotypic deviation from the population mean of the animal's own performance combined with all its relatives' performance. Blood samples were collected from East Friesian ewes. Genotypes were determined by PCR amplification of a 120bp fragment of ovine BLG and 2.5kb fragment of ovine PRL followed by restriction enzyme digestion. The frequency of A and B allele for BLG was 0.69 and 0.31, respectively and the frequency of P and p allele for PRL was 0.13 and 0.87, respectively. Genotypic frequencies for AA, AB, and BB genotypes for BLG were 0.43, 0.52, and 0.05, respectively, and 0.01, 0.23, and 0.76, respectively for PP, Pp and pp genotypes for PRL. The Least Square Means (LSM) for EBV of AA, AB, and BB genotypes in BLG were 112.16, 112.25, and 72.53g of milk per day, respectively, indicating that ewes with at least one A allele would produce 40g of milk per day more than ewes with no A allele. However, this difference was not significant (P = 0.28), possibly due to the low occurrence of BB genotype given the selection for high milk yield within this population. The LSM for weighted EBV of PP, Pp, and pp genotypes in PRL were 153.21, 167.44, and 91.17g of milk per day, respectively, indicating that ewes with no P alleles would produce 73.6g of milk per day more than ewes with at least one p allele (P = 0.0001). These results show an association between PRL gene and milk production in sheep suggesting that this polymorphism could be used in a marker assisted selection program. However, additional genotyping in a different population may be necessary to prove an association between BLG gene and milk production in sheep.

Key Words: β-lactoglobulin, prolactin, milk production

W59 An R package for fitting generalized linear mixed models in animal breeding. A. Vazquez*, D. M. Bates, D. Gianola, K. A. Weigel, and G. J. M. Rosa, *University of Wisconsin*, *Madison*.

Linear mixed models have been extensively used in animal breeding for estimation of genetic parameters and prediction of breeding values associated with normally distributed traits. A more general class of mixed models is represented by the generalized linear mixed models (GLMM), which are appropriate for analysis of data from additional members of the exponential family, such as the Poisson or binomial. This class includes discrete variables such as disease records (e.g., absence or presence of clinical mastitis during lactation) or reproductive traits (e.g., number of inseminations). A standard quantitative genetic model poses that the effects of levels of some random factor (e.g., sire) are correlated. For this reason, routines for mixed models available in standard packages cannot be used for genetic analysis. The pedigreemm package for R was developed as an extension of the lme4 package and allows fitting mixed models with correlated random effects for Gaussian, binary and Poisson responses among others. A correlation between levels of the grouping factor is induced by post-multiplying the incidence matrix of the levels of this random factor by the Cholesky factor of the corresponding (co) variance matrix, e.g., the numerator relationship matrix between sires. Estimation methods available in pedigreemm include approximations to maximum likelihood and restricted maximum likelihood. The pedigreemm also allows the extraction of inbreeding coefficients and relationship matrix from a pedigree. Additionally, the general methods applicable to lme4, as ranef(), plot(), or anova() to name a few, can be also used with pedigreemm.

Key Words: R package, generalized linear mixed models, pedigree

W60 Genetic analysis of lean tissue growth and carcass traits in Large White swine. T. M. Gonçalves*[1], A. L. L. Costa[1], A. I. G. Oliveira[1], and M. C. A. M. Bink[2], [1]*University of Lavras*, *Lavras, Minas Gerais, Brazil*, [2]*University of Wageningen*, *Wageningen, the Netherlands*.

A Bayesian approach was undertaken to estimate genetic parameters and detect major genes (MG) to dressing percentage (DP), carcass length by the Brazilian method of carcass classification (CLMB), average backfat thickness (ABT), backfat thickness at 6.5cm from the dorsal line (P2), loin eye area (LEA), ham yield (HY), lean (LP) fat (FP) and lean cut percentages (LCP), fat weight:lean weight ratio (FLR), and lean tissue growth rate (LTGR). Data from 711 Large White swine were analysed by fitting different genetic models, i.e., the Finite Polygenic Model (FPM), where the number of genes in the FPM is included as an additional random variable, the Infinite Polygenic Model (IPM) and a combination

of these two models. The heritability estimates in the IPM model were 0.17, 0.30, 0.15, 0.16, 0.33, 0.20, 0.51, 0.38, 0.38, 0.42 and 0.42 for traits DP, CLMB, ABT, P2, LEA, HY, LP, FP, LCP, FLR, and LTGR, respectively. The FPM model yielded clearly lower estimates for traits CLMB, ABT, P2, HY, LP, FP, LCP and FLR, respectively. The FPM model revealed posterior evidence for at least one MG at decisive level for traits CD, LEA, LCP and LTGR; at strong level for traits CLMB, FP and FLC; and at positive level for traits P2 and HY. The combined model yielded decisive evidence for presence of one MG for traits CD, LEA and LTGR, while the heritability estimates for these traits were 0.11; 0.36 e 0.17, respectively. These findings suggest that the genetics of growth and carcass traits may be better studied by using models that combine polygenic and major gene effects.

Key Words: swine, finite polygenic model, major genes

W61 Factors affecting weaning-to-first service interval in a Landrace-Large White swine population in Northern Thailand. C. Chansomboon[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand*, [2]*University of Florida, Gainesville.*

Non-productive sow days measured as weaning-to-first service interval (WSI) is an economically important trait in commercial swine production. Thus, a reduction in WSI would help increase efficiency and lower production costs. The aim of this study was to characterize factors affecting WSI in a Landrace-Large White commercial swine population in the province of Chiang Mai, Northern Thailand. The dataset contained 12,974 litter records from 2,596 sows collected from 1989 to 2008. Sows were raised in an open-house system and received the same feeding and management. Sows were from 4 breed groups: Landrace (L), Large White (Y), L × Y (LY), and Y × L (YL). Parity of sow was classified as 1, 2, 3, 4, 5, 6, and ≥ 7. Seasons were winter (November to February), summer (March to June), and rainy (July to October). Preliminary analyses showed no effect of age at farrowing of the sow and number piglets weaned on WSI. Thus, the model for WSI contained the fixed effects of farrowing year-season of the sow, parity of the sow, lactation length, and breed group of sow, and a random residual effect. Year-season of farrowing was an important source of variation ($P < 0.01$). Year-season effects for WSI ranged from 4.60 ± 0.51 days (1991-summer) to 9.22 ± 0.87 days (1989-rainy). The WSI was longer ($P < 0.01$) for first-parity sows (7.91 ± 0.12 days) than for sows of other parities (5.72 ± 0.15 days to 6.10 ± 0.12 days). Landrace sows had similar WSI (5.89 ± 0.09 days) to Y sows (6.00 ± 0.09 days). Crossbreds LY sows (6.23 ± 0.16 days) and YL sows (6.67 ± 0.16 days) had longer WSI than purebreds sows ($P < 0.01$). Heterosis estimates were 0.29 days (4.8%) for LY sows, and 0.73 days (12.2%) for YL sows. Reciprocal differences for WSI indicated that LY sows had lower production costs than YL sows. Crossbred sows had longer WSI than purebred sows, perhaps due to lower adaptability to tropical conditions and unmet higher nutritional requirements.

Key Words: swine, weaning-to-first-service interval, tropical

W62 Use of random regression models for the genetic analysis of weight gain from electronic swine feeders. C. Y. Chen*[1], I. Misztal[1], S. Tsuruta[1], B. Zumbach[1,2], M. Łukaszewicz[1,3], W. O. Herring[4], J. Holl[4], and M. Culbertson[4], [1]*University of Georgia, Athens*, [2]*Norsvin, Hamar, Norway*, [3]*Institute of Genetics and Animal Breeding, Polish Academy of Sciences, Wólka Kosowska, Poland*, [4]*Smithfield Premium Genetics Group, Rose Hill, NC.*

Body weights (BW) of 1,921 Durocs from electronic feeders were used for genetic analysis of weight with random regression models (RRM). Daily, weekly, and bi-weekly average daily gain (DG, DGW, and DGB) were calculated from the average daily BWs with 69,068 records of DG. Estimates from various RRM for DG were erratic. Subsequent tests using a repeatability model for DG, DGW and DGB indicated that heritability of daily gain averaged over d days is approximately 1/(3.3+100/d) and is very low for DG (< 1%) but higher for DGW (6%) and DGB (9%). Subsequent analyses with RRM used DGB. Two RRM were used: with quadratic Legendre polynomials (RRM-L) and with three knot (100, 125, and 150 d) linear splines (RRM-S). Effects in the model included fixed year-biweek-pen and random litter, animal, permanent environment. For both models, the residual variances at 100 d and 150 d were much bigger than at 125d while the genetic variance was the highest at 125d. For RRM-L, heritabilities were 8%, 33%, and 9% at 100 d, 125 d, and 150 d of age. Same estimates were 2%, 26%, and 7% with RRM-S models. Repeatabilities estimated at the three ages were similar (13% to 40% with RRM-L and 9% to 40% with RRM-S). Correlations of 100-125 d, 100-150 d, and 125-150 d of ages were 0.23, -0.07, and 0.66 with RRM-L and 0.39, -0.42, and 0.67 with RRM-S. Adaptation to the feeder in the beginning of test and crowded environment at the end of the test period could cause large residual variances observed in the study. Data from feeder stations can be used for longitudinal analysis of daily gain averaged biweekly. The genetics of daily gain at the beginning and at the end of trail can be different.

Key Words: daily gain, pig, random regression

Dairy Foods: Dairy Products/Chemistry/Enzyme

W63 Calcium reduces DMH-induced large intestinal tumors in male Wistar rats. K. Sivieri*[1] and E. Rossi[2], [1]*Universidade Norte do Paraná-UNOPAR, Londrina, Paraná, Brasil*, [2]*Universidade Estadual Pulista-UNESP, Araraquara, São Paulo, Brasil.*

Different dietary factors can affect colorectal cancer incidence. However, the effect of increased levels of dietary calcium on neoplasms is unclear. The present study was designed to examine the influence of the yogurt fermented with *Enterococccus faecium* CRL and added calcium (600mg/l) on experimental colon carcinogenesis induced by parenteral administration of dimethylhydrazine (DMH). 8-week old rat were given subcutaneous DMH injections at 20 mg/kg once a week during three months. Four groups were used: 1) non-treatment control; 2)DMH control; 3) yogurt fermented with *Enterococcus faecium* CRL 183-DMH plus calcium and induced with DMH (Calcium yogurt) and 4) yogurt fermented *Enterococcus faecium* CRL 183 and induced with DMH (yogurt). Animals were then sacrificed and the incidence of tumors and the number of tumors per tumor-bearing rat were determined. The all groups were compared histologically and TNF-α, IFN-γ and IL-4 cytokines. The non-treatment control not develop tumor. Calcium yogurt group showed a 50% inhibition in incidence in average number of tumors and significantly decreased the number of rats with multiple tumors and TNF-α, IFN-γ and IL-4 cytokines increasing in this group. We conclude that a low dietary calcium supplement in rats inhibits colon cancer carcinogenesis induced by DMH and enhanced the immune response.

Key Words: calcium, yogurt, colon cancer

W64 Effect of storage temperatures on ice cream quality. J. Buyck* and R. Baer, *South Dakota State University, Brookings*.

Ice cream quality is dependant on many factors including the storage temperature. Currently, the industry standard for ice cream storage is -28.9°C (-20°F). Ice cream production costs may be decreased by increasing the temperature of the storage freezer. Increasing the storage temperature of ice cream by one degree may lower energy consumption by about 5%. The objective of this research project was to evaluate the effect of four storage temperatures on storage quality of commercial light and full fat vanilla flavored ice cream. Storage temperatures used were -45.6°C (-50°F), -26.1°C (-15°F), and -23.3°C (-10°F) for the three treatments and -28.9°C (-20°F) as the control. Composition of light and full fat ice cream mixes averaged 5.18 and 10.35% milk fat, 3.99 and 2.98% protein, 0.93 and 0.87% ash, 25.67 and 24.51% total sugars, and 35.77 and 38.71% total solids, respectively. Light and full fat ice cream mixes averaged -2.66 and -2.67°C for freezing point, 6.92 and 6.50 for pH, 0.18 and 0.20% for titratable acidity, respectively. Ice crystal sizes were analyzed by a cold-stage microscope and image analysis at 1, 19.5, and 39 weeks of storage. A trained sensory panel evaluated the coldness intensity, iciness, creaminess, overall body/texture acceptance, storage/stale off-flavor, and overall flavor acceptance of the light and full fat ice creams at 39 weeks of storage. Average ice crystal sizes for light and full fat ice creams after one week of storage were 25.78 and 22.82 um, respectively. In a second study, light and full fat ice creams were heat shocked by storing at -28.9°C (-20°F) for 35 weeks and then alternated between -23.3°C (-10°F) and -12.2°C (10°F) every 24 hours. Heat shocked ice creams were analyzed at 2 and 4 weeks of storage for ice crystal sizes and evaluated by the trained sensory panel.

Key Words: ice cream, storage temperature, ice crystals

W65 Obtention of a dairy ingredient rich in milk fat globule membrane material from whey buttermilk. M. R. Costa*[1,2], R. Jiménez-Flores[3], and M. L. Gigante[2], [1]*Universidade Norte do Paraná, Londrina, Paraná, Brazil*, [2]*Universidade Estadual de Campinas, Campinas, São Paulo, Brazil*, [3]*California Polytechnic State University, San Luis Obispo*.

Milk fat globule membrane (MFGM) components are known for their technological and health properties, and there is interest in isolating and concentrating this material from dairy sources. Whey buttermilk contains triglycerides residues and hydrosoluble compounds from milk, including MFGM material, and it can be considered a suitable source of the latter. The objective of this work was to obtain a dairy ingredient rich in MFGM components from whey buttermilk using membrane filtration. Batches of sweet whey cream was obtained from a commercial source and churned into whey butter with resulting separation of whey buttermilk. The buttermilk was processed through an ultrafiltration (UF)/diafiltration (DF) system (10 KDa molecular weight cutoff) at 25 °C and 6 bar of transmembrane pressure and the final retentate was spray-dried. The whey buttermilk, the filtration retentates, and the whey buttermilk powder (WBP) were analyzed for composition, protein profile and phospholipids content. All the experiments were done in triplicate. The protein, lipid, phospholipid, lactose and ash contents in the whey buttermilk, in dry matter basis, were 24.9, 16.3, 2.0, 51.8 and 7.0%, respectively. The average transmembrane flux was 34 and 30 L.h-1.m-2 during UF and DF, respectively. The membrane filtration reduced the contents of lactose and ash in 94 and 77% ($p<0.05$), and increased the contents of lipids, phospholipids and proteins in 190, 90 and 300%, respectively ($p<0.05$). The final composition of the WBP was 47.4, 47.3, 7.2, 3.0 and 2.3% of protein, lipid, phospholipids, lactose and ash, respectively. SDS-PAGE showed small casein content in the whey buttermilk and that MFGM proteins represented large amount of the total protein in the whey buttermilk powder. The use of whey buttermilk as raw-material and the application of ultrafiltration and diafiltration yield a dairy ingredient with original features for its use in foods, especially considering that the powder had a protein:lipid ratio of 1:1, and high content of phospholipids.

Key Words: membrane filtration, supercritical fluid extraction, phospholipids

W66 Effect of pH on functional properties of regular and whey buttermilk powders. M. R. Costa*[1,2], R. Jiménez-Flores[3], and M. L. Gigante[2], [1]*Universidade Norte do Paraná, Londrina, Paraná, Brazil*, [2]*Universidade Estadual de Campinas, Campinas, São Paulo, Brazil*, [3]*California Polytechnic State University, San Luis Obispo*.

Buttermilk is a derivative product of butter production from cream. However, butter can also be produced from a by-product of cheese, the whey cream. The buttermilk produced from whey cream has been poorly characterized. The objective of this work was to evaluate the effect of pH on some functional properties of regular and whey buttermilk powders. Whey buttermilk powder was produced by ultrafiltration and 5X diafiltration (membrane of 10 KDa molecular weight cutoff, at 25 °C) of whey buttermilk followed by spray-drying of the final retentate. The regular buttermilk was a commercial powder. Protein solubility (5% protein solution), by the centrifugation method, and emulsion stability (20% canola oil and 1% protein emulsions), by creaming index and kinetics (QuickScan® optical analyzer), were evaluated at pH 5 and pH 7 for both powders. The pH did not significantly affect the protein solubility of the whey buttermilk solutions while the regular buttermilk solutions had its protein solubility reduced from 86.2 to 73.0% when the pH was decreased from 7 to 5. This protein solubility decrease was possibly due to the reduction of the residual casein solubility, found in higher quantity in the regular buttermilk than in whey buttermilk. At pH 7, regular and whey buttermilks showed similar protein solubility, while at pH 5 the whey buttermilk had the best solubility. The pH significantly affected the emulsion stability of the whey and regular buttermilk solutions. At pH 5, the emulsions made from both buttermilk powders had lower stability (creaming index ~ 38%) than at the highest pH. At pH 7, the whey buttermilk emulsion showed the best stability (creaming index of 0.2%) in comparison to the regular buttermilk (creaming index of 3%). Whey buttermilk powder showed better functionality than the regular buttermilk powder, which makes it an interesting ingredient to be used in food formulations as high quality protein and lipid sources, especially in low pH foods.

Key Words: protein solubility, emulsion stability, dairy ingredients

W67 Milk iodine concentration in goats supplemented with potassium iodide. A. Nudda*[1], F. Aghini-Lombardi[2], G. Battacone[1], M. Decandia[3], M. Frigeri[2], and G. Pulina[1,3], [1]*Dipartimento di Scienze Zootecniche, University of Sassari, Italy*, [2]*Dipartimento di Endocrinologia e Metabolismo, University of Pisa, Italy*, [3]*Agricultural Research Agency of Sardinia - AGRIS Sardegna, Sassari, Italy*.

Aim of this work was to evaluate the effects of continuous oral supplementation of potassium iodide (KI) on iodine levels in goat milk. Thirty crossbreed dairy goats were divided into 3 groups and each goat was supplemented with 0 (control; group 0), 450 (group 1), or 900 (group

2) µg of KI/day. The dose of KI (76.5% of Iodine) was orally administered in water every day for 8 weeks. Milk yield was recorded and milk samples were collected weekly. Iodine concencentration was determined using the Sandell–Kolthoff reaction. Data were analyzed with a GLM procedure including iodine level, week and their interaction in the model. Milk yield was not influenced by KI supplementation and averaged 1229, 1227 and 1179 g/d per head in groups 0, 1 and 2 respectively. Mean milk iodine concentrations throughout the experimental period (90 days) were 60.1 ± 50.5, 78.8 ± 55.4 and 130.2 ±62.0 µg/l in groups 0, 1 and 2, respectively. The extent of enrichment of iodine concentration in milk was about 31% in group 1 and 117% in group 2 compared to control. Milk iodine concentration within group showed a high variability among weeks, especially in the group that received the highest dose of KI. The carry-over (iodine excreted in milk/iodine supplemented), which averaged 32% in group 1 and 24% in group 2, was lower than the values previously reported in other ruminant species.

Key Words: milk, iodine, dairy goat

W68 Antioxidant properties of milk protein dispersions preheated with various sugars. H. J. Giroux*, J. Houde, and M. Britten, *Food Research and Development Centre, Agriculture and Agri-Food Canada, Saint-Hyacinthe, QC, Canada*.

Polyunsaturated fatty acids are susceptible to oxidation during heating. It has been shown that sterilization induced significant oxidative degradation in dairy beverages enriched with linseed oil. Nevertheless, during storage, sterilized beverages showed better resistance to photo–oxidation than unheated beverages probably as a result of the antioxidant activity of Maillard reaction products generated during heating. The objective of this study was to evaluate the effect of adding preheated milk protein–sugar dispersions to dairy beverages (enriched with linseed oil) in order to prevent oxidation during sterilization. Milk protein (MP) dispersions (3.5% protein) containing various concentrations of glucose–galactose (GG), glucose–fructose (GF) or sucrose (S) were heated at 110°C for 10 minutes. The preheated protein–sugar dispersions were added to dairy beverage formulations at 5% (v/v). Unheated protein–sugar dispersions were also tested. Color and hydroxymethylfurfural (HMF) content were measured to evaluate the extent of Maillard reaction. Propanal and hexanal (two volatile secondary oxidation products) were selected as indicator for linseed oil oxidation and analysed by GC–MS. The total colour difference (ΔE) and HMF content of the beverages increased (P<0.01) with increasing concentration of unheated or preheated MP–GG and MP–GF preparations, the effect being significantly higher in beverages containing preheated preparations. Unheated protein–sugar preparations did not reduce lipid oxidation during sterilization while preheated MP–GG and MP–GF preparations were most effective. The concentrations of hexanal and propanal resulting from the sterilization treatment were respectively reduced by 100 and 78% when GG or GF concentration in the beverage was 0.4%. The addition of preheated MP–S had no significant effect on color, HMF content or sterilization–induced oxidation. In conclusion, milk protein dispersion preheated in the presence of monosaccharide mixtures can be added to dairy beverages to efficiently inhibit oxidation during sterilization treatment.

Key Words: oxidation, sterilization, Maillard

W69 Main phospholipids content of sweet whey cream, butter and buttermilk. M. R. Costa*[1,2], R. Jiménez-Flores[3], and M. L. Gigante[2], [1]*Universidade Norte do Paraná, Londrina, Paraná, Brazil*, [2]*Universidade Estadual de Campinas, Campinas, São Paulo, Brazil*, [3]*California Polytechnic State University, San Luis Obispo*.

There is an increasing interest in phospholipids found in milk because of their technological functionality and potential health benefits. Whole milk has around 0.04% of phospholipids, of which distribute approximately 35% in the whey and 65% in the milk fat globule membrane (MFGM). When whey cream is churned into butter, an aqueous phase called whey buttermilk is separated. These products contain all the milk components, including MFGM material. The objective of this work was to quantify in sweet whey cream, butter and buttermilk the contents of the main phospholipids found in milk and dairy products: phosphatidylcholine (PC), phosphatidylethanolamine (PE), sphingomyelin (SM), phosphatidylinositol (PI) and phosphatidylserine (PS). Batches of sweet whey cream were taken from a commercial cheese plant and churned to obtain whey butter and buttermilk. The three products had their gross composition evaluated. The fat extracted from these samples was analyzed by High Performance Liquid Chromatography to identify and quantify their main phospholipids contents. The protein, lipid, phospholipid, lactose and ash contents, in dry matter basis, were, respectively, 3.6, 86.1, 4.9, 6.4 and 3.9% for the whey cream, 0.6, 96.9, 5.1, 2.4 and 0.1% for the whey butter, and 24.9, 16.3, 2.0, 51.8 and 7.0% for the whey buttermilk. As expected, the main phospholipids found were phosphatidylcholine, phosphatidylethanolamine and sphingomyelin, followed by phosphatidylinositol and phosphatidylserine. As a percentage of the total lipids, PC, PE, SM, PI and PS contents were, respectively, 1.90, 1.00, 1.23, 0.87 and 0.64% for the whey cream; 1.77, 0.94, 1.16, 0.84 and 0.61% for the whey butter; and 5.71, 2.11, 2.69, 0.88 and 1.00% for the whey buttermilk. These phospholipids represented 5.6, 5.3 and 12.4% of the total lipids in the whey cream, butter and buttermilk, respectively, showing that this class of lipids distributes preferentially to the aqueous phase. The relatively high phospholipids content makes the whey buttermilk interesting to be processed in a dairy ingredient that would be rich in compounds with good functionality and potential health benefits.

Key Words: milk fat globule membrane, dairy ingredients, chromatography

W70 Expression of milk-derived angiotensin-converting-enzyme-inhibiting peptide in *Lactococcus lactis*. X. Han[2], L. Yao[2], M. Wang[2], D. Sun[2], B. Li[2], and Y. Jiang*[1,2], [1]*National Dairy Engineering & Technical Research Center, Northeast Agricultural University, Harbin, China*, [2]*Key Laboratory of Dairy Science, Ministry of Education, Northeast Agricultural University, Harbin, China*.

Peptides derived from milk proteins can have Angiotensin-converting enzyme (ACE)-inhibiting properties and may thus be used as antihypertensive components. The objective of this study is to establish a new method to produce antihypertensive peptides (AHP) by DNA recombination technology in *Lactococcus lactic*. To produce a large quantity of the ACE-inhibiting peptide CEI_7, which consists of seven amino acids found from β-casein f(169-175), a high-level expression was explored with tandem multimers of CEI_7 gene in *Lactococcus lactic* . The genes encoding CEI_7 were tandemly multimerized to 4-mers, in which each of the repeating units in the tandem multimers was connected to the neighboring genes by a DNA linker encoding Ile-Glu-Gly-Arg for the cleavage of multimers by Factor Xa. The repeats gene was cloned into the expression vector pNZ8148, and expressed in *Lactococcus lactic* NZ9000 with nisin induction. Then the tandem multimers mRNA expression identified and the optimal induction-condition obtained by real time RT-PCR. Finally, using the protocol of protein electrophoresis

and Western Blot completes the further validation. The 4-mer's mRNA had completely expressed. Optimization of induction factors for this pNICE system was that the induction was caring out at the early exponential phase (2h after bacterial inoculation) by 2 ng/ml nisin, and the best time for analyzing the gene product after induction was the 1st h. At last, SDS-PAGE and Western Blot analyses showed the expressed protein, with a molecular weight of about 8kD, which was close to the 4-mer's theoretical molecular weight and had same immunogenicity. The aim of expression was came true, but the yield of the recombinant CEI_7 was lower than expectation causing the mRNA of tandem multimers being unstabilized.

Key Words: angiotensin-converting-enzyme-inhibiting peptide, expression, *Lactococcus lactis*

W71 Effect of tara gum and carrageenan addition on syneresis of non-fat set yogurt. C. L. Hatanaka, A. L. Cavallieri, R. L. Cunha, and M. L. Gigante*, *Universidade Estadual de Campinas*, *Campinas, SP, Brazil*.

The aim of this work was to evaluate the effect of tara gum and carrageenan addition on spontaneous syneresis during the cold storage. Three types of yogurts with 12.5% of dry matter, made of skim reconstituted milk, were manufactured: (1) yogurt control (no polysaccharides added); (2) yogurt with 0.02% of tara gum and (3) yogurt with 0.02% of tara gum and 0.02% of carrageenan. Solutions of polysaccharides and skim milk in distilled water were prepared at 85°C/30 min, cooled and stored (5°C) a day before the fermentation. The mixtures were inoculated with 2.5% of starter culture (*Streptococcus thermophilus* and *Lactobacillus bulgaricus*), and the fermentation was conducted at 45°C until pH 4.7±0.05. Total solids, protein, fat, ash and lactose content of yogurts were evaluated a day after the manufacturing. Spontaneous syneresis was evaluated during the cold storage at 1, 8, 15, 22 and 29 days after yogurt manufacture. A split-plot design with three replicates was used. The treatments did not affect the yogurt composition, which was 12.3±0.1% of total solids; 4.36±0.02% of protein; 0.098±0.001% of fat; 1.07±0.01% of ash and 6.43±0.09% of lactose. Treatments significantly affected yogurts syneresis. Yogurt with tara gum and carrageenan showed the lowest syneresis, followed by yogurt control and then by yogurt manufactured with tara gum. The highest syneresis observed when tara gum was added was probably due to depletion or excluded volume interactions among this polysaccharide and the casein, which may weakened the gel structure. The lowest syneresis in the yogurt containing tara gum and carrageenan may be due to an increase of system hydrophilic groups caused by the presence of the polysaccharides, which confers greater interactions among water and biopolymers segments. The addition of polysaccharides also led to casein and carrageenan interactions below the casein isoelectric point, since at these conditions they associate with each other and strengthen gel structure allowing an additional immobilization of water in the yogurt network.

Key Words: hydrocolloids, set yogurt, syneresis

W72 Improvement of emulsifying properties of sodium caseinate by conjugation with maltodextrins through the initial step in the Maillard reaction. Y. Lu* and J. Lucey, *University of Wisconsin*, *Madison*.

The objective of this study was to improve the emulsifying properties (e.g., stability) of sodium caseinate (SC) by conjugation with maltodextrin (MD) in an aqueous solution through the initial step in the Maillard reaction (by the method of Zhu et al. 2008. J. Agric. Food Chem. 56: 7113). Complexation was conducted in phosphate buffer using SC and MD and by varying the reaction conditions including: temperature (60-90°C), pH (6.5 to 8.5), reaction time (0-180 min), and solids content (9 to 19%, w/w). Conjugation was monitored using Difference UV (DUV) Spectroscopy by the formation of a peak at around 305 nm; conjugate formation was confirmed using SDS-PAGE with both protein and glycoprotein stains. Yellow color development (unwanted) was monitored using DUV spectroscopy as indicated by an increase in absorbance at λ450 nm. Conjugate formation increased with longer reaction time, and higher solids content, or temperature. There was no significant difference in conjugate formation between different pH values investigated. Emulsifying properties of the conjugates were determined using a particle size analyzer and the surface-weighted mean particle size, D[3,2], was measured. Compared to emulsions made with SD alone, the D[3,2] values of emulsions made with SD-MD conjugates were smaller at both the 1st day after manufacture and after storage at 4°C for 30 days. These results indicate that stability of SD emulsions was improved by conjugation with MD. This study could be significant in the development of a new type of food ingredient.

Key Words: sodium caseinate, protein-polysaccharide conjugates, emulsifying properties

W73 Chemical composition, probiotic survivability and sensory property of goat's milk kefir. Y. H. Bao[1,2], G. P. Yu[1,3], and M. R. Guo*[1], [1]*University of Verment*, *Burlington*, [2]*Northeast Forestry University*, *Harbin, Heilongjiang, China*, [3]*Northeast Agricultural University*, *Harbin, Heilongjiang, China*.

Kefir is an acidic and mildly fermented dairy product and considered as a functional food. As a specialty food, goat's milk and its products are getting popular in the U.S. In present study, formulation and processing technology of goat's milk kefir were developed using a commercial starter containing *L. lactis subsp. lactis* and *L. lactis subsp. diacetylactis* and probiotics *L. casei* and *L. plantarum*. Three different flavored kefir beverages were analyzed for chemical composition, changes in pH and viscosity, and probiotic survivability during storage. Mold, yeast and coliform counts were also evaluated weekly for these samples. The gross compositions of three products (blueberry, strawberry and plain) were: total solids: 16.28%, 14.78% and 16.03%; protein: 2.43%, 2.16% and 2.35%; fat: 1.99%, 1.87% and 2.15%; ash: 0.62%, 0.58% and 0.61%, respectively. There were no considerable changes in pH and viscosity during the 8-week storage at 4°C. Both *L. casein* and *L. plantarum* remained viable and their populations were above 10^6 cfu/g during storage. The mold, yeast and coliform were not detected in the products. The results showed that the addition of fruit flavor had no considerable effect on the probiotic survivability, coliform, and viscosity during the storage. The results of sensory evaluation showed that the fruit-flavored goat's milk kefirs were stable without losing its desired flavor qualities.

Key Words: goat's milk, kefir, probiotics

W74 Optimizing the organoleptic and nutritional qualities of a dairy-based ready-to-eat food product. J. Heick*, M. Cleveland, H. Khalil, and R. Jiménez-Flores, *California Polytechnic State University*, *San Luis Obispo*.

Providing high quality dairy protein in a ready-to-eat (RTE) form is desirable when delivering convenient nutrition to active consumers

as well as providing probiotic organisms as a functional component. The main challenge in developing such a product is the relatively high concentration of protein, which negatively impacts flavor, texture and overall acceptability throughout the product shelf life. Another challenge is the survival of active probiotic organisms, limited by relative instability of organisms in processed foods. We have developed a unique formulation and processing technique that eliminates the unappealing dense texture of high protein food, while extending the products' shelf life. The optimized RTE delivers a minimum of 25 grams of protein per serving. It includes milk phospholipids, which have been shown to enhance the survival of probiotic lactic acid bacteria (LAB). Our experimental design was a 2 x 2 x 3 factorial experiment that included two processing methods; freeze drying and vacuum drying; two levels of dairy ingredients; buttermilk powder (BMP) rich in milk phospholipids and skim milk powder (SMP); and three strains of LAB. Our results show that drying the RTE below five percent moisture results in a clean tasting lightweight energy-dense product. Results indicated that the impact of the drying method on flavor and texture profiles was not significant, the final moisture being the most important factor. In addition enumeration of the probiotic organisms displays a two to three log reduction after processing with a difference of one log between the two methods. Statistical analysis of the various formulations and drying parameters show that the BMP and freeze-drying combination produces the most acceptable product in terms of flavor, texture, and probiotic survival.

Key Words: probiotics, freeze drying, phospholipids

W75 Milk fatty acid composition of whole fluid milk in the United States. A. M. O'Donnell*, D. M. Barbano, and D. E. Bauman, *Cornell University*, *Ithaca, NY*.

Consumers are increasingly aware that food components have the potential to influence human health maintenance and disease prevention, and dietary fatty acids (FA) have been of special interest. It has been 25 years since the last survey of US milk fatty acid composition, and during this interval there have been substantial changes in dairy rations, including increased use of total mixed rations and by-product feeds as well as the routine use of lipid and FA supplements. Furthermore, analytical procedures have improved allowing greater detail in the routine analysis of FA, especially *trans* fatty acids. Our objective was to survey US milk fat and determine its fatty acid composition. We obtained samples of fluid milk from 56 milk processing plants across the US every 3 months for one year to capture seasonal and geographical variations. Processing plants were selected based on the criteria that they represented the major volume of milk produced in that area. An overall summary of the milk fat analysis indicated that saturated fatty acids (SFA) comprised 63.7% of total milk FA with palmitic and stearic acids representing the majority (44.1% and 18.3% of total SFA, respectively). Unsaturated fatty acids (UFA) were 33.2% of total milk FA with oleic acid predominating (71.0% total UFA). *Trans* FA (TFA) represented 3.2% of total FA, with vaccenic acid being the major *trans* isomer (46.6% total TFA). *Cis*-9, *trans*-11 18:2 conjugated linoleic acid represented 0.56% total milk FA, and the major omega-3 FA (linolenic acid, 18:3) composed 0.39%. Analyses for seasonal and regional effects indicated statistical differences for some FA, but these were minor from an overall human nutrition perspective as the FA profile for all samples were numerically similar. Overall, the present study provides a valuable database for current fatty acid composition of US fluid milk, and results demonstrate that the milk fatty acid profile is remarkably consistent across seasons and geographic regions from the perspective of human dietary intake of milk fat.

Key Words: fatty acids, milk fat composition, survey

W76 Shelf life of milk. C. A. Boeneke*, J. L. Vargas, and K. J. Aryana, *Louisiana State University Agricultural Center*, *Baton Rouge*.

The objective of this work was to assess the shelf life of milk. Whole and two percent milks were received from 17 dairy processing plants located in the west, midwest, and southern regions of the U.S in duplicate. All milks were shipped overnight in styrofoam coolers filled with ice to maintain the temperature of the samples. The samples were pasteurized at the processing plants by high-temperature short-time pasteurization. The first set of milk samples was evaluated for standard plate count, coliforms, and psychrotrophic counts (using a standard method as well as a rapid method), heat-resistant spore-forming psychrotrophs, aerobic spores, HR testing (HR-1, HR-2 and HR-3), fat percentage, protein percentage, somatic cell count and sensory evaluation. Milks were evaluated for flavor using the Collegiate Dairy Products Evaluation Score Sheet. The duplicate set was evaluated for standard plate count, coliform count and a sensory evaluation at the end of two weeks storage time at seven degrees C. Three replications were conducted. Five percent of the 2% milk samples presented psychrotrophic counts (three samples in the first replication of the study, two samples in the third replication) with a mean values of approximately 2 CFU (colony forming units)/ml. For heat resistant spore forming psychrotrophs, ten percent of the samples showed the highest counts of approximately 1 CFU/ml, mainly in the second replication of the study. Ninety percent of the samples showed zero counts. Sensory evaluation scores ranged from 1 to 10 out of 10 possible points. The most common flavor criticism found by the panelists was a cooked off-flavor as well as rancid and oxidized criticisms.

Key Words: shelf life, fluid milk

W77 Influence of resistant starch on the characteristics of fat free plain yogurt. M. Moncada[1], K. Aryana*[2,1], M. Keenan[2,1], R. Martin[2,1], F. Greenway[3], and N. Dhurandhar[3], [1]*Louisiana State University*, *Baton Rouge*, [2]*Louisiana State University Agricultural Center*, *Baton Rouge*, [3]*Pennington Biomedical Research Center*, *Baton Rouge, LA*.

Resistant starch is a starch that escapes digestion in the small intestine and can deliver some benefits of insoluble and soluble fiber. Objective was to study the influence of resistant starch on the physico-chemical, microbiological and sensory characteristics of yogurt. Three types of resistant starches namely; Hi maize, Amioca, and Novelose were incorporated at 30 g per 8 oz of yogurt. Total solids in the control were kept constant with non fat dry milk. Apparent viscosity, pH, syneresis, sensory properties (flavor, body and texture, and appearance and color), lactic acid bacterial counts and color (L*, a*, and b*) of yogurts were determined at 0, 1, 3, 5 and 7 week after yogurt manufacture. Yogurts with Amioca had significantly the lowest apparent viscosity values, while there were no significant difference among the other yogurts. Yogurts with Hi maize and Novalose had significantly the highest syneresis which were not different from each other. The pH values of the yogurts with the resistant starches were significantly lower compared to the control but were not different compared to each other. Control and yogurts with Amioca had significantly the highest flavor scores compared to the other yogurts. Control had significantly the highest sensory body texture

score compared to the other yogurts. Body and texture scores of yogurts with resistant starches were not significantly different from each other. Control and yogurts with Amioca had significantly the lowest a* values which were not different from each other, while yogurts with Hi maize and Novalose had significantly the highest a* values which were not different from each other. Control had significantly the highest b* values, while yogurts with Amioca had significantly the lowest b* values. Type of resistance starch influenced different characteristics of yogurt.

Key Words: resistant starch, fermented, yogurt

W78 Acceptability of yogurt containing resistant starch. K. Aryana*[1,2], D. Olson[2], M. Keenan[1,2], R. Martin[1,2], F. Greenway[3], and N. Dhurandhar[3], [1]*Louisiana State University Agricultural Center*, *Baton Rouge*, [2]*Louisiana State University*, *Baton Rouge*, [3]*Pennington Biomedical Research Center*, *Baton Rouge, LA*.

Objective was to study the acceptability of yogurt containing Hi maize resistant starch. Resistant starch (RS) Hi maize was incorporated in yogurt manufacture at 30 g per 227 g of yogurt. Total solids in the control were kept constant with non fat dry milk. One hundred participants (without allergy to dairy or starch) used a 9-point hedonic scale (1=dislike extremely; 5 = neither like nor dislike; 9 = like extremely) for overall liking, appearance, color, aroma, taste, thickness, graniness, product acceptability. Yogurt with or without RS was placed in separate 85g cups which were assigned 3-digit random number codes. The sensory data were analyzed using the GLM procedure of SAS 9.1 for Windows as a Randomized Block Design using participants as blocks. There were no significant ($P > 0.05$) differences in appearance, color and aroma scores for the control yogurt compared to the RS yogurt. Taste, thickness, graininess and likeness scores for the control yogurt were significantly ($P < 0.0001$) higher than the RS-yogurt. The RS-yogurt was acceptable to the consumers.

Key Words: resistant starch, yogurt, acceptability

W79 Improving the quality of yogurt with modified whey protein ingredients. P. T. Matumoto-Pintro*, L. Rabiey, G. Robitaille, and M. Britten, *Agriculture and Agri-Food Canada*, *St-Hyacinthe, QC, Canada*.

Fermented milk products are widely consumed as healthy food, and represent a growing market for the dairy industry. Denatured whey protein concentrates or isolates are used in yogurt formulations to decrease costs, improve nutritional value or reduce syneresis. However, high concentrations of whey protein usually results in unpleasant elastic textures. In order to increase the viscous character of yogurts supplemented with denatured whey protein, alteration of composition (increased proportion of α–lactalbumin) and proteolytic treatment (using α–chymotrypsin) of whey protein isolate were studied. Whole milk was standardized to 4.2% protein with heat–treated whey protein isolates, or milk protein concentrate as a control. The proportion of α–lactalbumin in the whey protein isolate and the degree of hydrolysis were the main factors under study. Rheological properties, rate of sedimentation and syneresis were monitored on set–style and stirred–style yogurts during a three weeks storage period. Controlled protein hydrolysis and increasing proportion of α–lactalbumin in the whey protein isolate reduced the stress and the deformation at rupture point in set–style yogurts, bringing the rheological characteristics close to those of control yogurt. Similar trend was observed for stirred–style yogurts. High proportion of α–lactalbumin and hydrolysis treatment also reduced yogurt particles sedimentation rate, suggesting a finer structure, less prone to syneresis. In conclusion, this study showed that the modification of whey protein composition or appropriate hydrolysis treatment can be used to improve the texture attributes of set–style and stirred–style yogurts.

Key Words: yogurt, α-lactalbumin, proteolysis

W80 Effect of starch spherulites on survival of bifidobacteria in the presence of acid or bile. S. Chittiprolu, R. F. Roberts*, and G. R. Ziegler, *The Pennsylvania State University*, *University Park*.

Strains of the genus Bifidobacterium are widely added to ferment dairy products such as yogurt because of their potential probiotic activity. Bifidobacteria are often sensitive to stresses encountered during production and storage of food and during passage through the gastrointestinal tract. The objectives of this study were to develop conditions for production of starch-based spherulites, to determine if bifidobacteria adhere to spherulites and to determine if adhesion to spherulites could improve their survival when exposed to acid or bile. First, conditions were developed to produce starch-based spherulites successfully in a pressure vessel using purified potato amylose. These spherulites were further dried, characterized and stored until adequate quantities were obtained for use in adhesion and survival studies. A total of 38 Bifidobacterium strains were analyzed for their ability to adhere to potato amylose spherulites and native high amylose maize starch granules (Hylon VII). The strains differed in their ability to adhere to spherulites and Hylon VII with adhesion to spherulites significantly higher than Hylon VII for the majority of the strains. The protective effect of adherence of 4 bifidobacterial strains to spherulites or Hylon VII on their survival when exposed to acid or bile was investigated. The number of bifidobacteria surviving after 3 h exposure to acid (pH 1.8, 2.9 and 7.2) or bile (0 and 0.5% oxgall) was significantly affected by type of strain used, pH and bile concentration. The strains analyzed were not tolerant to pH 1.8 but survived well at pH 2.9 and 7.2 and in bile solutions containing 0 and 0.5% oxgall. Overall, adhesion to spherulites or Hylon VII did not improve the survival of bifidobacteria in the presence of acid or bile. This is the first study on protective effects of spherulites on survival of bifidobacterial strains.

Key Words: bifidobacteria, spherulites, adhesion

W81 Determination of free fatty acid profiles of reduced-fat and whole goat milk cheeses aged for 3 months under refrigeration. W. Nouira[1], Z. Guler[2], and Y. W. Park*[1], [1]*Fort Valley State University*, *Fort Valley, GA*, [2]*Mustafa Kemal University*, *Hatay, Turkey*.

Implication of dietary fat with coronary heart diseases, strokes and other health concerns has increased the demand for reduced-fat dairy products. Few reports are available for free fatty acid profiles of reduced fat goat milk products. The study was conducted to evaluate differences in free fatty acid (FFA) compositions between skim milk (SM) and whole milk (WM) goat cheeses aged at 4°C for three months. The two types of cheeses were manufactured using a bulk goat milk from a mixed herd of Saanen, Alpine, and Nubian breeds. Cream was separated from the whole milk by a cream separator (Model 17584, Clair Co., Austria) before manufacture of SM cheeses. FFAs of all cheeses were extracted in diisoprophyl ether using polypropylene chromatography column (Bio-Rad Labs, Los Angeles, CA), and FFA concentrations were quantified using a gas chromatography (17A-GC, Shimadzu Co., Japan) equipped

with a fused silica capillary column (DB-FFAP; 30 m x 0.25 mm i.d. x 0.25 Î¼m, Agilent Technologies, Wilmington, DE). FFA contents (mg/g cheese) of fresh WM and SM cheeses for C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C18:0, C18:1, C18:2 were: 0.020, 0.072; 0.070, 0.035; 0.061, 0.055; 0.181, 0.167; 0.073, 0.047; 0.174, 0.112; 0.579, 0.152; 0.308, 0.202; 0.521, 0.174; 0.057, 0.026, respectively. The respective % FFA in total fatty acids for 0, 1 and 3 months aged WM and SM cheeses were 8.44, 12.4; 6.31, 16.91; 12.03, 14.19, indicating that the reduced-fat cheeses had significantly higher proportions of FFA than those in the corresponding WM cheeses. The respective ratios of SM:WM cheeses in FFA concentrations for 0, 1 and 3 months aging were 0.48, 1.21 and 0.364, suggesting that SM cheeses had higher levels of FFA than WM cheeses. The higher proportions of FFA in SM cheeses compared to WM counterparts may account for the released FFAs from the fat globule membrane during cream separation.

Key Words: goat cheese, reduced-fat, free fatty acids composition

W82 Heat stability of mixtures of different milk protein concentrates (40–90% protein) and whey protein concentrate (80% protein). Y. H. Yong* and E. A. Foegeding, *Department of Food, Bioprocessing and Nutrition Sciences, North Carolina State University, Raleigh*.

Meal replacement beverages generally contain a mixture of proteins that are at neutral pH and processed by retorting. Low heat stability of whey protein ingredients limits their application in these products. The goal of this investigation was to determine if combining whey protein concentrate 80 (WPC80, containing minimum 80% w/w dry basis protein) at a proper ratio with milk protein concentrate (MPC) will improve heat stability and thereby allow for a higher percentage of whey proteins in these beverages. Five types of MPC (containing 40, 56, 70, 80 and 90% w/w dry basis protein) and four types of WPC80 (regular types A, B, C and heat stable/gelling type H) were collected from U.S. companies. At pH 7, single protein solutions of WPC80 (4–10% w/v protein), MPC (5–12.5% w/v protein) and their mixtures (particularly WPC80 and MPC80) at different ratio (10% w/v total protein) were retorted for 26±1 min (including sterilized at 121+2°C for 10 min). For single WPC80 solutions, all four types of WPC80 showed different thermal stabilities. The two most stable samples, WPC80-A and H, formed gels at 9 and 7% w/v protein, respectively. WPC80-A, B and C showed similar destabilizing trends from stable fluids, to fluid aggregates, to gels, with increasing protein concentrations. In the case of MPC solutions, MPC-40 and 56 gelled at 7.5 and 12.5% w/v protein, correspondingly, but MPC-70, 80 and 90 remained stable at 12.5% w/v protein. Mixtures of WPC80 and MPC80 at 10% w/v total protein improved the heat stability of WPC80-A, B and C but, surprisingly not WPC80-H. When ratios of WPC80-A to MPC80 were 7:3 or lower, all the mixtures remained as stable fluids after thermal processing. Viscosity of the retorted solutions became higher when the concentration of WPC80-A in the mixtures increased. The results showed that at 10% w/v protein, up to 70% of MPC80 can be replaced with a WPC80 and still produce a stable fluid after retorting.

Key Words: milk protein concentrate, whey protein concentrate, heat stability

W83 Effect of processing on the structure and functional properties of milk phospholipids. S. Gallier*[1,2], D. Gragson[3], D. W. Everett[1], and R. Jiménez-Flores[2], [1]*Department of Food Science, University of Otago, Dunedin, Otago, New Zealand*, [2]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo*, [3]*Department of Chemistry and Biochemistry, California Polytechnic State University, San Luis Obispo*.

Bovine raw milk is a very nutritious food, however consumers are concerned about any health benefit derived from consumption of this product. There are many questions about whether current processing conditions, such as pasteurization, have benefits other than microbiological safety. One of the components of milk that has been associated with several biological functions is milk fat, and in particular, the milk fat globule membrane (MFGM). In this study, we compared phospholipids from bovine raw milk, raw cream, whole homogenized pasteurized milk and buttermilk powder. The basis for our comparative study is the physical and structural properties of the phospholipids from each of these products. We used a combination of Langmuir trough studies, atomic force microscopy and confocal laser scanning microscopy to probe the changes in function and structure due to processing (centrifugation, homogenization, pasteurization and churning). By studying the behaviour of phospholipids using these techniques, when MFGM proteins are added to the mixture, our study has the potential to improve our understanding of the structure, dynamics, and composition of the lipid domains of the MFGM. The phospholipids were obtained by solid-phase extraction from each dairy product. The Langmuir film balance mounted on an epifluorescence microscope was used to characterize the physical behaviour of the phospholipid monolayer films and the coexistence of different phases within these films. We have evidence that the shape and size of the lipid domains vary according to the temperature of the trough, the pressure applied to the monolayer, but most importantly, the properties differ according to the milk product source of the phospholipids. Multilamellar and large unilamellar vesicles were also made from these phospholipids and observed under a confocal laser scanning microscope to compare their morphology and structure to the native MFG. We are confident that this information will help scientists and technologists to decide how to best process milk to keep valuable biological functionality.

Key Words: milk phospholipids, monolayer, dairy processing

W84 Investigation of self-assembly properties of a β–lactoglobulin tryptic peptide. M.-M. Guy*[1,2], M. Tremblay[3], N. Voyer[3], S. Gauthier[1,2], and Y. Pouliot[1,2], [1]*Institute of Nutraceuticals and Functional Foods (INAF), Quebec City, QC, Canada*, [2]*Dairy Science and Technology Research Center (STELA), Quebec City, QC, Canada*, [3]*Protein function, Structure and Engineering Research Center (CREFSIP), Quebec City, QC, Canada*.

Tryptic hydrolysis of β–lactoglobulin (β–lg) generates a number of peptides having specific functional and biological properties. Spontaneous peptide precipitation has been observed during the concentration of a tryptic hydrolysate of β–lg by reverse osmosis (RO). The analysis of the insoluble fraction has allowed the identification of β–lg N-terminal fragment 1—8 as the major peptide involved in the formation of aggregates. Structural analyses showed that peptide β–lg f1—8 forms aggregates via an efficient self-assembly process. Nanostructures formed by self-assembly of peptide β–lg f1—8 were observed by transmission electron microscopy (TEM). Circular dichroïsm (CD) characterization of the secondary structure of peptide β–lg f1—8 showed significant changes in the secondary structure of the peptide which can adopt β–sheet or random coil conformations under specific conditions. Self-assembly properties of the peptide β–lg f1—8 are triggered by some key parameters such as pH, peptide concentration, ionic strength and solvent polarity. The self-assembly properties of peptide β–lg f1—8 suggest that this peptide

could be suitable for biomedical applications. Moreover, the study of aggregation of peptide β–lg f1—8 is providing new clues for the development of large-scale methods of peptide purification using membrane separations (RO) under specific physicochemical conditions.

Key Words: β–lactoglobulin, peptides, self-assembly

W85 Identification of chemical components responsible for cardboard flavor in whey proteins. M. E. Whitson*, R. E. Miracle, and M. A. Drake, *North Carolina State University*, *Raleigh*.

Off flavor of whey proteins is a major obstacle to widespread utilization. Cardboard flavor is one of the most commonly described off-flavors. Precise knowledge of the volatile compounds that cause cardboard flavor is still not known. The objective of this research was to identify volatile components responsible for cardboard flavors in whey protein concentrates and isolates (WPC, WPI). Actual cardboard and brown paper samples (n= 5 types) were soaked in deionized water and analyzed by headspace solid phase micro extraction with gas chromatography mass spectrometry (SPME GC-MS) and descriptive sensory analysis. An array (n= 60) of stored (> 12 mo) and fresh (< 2 mo) WPC and WPI were rehydrated and evaluated by sensory analysis and SPME GC-MS. Univariate and multivariate analyses were applied to identify volatile compounds associated with cardboard flavor. Subsequently, sniff jars were created for potential cardboard compounds using pure chemical standards and filter paper. Compounds were screened for cardboard aroma by the trained sensory panel and then spiked into fresh WPC80 previously identified as free of cardboard flavor. Results from the real cardboard and brown paper reference samples indicated that aldehydes: pentanal, hexanal, heptanal, octanal, nonanal and decanal, were present at highest concentrations in cardboard samples which scored the highest sensory panel cardboard intensity and similarity to whey protein cardboard flavor. Analysis of volatile compounds from stored and fresh whey proteins with and without cardboard flavor also suggested aldehydes as the contributors to cardboard flavor. Sensory analysis of the aroma of the chemical standards yielded no single aldehyde as exhibiting a cardboard aroma, suggesting that cardboard flavor does not result from one compound, but a combination. Combinations of pentanal/heptanal, heptanal/hexanal, heptanal/nonanal, and pentanal/heptanal/nonanal were all characterized by fatty/cardboard aromas when added back to rehydrated whey protein solutions. These results suggest that lipid oxidation aldehydes are the source of cardboard off flavor in whey proteins.

Key Words: off flavors, whey protein, cardboard flavor

W86 Salty taste in dairy foods: Can we reduce the salt? S. L. Drake*, K. Lopetcharat, and M. A. Drake, *North Carolina State University*, *Raleigh*.

Sodium can be found in many sources of the diet. Dietary guidelines currently suggest a maximum intake of 2300 mg of sodium per day, while the average consumer intake is 9 g per day. The main health concern with high consumption of sodium is hypertension. The objectives of this study were to identify the salty taste intensity of sodium chloride in water and various dairy food matrices, and to identify the just-noticeable difference (JND) in concentration where consumers notice a decrease in salty taste in these foods. Solutions and foods (cheese sauce, cottage cheese and milk-based soup) were prepared with sodium chloride ranging in concentration from 0.008 M to 0.06 M. Fifteen panelists evaluated the salty intensity of each product in triplicate using a magnitude estimation scale (MES). In subsequent tests, panelists (n=25) evaluated salty intensity of these food products in separate sessions using an ascending force choice method to determine the JND. MES data was log-transformed, and all data was analyzed by analysis of variance with Fisher's least significant difference for means separation. The linear proportion of the power function in the salty taste intensity curve established for sodium chloride solutions and the three foods was between 0.03 M and 0.08 M. Consumers were able to notice and correctly identify a 25% reduction in salt concentration in all products. These results suggest that reducing sodium in cheese sauce, cottage cheese, and milk-based soups may be challenging and that exploration of sodium chloride alternatives in these foods is warranted.

Key Words: sodium reduction, salty taste, salt

W87 Binding affinity of various strains of lactic acid bacteria to phospholipids found in buttermilk. M. Cleveland* and R. Jiménez-Flores, *California Polytechnic State University*, *San Luis Obispo*.

Milk products are an important source of phospholipids (PL). PL are potentially excellent ingredients in food formulations due to the emulsifying power of their amphiphilic structure, and are particularly abundant in sweet buttermilk. Dairy foods are also an excellent medium for the survival and delivery of lactic acid bacteria (LAB), also known as probiotics. LAB have well-established roles in human health, especially in digestive and immune function, and have become a popular addition to many processed foods. If LAB are to benefit the host, however, it may be helpful if they are bound to a component in the food which enhances their survival during product shelf-life and during digestion. Previously in our lab, we observed specific binding of LAB to PL. We were recently interested in developing an assay to evaluate the binding affinity of various strains of LAB to the most abundant PL in buttermilk, including sphingomyelin (SM), phosphatidylcholine (PC), and phosphatidylethanolamine (PE). An immunoblotting technique was used to quantitatively measure this binding. Five PL standards were applied to both polyvinylidene fluoride (PVDF) and nitrocellulose membranes (NCM) and incubated with eight strains of biotinylated LAB, including Lactobacillus reuteri and Lactobacillus acidophilus. The interaction between them was measured using two methods of signal development. These included HRP-conjugated streptavidin with a diaminobenzidine color reaction, and fluorescent streptavidin with signal visualized under ultraviolet light. Binding affinity was assessed using densitometry. We found that L. reuteri had an especially strong affinity for most PL, and that SM was preferred by most LAB strains. From these results, we conclude that we have established a unique tool useful to researchers in determining which probiotic strains have optimal bioactivity in the desired application.

Key Words: phospholipids, lactic acid bacteria

W88 Non-casein nitrogen analysis of microfiltration and ultrafiltration retentate. H. Zhang*[1,2] and L. E. Metzger[1,2], [1]*Midwest Dairy Foods Research Center*, *Brookings, SD*, [2]*South Dakota State University*, *Brookings*.

Previous research has suggested that the standard non-casein nitrogen (NCN) method for milk overestimates the NCN content of ultrafiltration and microfiltration retentate samples. The objective of this study was to develop a modified method to more accurately measure the

NCN content of retentate products. In the standard method, a 10g milk sample (or equivalent protein content of retentate sample) and 75mL of 38 °C water are placed in a 100-mL volumetric flask. 1 mL 10% acetic acid solution is added and the flask is incubated at 38 °C for 10 min. Subsequently, 1mL of 1N sodium acetate solution is added and mixed. After cooling the content to 20 °C, the flask is made up to 100 mL, mixed, and then filtered (Whatman No1). The nitrogen content of the filtrate is then determined by Kjeldahl analysis. In preliminary research, a method was developed that used a 50mL centrifugal tube instead of the volumetric flask. This modification facilitated measurement of the pH after addition of acetic acid. Additionally, the sample was centrifuged (800 x g) for 10min to facilitate filtration with a smaller pore size filter paper (Whatman No 6). Subsequently, a study was completed to evaluate the impact of :1) pH after addition of 1% acetic addition solution and 2) pH of filtrate on NCN analysis. In this study, a microfiltration retentate sample (10% protein) was analyzed using four pH levels after acetic acid addition (4.0, 4.2, 4.4, and 4.6) and two pH levels after sodium acetate addition (4.6 and 4.8). Each pH combination was performed in triplicate. In this study we found that as the pH after acetic acid addition was increased from 4.0 to 4.6 the NCN content decreased. Additionally, the NCN content tended to decrease when the final pH of the filtrate was increased from 4.6 to 4.8. These results indicate that modifications in the standard method for NCN analysis may improve the accuracy of NCN analysis of retentate products.

Key Words: non-casein nitrogen, retentate, pH

W89 Effect of processing and refrigerated storage on isoflavone and stachyose contents of yogurt fortified with nongerminated or germinated whole soy powder. U. Nsofor* and Z. Ustunol, *Michigan State University*, *East Lansing*.

Fortification of yogurt with soy and soy ingredients has been of interest to combine health benefits of soy with dairy ingredients. Dairy yogurts fortified with germinated or nongerminated spray dried whole soy powders (50:50 blend) and cultured with *Streptococcus salivarius* subsp. *thermophilus*, *Lactobacillus delbreuckii* subsp. *bulgaricus* and a probiotic *Lactobacillus acidophilus* NCFM were manufactured using standard yogurt manufacturing procedures. The soybean varieties utilized for yogurt making were Vinton 81, DF 222 and E05276-T. All soy and all dairy yogurt controls were also included. All yogurts manufactured were evaluated for isoflavones (genistein, daidzein, genistin, daidzin) at one week of manufacturing and after six weeks of storage at 4°C using reverse-phase HPLC. Stachyose content was also determined. Total concentration of the four isoflavones evaluated increased ($p<0.05$), after 6 weeks of storage in all soy fortified dairy yogurts. The isoflavones retained in the soy and soy- fortified yogurts were significantly ($p < 0.05$) higher after 6 weeks of refrigerated storage compared to the isoflavone contents of the corresponding soy powders that was utilized in the yogurt base. There were differences in isoflavone concentrations between the yogurts due to the different soybean varieties used. All the yogurt samples containing germinated soy powders had lower stachyose contents than non-germinated soy-fortified yogurts. Germination of soybeans and subsequent fermentation by lactic acid bacteria during yogurt making was shown to enhance isoflavone content and reduce the stachyose contents soy fortified dairy yogurts.

Key Words: yogurt, soy, isoflavones

W90 The effect of pH and whey protein nitrogen (WPN) on the heat stability of medium heat nonfat dry milk powders. V. Sikand*[1], E. Ng[1], S. Gualco[1], A. Hui[1], P. S. Tong[1], and J. H. Walker[2], [1]*Dairy Products Technology Center, Cal Poly State University*, *San Luis Obispo*, [2]*Statistics Department, Cal Poly State University*, *San Luis Obispo*.

Heat stability (HS) of milk is the ability to withstand high temperature without coagulation. Almost every dairy product is heat-treated for food safety and specific functional properties. This study assesses how HS is related to pH and WPN in medium heat nonfat dry milk (NFDM) powders. The NFDM powders were reconstituted into an unconcentrated fluid milk (UFM) containing 9% total solids (TS) and a concentrated fluid milk (CFM) containing 18% TS. Samples were studied at their natural pH and at adjusted pH values from 6.5 to 6.8 for UFM and between 6.3 and 6.6 for CFM. The pH of the samples was adjusted by drop wise addition of either 1N NaOH or HCl. HS is defined as the heat coagulation time (HCT), which is the time between inserting the samples in a hot oil bath and the onset of visible clots. HCT was measured at 140°C for UFM and at 120°C for CFM. For UFM, the HCT of the natural and pH adjusted samples was positively related to WPN ($p < 0 .0001$) and quadratically related to adjusted pH ($p < 0.0001$). For unconcentrated milk, the HCT - pH curve maximum was found to be at 6.6. For CFM, the HCT of the natural and pH adjusted samples was also positively related to WPN ($p < 0.0001$) and quadratically related to adjusted pH ($p < 0.0001$). The HCT - pH curve maximum for concentrated milk was found to be at 6.5. In both concentrated and unconcentrated samples, the shape of the HCT - pH curve changes as WPN increases. In sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) under non-reduced conditions, decreased band intensities for the β-lactoglobulin and α-lactalbumin were observed for less heat stable samples. These results complement the low WPN values obtained for less heat stable samples. The lower band intensities of β-lactoglobulin and α-lactalbumin suggest that a portion of these proteins could not enter the gel. This is likely due to differences in degree of protein aggregation that could have occurred during powder manufacture and/or storage. These results indicate that the HS of UFM and CFM depends upon pH and WPN. This information forms the basis for better selection of nonfat dry milk powder for optimum HS.

Key Words: heat stability, WPN, NFDM

W91 Dietary milk fat globule membrane (MFGM) reduces the incidence of aberrant crypt foci (ACF) in Fisher-344 rats. K. J. Hintze*[1], D. Snow[1], R. Jimenez-Flores[2], J. Campbell[1], and R. E. Ward[1], [1]*Department of Nutrition and Food Sciences, Utah State University*, *Logan*, [2]*Dairy Products Technology Center, Department of Agriculture, California Polytechnic State University*, *San Luis Obispo*.

The aim of this study was to determine if MFGM as a dietary fat source confers protection against chemically induced colon cancer compared to anhydrous milk fat (AMF) and corn oil (CO). Milk fat globular membrane (MFGM) is a complex mixture of membrane lipids (phospholipids, sphingolipids, plasmalogens, gangliosides) and glycoproteins which surround fat globules in milk. Butter production generates substantial amounts of MFGM by lysis and disaggregration of the fat globule. MFGM may be recovered from the buttermilk for use as a nutraceutical. Previous studies have shown that sphingomyelin and glycosphingolipids purified from milk inhibit chemically induced colon cancer in the rodent ACF model. ACF are pre-neoplastic lesions that can develop into tumors; the ACF model is well established and has been used extensively in nutritional studies to model colon cancer. Male, weanling Fisher-344 rats were randomly assigned to one of three

dietary treatments: 1) AIN 93 diet, CO as the fat source; 2) AIN 93 diet, AMF as the fat source and 3) AIN 93 diet, 50% MFGM, 50% AMF as the fat source. MFGM was isolated from buttermilk by ultrafiltration. Diets were balanced for micro and macro nutrients including casein and lactose. Diets differed only in fat source. Rats were fed experimental diets for 15 weeks and injected with the carcinogen 1,1-dimethylhydrazine at weeks 3 and 4. After sacrifice, colons were harvested and aberrant crypt foci were counted by microscopy. There were no significant effects of dietary treatment on feed consumption or weight gain. Rats fed the MFGM diet (n=15) had significantly less aberrant crypt foci (20.9 ± 5.7, mean ± std. dev.) compared to rats fed CO (n=16) or AMF (n=15) diets (31.3 ± 9.5 and 29.8 ± 11.4 respectively; $P < 0.05$). These results indicate that MFGM may be protective against colon cancer, possibly by providing dietary sphingolipids.

Key Words: milk fat globular membrane, anhydrous milk fat, colon cancer

W92 Codon optimization of bovine prochymosin gene and its expression in *Kluyveromyces lactis*. F. Zhen*[1] and Z. Lanwei[2], [1]*College of Food Science, Northeast Agricultural University, Harbin, Heilongjiang Province,China*, [2]*College of Food Science and Technology, Harbin Institute of Technology, Harbin, Heilongjiang Province,China*.

Chymosin as an important industrial enzyme has been widely used in cheese manufacture. To improve expression efficiency of recombinant bovine chymosin in *Kluyveromyces lactis* GG799, the DNA sequence encoding prochymosin was designed and synthesized based on the codon bias of *K. lactis*, the codons encoding 315 amino acids were optimized, in which a total of 333 nucleotides were changed. At shaking flask level, chymosin activity is 575U/mL. Compared to the nonoptimized control, expression level of the optimized chymosin based on preferred codons in *K. lactis* shown a 7-fold higher level. The purified enzyme had a molecular mass of 36.5 kDa on SDS-PAGE. Whole bovine casein was incubated with the recombinant chymosin or bovine chymosin and some breakdown products were analysised by SDS-PAGE, as does bovine chymosin.

Key Words: prochymosin, codon optimization, *Kluyveromyces lactis*

W93 Effect of carbon dioxide addition on refrigerated raw milk proteolysis. P. C. B. Vianna, M. T. Ruiz, and M. L. Gigante*, *State University of Campinas, Campinas, SP, Brazil*.

Proteolysis in raw milk can be caused by plasmin and by psychrotrophic bacteria enzymes. These bacteria are inhibited through dissolution of carbon dioxide (CO_2) in milk. The objective of this study was to evaluate the effect of CO_2 addition and the storage temperature on proteolysis of raw milk. Control (without CO_2 addition) and treated (added with CO_2 until pH 6.2) milk samples were placed in 300 ml glass bottles fitted with metal lids and stored at 4±1°C and 7±1°C. Proteolysis was evaluated every other day until the standard plate count (SPC) had reached 7.5×10^5 ufc/ml, which corresponds to the raw milk microbiological standard established by the Brazilian legislation. Split-split-plot design was used and the complete experiment was replicated two times. Decreased in casein as a percentage of true protein (CN/TP) was used as an index of proteolysis. The treatments effects on the proteolysis were evaluated by multivariate variance analysis. Raw milk presented typical whole milk composition and the standard plate count was 3.7×10^3 ufc/ml. After the addition of CO_2, its concentration in milk was 1190 ppm and remained constant during the whole analysis period. The shelf life for samples stored at 4°C, with and without CO_2 addition, was 14 and 12 days, respectively, while for samples stored at 7°C was 8 and 6 days, respectively. CO_2 addition and storage temperature did not affect the proteolysis but the storage time and the interaction CO_2 x storage time significantly affected it. CN/TP decreased during storage time for all samples, however, this decrease was faster for samples without CO_2 addition. Independent of temperature, milk with CO_2 addition had a CN/TP reduction of 1.6% at the end of its shelf life (SPC $\geq 7.5\times10^5$ ufc/ml), while samples without CO_2 addition showed a reduction of 5.0%. The CO_2 addition showed efficiency to delay the proteolysis in refrigerated raw milk probably because of the inhibition of psychrotrophic bacteria growth.

Key Words: carbon dioxide, psychrotrophic bacteria, proteolysis

W94 Expression of bovine trypsin in *Lactococcus lactis*. L. Yao[2], X. Han[2], X. Qu[2], B. Li[2], Y. Jiang[2], and Y. Jiang*[1,2], [1]*National Dairy Engineering & Technical Research Center, Northeast Agricultural University, Harbin, China*, [2]*Key Lab of Dairy Science, Ministry of Education, Northeast Agricultural University, Harbin, China*.

Bioactive peptides derived from milk have remarkable ability to lower blood pressure, regulate immue system, stimulate calcium absorption and so on. Protease of lactobacillus can produce bioactive peptides by hydrolyzing milk protein casein in fermented dairy products. To produce bioactive peptides more effectively, we should improve the hydrolysis ability of lactobacillus. The objective of this study is to construct a *Lactococcus lactis* (*L. lactis*) which can express bovine trypsin. The bovine trypsin gene was synthesized artificially based on its amino acid sequence and bias codon of *L. lactis*, with restriction sites *Nsi* I and *Spe* I at 5′ and 3′, respectively, for subsequent cloning in expression vector pSEC-E7. The gene was directly digested with *Nsi* I and *Spe* I enzymes and cloned into purified *Nsi* I - *Spe* I -cut pSEC-E7 vector , resulting in the pSEC: Trypsin plasmid. Then this recombinant plasmid was transformed into *L. lactis* strain NZ9000 carrying regulatory genes *nisR* and *nisK* to obtain the strain NZ(pSEC: Trypsin) by electroporation. The expression of trypsin gene induced by nisin was identified by RT-PCR, SDS-PAGE and Western blot. RT-PCR showed that the bovine trypsin was expressed at the RNA level. Analysis of induced cultures of *L. lactis* strain NZ(pSEC: Trypsin) revealed a band of ~ 27kDa in the cell fraction, whereas no signal was detected in the supernatant. As expected, Western blot analysis revealed a one major band of ~ 27kDa corresponding to SP_{Usp45}-Trypsin. The recombinant expression vector has been obtained and the expression of bovine trypsin has been detected in *L. lactis* strain NZ9000. *The work was supported by Hi-Tech Research and Development Program of of China (2008AA10Z311), the Science and Technology Program of Heilongjiang Province (GB07B406) and the Innovative Research Team Program of Northeast Agricultural University (CXT007-3-2).*

Key Words: bovine trypsin, *Lactococcus lactis*, expression

W95 Effect of the protein fractions of the milk serum, alpha-lactalbumin and beta-lactoglobulin, on the *Escherichia coli* O157:H7 colonization in the intestinal mucosa of mice. J. P. Teixeira[2], N. Silva[2], L. M. Fonseca*[1,3], and R. L. Bradley Jr.[4], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection, Belo Horizonte, MG, Brazil*, [2]*Federal*

University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Preventive Veterinary Medicine, Belo Horizonte, MG, Brazil, [3]Laboratory of Milk Quality Analysis, UFMG, Belo Horizonte, MG, Brazil, [4]University of Wisconsin, Madison.

The effect of dietary whey protein concentrate on adhesion and colonization of enterohemorrhagic *Escherichia coli* O157:H7 in small intestine of Balb/C mice was evaluated. Eight groups containing six females each one were separated and randomly assigned to the following diets (two groups for each diet): standard diet (AIN93G; control group) and three groups with modified diet (AIN93 modified with addition of alpha-lactalbumin fraction; AIN93 modified with addition of beta-lactoglobulin fraction, and AIN93 modified with addition of whey protein concentrate - WPC). The protein fractions were obtained as described in US Patent n.6,900,290. Water was administered ad libitum during the experimental period of seven days. The experimental groups received aliquot of 0.5ml of *Escherichia coli* O157: H7 (ATCC 43895), in the concentration of 7 x 10^{10} CFU/mL using a gavage cannula. The animals had been examined clinically and sacrificed in the 8th experimental day, following recommendations of the bioethics committee (CETEA/UFMG). Samples of intestinal portions were submitted to histopathology and morphometry. The statistical analyses was done by the t-Student Test and by ANOVA including analysis of variance and test of multiple comparison according to Tukey (Software GraphPad Prism® 3.0.3 - San Diego). The diet containing fractions of beta-lactoglobulin and alpha-lactalbumin resulted in protective effect on the intestinal vilosity, respectively, of the distal part of the jejune and the ileum ($p \leq 0,05$) in Balb/C mice infected by *Escherichia coli* 0157:H7. On the other hand, the WPC did not demonstrate protective effect on the intestinal vilosity. Results showed that whey proteins present great potential for the control of intestinal infections caused by *Escherichia coli* 0157:H7.
Acknowledgements: FAPEMIG; CNPq; CAPES.

Key Words: whey protein, labctalbumin, *Escherichia coli*

Extension Education

W96 Effects of heat mount detectors, season, breed, and lactation on reproductive efficiency in summer and winter of dairy cows marked with chalk.
J. A. Pennington*[1] and Z. B. Johnson[2], [1]*University of Arkansas, Little Rock*, [2]*University of Arkansas, Fayetteville*.

To determine effects on reproduction, cows (n=410) housed in free stalls and milked in a rotary parlor were assigned on May 26 (S) or January 6 (W) to treatments as cows (C) marked with chalk as an aid to detect estrus or cows (MD) fitted with mount detectors plus marked with a 7-cm wide by 25-cm long chalk along the tail and backbone, beginning at the fifth coccygeal vertebra as the tail curves to form the backbone. Early in the trials, open cows at least 40 days post-partum with no prior breeding or declared open by palpation per rectum were synchronized for estrus and bred at 72 h after PG, unless bred earlier based on detection of estrus. Changes in status of detection aids and estrous activity were recorded at least 2× daily. Holsteins (H; n=134), Jerseys (J; n=189), crossbreds (X; n=38), and other breeds (O; n=49) were assigned 62% to C and 38% to MD. Status of cows following the 96-day spring/summer (S; n=152) and 86-day winter (W; n=258) trials was based on return to estrus and/or results of palpation of reproductive organs. Days from calving to assignment of treatment was not affected (P>0.10) by treatment (T) and lactation number (L) but was affected (P<0.01) by season (S), breed (B), and T×B. Treatment did not affect traits observed but T×L affected days between 1st and 2nd breeding (P<0.05) and days to pregnant (P<0.01). Days from start of trials to 1st breeding were affected (P<0.05) by TxB. Season affected days from start of trials to first detected breeding (P<0.05; S=33.2; W=27.1), days to 2nd breeding (P<0.01; S=61.6; W=48.3), and days to pregnant (P<0.01; S=49.9; W=35.6). Breed affected (P<0.05) days from calving to 1st breeding after treatment (H=113.8; J=102.6; X=90.9; O=98.8) and days from treatment to pregnant (H= 49.9; J= 38.7; X= 38.5; O= 43.8). Pregnancy rates were not affected (P>0.10) by T (C=54.7%; MD=52.6%). Overall, results indicated that heat mount detectors did not improve reproductive performance of dairy cows marked with chalk in the spring/summer and winter. Season, breed, and lactation number affected reproductive efficiency of the dairy cows.

Key Words: dairy, heat detection, estrus detection aid

W97 Improving IPM of house flies at commercial dairy operations through pest monitoring and determination of nuisance threshold.
G. E. Higginbotham*[1], L. N. Pereira[2], and A. C. Gerry[3], [1]*University of California Cooperative Extension, Fresno*, [2]*California State University-Fresno, Fresno*, [3]*University of California, Riverside, Riverside*.

House fly abundance was monitored at three large dairy operations in Fresno County during the summer of 2005. Spot cards, fly tapes, and fly bait traps were simultaneously compared to detect early increases in house fly abundance while still providing manageable information during peak fly activity in mid-summer. Ten spot cards, five fly tapes, and five bait traps were placed to provide full coverage of each dairy. Spot cards and traps were replaced weekly. Fly counts varied significantly by trap location for all monitoring methods ($P < 0.006$). The correlation between fly counts at each trap location also varied considerably for all monitoring methods, with trap locations in near proximity or placed near similar habitats generally having significant correlations ($P < 0.05$). Spot cards and bait traps were similarly effective over a range of fly abundance. Spot card counts ranged from 35 to 5,940 spots per card across all dairies and weeks sampled, with mean spot card counts per dairy of 174 (±85), 461 (±221), and 1612 (±853) spots per card. Mean weekly spot card counts between dairies was significant ($P < 0.001$). Fly bait traps ranged from 41 to 4,545 house flies per trap across all dairies and weeks sampled. Mean bait trap counts per dairy were 600(±317), 1473 (±840), 2040 (±1275) with significant differences in mean weekly bait trap counts between dairies ($P < 0.001$). Fly tapes were ineffective due to tape failure (18% failure rate) caused by wind, dust, and heat. Spot cards required the least effort and cost to deploy while still providing acceptable resolution of changes in house fly abundance. An automated spot card counting system is needed to improve efficiency of this monitoring tool so that it might be adopted by the industry.

Key Words: fly control, IPM, pest monitoring

W98 Pizza Ranch is an educational tool to teach fourth graders about proper nutrition and where food originates. J. A. Pennington* and J. Buffalo, *University of Arkansas Cooperative Extension Service, Little Rock.*

Pizza Ranch is an educational class for fourth graders which teaches them about the nutritional value of the components of pizza, where the components originate, and the importance of eating properly. Teachers of the youth, primarily from Pulaski County but also some from adjacent counties, are invited to bring their classes to the one-day activity conducted at the Arkansas State Fairgrounds. The 1000-1500 youth attend 20-minute stations for (1) milk, (2) wheat and dough,(3) vegetables and sauce, (4) meat, and (5) cheese before eating pepperoni pizza which is served with milk and ice cream. At each station, the fourth graders are taught about the specific components of the pizza, where the components originate on the farm, how the components are processed into food (wheat into flour or milk into cheese), and the nutritional value of the specific food components. The youth are also told why it is important to eat properly. Extension specialists are the instructors except for the milk and cheese stations where dairy promotion personnel are the instructors. During the breaks between classes, youth are allowed to milk an artificial cow and pet dairy goats. In some years, other animals are also present. Teachers are provided with education materials that they can use in their classroom to further explain the nutritional value of a pizza and the importance of eating according to USDA dietary guidelines. Evaluations for the Pizza Ranch range from 4.3 – 4.8 for the last nine years on a scale of 5.0 and average 4.6 (SD=0.2); comments by teachers are very positive.

Key Words: nutrition education, youth education, dairy

W99 Economic importance of some traits of dairy cattle. F. Szabó* and Z. Fekete, *University of Pannonia, Keszthely, Hungary*.

The economic value of 7 traits was calculated for the dairy cattle population in Hungary in 2008, using a bioeconomic model based on the program package ECOWEIGHT (Wolf et al. 2005). The importance of the study was due to more than 70% of the cattle in the country belonging to the dairy industry.The study was based on the typical dairy farm size of 330 Holstein-Friesian cows, with a production level of 7000 kg annual milk yield. Cows were managed in a loose-housing system with parlour milking, representing current commercial dairy enterprises. A total mixed ration based on maize silage and concentrates, with some alfalfa hay, was offered to 4 groups (first-, second-, third-phase of the lactation and a dry group). Besides the dairy enterprise, calf and replacement rearing were also taken into consideration. Income came from milk, calves, culled cows and manure sale. About 50% of the total costs related to feed, with the remainder due to factors such as management, reproduction and health services, labor, interest and amortization. Annual revenues and costs were used for the economic calculations. Gross margin was taken as a difference between income and variable costs. Marginal economic value of a given trait was defined as the partial derivative of the profit function, which was standardized by multiplying by the genetic standard deviation of the trait. The relative economic values for traits were expressed as a percentage of the standardized economic value of 305-d milk yield. The relative economic importance of the evaluated traits were as follows: 305-d milk yield 100%, length of productive life 51%, conception rate of cows 36%, 305-d protein yield 35%, 305-d fat yield 20%, stillbirth 13%, pregnancy rate of replacements 3%.

Key Words: dairy cattle, functional and production traits, relative economic weight

W100 Financial performance of dairies in Florida and Georgia in 2007. L. O. Ely*[1], A. DeVries[2], R. Giesy[2], M. Sowerby[2], B. Broaddus[2], and C. Vann[2], [1]*University of Georgia, Athens*, [2]*University of Florida, Gainesville*.

The Dairy Business Analysis Project (DBAP) includes an annual survey of the financial performance of dairies primarily located in Florida and Georgia. Its objective is to document the dairies' financial success using standardized, accrual accounting methods in order to calculate benchmarks and provide feedback on the dairies financial strengths and weaknesses. Twenty-three dairies submitted financial data in 2007. Twenty-one dairies were included in the summary results. Of these, 16 were located in Florida, and 5 in Georgia. The average herd size was 1,399 cows and 708 heifers with 18410 lbs. milk sold per cow. The average culling rate was 35%. There was an average of 22 FTE workers per farm and 1.06 million lbs milk sold per FTE worker. Total revenue per cwt. was $24.67 / cwt with $22.59 / cwt milk income. The average total expense was $21.09 / cwt. The largest expense items were purchased feed ($9.20 / cwt), labor ($3.57 / cwt), livestock ($1.62 / cwt) and milk marketing ($1.14 / cwt). Net farm income from operations was $3.58 / cwt and net farm income was $3.57 / cwt. The debt to asset ratio was 0.29, the rate of return on assets was 0.15, the rate of return on equity was 0.26, and the operating profit margin ratio was 0.13. Total revenue increased and expenses decreased with herd size in 2007 resulting in the largest herds having the largest net farm income ($4.98/ cwt). The herds with the highest milk production (>20,600 lbs / cow / year) had the highest total revenue ($25.08 / cwt) and the lowest expenses ($19.87/ cwt) resulting in the highest net farm income ($5.20 / cwt).

Key Words: dairy, financial, management

W101 Profitability of milk production considering different prices and yield. F. Szabó*, G. Buzás, and I. Heinrich, *University of Pannonia, Keszhely, Hungary*.

The profitability of milk production was calculated for the dairy cattle population in Hungary using input-output analysis based on budgeting bioeconomic program package. A higher ($0.35/kg) and a lower ($0.30/kg) milk prices were taken into consideration. Calculation was done for 6000, 7000 and 8000 kg annual milk yield per cow. Price and cost data were collected on different farms in the country. Cows were managed in a loose-housing system with parlour milking, representing the typical, current commercial dairy enterprises. A total mixed ration based on maize silage and concentrates, with some alfalfa hay, was offered to cows. Besides the dairy enterprise, calf and replacement rearing were also taken into consideration. Income came from milk, calves, culled cows and manure sale. Total variable costs including feed, replacement cow, and other variable costs (such as management, reproduction and health services, interest and amortization) were used for the economic calculations. Feed costs were calculated from the nutrient requirements of cows. Labor costs weren't taken into consideration. Annual revenues and costs were used for the profitability evaluation. Gross margin (GM), in which labor costs and profit of the farmer are included, was taken as a difference between income and total variable costs. Profitability was calculated as a percentage of total variable cost in the income. The ratio of the feed, replacement and other variable costs in case of 6, 7 and 8 thousand kg annual milk yield were: 56:23:21%, 60:21:19% and 62:20:18%, respectively. GM and profitability values, when milk price was high, were: $789, $935, $1025 /cow, 43.5%, 46.1%, and 45,1%, when milk price was low, were: $488, $570 and $625 /cow, 26.9%, 28.1%, and 27.5% in case of 6, 7, and 8 thousand kg milk yield per cow, respectively. However, gross margin per cow increased with increasing

milk production, the profitability from 7 to 8 thousand kg milk yield decreased due to the higher feed costs.

Key Words: dairy cattle, gross margin, profitability

W102 Livestock gross margin insurance for dairy cattle: Analysis of program performance and cost under alternative policy configurations and market conditions. M. Valvekar*, V. E. Cabrera, and B. W. Gould, *University of Wisconsin, Madison*.

Livestock Gross Margin insurance for dairy cattle (LGM-Dairy) is a new risk management tool that can be used to establish a lower bound on a dairy producer's gross margin (defined as milk revenue minus imputed purchased feed costs). A producer's decision of the level of gross margin to insure has a significant impact on the gross margin guarantee (GMG) and resulting premium. An analysis of the relationship between these decision parameters is important to understand how this program could potentially benefit dairy producers. Objectives of these analyses are to (1) review the basic structure of LGM-Dairy (2) examine sensitivity of GMG and premium to changes in insured feed quantity and (3) quantify the impacts of changes in deductible level on important program characteristics. Although this program has been available only since August 2008, we review program performance under a variety of market conditions over the 2000-2008 period for a hypothetical Wisconsin dairy to provide an indication of the usefulness of this program under alternative market conditions. The level of corn and soybean meal equivalent fed are divided into discrete ranges to allow for a sensitivity analysis of GMG and insurance premium to feed quantities. GMG and premium are then calculated for different combinations of feed use and deductible levels, using the University of Wisconsin's LGM-Dairy premium calculator. Correlation coefficients analyze key relationships between different program parameters. Preliminary analysis using 2008 data indicates a negative association between deductible level and premium, a negative association between insured corn equivalents and GMG and a low correlation between insured soybean meal equivalents. Preliminary analyses of the impact of gross margin deductible on payout probability shows that maximum deductible corresponds with lesser payout probabilities.

Key Words: price risk, risk management, revenue insurance

W103 Description of Kentucky dairy management systems and producer demographics. R. A. Russell* and J. M. Bewley, *University of Kentucky, Lexington*.

To characterize the management of Kentucky dairy operations, a survey was distributed to all licensed milk producers in the state. Two hundred and twenty-nine producers responded to the survey. Mean age of responding producers was 50.9 (± 12.9) with a range of 22 to 82. Mean 2008 herd size (milking and dry cows) was 83.0 (± 101.8) with a projected herd size of 102.1 (± 114.4) in 2013. Mean daily milk yield (pounds per cow) was 52.7 (± 11.8) with a range of 15 to 85 pounds. Mean somatic cell count (cells/ml) was 304,524.6 (± 123,306.7) with a range of 75,000 to 750,000. When asked to describe how much of their income came from farming, 54.9% reported all of their income was from farming, 30.1% said more than half of their income was from farming, 9.3% indicated their income was evenly split between farm and off-farm sources, and 5.8% said most of their income came from off-farm sources. Forty-eight respondents (22.4%) said they intended on staying in the business for more than 20 years, 61 (28.5%) for 10 to 20 years, 71 (33.2%) for 5 to 10 years, and 34 (15.9%) for less than 5 years. One hundred thirty-seven respondents (63.4%) indicated they would improve efficiencies in the next 5 years while 64 (29.6%) said they would expand, 41 (19.0%) would modernize and 36 (16.7%) said they would leave farming in the next 5 years. One hundred and seventy-six (84.6%) producers indicated that Holstein was their primary breed followed by Jersey (8.2%), crossbred (3.4%), mixed (1.9%), Guernsey (1.0%), Brown Swiss (0.5%), and Milking Shorthorn (0.5%). Producers characterized their housing systems as follows: no housing (cows are outside year-round) (40.1%), new (<10 years) or modern freestall barns (22.2%), existing building(s) converted to freestall housing (17.9%), tie-stall or stanchion barns (8.7%), compost bedded pack (sawdust) housing (6.8%), and bedded pack (straw) housing (4.3%). The majority of producers milked cows in a pit parlor (77.7%) with the remaining milking in a stall barn with buckets or pipeline (14.3%) or flat parlor (8.0%). These results provide new insight into the management of Kentucky dairy operations.

Key Words: survey, dairy extension, management systems

W104 Characterization of the decision making behavior of Kentucky dairy producers. R. A. Russell* and J. M. Bewley, *University of Kentucky, Lexington*.

A survey was distributed to all licensed milk producers in Kentucky to gain a better understanding of the factors that influence decisions made by dairy producers. Two hundred and twenty-nine producers responded to the survey. When asked to describe criteria used to evaluate the success of their dairy operation, the criteria selected by the highest percentage of respondents were (1) ability to pay operating expenses without incurring unnecessary debt (91.6%), (2) well-being of animals in the herd (82.8%), (3) producing superior quality milk (75.8%), (4) keeping a balance in the checking account (73.1%) and (5) quality of life (67.0%). The top three sources of influence or information in decision making (with mean response calculated after assigning the following numeric values to producer response categories: not important-1; important-3, very important-5) were (1) advice from consultants, nutritionists, and veterinarians (3.70 ± 1.23), (2) consultation with business partners and family members (3.68 ± 1.29) and (3) intuition and gut feeling (3.10 ± 1.45). When asked about criteria used to evaluate decisions, the criteria selected by the highest percentage of respondents were (1) ability to cash flow (94.7%), (2) availability of funds to pay for investments (80.5%) and (3) impact on the business's long-term financial performance (70.8%). Respondents were asked how frequently they reevaluated their long-term business strategy. The percentage of producers who listed annually was 29.4%, while 16.2% stated never, 14.7% monthly, 13.7% twice a year, 13.2% more than once per month, and 12.7% quarterly. With regard to adoption of automated monitoring technologies, producers indicated that modest adoption rates were a result of (1) not being familiar with technologies that are available (54.9%), (2) undesirable cost to benefit ratios (41.8%) and too much information provided without knowing what to do with it (35.9%). Utilizing this insight into dairy producer decision making should help industry professionals address dairy producer issues and concerns.

Key Words: survey, dairy extension, decision making behavior

W105 A Spanish language artificial insemination school for Idaho dairy employees. J. C. Dalton*[1], K. S. Jensen[2], M. Chahine[3], and M. de

Haro Marti[4], [1]*University of Idaho, Caldwell*, [2]*University of Idaho, Marsing*, [3]*University of Idaho, Twin Falls*, [4]*University of Idaho, Gooding*.

Idaho is the second largest milk producing state in the western United States, and currently ranks as the third largest in the entire country. The Idaho dairy industry relies on a Spanish-speaking workforce. Coincident with the recent rapid growth of the Idaho dairy industry, the demand from dairy producers for new educational opportunities for dairy employees has increased. To identify critical topic areas, University of Idaho Extension personnel consulted 1) a dairy advisory board, consisting of producers and members of allied industry, and 2) participants in a Spanish language milker's school. Consequently, a Spanish language artificial insemination school for Idaho dairy employees was developed. The program consisted of 10 h of classroom teaching followed by a minimum of 8 h of practical live animal and semen handling experience. The registration fee was $250 and the program was held in Caldwell and Twin Falls, Idaho. Topics included collection and processing of semen, reproductive anatomy and physiology, semen handling, heat detection, and artificial insemination technique. All material was presented in Spanish. A pre- and post-test (true or false, and fill in the blank) was administered to participants at the beginning and end of each topic area. Twenty-one students completed the pre- and post-tests. The overall mean score for the pre-tests was 76.7%, while the mean score for the post-tests was 90.2%. The mean difference (Post-test – Pre-test) was 13.5%, providing evidence of increased knowledge gained by the participants. At the conclusion of the program, a certificate was awarded to all participants who completed both the classroom and live animal instruction.

Key Words: Spanish, artificial insemination, dairy

W106 Hoof care workshop in English and Spanish. M. Chahine*[1], T. S. Hirsch[2], J. M. DeFrain[2], T. Fife[1], and M. E. de Haro Marti[3], [1]*University of Idaho, Twin Falls*, [2]*Zinpro Corporation, Eden Prairie, MN*, [3]*University of Idaho, Gooding*.

Milk sales are the number one revenue on a dairy operation. However, there are many different factors that can impair milk production and thereby reduce profits. One of the most significant among these factors is lameness. The University of Idaho and Zinpro Performance Minerals® teamed together to address the lameness issue in dairy herds by conducting a Hoof Care Workshop. This workshop was a one day event held in both English and Spanish at a dairy in Jerome, ID. The first half of the workshop was lecture-based and included presentations on the economics of lameness, the overall anatomy of the foot, claw horn lesions, both infectious and non-infectious, hoof and claw care (claw trimming and foot baths), effects of nutrition on hoof health, cow comfort, record keeping, and locomotion scoring. The workshop concluded with a demonstration on locomotion scoring and hoof trimming where the participants received hands-on experience. On the first day 23 people attended the English version of the Hoof Care Workshop. On the second day there were 20 people in attendance for the Spanish presentation of the workshop. Follow-up surveys were conducted in English and Spanish to assess the value of the workshop and what the participants had implemented as a result. Fourteen of the 43 surveys were returned. The overall value of the workshop was 4.2 on a 1 to 5 scale (1 being of little value and 5 being of great value). All the respondents indicated that dairy management practices have been changed or initiated to deal with lameness based upon information they received from the workshop. Several people emphasized the connection they made between cow nutrition and hoof health, such as the amount of fiber in the ration affecting the amount of cud chewing, and ultimately hoof health. Others commented on the importance of detecting problems early on, diagnosing them, and therefore providing the correct treatment. This educational program has the potential to increase revenues for the dairies through increased milk production, decreased days open, decreased death loss, cows staying on the dairy longer, reducing the number of culls and ultimately improving animal well being.

Key Words: hoof care, lameness

W107 TMR feeder schools in English and Spanish. R. J. Norell*[1], M. Chahine[2], and M. E. de Haro Marti[3], [1]*University of Idaho, Idaho Falls*, [2]*University of Idaho, Twin Falls*, [3]*University of Idaho, Gooding*.

Feed cost is the largest single expenditure on a dairy, accounting for 50 to 60% of the total cost of producing milk. On-farm training programs for feeders are limited in number and scope. Hispanic workers comprise 85% or more of the Idaho dairy workforce, most of them with little or no proficiency in English. Dairies also have English speaking feeders with no knowledge of Spanish. Based on this situation, it was determined that training programs for dairy feeders should be offered in both languages. The University of Idaho Extension developed and pilot tested the TMR/Mixing Feeding School. The school included presentations and written materials on nutrition and metabolic diseases, Total Mixed Ration mixing techniques and Standard Operation Procedures, feed bunk management, dry matter determination, particle size determination, farm safety, and nutrients and the environment. In total, 17 participants attended the Spanish workshop, and 12 participants attended the English workshop. A one page questionnaire was used in the English workshop to assess how often feeders used best management practices before attending the school, and how often they planned to use the practice after attending it. Participants in the Spanish version of the feeder school indicated they preferred to use a pre/post test format for evaluating their knowledge. Based on their input, an 18 question pre/post test was developed in Spanish and covered various aspects of feeding management. Scores improved from 33.3% correct to 71.1% correct, indicating a significant increase in knowledge. Based on the questionnaire responses, significant improvements in planned practice adoption were also observed in the English workshop for eleven out of twelve categories, and for the overall school. To assess learning, we also asked each attendee to indicate how much they may have learned from the workshop. The feeder school received an overall rating of 3.2 on a 1 to 4 scale (1 being nothing new and 4 being a lot). We anticipate that this educational program will increase revenues on dairies through improved feeding management, increased milk production, decreased feed cost and decreased metabolic diseases.

Key Words: feeder school, Spanish education

W108 Educating Oklahoma producers on radio frequency identification. P. K. Camfield*, A. Preator, D. Stephens, and J. Townsend, *Oklahoma Panhandle State University, Goodwell*.

National Animal Identification (NAID) is a system that will effectively allow animals to be tracked from birth to death in a timely manner. Benefits of NAID include quick response to disease outbreaks, preventing disease outbreaks, and maintaining domestic and foreign consumer confidence in the U.S. beef industry. Objectives for our Radio Frequency Identification (RFID) research were to compare 3 different ear tags and 2 electronic readers over a 2 year period. The working ease, readability, and durability of these RFID materials were tested. Methods of testing

were: tagged cattle (n=5000) in both large and small operations, located within different geographic regions of Oklahoma, were tracked through all stages of production. Two types of RFID readers were used during this trial, one was battery operated and has the capability of storing 5000 data points. The other utilizes Bluetooth technology and sends all data points directly to a spreadsheet. The battery operated reader was the easiest to operate in all production scenarios. It was necessary to have a clear line of site to the computer with the Bluetooth reader. Both readers were very easy to operate and can be utilized in all cattle production phases. There was no difference between the 3 ear tags used, with less than 1% loss and/or damage regardless of operation size, geographic region, or stage of production ($P > 0.05$). No difference ($P > 0.05$) was observed between either reader's ability to identify and read tags. The only operational difference was the capability for one reader to store data in the reader, compared to the Bluetooth reader's ability to only store data directly to the computer. The main concern of producers was the overall cost of implementing, maintaining, and educating users to properly operate this technology. The RFID technology tested was equally effective in working ease, readability, and durability, regardless of size of the business and geographic location.

Key Words: animal identification, electronic tags, tag readers

W109 The integration of beef cattle into a peanut and cotton crop rotation that involves a perennial grass: A farm scale demonstration. R. O. Myer*[1], D. Zhao[1], K. S. Balkcom[2], C. L. Mackowiak[1], J. L. Foster[1], D. L. Wright[1], J. J. Marois[1], J. A. Howe[2], G. C. Lamb[1], A. R. Blount[1], and M. K. Maddox[1], [1]*University of Florida*, *Marianna*, [2]*Auburn University*, *Headland, AL*.

Use of perennial grasses in row crop rotations can reduce economic risk, enhance crop yields and protect the environment. Integrating beef cattle into the system can make for more efficient use of farm resources, and reduce risk by diversification. Two, irrigated farm-size fields (NW Florida; 61 ha and SE Alabama; 20 ha) have been involved in a sod-based rotation project since 2000, mainly focusing on the agronomic aspects of the system. Results to date indicate that including bahiagrass (Paspalum notatum) in the rotation improves cotton and peanut yields, and water quality. The present focus is to demonstrate how best to integrate beef cattle (cow/calf system) into the rotation system, and to evaluate how grazing might impact subsequent yields of cotton and peanut. Each field is divided into four sections and a 4 yr rotation of bahiagrass (bahia1), bahiagrass (bahia2), peanut and cotton has been and is being utilized. The cows are used in the rotation to utilize the bahiagrass as well as the winter cover crops (rye and oat blend) planted after the peanut and cotton harvests. The fields have non-grazed (exclusion) areas to evaluate the impact of grazing. The cattle graze bahia2 starting May, continue grazing until Aug., graze bahia1 until frost (Nov.), and fed hay (oat or bahiagrass) until calving (Jan. thru Mar). After calving, cows and calves graze winter cover crops until May, and cycle repeats. Calves are weaned in Aug. Each site uses a constant number of cows through the summer and winter/spring. Put and take cows are used during the winter/spring to utilize the excess forage. Hay is harvested from Bahia2 in Oct. and this field is planted into Oat (sod-seeded) which is harvested for hay (FL) in April or grazed (AL). After 2 yr at the FL site, 45 calves per yr have been raised, and the winter cover crops provided extra grazing days (mean of 2548 d). No impact ($P<0.05$) on subsequent peanut or cotton yields were noted.

Key Words: beef cattle, farming systems, forages

W110 Incorporation of Tifton 85 greenchop in least-cost rations for Florida dairy producers. J. Clavijo*[1], Y. Newman[1], L. Ortega[2], C. Staples[1], A. Adesogan[1], and L. Sollenberger[1], [1]*University of Florida*, *Gainesville*, [2]*National Mango Board*, *Orlando*.

Due to the dependence on purchased feeds that is typical of Florida dairies and the declining trend of milk prices, farmers are increasingly interested in analyzing the feasibility of growing forages for their rations. Predictive tools can help the decision making process by providing insight into the potential outcomes of using perennial warm-season forages as feeding alternatives in dairies. To address the need for such tools, a least-cost ration formulation model that assessed the incorporation of Tifton 85 bermudagrass greenchop into dairy rations was developed. The linear program model was based on information from nutrient requirements of dairy cattle (NRC, 2001) feedstuff nutritive value profiles, as well as the nutritional requirements of Holstein cows at different production levels and lactation stages. Yields (DM, Mg ha^{-1}) and nutritive value (crude protein, CP; neutral detergent fiber, NDF; acid detergent fiber, ADF; phosphorus, P) from an on-farm Tifton 85 defoliation management trial were incorporated into the model. Production costs and prices for readily available feedstuffs in the region were obtained from producer interviews and local distributors. On average, rations that incorporated Tifton 85 greenchop harvested at 35 d intervals cost \$4.3 $cow^{-1}d^{-1}$, resulting in an 18.1 and 28.7% reduction when compared to those formulated with purchased Tifton 85 or alfalfa hay, respectively. These results suggest that Tifton 85 greenchop can replace other high quality forage sources in dairy rations, benefiting producers by lowering production costs and nutrient imports. Least-cost ration models that incorporate on-farm forage cropping alternatives and that simulate Florida dairy farm conditions can serve as predictive tools that facilitate decision making in milk production.

Key Words: Tifton 85 bermudagrass, greenchop, least-cost ration

W111 Master goat producer's training certification program at Tuskegee University. O. U. Bolden-Tiller*, S. Solaiman, and N. K. Gurung, *Tuskegee University*, *Tuskegee, AL*.

The Tuskegee University (TU) Master Goat Producer's Training Certification (MGPC) Program was held in August 2008 to provide new and established producers an opportunity to access up-to-date and accurate information on how to raise healthy, productive meat goats. Although much information such as that provided in the MGPC Program is available via the internet, to date more than 50% of Alabamians, particularly those in the more rural areas which boast most of Alabama's farms, do not have access to high speed internet. Program participants took part in a comprehensive three-day intensive course (lecture and hands-on) in meat goat production, covering topics such as marketing, enterprise budgets, record keeping, facilities, livestock evaluation, parasite management, pasture management, nutrition, reproduction, predator management and more. Three levels of certification were offered: One - completion of the three-day MGPC program; Two - completion of level one and a farm inspection; Three - completion of Levels One and Two, an exam evaluating the ability to apply the newly learned information, and a second farm inspection. Producers completed surveys to assess the likeability of the events and to ascertain demographic information. Twenty-four participants took part in the program, representing 20 farms and three states (AL-20; GA-1; FL-2). Based on survey results, participants found the presentations to be of quality and value and the presenters knowledgeable with adequate materials (3.6±/4.0); and they would recommend the program to others. An increase in post-test scores compared to pre-test scores, indicated that producers acquired knowledge that could result in

improved herd management. To date, five of the 20 farms have received Level Two Certification. In conclusion, the TU MGPC program provided producers with valuable information necessary for meat goat producers to become competitive in this global economy.

Key Words: goats, extension, producer education

W112 Influence of citronella and geranium essence treatment on milk aroma. S. Carpino[1], G. Belvedere[1], T. Rapisarda*[1], G. Azzaro[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*D.A.C.P.A. University of Catania, Italy*.

A commercial mix containing geranium and citronella essence was used in a farm against flies. Several authors report volatile compounds can be transferred by breath and skin to blood and consequently to milk. This study was performed in a dairy cow farm located in the South of Sicily. The aim of this study was to detect the influence of geranium and citronella essence treatment on milk aroma profile at different times. Geranium and citronella mix was spread on lactating cows trough the farm cooling system. Milk samples were collected at 0 (M0), 12 (M12), 24 (M24) and 36 (M36) hours from mix spreading and then analyzed. SMart Nose system (LDZ, Switzerland) allowed the direct analysis by MS of volatile organic compounds (VOCs). Dynamic headspace extraction (Purge&Trap) (Tekmar 8900) in combination with a gas chromatograph olfactometry/mass selective detector (GC/MSD/O) were also used to analyze the odour active compounds of milk samples. Sensory analysis, using triangle test technique, was also performed on M0 and M12 milk samples, by CoRFiLaC staff in Ragusa, Italy. Principal Component Analysis (PCA) applied to SMart Nose results had a good separation (PC1 55.96%; PC2 12.04%) among the four group of milk samples. This result clearly indicated that, at different time of treatment, samples showed different volatile compounds. Moreover, GCO results demonstrated that M0 milk samples had the richest profile among the M12, M24 and M36 respectively. Triangle test confirmed ($p<0.001$) all the instrumental results and clearly indicated a difference between treated and no treated milk. The different aroma profiles in milk samples are strongly correlated to the volatile components of the mix treatment. Further, studies are needed to better understand if different concentrations of these mixes might be used without interfering with milk and eventually cheese flavour. This would be a good practical application for farmers in order to improve cow comfort, health and safety in their farm.

Key Words: milk, volatile compounds, geranium citronella essence

Forages and Pastures: Silages

W113 Relationship of corn silage dry matter content to density in bunker silos. K. E. Griswold*[1], P. H. Craig[2], and S. K. Dinh[1], [1]*Penn State Cooperative Extension, Lancaster*, [2]*Penn State Cooperative Extension, Dauphin*.

Dry matter (DM) content and density of corn silage (CS) was investigated in 103 bunker silos and piles over a 5-year period. For each silo/pile, 12 samples were collected using a 5.08 cm diameter stainless-steel coring tube driven by a gas-powered drill. Core depth was recorded to the nearest 0.64 cm, and wet weight was determined on a digital scale. Sample DM was determined with a Koster Crop Tester. Density was calculated by dividing core dry weight by core volume. Cores were collected at three vertical levels, bottom ≈ 1 m from silo floor, top ≈ 1 m from top edge, and middle ≈ equidistant between bottom and top. At each level, cores were collected horizontally at four locations, I and IV within 2.4 m of the outside edges, and II and III equidistant between I and IV. Data were analyzed using PROC REG and RSREG within SAS. When individual core density and DM content were regressed, there was a significant quadratic relationship ($P < 0.0001$, $R^2 = 0.13$). However, when level and location were included in the model as covariates, the strength of the relationship increased ($R^2 = 0.43$). Location was not significant in the model. These results suggest that DM content of corn silage is weakly related to density within bunker silos/piles and that level at which density is measured has a greater impact on density than DM content. Regression of the silo/pile average density and DM content showed a significant quadratic relationship ($P < 0.0001$, $R^2 = 0.28$), which suggested that DM content of corn silage may have greater impact on overall density of corn silage in silo/pile than density at specific positions within a silo/pile.

Key Words: corn silage, dry matter, density

W114 Biomass yield and nutritive value of three forages for silage. R. L. Holness*, N. C. Whitley, and K. Baldwin, *North Carolina A&T State University, Greensboro*.

A two yr study was conducted to measure the biomass yield and nutrient content of three forages for potential silage use. Forages used were conventional (Round-Up Ready®; CC) and organic (OC) corn (*Zea mays*) and pearl millet (*Pennisetum americanum*; PM). Plots measuring 18x18 m were used in a completely randomized design with four replications. Fertilization considered organic status as well as soil test recommendations. Forages were seeded at recommended rates and harvested at the same time both years. Four weeks after planting, CC was treated with glyphosate. Areas of 3.05 x 3.05 m were manually sampled to a 10-cm stubble height. Samples were weighed to determine fresh biomass accumulation, fed into a silage flail-type mower conditioner and sub-sampled for nutritional content analysis by near infrared reflectance spectroscopy (Dairy One, Ithaca, NY). Biomass yield was influenced by a forage × yr interaction ($P < 0.01$). Corn forages had greater ($P < 0.05$) yields than PM for both years, however, CC and OC yield were similar in yr 1 but CC was greater than OC for yr 2 (a year with less rainfall). Both forage type and year influenced CP, TDN and NSC ($P < 0.05$) with values higher for yr 1 than yr 2 and higher for CC and OC (which were similar) than for PM. Values for ADF, NDF and Ca were influenced by treatment ($P < 0.001$) with CC and OC values being similar but lower than that for PM. Variety and year both influenced levels of P, K, and Mg ($P < 0.05$). Corn forages had similar levels for both years but P was higher than PM in yr 1, lower in yr 2; K was lower in PM for yr 1 than yr 2 and PM Mg was similar to CC but lower than OC in yr 1 and lower than both CC and OC in yr 2. Overall, corn produced silage with greater biomass and better nutritional values than PM with organic and conventional corn silage forages having similar nutrient profiles.

Key Words: organic corn, pearl millet, silage

W115 Selection of bacterial strains to improve ensiling of alfalfa under sub-optimal conditions. S. Hansen*, A. Smith, and T. Rehberger, *Agtech Products Inc., Waukesha, WI.*

The quality of fermented forage is important in the dairy industry, with 40-60% of the diet consisting of ensiled field crops. The objective in this study was to identify and isolate bacteria unique to well-ensiled alfalfa and test them under optimal and sub-optimal conditions in order to develop a silage inoculant capable of fermentation over a broader moisture range. Previous studies using DGGE (Denaturing Gradient Gel Electrophoresis) reported a unique bacterial banding pattern associated with well-ensiled haylage when compared to haylage ensiled at sub-optimal moisture conditions. These unique DGGE bands mainly corresponded to the genus *Weissella*, previously *Leuconostoc*. Two *Weissella* strains were selected for testing in mini silos, air tight 5 gallon buckets containing haylage at a density of 46.5 pounds/cubic foot. Strains were tested in combination and applied at 2.0×10^5cfu/gram of haylage. Alfalfa was wilted for 24 hours in the field before it was chopped. The moisture level of the alfalfa upon arrival was 53%, within the ideal level for ensiling of alfalfa (45-55%) and was packed immediately (normal treatment). To simulate sup-optimal ensiling; alfalfa was laid out in the sun to dry for an additional two hours and ensiled at 43% moisture (dry treatment). Furthermore, water was sprayed on alfalfa to simulate a quarter inch of rain, dried for one hour and ensiled at 61% moisture (rain treatment). Each mini silo was sampled on day 0, 4, 2, 6, 11, 13, 32 and 98 post ensiling. Volatile fatty acids (VFAs) and pH were measured at each time point, as well as the enumeration of lactic acid bacteria and spoilage organisms (coliforms, yeasts, molds) on selective media. Analysis of the pH and VFAs indicated that the inoculated alfalfa had an improved fermentation under the dry and normal treatments. The inoculant decreased the pH and increased the rate and total concentration of lactic acid ($P < 0.05$) compared to the uninoculated alfalfa. The tested bacterial strains improved alfalfa fermentation, ensuring higher quality forage even under sub-optimal conditions of ensiling.

Key Words: alfalfa, forage, inoculant

W116 Effect of additive inclusion on dry matter loss of sugarcane silage. L. Borgatti*[1], A. Conrado[1], J. Pavan Neto[1], P. Meyer[2], C. Marino[1], and P. Rodrigues[1], [1]*University of São Paulo, Pirassununga, São Paulo, Brazil*, [2]*Brazilian Institute of Geography and Statistics, Pirassununga, São Paulo, Brazil*.

This study aimed to evaluate the effects of adding alkalis to sugarcane silage on dry matter loss. A completely randomized design was used, with 6 additives in two different concentrations (1 or 2%), plus a control group, totaling 13 treatments with four repetitions. The tested additives were: sodium hydroxide, limestone, urea, sodium bicarbonate, quicklime and hydrated lime. The experimental silos were stored and opened at 53, 60, 67 and 74 days after ensiling. Before opening, the silos were weighed for dry matter loss determination, calculated as the difference between the mass weight at ensiling and at opening multiplied by the respective dry matter contents. The loss was transformed on percentage of initial mass. Data were submitted to polynomial regression analysis by GLM procedure, which decomposed the effects in linear and linearity deviation. Differences were declared at $P<0.05$. All additives caused a decrease in total dry matter loss of silages ($P<0.05$) in relation to control (Table 1). Sodium hydroxide decreased by 43.5% dry matter loss in relation to control when added at 1% and by 62.5%, when was added in 2%. The decrease in dry matter loss caused by additives mainly occurred by a decrease in digestible dry matter loss (especially nonstructural carbohydrates). It could also be due to, in less scale, result of a decrease in hemicellulose and cellulose losses. The tested additives were efficient in the reduction of dry matter loss resulting from sugarcane silage fermentation.

Table 1.

Additive	Doses (%GM) 0	1	2	CV	Prob. Linear	Dev.	Equation	R^2
				DM LOSSES (%)				
Sod. hydroxide	33.1	18.7	12.4	43.2	0.0001	0.0121	$Y=33.1-18.4x-4.1x^2$	0.96
Limestone	33.1	19.4	20.3	27.3	0.0001	0.0001	$Y=33.1+21.1x-7.3x^2$	0.97
Urea	33.1	23.8	20.7	23.0	0.0001	0.0655	$Y=32.1+6.2x$	0.80
Sod. bicarbonate	33.1	20.5	24.6	21.9	0.0001	0.0001	$Y=33.1+21.0x-8.4x^2$	0.92
Quicklime	33.1	20.7	23.5	21.9	0.0001	0.0001	$Y=33.1+19.9x-7.6x^2$	0.97
Hydrated lime	33.1	20.8	25.7	17.3	0.0001	0.0001	$Y=33.1+16.8x-6.6x^2$	0.92

Key Words: alkalis, fermentation, silage

W117 Effects of microbial inoculants and dry matter content at harvest on the fermentation, aerobic stability and digestion of NDF of two corn silage hybrids. M. C. Santos*[1], L. T. Tatit[2], M. C. Der Bedrosian[1], W. Hu[1], O. G. Pereira[3], L. A. Williams[1], M. A. Gilinsky[1], and L. Kung Jr.[1], [1]*University of Delaware, Newark*, [2]*Univerisdade de Sao Paulo, Piracicaba, SP, Brazil*, [3]*Universidade Federal de Vicosa, Vicosa, MG, Brazil*.

The objective of this study was to compare the effects of microbial inoculants on the ensiling process of two corn silages ensiled at different DM contents. Two hybrids (DeKalb 6339 and Pioneer 33A88) were harvested at four DM contents (30, 32, 37 and 42%) and untreated or treated with 11CFT (Pioneer Hi-Bred International, Inc., Johnston, IA) at a rate of 1×10^5 cfu of *L. buchneri* PTA6138 and 1×10^4 cfu of *L. casei* PTA6135 or with Buchneri 500 (Lallemand Animal Nutrition, Milwaukee, WI) at a rate of 4×10^5 cfu of *L. buchneri* 40788 and 1×10^5 cfu of *P. pentosaceus* 12455 per g of wet forage. Approximately 600 g of fresh forage was ensiled in vacuumed and heat sealed bag silos (quadruplicate per treatment) and stored for 150 days. At the time of opening, a representative sample was taken and analyzed for fermentation end products, microbial populations, aerobic stability and nutritive value. NDF digestion was determined using dried samples ground through a 6-mm screen in a Wiley mill, weighed into in situ bags and incubated in the rumen of fistulated steers for 48 h. There were hybrid × DM × treatment interactions for all fermentation end products except lactic acid, numbers of lactic acid bacteria and aerobic stability. Over all hybrids and DM contents, corn silages treated with Buchneri 500 and 11CFT had higher ($P < 0.0018$) concentrations of acetate when compared with untreated silages (1.52 and 1.55 vs. 1.05% of DM). The same response was observed for 1,2-propanediol (0.57 and 0.52 vs. 0.24% of DM) and the number of lactic acid bacteria (8.22 and 8.01 vs. 6.30 $\log_{10}$ CFU/g). Buchneri 500 and 11CFT silages were also more stable when exposed to air (291 and 269 h for silage temperature to reach 2°C above ambient vs. 203 h for control) and had fewer yeasts at the time of opening (0.84 and 0.76 vs. 2.35 $\log_{10}$ CFU/g in untreated silages). Inoculation did not statistically improve NDF-D for either hybrid, but when combined as a main effect there was a trend ($P < 0.1026$) for silage treated with 11CFT to be more digestible than untreated silage (45.49 vs. 43.96% of NDF).

Key Words: ferulic acid esterase, silage, digestibility

W118 Using molecular techniques to identify and differentiate bacterial species and strains used in commercial silage inoculants. N. D. Walker*[1], M. E. Quintino Cintora[1], R. Schmidt[2], and R. Charley[2], [1]*Lallemand Animal Nutrition, Montreal, QC, Canada*, [2]*Lallemand Animal Nutrition, Milwaukee, WI.*

One of the problems encountered when analyzing the bacterial profiles found in silage inoculants is that they may contain a mixture of closely related species and strains which exhibit similar biochemical properties. However the advancement in molecular techniques has led to the development of a number of methods which enable this problem to be overcome. In this study, a DNA fingerprint method was used to identify species of bacteria present in commercially available silage inoculants; specific primers were used to identify isolates of *Lactobacillus buchneri* from these samples, and RAPD-PCR was used to differentiate closely related isolates of this organism and compare them to *L. buchneri* 40788. Commercial preparations (5) which contained *L. buchneri* were plated out. DNA was extracted from each plate and amplified. The resulting amplicons were separated by TTGE and the band positions compared with known standards (*L. buchneri, L. casei, E. faecium, L. plantarum*). In most instances, the package label corresponded to what was found in the packet except one sample which was supposed to contain *L. buchneri* did not appear to contain any viable cells of this organism as seen by the absence of a *L. buchneri* band. Further attempts to use *L. buchneri* specific primers on this preparation also did not produce a reaction, confirming this. To differentiate between strains of *L. buchneri*, single colonies were isolated from each commercial sample. Each isolate was Gram stained and those which resembled *L. buchneri* in morphology were selected, their DNA extracted and amplified using specific primers. Those which gave a positive reaction were then subjected to RAPD-PCR using 5 different primers and compared with the corresponding fingerprint of *L. buchneri* 40788. All were different to 40788 however, some of these new isolates only exhibited minor differences to each other, indicating that they were very closely related. A rapid method has been developed which can enable the identification and differentiation of different species of lactic acid bacteria and strains of *L. buchneri* commonly used in commercial silage inoculants.

Key Words: *L. buchneri*, silage, fingerprint

W119 Sorghum forage as an alternative to corn silage in dairy cows feeding. S. Colombini, G. Galassi, G. M. Crovetto*, and L. Rapetti, *University of Milan, Milan, Italy*.

Aim of the study was to study the possibility of substituting corn silage with low lignin (brown midrib, BMR)-sorghum silage in the diet of lactating cows. Two TMRs containing BMR333 single harvest sorghum forage silage (SF) or corn silage (CS) were fed to 60 Holstein dairy cows in a change-over design. Diets included (dry basis) 26.3% CS or 17.3% SF, 6.0% alfalfa hay, 11.0% Italian ryegrass hay and 56.6% or 65.7% concentrate for CS or SF diet, respectively. Diets had 15.5% CP, 31.5% aNDFom and 24.2% starch, on DM. Due to the low SF starch content (2.8% on DM), a higher amount of corn meal was included in the SF diet (5.7 *vs* 8.0 kg/d). Forages were also incubated *in situ* to determine rumen degradability and degradation rate (k_d) of NDF. All data were statistically analyzed by SAS-GLM procedure. DMI was not affected by diet (24.4 *vs* 25.4 kg/d for CS and SF fed cows). Milk yield (32.6 and 33.1 kg/d for CS and SF diets), milk fat (4.16% for both diets) and milk protein (3.42 and 3.40% for CS and SF diets) were not affected by dietary treatment (NS). MUN was lower in the diet CS (9.2 *vs*9.9 mg/dl; $P<0.001$); this was probably due to the higher starch fermentability of corn silage as compared to corn meal, included at a higher proportion in the SF diet, resulting in a better N utilization for CS diet. The rate of aNDFom degradability (k_d) was higher for SF, although only a trend was detected. On the other hand potentially degradable aNDFom (a+b) was higher for CS; thus, effective degradability was not different between the two forages (table 1), confirming the results obtained *in vivo*. BMR sorghum silage can be effectively used in dairy cow feeding, provided starch content of the diet is balanced.

Table 1. *In situ* rumen DM and aNDFom degradability

	DM				aNDFom			
	CS	SF	SE	P	CS	SF	SE	P
a[1] (%)	33.1	23.7	0.44	***	3.63	3.27	1.08	NS
b[2] (%)	46.3	48.7	0.23	**	67.3	63.3	1.55	NS
k_d (%/ h)	3.3	3.3	0.19	NS	2.5	3.10	0.17	0.07
a+b[3] (%)	79.4	72.4	0.39	***	70.9	66.6	0.71	*
Effective deg[4]	49.5	40.8	0.73	**	21.5	21.8	1.11	NS

*$P<0.05$; ** $P<0.01$; *** $P<0.001$. [1]soluble fraction; [2]degradable fraction; [3] potentially degradable fraction; [4]effective degradability with a passage rate of 6%/h

Key Words: sorghum forage BMR, dairy cow, NDF degradability

W120 Nutritive value and fermentation profile of sorghum silages with urea and two storage periods. F. E. P. Fernandes[1], R. Garcia*[1], A. J. V. Pires[2], O. G. Pereira[1], and C. S. Fernandes[1], [1]*Federal University of Viçosa, Viçosa, MG, Brazil*, [2]*State University of Bahia, Itapetinga, Ba, Brazil*, [3]*Fapemig, Belo Horizonte, MG, Brazil*.

The objective of the study was to determine the effects of doses of urea (0.0, 2.5, 5.0, and 7.5%, DM base) and storage periods (30 and 60 days) on the chemical composition, IVDMD, NH3-N, pH values and WSC of the silages. The addition of urea doses showed a quadratic effect upon DM content. The smallest estimated DM content of silage (21,87%) was observed at 5,69% of urea dose added. The urea addition in the ensiling process of sorghum increased the CP, NDIP, and IVDMD and reduced the NDF, ADF, cellulose and lignin contents. To the fermentative charactericts of the silages, the urea doses had a quadratic effect in the NH3-N contents. The pH values of the silages increased lineary. There was effect of the silage periods on the NH3-N content and pH value. However, the urea addition in the ensiling process of sorghum did not cause any significative change in reducing the fermentative characteristics of the silages. The nitrogen fractions of the silage were influenced by the urea addition, being verified positive linear effect for the A fraction, negative linear effect for B1+B2, B3 and C fractions. It was detected a linear reduction of CT contents in function of the urea addition. The fractions of CT were influenced by urea addition, being verified negative linear effect on the content of A+B1 fractions; positive linear effect on the B2 and C fractions for the storage period of 60 days. The addition of urea in the ensiling process of sorghum can reduce losses by fermentation and increasing the nutritive value of the silage.

Key Words: ensilage, digestibility, ammoniation

W121 Elephantgrass with and without wilting, added of cassava meal in silage production. R. Garcia*[1], A. C. Oliveira[1], A. J. V. Pires[2], O. G. Pereira[1], and F. E. P. Fernandes[1], [1]*Federal University of Viçosa*, *Viçosa, MG, Brazil*, [2]*State University of Bahia*, *Itapetinga, Ba, Brazil*.

Two experiments were conducted, using a completely randomized design, to evaluate the nutritive value, fermentative characteristics and losses in elephantgrass with and without wilting and added cassava meal (0; 7.5; 15 and 22.5% natural base), in the ensiling process and to determine protein and carbohydrate fractions of silage. In experiment I, wilting associated with cassava meal was efficient to increase dry matter (DM) content, to minimize DM losses and to reduce crude protein (CP), acid detergent insoluble nitrogen, neutral detergent fiber, neutral detergent fiber ash and protein free, acid detergent fiber, and celluloses contents. Cassava meal addition in elephantgrass silage production caused reduction in ether extract, hemicellulose and lignin contents and increased organic matter content, in vitro DM digestibility, and total digestible nutrients. The wilting treatment had effect only in neutral detergent insoluble nitrogen content. It was observed quadratic effect of without wilting on pH and butyric acid, with pH showing minimum value of 3.7% in 15.9% cassava meal level. It was observed quadratic effect of without wilting on ammonia nitrogen and acetic acid but linear effect of wilting on ammonia nitrogen and acetic acid. In experiment II the regression analysis detected a linear increase of total carbohydrates (TC) content as a function of cassava meal addition. The association of wilting with different levels of cassava meal influenced the TC fractions (A+B1 and B2), but did not have effect on nitrogen fractions (A and B1+B2). The wilting of elephantgrass associated to cassava meal was efficient to reduce the moisture and the losses in the silage. The cassava meal improved the in vitro DM digestibility. The level of 22.5% of cassava meal (natural base) in the ensiling process of elephantgrass (19.5% DM) can be recommended to improve the nutritive value and fermentative characteristics of silage.

Key Words: digestibility, *Pennisetum purpureum*, by-product

W122 Effects of ensiling corn and sorghum silages under normal or adverse conditions on proportions of long chain fatty acids. B. C. do Amaral[1], S. C. Kim[2], O. F. Zacaroni[1], A. T. Adesogan[1], and C. R. Staples*[1], [1]*University of Florida*, *Gainesville*, [2]*Gyeongsang National University*, *Jinju, South Korea*.

The objective was to determine the effect of ensiling regime and storage duration on long chain fatty acid (LCFA) profiles of corn (CS) and sorghum silages (SS). Corn (Pioneer 30F34) and sorghum (NK300) forages, grown at the University of Florida, were ensiled at 31 and 36% dry matter, respectively. Chopped forages were packed into 20-L silos in triplicate and ensiled for 0, 7, 21 and 156 d. Half of the silos were sealed immediately and stored at 24°C (normal ensiling) and half were placed in a 30°C room for 48 h before sealing and storage at 30°C (adverse ensiling). Silages were subsampled, freeze-dried, ground, and analyzed for FA using gas chromatography. Sorghum silage had greater ($P < 0.05$) concentrations of total FA (1.90 vs. 1.80% of DM), 18:1n-9 (20.9 vs. 19.5% of FA), and C18:3n-3 (17.9 vs. 15.6% of FA) than CS whereas CS had greater concentrations of C16:0 (23.8 vs. 20.0% of FA) than SS. Adverse ensiling tended to increase ($P=0.06$) total FA concentration over time (18.9 vs. 18.2% of DM), increased proportions of C16:0 (22.3 vs. 21.5% of FA) and C18:0 (3.1 vs. 2.7% of FA) but decreased proportions of C18:2n-6 (36.6 vs. 38.5% of FA) across both silage types. The effect of storage duration on the proportions of individual FA differed between CS and SS. The proportions of C18:3n-3 decreased linearly with storage duration but the decrease was greater for SS (20.2, 19.7, and 13.8% of FA) than for CS (16.2, 16.5, and 14.1% of FA for 0, 7, and 156 d of ensiling, respectively). In contrast, proportion of the other unsaturated FA, C18:1n-9 and C18:2n-6, increased with storage duration. In silages prepared under adverse conditions, the proportion of C18:3n-3 in silage did not decrease dramatically until 156 d whereas proportions of C18:3n-3 decreased at both 7 and 156 d of ensiling in silos ensiled under normal conditions. Approximately 13 to 31% of linolenic acid was degraded in corn and sorghum silage during ensiling but proportions of linoleic acid remained relatively unchanged.

Key Words: silage, ensiling time, fatty acid

W123 Nutritive value of corn hybrids for silage production according to the maturity stage. M. Zopollatto*[1], L. G. Nussio[1], J. O. Sarturi[2], G. B. Mourão[1], A. P. Duarte[3], C. M. M. Bittar[1], and V. P. Santos[1], [1]*University of Sao Paulo/ESALQ*, *Piracicaba, SP, Brazil*, [2]*University of Nebraska*, *Lincoln*, [3]*Apta Regional*, *Assis, SP, Brazil*.

The objective of this study was to evaluate the nutritive value of corn hybrids for silage production harvested across maturity stages A randomized block design, with an 8×6×2 factorial scheme based on eight harvesting ages, six corn silage hybrids and two harvesting years (2001/02 and 2002/03) was performed. The hybrids CO 32, semi–hard endosperm; AG 5011 – soft endosperm; P 3041 – hard endosperm; DKB 333B – semi–hard endosperm; AG 1051 – soft endosperm and Z 8550 – semi–soft endosperm were harvested when they reached 50% tasseling, 15 days later and weekly, totalizing eight harvesting times. Maturity advance resulted in increases ($P<0.05$) in the mean starch content (1.8 to 26.1%) and digestible dry matter production (5.9 to 16.3 t/ha –DDMP). However, decreases ($P<0.05$) in forage neutral detergent fiber – NDF (71.9 to 52.8%); digestible NDF (64.7 to 54.4%) and crude protein (12.5 to 7.0%) were observed across the time. The in vitro true dry matter digestibility (IVTDMD) did not ($P>0.05$) changed along maturity stage (71.8 to 72%) At the ensiling stage (30–35% DM – at the 5th harvesting age, from 94 to 105 days after seeding) P 3041, AG 1051 and Z 8550 hybrids showed the most desirable quality characteristics for silage production: the lowest ($P<0.05$) NDF content (54.9; 55.2 and 55.1%, respectively) and the highest ($P<0.05$) digestible NDF content (60.0; 62.4 and 61.0%, respectively), IVTDMD (75.4; 74.3 and 75.6%, respectively) and DDMP (14.4; 14.3 and 13.9 t/ha, respectively). Furthermore, AG 1051 and CO 32 hybrids showed the highest ($P<0.05$) starch content (23.5 and 20.9%, respectively) at the ensiling stage. The forage nutritive value is a result of the interactions between fiber and starch kernel contents and differences observed across the maturity indicated that the maximum forage nutritive value for setting a harvesting window may differ among cultivars.

Key Words: digestibility, fiber, starch

W124 Nutritional quality of sunflower silage associated with additives. R. H. de Tonissi e Buschinelli de Goes*[1], K. A. de Souza[1], E. S. Myagi[3], R. A. Patussi[1], K. C. da Silva Brabes[1], A. C. Martinez[2], C. O. de Abreu[2], E. R. de Oliveira[1], and D. D. Alves[4], [1]*Universidade Federal da Grande Dourados*, *Dourados, Mato Grosso do Sul, Brazil*, [2]*Universidade Estadual de Maringá*, *Umuarama, Paraná, Brazil*, [3]*Universidade Federal de Goiás*, *Goiânia, Goiás, Brazil*, [4]*Universidade Estadual de Montes Claros*, *Janaúba, Minas Gerais, Brazil*.

Sunflower (20.0% DM and 10.0% CP) was ensiled in 36 experimental silos in a randomized design, in a factorial square 4x3 (four treatments,

three days of opening) with three replicates; to evaluate the effect of the addition of soybean hulls, sunflower crushed seeds and urea on the nutritional quality of sunflower silage. The averages were analyzed by the Tukey test to 5% of probability. The treatments were: Control (100% of Sunflower plants - SS), SS + 5% of soybean hulls, SS + 5% of crushed sunflower seeds and SS + 5% of urea. The silos were opened at 14, 21 and 28 days after ensilage. There was no effect (P>0.05) for day of opening, or addition on organic matter (OM), neutral detergent insoluble protein (NDIP), mineral matter (MM), neutral detergent fiber (NDF) or acid detergent fiber (ADF), (mean = 91.12, 8.66, 9.29, 62.54, 46.02%, respectively). Dry matter (DM) and ether extract (EE) presented interaction for addition and days of opening (P<0.05). 5% of soybean hulls increased the DM after 28 days of ensilage (34.9%), for the crushed sunflower seeds the MS were higher after 21 days (31.7%). The DM of SS at 28 days was 26.4%. The addition of 5% crushed sunflower seeds presented higher EE to the 28 days of ensilage (6.96%) The control presents at 28 silage day of 4.8% EE and 26.4% DM. There was an effect on crude protein (CP), acid detergent insoluble protein (ADIP) and total carbohydrates (TC), for additions (P<0.05), but not for opening dates. Urea provided increment of nitrogen′s fractions, and consequently larger crude protein and acid detergent insoluble protein (23.5 and 1.3% DM), while others treatments presents a media of 11.8% and 0.8% of AIPD. The addition of 5% of soybean meal and crushed sunflower seeds increased the total carbohydrates in sunflower silage (76.9 and 71.5%), this didn't happen with the urea addition (63.1%). The SS presents total carbohydrates of 73%. The addiction of urea provides a higher CP and ADIP and 5% of sunflower crushed seeds and soybean hulls increases DM and EE after 21 days of silage and the total carbohydrates of sunflower silage.

Key Words: crushed sunflower seeds, soybean hulls, urea

W125 In situ dry degradation coefficients of whole crop barley silage treated with *Lactobacillus plantarum* or mixed with *Pediococcus pentosaceus* plus *Propionbacter freudenreichii*. M. Vatandoost, M. Danesh Mesgaran*, A. Heravi Mousavi, and A. R. Vakili, *Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The aim of the present study was to determine the chemical composition and in situ dry matter (DM) degradation of whole crop barley silage (WCB, 35% DM) as untreated or treated with *Lactobacillus plantarum* (8×1010 CFU (LP8) or 16×1010 CFU (LP16) per g of DM) or mixed with *Pediococcus pentosaceus+Propionbacter freudenreichii* (5.5×1010 CFU (PP5.5) or 11×1010 CFU (PP11) per g of DM) for 30 days (n = 4). Standard procedures were used to determine the chemical composition of the samples. The pH of the silage extract was determined using a pH meter (Metrohm 691, Swiss). NH3-N concentration was determind in acidified silage extract (5 ml of the extract + 5 ml of 0.2 M HCl) using a distillation method (Kjeltec 2300 Autoanalyzer, Foss Tecator, Sweden). The rumen degradable parameters of DM of the silages were determined using in situ procedure. Four sheep (44±5 kg liveweight) fitted with rumen cannula were used in the present study. About 5 g DM of each sample was placed in each polyster bag (10×12 cm, 52 µ por size), then incubated (n = 4) for 2, 4, 8, 16, 24, 48, 72 and 96 h. For zero time, bags were washed using cold tap water. The equation of $P=a+b(1-e^{-ct})$ was applied to determine the coefficients (a = quickly degradable fraction, b = slowly degradable fraction, c = fractional degradation rate constant). The inoculants caused to decrease the pH and NH3-N concentration (mg/dl) (WCB = 4.07 and 9.10, LP8 = 3.69 and 8.47, respectively). Neutral detergent fiber content of the treated silages was significantly increased (P< 0.05) than WCB (WCB = 554, LP8 = 581, LP16 = 627, PP5.5 = 542 and PP11 = 617 g/kg DM; SEM = 6.22). Treated silages had a greater slowly degraded fraction of DM compared with WCB samples (WCB = 0.44 ± 0.03, LP8 = 0.48 ± 0.02, LP16 = 0.49 ± 0.01, PP5.5 = 0.47 ± .02 and PP11 = 0.49 ± 0.02 g/kg DM; SEM = 6.22).

Key Words: silage, *Lactobacillus plantarum*, degradation

W126 The effect of propionic acid or propionate ammonium on chemical composition and in situ dry matter degradation of whole crop barley silage. M. Vatandoost, M. Danesh Mesgaran*, A. Heravi Mousavi, and A. R. Vakili, *Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The aim of this study was to evaluate the effect of propionic acid or ammonium propionate on chemical composition and in situ dry matter (DM) degradation of whole crop barley silage. It was harvested (about 35% DM), chopped, and then ensiled as untreated (UT) or treated with propionic acid (3 or 6 g per Kg of DM; P3 or P6, respectively) or ammonium propionate (1 or 1.5 g per Kg of DM; AP1 or AP1.5, respectively) for 30 days (n = 4). Standard procedures were used to determine the chemical composition of the samples. Silage extract pH was determined using pH meter (Metrohm 691, Swiss). NH3-N concentration was determined in acidified silage extract (5 ml of the extract + 5 ml of 0.2 N HCl) using distillation method. The ruminal degradable parameters of DM of the silages were determined using in situ procedure. Four sheep (44±5 Kg Body Weight) fitted with the rumen fistulae were used in the present study. Bags (10 × 12 cm) were made of polyester cloth with a pore size of 52 µm. About 5 g DM of each sample was placed in each bag, and four bags for each treatment were incubated for each time (2, 4, 8, 16, 24, 48, 72, 96 h). For zero time, bags were washed using cold tap water. The equation of $P=a+b(1-e^{-ct})$ was applied to determine dry matter degradation coefficients (a = quickly degradable fraction, b = slowly degradable fraction, c = fractional degradation rate constant). Both additives did not have any significant effect on pH (UT = 4.07, P3 = 4.05, P6 = 4.03, AP1 = 3.95 and AP1.5 = 3.93; SEM = 0.15) or crude protein concentration (UT = 7.98, P3 = 8.03, P6 = 8.11, AP1 = 8.06 and AP1.5 = 8.08 g/kg DM; SEM = 0.09). However, these additives caused a significant (P < 0.05) increase in neutral detergent fibre content (UT = 554, P3 = 661, P6 = 664, AP1 = 577 and AP1.5 = 595 g/kg DM; SEM = 7.7). NH3-N concentration (mg/dl) was significantly increased when ammonium propionate was applied (UT = 9.10, AP1 = 11.69; SEM = 0.53). The additives caused an increase in slowly degradation faction of DM (UT =0.46 ± 0.03, P3 = 0.56 ± 0.03, P6 = 0.57 ± 0.04, AP1 = 0.49 ± .02 and AP1.5= 0.52 ± 0.03).

Key Words: silage, propionic acid, propionate ammonium

W127 Antioxidant activity and white blood cells on plasma of lambs fed with Manzarina. H. E. Rodríguez-Ramírez*[1,2], C. Rodríguez-Muela[1], R. Bocourt-Salabarría[3], C. Chávez-Hernández[2], O. Ruiz-Barrera[1], C. Hernández-Gómez[1], R. Jasso-Ibarra[2], and C. Holguín-Licón[1], [1]*Universidad Autónoma de Chihuahua*, *Chihuahua, México*, [2]*INIFAP, Campo Experimental Delicias*, *Delicias, Chihuahua, México*, [3]*Instituto de Ciencia Animal*, *Habana, Cuba*.

Apples have positive effects as a natural antioxidant. Manzarina (Mzn) is a solid state fermentation product of apple byproducts. Mzn could preserve some of the apple properties; in addition, it has high yeasts content. The objective was to evaluate Mzn influence over plasma antioxidant activity (AA) and white blood cells concentration on lambs

(n=24 lambs), during a feedlot trial. Six males (M) and six females (F) were fed with a ≈10% of Mzn in diet (n=12; t1), six M and six F were fed with a common diet (t2). Animals remained on individual stalls with water and feed *ad libitum* during 56 d. Samples of blood were taken on July 31 (1), August 30 (2) and September 26 (3) of 2007 to determinate AA (FRAP technique) and white blood cells count (Beckman Coulter® A^c•T 5diff AL device). Data analysis was done with a multivariate procedure for repeated measures (SAS 9.0 GLM, REPEATED statement); the effects were treatment, sex and their interaction. Blood sampling moment (1, 2 or 3) was used as repeated measure. On sampling 3, plasma AA (mM Fe_2 eq.) of t1 lambs (7.40±0.25) was higher (P≤0.08) than t2 lambs (6.61±0.23) plasma AA. There was not difference (P≥0.05) between t1 and t2 Leukocyte counts ($L*10^3*\mu L^{-1}$ of blood). t1 lambs had $8.0\pm0.6*10^3$, $7.1\pm0.4*10^3$ and $8.7\pm0.4*10^3$ $L*\mu L^{-1}$ on samplings 1, 2 and 3; t2 lambs had $8.7\pm0.6*10^3$, $7.6\pm0.4*10^3$ $L*\mu L^{-1}$ and $8.0\pm0.4*10^3$ $L*\mu L^{-1}$ on the same moments. On sampling 3, Neutrophiles proportion (Ne%) was higher (P≤0.025) on t1 F (53.8±5.0%), compared with t1 M (34.8±5.0%) and t2 F (32.3±5.0%) Ne%, t2 M had 45.3±5.0%. On sampling 3, Lymphocytes proportion (Ly%) was lower (P≤0.05) on t1 F (41.3±5.6%) compared with t1 M (62.0±5.6%) and t2 F (61.2±5.6%) Ly%, t2 M had 49.5±5.6%. On sampling 2, Eosinophils proportion (Eo%) was higher (P≤0.05) on t1 lambs (2.3±0.2%) compared with t2 lambs (1.4±0.2%). Monocytes and Basophils proportions were similar (P≥0.05) between treatments. We conclude that there is a positive influence of the diet with Mzn (t1) over the AA of lambs′ plasma and there is an influence of the diet over the leukocyte profile.

Key Words: antioxidant, leukocyte, lambs

W128 Inoculant-treated corn silage quality and performance of lactating cows. A. Ghaempour[1], G. R. Ghorbani[1], M. Khorvash[1], and A. Nikkhah*[2], [1]*Isfahan University of Technology*, *Isfahan, Iran*, [2]*Zanjan University*, *Zanjan, Iran*.

It has been a question for large dairy holders if applying inoculants to low-DM corn crop can improve preservation quality. The objective was to determine the effect of microbial inoculant application to high moisture corn crop on silage quality and performance of lactating cows. Crop corn was harvested at milk stage of maturity with 21% DM, cut at a theoretical particle length of 2 cm, filled in four 60-tone bunker silos, and treated with 1) no inoculants, 2) inoculant A (Ecosyl) containing Lactobacillus plantarum, 3) inoculant B (Biotal) containing Pediococcus pentosanus, Lactobacillus plantarum and Propionibacter freudenreichii or 4) the combination of inoculants A and B. Eight multiparous lactating Holstein cows at 100 ± 20 days in milk with an average body weight of 650 kg were used in a 4 × 4 Latin square design with four 20 d periods, 14 d of adaptation and 6 d of sampling. Treatments were total mixed rations (TMR) with inoculant-treated corn silages as above. Diets contained 32.9% corn silage, 14.3% alfalfa hay, 15% ground barley, 13.1% ground corn, 17.4% soybean meal, 3.4% cottonseeds, 1.8% fat powder, 0.8% sodium bicarbonate, 0.45% calcium carbonate, and 0.8% vitamin and mineral supplement. Orts were adjusted to not exceed 10% of the daily TMR. Cows were milked in a milking parlor three times daily at 0500, 1300 and 2100 h. Rumen fluid was sampled by rumenocentesis at 4-h post-feeding. Inoculants did not affect silage pH, and concentrations of ammonia, lactate, acetate, CP, NDF, ADF, ash and water soluble carbohydrates. Dry matter intake (21.5, 22.8, 21.7 and 21.7 ± 0.6 kg/d) and milk yield (33.7, 32.8, 32.3 and 33.6 ± 1.4 kg/d), and milk percentages of fat (3.32, 3.14, 3.32, and 3.15 ± 0.16), protein (3.05, 3.08, 3.06 and 3.08 ± 0.06) and lactose (5.44, 5.45, 5.47 and 5.44 ± 0.08) were unaffected by corn silage inoculant treatment. Applying inoculants to corn crop before ensilage did not significantly affect rumen pH VFA concentrations, and total tract nutrient digestibility. Results suggest little effect of inoculants on corn silage quality and performance of mid lactation dairy cows on diets with 32.9% corn silage.

Key Words: corn silage, inoculant, dairy cow

W129 Fitted models for description of cumulative gas production profiles from silages of sunflower and corn. R. Mello*[1], A. L. R. Magalhães[2], F. C. Breda[1], A. J. Regazzi[3], A. C. de Queiroz[3], and J. L. Nörnberg[4], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Universidade Federal Rural de Pernambuco - Unidade Acadêmica de Garanhuns*, *Garanhuns, Pernambuco, Brazil*, [3]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [4]*Universidade Federal de Santa Maria*, *Santa Maria, Rio Grande do Sul, Brazil*.

The aim of this work was to identify among the Brody, Von Bertalanffy, Gompertz, France, Logistic, Modified logistic and Dual-pool logistic models, the one that presents the highest quality of fit for description of cumulative gas production curves from silages of sunflower and corn. Twelve different sunflower silages and two different corn silages samples were obtained from different ensiling experiments using laboratory silos. Substrates were incubated with ruminal fluid buffered in triplicate, resulting in 42 individual curves. Gas production was followed over time in a semi-automated in vitro system with pressure transducer. Parameters of the models in question were estimated through the Marquadt algorithm implemented in the NLIN procedure of SAS® software. The quality of fit was evaluated by coefficient of determination, residual mean square, graphic analysis of the observed and estimated curves, graphic analysis of dispersion of the studentized residual, average percentage error, relative efficiency and number of iteractions to converge. Brody, France and Dual-pool logistic models showed the largest values of coefficient of determination in both substrates, and the difference among them was considered worthless. They also showed the smallest values of residual mean square in sunflower silages, being the difference among them was considered worthless. Brody and France models presented smaller residual mean square in corn silages, but these models estimated negative gas production on initial times of incubation in both substrates, being biologically impossible. All the models showed positive dispersion of the residual in both substrates after 144 hours of incubation. The Brody model showed smaller average percentage error and number of iterations in both substrates. The Dual-pool logistic and France models showed higher relative efficiency, respectively, in sunflower and corn silages. Thus, the Dual-pool logistic model showed higher quality of fit to the cumulative gas production curves in sunflower and corn silages.

Key Words: fermentation kinetics, mathematical models, nonlinear models

W130 Nitrogenous compounds and fermentation characteristics of king grass - leucaena silages. T. Clavero* and R. Razz, *Universidad del Zulia*, *Maracaibo, Estado Zulia, Venezuela*.

In order to increase nitrogenous compounds and improve fermentation quality of king grass (*Pennisetum purpureum* × *Pennisetum typhoides*) silage, ensiling with *Leucaena leucocephala* was tested. King grass and leucaena were cultivated in a very dry tropical forest in north west of Venezuela. The treatments for silage making were: 100% king grass (KG), 30% leucaena (L)-70% KG, 70%L-30% KG and 100% L. Fresh plant materials were chopped to 1 cm length, mixed according to treat-

ments, ensiled in laboratory silos and stored a 25 °C for 45 d. After opening the silos, dry matter (DM), pH, temperature (T), total nitrogen content (TN), protein nitrogen (PN), soluble nitrogen (SN),ammonia nitrogen (AN), PT/TN and N-NDF/TN were determined. The data were analyzed according to a completely randomized design with three replications, significance among mixing levels was determined by Tukey test. DM content of the resultant silages significantly increased ($p \leq 0.001$) with the inclusion of leucaena in the mixtures, reached the highest values (26.49%) with 70%, which is considered as optimal for a good conservation. The introduction of leucaena produced a trend towards a significantly ($p \leq 0.05$) decreased of pH levels of the silages, showing the lowest values (3.48) with 100% leucaena. T was not affected by treatments. TN, PN, SN, PN/TN and N-FND/TN contents increased with increasing proportion of leucaena in the mixtures. However, there were not significant differences ($p \geq 0.05$) among 70-100% levels of leucaena. AN was not detected or only in small amount during ensiling period. Those results indicated that mixing leucaena with king grass would inhibit proteolysis and reduced the loss of nitrogen compounds during fermentation of the silage also leucaena material might inhibit clostridia growth during storage and stimulate lactic acid fermentation, resulting in a decreased pH value of the silage. In this study, the inclusion of leucaena at the rate of 30% or more, increased nitrogenous compounds and improved silage fermentation.

Key Words: silage, *Leucaena leucocephala*, nitrogenous compounds

W131 The effect of sewage irrigation on mineral composition and in-vitro digestibility of two corn forage varieties. E. Yosef*[1], E. Zukermann[2], J. Miron[1], M. Nikbahat[1], and D. Ben-Ghedalia[1], [1]*The Volcani Center, ARO, Bet Dagan, Israel*, [2]*Extension Service-Ministry of Agriculture and Rural Development, Bet Dagan, Israel*.

Summers in Israel are dry and forage crops must be irrigated. The usage of sewage irrigation of summer forages, increased in Israel due to regional droughts and the necessity to eliminate the excess of urban waste waters. The purpose of this study was to evaluate the effect of secondary-treated sewage water irrigation on the composition and in vitro digestibility of two corn forage varieties: Oropesa (Europe origin) and 32P75 (USA Pioneer). The irrigation treatments were sewage vs. flood water at a level of 3380m^(3)^/ha. In each treatment, both corn varieties were grown as five replicated plots and sampled by manual harvesting at the soft dough stage of maturity. The conductivity of the sewage and flood water used was 1.41 and 0.81 ds/m, respectively. Within each variety, plant morphology, plant yields and cell wall content and composition were not affected by type of irrigation. Despite of the several folds higher mineral concentrations in sewage water as compared with flood water: Na (× 5.4), S (× 2.6), K (× 14), P (× 473), Al (× 5.6), B (× 2.4), Mn (× 24.3), Cu (× 31.9) etc., the mineral composition in both irrigation treatment of corn plants was similar. The sewage treatment improved dry mater and NDF in vitro digestibility of corn Oropesa as compared with flood water treatment (71.2% vs. 68.8% and 53.8% vs. 45.7%, respectively). However, sewage treatment decreased in vitro digestibility of 32P75 as compared with flood treatment (66.5% vs. 71.6% and 51.3% vs. 57.6%, respectively). In both treatment of each variety the nitrate contents were similar, but Oropesa contained 2-3 folds higher nitrate content then 32P75. In this study the mineral concentrations of secondary-treated sewage water were below the critical level which may damage the corn plants quality.

W132 Biomin® BioStabil Mays enhanced the fermentation and the aerobic stability of corn silage under tropical laboratory conditions. A. A. Rodríguez*[1], Y. Acosta-Aragón[2], and E. Valencia[1], [1]*University of Puerto Rico, Mayaguez, PR*, [2]*Biomin GmbH, Austria*.

An experiment was conducted to determine the effects of the silage additive Biomin® BioStabil Mays (BSM, blend of homo- and heterofermentative bacteria) on the fermentation characteristics and aerobic stability of corn whole plant (QPM variety) growth and ensiled in Puerto Rico. Corn was harvested 75 d after planting and chopped finely. Prior to ensiling, the vegetative material was treated or not with BSM (1 x 105 cfu/ g silage). Treatments were applied to weighted portions of corn forage, manually mixed, and packed into PVC laboratory silos. Samples of fresh forage and triplicates silos of each treatment were taken at 0, 3, 45 and 90 d of fermentation, analyzed for pH, chemical composition, and fermentation products. Statistical analysis was performed as a completely randomized design with a 2 by 4 factorial arrangement of treatments. Tukey t-test was used for mean separation. For aerobic stability determination, triplicate silos from each treatment were emptied after 45 and 90 d of ensiling, placed into styrofoam containers lined with a plastic bag and exposed to air for 5 d. Temperature was monitored every 6 hours during the 5 d with a thermometer embedded in the surface of the exposed silage. pH was measured after 0, 1, 3 and 5 d. Statistical analysis of pH data was performed as a completely randomized design with a 2 by 5 factorial arrangement of treatments. The same model was utilized for temperature data except that 19 times of aerobic exposure (hours) were utilized instead of 5 d. Tukey t-test was also used for mean comparison. BSM enhanced the fermentation characteristics of corn ensiled during 45 d as evidenced by lower pH ($P<0.05$) and higher lactic acid content ($P<0.05$). After 90 d of fermentation BSM lowered the ratio of NH3-N/total-N ($P<0.05$) as compared with corn ensiled without additive. After the opening of the silos at the d 45 and 90 the temperature of silages treated with BSM was lower than that of the control silage ($P<0.05$). In summary, BSM improved the fermentation characteristics and the aerobic stability of corn ensiled under tropical laboratory conditions.

Key Words: corn silage, additive, tropical environment

International Animal Agriculture

W133 Dairy farm milk quantity, quality, and revenue within a private organization in Central Thailand. S. Yeamkong[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand*, [2]*University of Florida, Gainesville*.

Survival of dairy farming in Thailand depends on the ability of dairy farmers to increase profitability and efficiency of their dairy operations. Revenues are primarily related to amount of milk produced, and secondarily to milk quality. The objective here was to determine factors affecting milk quantity, quality, and revenue in dairy farms from a private organization in Central Thailand. The dataset had 34,133 farm monthly records for milk yield per cow (MC), fat percentage (FP), protein percentage (PP), lactose percentage (LP), solids-not-fat percentage (SP), total solids percentage (TP), somatic cell count (SC), and milk revenue per cow (RC) collected from September 2003 to December 2007 in 1,101 dairy farms. Seasons were winter (November to February),

summer (March to June), and rainy (July to October). Farm locations were Muaklek (ML), Wang Muang (WM), Phattana Nikhom (PN), and Pak Chong (PC). Farms were classified by number of milking cows into small (< 10 cows), medium (10 to 19 cows), and large (> 19 cows). The model for each trait had year-season (YS) and farm location-farm size (FLFS) as subclass fixed effects, and farm and residual as random effects. Year-season and FLFS effects significantly affected all traits ($P < 0.05$), except for PP. Least squares means for FLFS ($P < 0.0001$) ranged from 162.3 ± 47.4 kg (small, PN) to 378.3 ± 14.5 kg (medium, PC) for MC, 3.36 ± 0.04% (medium, PC) to 3.60 ± 0.10% (large, PN) for FP, 4.54 ± 0.02% (medium, PC) to 4.61 ± 0.01% (small, PN) for LP, 8.19 ± 0.03% (medium, PC) to 8.33 ± 0.07% (large, PN) for SP, 11.64 ± 0.05% (medium, PC) to 12.01 ± 0.14% (large, PN) for TP, 536,450 ± 48,500 cells/ml (small, PN) to 1,062,780 ± 114,030 cells/ml for SC and 2,015.3 ± 549.3 baht (large, PN) to 4,483.7 ± 168.3 baht (medium, PC) for RC. Positive trends across YS existed for FP (0.015 ± 0.006%/YS; $P < 0.04$) and SC (11,309 ± 3,067 cells/ml/YS; $P < 0.004$), whereas a negative trend existed for MC (-6.2 ± 1.4 kg/YS; $P < 0.001$).

Key Words: dairy cattle, milk revenue, tropical

W134 Hormonal profile in superovulated buffalo heifers using pFSH and LH. A. M. Osman* and S. H. Shehata, *Assiut University, Assiut, Egypt*.

Literature show contrasting results with superovulation in buffaloes. Estrogen (e) and progesterone (p) were studied in 15 superovulated buffalo heifers to predict state of ovarian response. Ten heifers injected by pFSH (65 NIH unit divided into 6 equal doses for 3 consecutive days) and Lutalyse (25 mg given with 5th injection). LH (2-10 thousands USP unit) injected 12 hour (h) from treatment. Rest 5 heifers stayed as control. Blood taken before treatment (0h) then after 12, 24, 48, 72, 96, 120 and 144h. Sera separated and kept at -20C° for e and p determinations using IMMULITE Immunoassay. All heifers slaughtered and ovaries studied for new corpora lutea (CL) and unovulated follicles (UF). Data statistically analyzed using SAS computer system version 3.2. In control group, e levels (pg/ml) were 24.6±1.04 at 0h, 30±1.78 at 72h and 18.2±0.89 at 144h. The p levels (ng/ml) were 1.57±0.23 at 0h,2.93±0.26 at 120h and 2.58±0.25 at 144h.In superovulated heifers, results classified into high response group(HRG) >2CL(3.8±0.49) and low response group(LRG) <3CL(1.2±0.2). Difference was significant ($P<0.05$). There was significant increase in e at 72 h in HRG followed by decrease. The increase of e in the LRG continued till the last sample with significant difference ($P<0.05$). Significant correlation between e and UF presents ($r = 0.65$) during last 2 days. Total number of UF is lower in HRG than LRG (23 versus 37). One day after LH, e levels decreased in all animals without relation to injected doses. Overall p levels (ng/ml) significantly lower ($P<0.01$) in HRG than other groups (0.86±0.15 versus 2.3±0.21 control and 2.97±0.38 LRG). Lutalyse induced significant reduction in p after 2 days from injection in HRG only. Significant correlation between p and CL present in treated groups ($r=0.85$) during last 2 days. The overall ratios between p and e were larger in HRG than other groups (1:33 versus 1:11 control and 1: 9.5 LRG). Low levels of p in relation to e before superovulation regime in buffalo might be an indicator for the successful response of the ovaries.

Key Words: superovulation, buffalo, estrogen

W135 Semen quantity and quality of dairy bulls raised in tropical Central Thailand. T. Kongnoi[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand*, [2]*University of Florida, Gainesville*.

Widespread use of Holstein (H) and high percent H sires has been used to increase milk production in Thailand. As part of this mating strategy, semen production within Thailand has been promoted by the government. Thus, the objective here was to determine factors that affect semen quantity and quality traits in dairy bulls raised under tropical conditions in Central Thailand. The dataset contained 5,127 records from 57 bulls for semen volume (VOL), semen appearance (APP), semen concentration (CON), abnormal sperm (ABN), active motile sperm (MOT), and active motile sperm after freezing for 24 hr (M24) collected from October 2001 to April 2007. Bulls were grouped by H fraction into BG1 (0.96 to 1.0 H), BG2 (0.91 to 0.95 H), BG3 (0.86 to 0.90 H), BG4 (0.81 to 0.85) and BG5 (0.75 to 0.80 H). All bulls received the same nutrition and management. Semen was collected and evaluated using standard procedures from the Dairy Farming Promotion Organization of Thailand. The statistical model contained year-month of semen collection, ejaculation number (1 to 2), age of bull (339 to 2,988 d), ambient temperature at collection time (11 to 38°C), and breed group as fixed effects, and residual as a random effect. All factors in the model were important for all traits ($P < 0.01$), except for ambient temperature, which affected only CON, ABN and MOT ($P < 0.01$). Older bulls had higher VOL, APP, CON, and MOT, and lower ABN and M24 than younger bulls ($P < 0.001$). Semen collected at higher ambient temperatures had higher CON, higher MOT, and lower ABN ($P < 0.01$). Least squares means (LSM) indicated that BG5 was as good as or better than any other breed group for all traits ($P < 0.05$; VOL = 6.18 ± 0.11 ml; APP = 2.83 ± 0.05 score; ABN = 11.50 ± 0.15%; CON = 1,173.83 ± 13.26 × 10^6 cells/ml; MOT = 45.43 ± 0.56%), except for M24 (51.75 ± 0.17%) where it was second to BG1 (52.41 ± 0.15%). Breed groups 1 to 3 tended to have similar LSM, and BG4 yielded the worst results of all breed groups ($P < 0.05$).

Key Words: dairy cattle, tropical, semen

W136 Effect of proportion of females on number of piglets born alive and pre-weaning growth traits in Pietrain swine in Thailand. T. Punsanit[1], S. Koonawootrittriron[1], T. Suwanasopee[1], and M. A. Elzo*[2], [1]*Kasetsart University, Bangkok, Thailand*, [2]*University of Florida, Gainesville*.

The proportion of female piglets in a litter is important for producing replacement gilts. Different sex ratios in a litter may influence the level of competition among piglets and affect their growth performance. The objective was to assess the effect of proportion of female piglets born alive (FPB) on litter size and pre-weaning growth traits of piglets in a litter. Traits were total number of piglets born alive (NBA), average birth weight per litter (BW), average weaning weight per litter (WW) and average daily gain per litter (ADG). There were 3,521 litters from 1,252 negative halothane Pietrain sows that farrowed from 2004 to 2007 in a commercial population in Thailand. Sows were raised in an open-house system and received the same management and health care. The FPB was defined as the proportion of female to all piglets in a litter, and classified as LG1 ($0 \leq FPB \leq 20\%$), LG2 ($20 < FPB \leq 40\%$), LG3 ($40 < FPB \leq 60\%$), LG4 ($60 < FPB \leq 80\%$) and LG5 ($80 < FPB \leq 100\%$). Seasons were summer (March to June), rainy (July to October), and winter (November to February). Parity was classified as 1, 2, 3, 4, 5, 6, 7, and ≥ 8. The model had year-season, parity, and FPB as fixed effects, and boar and residual as random effects. First parity sows had the lowest least squares means (LSM) for all traits and increased in later parities ($P < 0.05$). The LSM for NBA of sows in LG3 (8.41 ±

0.07 piglets) was the highest of all litter groups (P < 0.05), and sows in LG2 (8.04 ± 0.08 piglets) and LG4 (7.95 ± 0.09 piglets) had higher NBA LSM than sows in LG1 (6.61 ± 0.13 piglets) and LG5 (6.42 ± 0.17 piglets). However, LSM for BW were lower for sows in LG2 (1.73 ± 0.01 kg), LG3 (1.72 ± 0.01 kg) and LG4 (1.73 ± 0.01 kg) than those for sows in LG1 (1.77 ± 0.01 kg) and LG5 (1.75 ± 0.02 kg). Similar trends were found for WW and ADG. Sows in LG1 had the highest LSM for WW (7.35 ± 0.08 kg) and ADG (234.51 ± 3.05 g/d), and then declined towards LG4 and LG5.

Key Words: pig, females born alive, growth

W137 The effects of four kinds of NSP enzymes based β-glucanase and xylanase on the performance and meat yield of broilers fed wheat/barley-based diet. H. Shirzadi, H. Moravej*, and M. Shivazd, *Tehran University*, *Karaj, Tehran, Iran*.

The aim of this research was to compare the effects of four enzyme preparations containing β-glucanase and xylanase activities [1] on performance and meat yield of broiler chicks fed wheat/barley-based diet with and without enzyme. 195 day-old male broiler chicks (Ross 308) were randomly allocated to 5 treatment groups, with 3 replicates and 13 birds per replicate in floor pen. All data was analyzed through the General Linear of Model procedure SAS for a randomized complete block design. The five dietary treatments consisted of the wheat and barley (30, 30%) supplemented with and without enzyme (A, B, C, and D added over the top to diets). Measured traits were body weight (BW), feed intake (FI), feed conversion ratio (FCR) and meat yield. All parameters were measured at 42d. BW was increased by addition all enzymes (P<0.05). However, FI was not significantly affected by enzyme supplementation. FCR were lower in diets containing enzymes compare to the barley-based diet without enzyme (P<0.05). Carcass weight, carcass yield, relative weight of the breast, legs, liver, and gizzard as percentage of live weight were not affected by enzyme supplementation, except enzyme A that reduced the relative weight of the breast (P<0.05). However, relative weight of the abdominal fat was increased by all enzymes addition (P<0.05). Our results led to the conclusion that there were similar improvements on performance of birds fed diets with enzyme supplementation, and performance of them were improved more than birds fed barley-based diet without enzyme supplementation, and choice preference of supplementation should be based on its economic value. [1] Enzyme A provided per kilogram of diet (Endo-1, 4- β-glucanase activity: min 800 units; Endo-1, (4) - β-glucanase activity: min 1800 units; Endo-1, 4- β- xylanase activity: min 2600 units), Enzyme B (Endo-1,3 (4)- β-glucanase: 100 AGL; Endo-1,4- β- xylanase: 1100 visco Units), Enzyme C (Endo-1, 4- β-glucanase: 1500 BGU; Endo-1,4- β- xylanase: 3600 FXU), Enzyme D (1420 units; xylanases: 660 units).

Key Words: β-glucanase, xylanase, broilers

W138 Consumers' preference for egg shell and yolk colour in Nigeria: A case study of Isolo and Alimosho local government area of Lagos State Nigeria. A. A. Mako*[1], O. K. Awobajo[1], O. I. Abiola-Olagunju[1], I. O. Ewebiyi[1], R. O. Ettu[1], R. A. Hamzat[2], and A. O. Akinsoyinu[3], [1]*Tai Solarin University of Education*, *Ijebu-Ode, Ogun State, Nigeria*, [2]*Quadbis Farms*, *Ibadan, Oyo State, Nigeria*, [3]*University of Ibadan*, *Ibadan, Oyo Sate, Nigeria.*

The objective of the study was to evaluate the preference for egg shell and yolk colour in the study area. Two hundred and fifty (250) respondents that consume eggs were randomly selected in the study area. The result shows revealed that the respondentsâ€™ age ranged between 15 to 55 years. 190 (76%) were males while 60 (24%) were females. Not all respondents had formal education, with 20 (8%) illiterates, 38 (15.2%) primary education, 50 (20%) HND, 100 (40%) B.SC, while 32 (12.8%) M.SC qualifications. Majority 180 (72%) of the respondents rear birds, while 70 (28%) do not rear birds. Among the respondents that rear birds 120 (55.56%) rear layers, 60 (33.33%) rear broilers and 20 (11.11%) rear cockerels. All respondents agreed that brown egg shell are more preferable to other colour of egg shell and majority 200 (80%) of the respondents agreed that white shell egg cracks faster than brown shell egg. The result shows that majority 215 (86%) agreed that yellow yolk eggs has better aroma than white yolk eggs. In conclusion, most of the respondents prefer brown egg shell due to its attractiveness and hardness, while yellow yolk is preferred due to its aroma. It us recommended that feed ingredients that produce brown eggs shell and yellow yolk should be used in layers mash to increase market for eggs and enhance large profit.

Key Words: egg shell and yolk, consumer preference, Nigeria

W139 Elaboration of ruminant supplements with byproducts and residues of bio-ethanol produced on farm settings. H. O. Patino*[1], B. P. Ospina[2], E. C. Mallmann[3], and A. Roa[4], [1]*Dep. Zootecnia,UFRGS*, *Porto Alegre, RS, Brazil*, [2]*Latin American and Caribbean Consortium to support Cassava Research and Development, CLAYUCA*, *Cali, Valle del Cauca, Colombia*, [3]*Usinas Sociais Inteligentes, USI*, *Porto Alegre, RS, Brazil*, [4]*Soil Net LLC*, *Madison, WI*.

To establish, validate and evaluate the technical and economic efficiency of a decentralized approach for production of hydrated and anhydrous ethanol (95% and 96% concentration, respectively) a low-cost, small-scale processing plant was built, with a processing capacity of approximately 1,000 liters/day. The plant is easy-to-manage and operate with different feedstock crops (cassava, sweet potato, beet, sugar cane and sweet sorghum) thus avoiding the dependency on just one crop. By transforming crops into a liquid biomass and bio-ethanol, which could be use in power generation (electric or mechanical) or can be sold as biofuel (anhydrous ethanol), farmers can increase their income. The approach proposed also includes a sustainable, added-value management of co-products (leaf, stover, etc) and residues generated (bagasse, vinasse) in the process, using them for the elaboration of products can be used as animal feed and/or fertilizer. Per tonelda de substrate are produced 30 liter of ethanol, 270 liter of vinasse and 700 kg of bagasse. Current approaches to biofuel production are a source of contamination for soils and waters because of the great volumes of effluents generated (8-10 liters/liter bio-ethanol produced) and the very high costs of currently available technologies for managing effluents. In this approaches, the organic content of the effluents is flocculated and agglomerated through the use of a biopolymer-based technology. This organic load is used to prepare multinutritional blocks (10-30%CP; 65-70% TDN) and supplements (17-40% CP; 60-65% TDN) for ruminants. The use of supplements in ruminants has allowed weights gains in calves and steers between 350 and 550 g/day. The remaining waters are cleaner and non-pollutant. Producing biofuels in farms has a great potential to generate added-value, stimulating social inclusion programs and socioeconomic development of family agriculture.

Key Words: biofuels, byproducts, animal feed

W140 Factors affecting milk production in Brazil. R. P. Lana*[1,2], G. Guimarães[1,2], A. V. Guimarães[1], and M. A. Santos[1], [1]*Universidade Federal de Viçosa - UFV, Viçosa, MG, Brazil*, [2]*Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq, Brasília, DF, Brazil*.

Brazil is the 6th milk producer in the world, based on crossbred Holstein-Zebu cows maintained in tropical pastures. This study has as objective to evaluate some factors that affect milk production in farm level and by state of federation. In the first case, data was collected from 50 farmers that sell milk for a dairy plant in the south region of Rio de Janeiro state, including daily milk production per producer, per cow by producer, and per area by producer, total area of farm and for the herd, total of milking cows, total cows in the herd, and breed. In the second case, data was collected from the Brazilian agencies (EMBRAPA and IBGE) in the year of 2004-2006, in which the emphasis was in milk production per state instead of per farmer. In the farmer level (1st case), the daily milk production ranged from 60 to 4000 kg of milk. The increase in milk production was linearly affected by increase in the number of milking cows (kg of milk/producer/day = 12 kg/cow * number of cows - 19.6; r = 0.94) and by increase in the area of pasture for the herd (kg of milk/producer/day = 4.92 kg/ha * number of hectares + 89; r = 0.67) and, surprisingly, the mean productivity per cow and per area did not correlate with milk production per producer (r = 0.11 and 0.06, respectively). In the country level (2nd case), the result repeated, in which there was high correlation of milk/state/year with total of milking cows compared with milk/km^2/year and milk/cow/year (r = 0.95, 0.55 and 0.51, respectively). Concluding, due to the large territorial extension of Brazil, the milk production is still more dependent on pasture extension than in productivity indexes.

Key Words: dairy cattle, milk production, pasture

W141 Bulk tank milk quality in Brazil - 2007/2008. L. M. Fonseca*[1,2], R. Rodrigues[1,2], M. M. O. P. Cerqueira[1,2], M. O. Leite[1,2], M. R. Souza[1,2], and C. F. A. M. Penna[1,2], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis, UFMG*, *Belo Horizonte, MG, Brazil*.

Brazil is facing a transition phase for new standards of milk quality. The objective of the present work was to evaluate the quality of the bulk tank raw milk produced in Brazil. The dairies were located mainly in Minas Gerais State, the largest milk producer in Brazil (approximately 30% of the national production). From January 2007 to July 2008, 1,176,000 samples were collected from 125 dairy industries and analyzed in the Laboratory of Milk Quality Analysis from the School of Veterinary Medicine, Federal University of Minas Gerais, Brazil. The raw milk samples for individual bacteria count (IBC) were preserved with azidiol (sodium azide, chloramphenicol), while the samples for composition and somatic cell count (SCC) were preserved with bronopol. After collection, the samples were properly stored, and sent to the laboratory. The bacteria analyses were done by flow cytometry (BactoCount IBC, Bentley®). The SCC were obtained by flow cytometry and the composition by infrared measurement (Combisystem 2300, Bentley®). Average values for milk composition were, in g/100g (average;SD): fat (3.67;0.52); protein (3.25;0.24); lactose (4.46;0.18); total solids (12.30;0.71), and nonfat solids (8.63;0.35). Geometric mean for microbial population was 347,000 CFU/mL, while for SCC was 380,000 cells/mL. The standard deviation was large for microbial and cellular counting, because of the high variability of these parameters. There was a negative correlation between SCC and lactose and between SCC and total solids ($p \leq 0.05$), and a positive correlation for CCS and fat content ($p \leq 0.05$). The Fat/Protein ratio was altered mainly at the end of the dry season in Brazil, because of nutritional deficiencies in some herds. Although the data show need for improvement, there has been an increasing awareness by the Brazilian dairy producers, with improvement in dairy practices, besides the payment of milk based on quality by some industries. It is believed that the majority of the milk producers will comply with the legal timeline required for 2011, when Brazilian requirements for milk quality will be similar to European standards. *Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq.*

Key Words: Brazil, milk quality, milk standards

W142 Multivariate analysis applied to milk quality evaluation in Brazil. A. M. G. Oliveira[1,4], L. M. Fonseca*[1,2], I. B. M. Sampaio[1], and Célia L. L. F. Ferreira[3], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis, UFMG*, *Belo Horizonte, MG, Brazil*, [3]*Federal University of Viçosa*, *Viçosa, MG, Brazil*, [4]*LANAGRO, Ministério da Agricultura, Pecuária e Abastecimento*, *Pedro Leopoldo, MG, Brazil*.

Milk quality data from 723 dairy farms, located in five regions of Minas Gerais State, Brazil, were used to access, in a multivariate space, the association between milk quality variables. Levels of fat, protein, lactose, total solids and nonfat solids were evaluated with somatic cell count (SCC), and total bacterial count (TBC). Three main components, obtained from the correlation matrix, showed variance lower than 0.7. The model was selected by excluding only two variables, solids and nonfat solids, which showed high correlation with protein and fat. After these adjustments, associations between lactose and somatic cell count, and between lactose and TBC were inversely related, with lactose levels decrease correlated with high somatic cell counts and high TBC. Associations for protein and fat levels, and for somatic cell counts and TBC were directly related, with higher intensity for protein and fat. *Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq; CAPES.*

Key Words: multivariate analysis, milk quality, Brazil

W143 Azidiol in tablet form as a preservative for milk quality analysis. J. F. Castro[1], L. M. Fonseca*[1,2], R. Rodrigues[1,2], and C. S. P. Fonseca[1], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis, UFMG*, *Belo Horizonte, MG, Brazil*.

The use of azidiol as tablet in the solid form results in several advantages, including safety for operator and milk collectors, viability to be sterilized inside collecting bottle, reduced manipulation during milk collection, and low cost. The objective of the present work was to compare azidiol, liquid and tablet, as a bacteriostatic of raw milk for the analysis of microbial counting by flow cytometry. The tablets of Azidiol were sterilized in the collecting bottle with gamma radiation or ethylene oxide. A total of 76 samples of raw milk were collected from bulk tank milk from a dairy industry in Belo Horizonte, Minas Gerais, Brazil during a period of two months. The efficiency of the tablet azidiol was compared to the traditional azidiol (liquid). The results of individual bacteria count were automatically converted to Colony Forming Units using a curve of linear regression (Bactocount IBC 150®, Bentley Inc.). Seven experimental groups were used: Control

(no azidiol added), Azidiol liquid (130µL/40mL), Azidiol tablet not sterilized, azidiol tablet sterilized by gamma radiation in the levels of 10, 15 and 20 kGy, and azidiol tablet sterilized by ethylene oxide. The results and variance analysis were compared using Duncan's Test. It is concluded that the treatments did not show any statistical difference ($p \geq 0,05$) in the several ranges of bacteria counting tested, concluding that azidiol liquid can safely be replaced by the tablet. The sterilization using gamma radiation is more feasible with lower levels, such as 10kGy, to reduce exposition of the tablets to high doses of radiation, which could result in the fusion of the crystal components, and less solubility. The tablet sterilization for ethylene oxide is also viable. *Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq; CAPES.*

Key Words: azidiol, milk quality, bacteria counting

Nonruminant Nutrition: Feed Additives II

W144 Effect of dietary medicinal plants or an organic acid on ileal nutrient digestibility of Ross broiler chickens. H. Ziaei*[1], M. Bashtani[2], M. A. Karimi Torshizi[3], H. Farhangfar[2], H. Naeemipour[2], and A. Zeinali[2], [1]*Agricultural Research Center*, *Birjand, Iran*, [2]*Birjand University*, *Birjand, Iran*, [3]*Tarbiat Modares University*, *Tehran, Iran*.

An experiment was conducted using 240 one-day old male Ross broiler chickens to evaluate the effect of dietary medicinal plants or an organic acid on ileal nutrient digestibility of Ross broiler chickens. Chicks were allocated to a randomized complete block design with 4 replicate pens (15 birds per pen). The experimental treatments were: T1= control, T2= control + 15 ppm of Virginiamycin, T3= control + 450 mg medicinal plants (digestrom) per kg diet and T4= control diet + 400 mg organic acid (Formycine) per kg diet. At age 21 and 42 d, ileal digestibility of nutrients was measured by Titanium oxide marker. Data was statistically analyzed using the GLM models of SAS. Duncan's multiple range test was used for pair-wise comparisons of treatment means. The results showed that supplemental diets significantly ($P<0.05$) improved bioavailability of energy and ileal digestibility of protein. At 21 days of age, broiler fed with treatments 3 and 4 had lower bioavailability of energy and ileal digestibility of protein as compared to treatment 2, but their differences were not significant at 42 d of age. The experimental diets had no effect on ileal digestibility of fat. In conclusion, using medicinal plants or an organic acid in broiler diets could improve nutrient digestibility indicating that these compounds may be an alternative to antibiotics.

Key Words: Ross broiler, medicinal plants, organic acid

W145 Effect of a dietary herbal medicine and an organic acid on bone characteristics of Ross broiler chickens. H. Ziaie*[1], M. Bashtani[2], M. A. Karimi Torshizi[3], A. Zeinali[2], H. Naeemipoure[2], and H. Farhangfar[2], [1]*South Khorasan Agricultural and Natural Resourses Researches Center*, *Birjand, Khorasan , Iran*, [2]*Birjand University*, *Birjand, Khorasan , Iran*, [3]*Tarbiat Modares University*, *Tehran, Iran*.

An experiment was conducted on 240 one-day old male Ross broiler chickens to evaluate the effect of dietary herbal medicine and or an organic acid on bone characteristic of Ross broiler chickens. Chicks were fed in a completely randomized block design with 4 replicate pens (15 birds per pen) for 42 days. Experimental treatments were: (T1= control, T2= control + 15 ppm of Virginiamycin, T3= control + 450 mg herbal medicine Digestrom /kg diet and T4= control diet + 400 mg organic acid Formycine /kg diet). At the end of the experiment, two birds from each replicate were randomly selected and sacrificed to determine the bone characteristics (modulus of elasticity, yield stress and percentage of ash, calcium and phosphorous). The results of our experiment showed that all parameters increased in supplemental diets ($P<0.05$). The differences between the antibiotic diet and treatments 3 and 4 were not significant ($P>0.05$). Therefore, supplementation of broiler diets with antibiotics and their alternatives such as a herbal medicine or an organic acid resulted in increased resistance of broiler bones.

Key Words: organic acid, herbal medicine, bone characteristic

W146 The effect of ractopamine and ileal digestible lysine levels on growth performance and carcass characteristics of finishing pigs. D. Fontes*[2], E. C. Almeida[1], E. T. Fialho[1], M. A Zangeronimo[1], N. O. Amaral[1], L. M. Pereira, Jr.[1], and P. B. Rodrigues[1], [1]*University Federal of Lavras*, *Lavras, MG, Brazil*, [2]*University Federal Minas Gerais*, *Belo-Horizonte, Brazil*.

A total of 50 hybrid barrows and 50 gilts (TOPIGS; initial and final weight of 90.2±0.90 and 117.8 ±1.2 kg) were used to evaluate the effects of ractopamine (Paylean®, PAY) and ileal digestible lysine (IDL) levels on late finishing pig performance and carcass characteristics. Pigs were blocked by weight and sex and randomly allotted to one of ten dietary treatments in a 28d experiment. There were two pigs (one barrow and one gilt) per pen and five pens per treatment. Pigs were fed corn and soybean meal based diets formulated to meet the NRC (1998) requirements, with the exception of ileal digestible lysine, methionine and threonine which were adjusted to satisfy the ideal relationship to lysine. Treatments were arranged as a 2 × 5 factorial with main effects of PAY (0 or 5 ppm) and ileal digestible lysine (0.68, 0.78, 0.88, 0.98, and 1.08%). There were no PAY × ileal digestible lysine interactions ($P>0.36$) observed. For the overall study, ADG and final weight were increased ($P<0.05$) for pigs fed Paylean®. For the carcass measurements, the results showed that barrows fed PAY had better carcass yield ($P<0.05$) than gilts. Pigs fed PAY had increased ($P<0.05$) hot carcass weight (HCW), yield and longissimus muscle area at the 10th rib than those fed diets not supplemented with PAY. Average backfat thickness decreased ($P<0.05$) for pigs fed PAY. Increasing ileal digestible lysine level did not affect ($P>0.05$) the growth performance or carcass characteristics. In conclusion, pigs fed 5 ppm PAY had improved growth performance and carcass characteristics. The diet containing 0.68% ileal digestible lysine (30 g/day) was enough to meet the requirement for finishing pigs weighing 90 to 117 kg.

Key Words: B-adrenergic, metabolism Assay, performance

W147 Influence of ractopamine on carcass characteristics and economic viability of finishing pigs fed ad libitum or restricted feeding system. E. T. Fialho*, V. S. Cantarelli, E. C. Almeida, M. G. Zangeronimo, N. O. Amaral, and L. V. C. Girão, *University Federal of Lavras*, *Lavras, MG, Brazil*.

A total of 30 barrows (TOPIGS; initial weight - 107.2 ± 4.2kg) were used to evaluate the influence of ractopamine (Paylean®) and feeding system (restricted vs ad libitum) on late finishing pig carcass characteristics

and economic viability. Pigs were blocked by weight and randomly allotted to one of five dietary treatments in a 28d experiment. There was one barrow per pen and six pens per treatment. Pigs were fed corn and soybean meal based diets with 1.04% total lysine. Treatments were arranged as a 2 x 2 factorial (main effects of Paylean® [0 or 5.0 ppm] and feeding system [ad libitum vs restricted by 15%]) plus a control diet with 0.80% total lysine and no Paylean® in an ad libitum system. There were no Paylean® and feeding system interactions (P>0.38) observed. The economic viability was determined based on diets and pig production costs, as well as considering carcass quality. Throughout the study, pigs which were fed Paylean® had increased (P<0.05) hot carcass weight, carcass yield, longissimus muscle area at the 10th rib, and standardized fat:free lean. Average backfat thickness decreased (P< 0.05) for pigs fed Paylean®. Tenth-rib backfat was also reduced (P<0.05) in pigs fed diets with Paylean® in a restricted feeding system. In conclusion, pigs fed 5 ppm Paylean® associated with the restricted feeding system had improved carcass characteristics and prove to be more economically viable for the production of finishing pigs from 107 to 120Kg.

Key Words: β-adrenergic, metabolism assay, carcass

W148 Effects of probiotics in lactating sow diets on litter growth performance. M. L. F. Silva, J. A. F. Lima, E. T. Fialho*, N. O. Amaral, V. S. Cantarelli, P. F. A. Souza, and C. H. T. Barbosa, *University Federal of Lavras*, *Lavras, MG, Brazil*.

The experiment was designed to evaluate the effects of antibiotics and probiotics during late gestation and lactation periods on litter growth performance during lactation through 14 and 28 days post-weaning. A total of 42 sows and 120 piglets were used . Early-weaned pigs (n = 120; 6.2 ± 0.72 kg of BW) were randomly distributed into 24 pens. Each pen was assigned one of three dietary treatments. The experimental diets were: two sow diets (with or without probiotics) fed 14 days before parturition until 21 days of lactation, and three piglets diets (1. with antibiotics, 2, with probiotics, or 3. both). The diets were formulated to meet the requirements of gestating and lactating sows and weanling piglets (NRC,1998) based on corn and soybean meal. Sows were fed the diets starting on day 100 of gestation through 21 days of lactation. There were no differences in ADG, and gain:feed ratio (G:F) among treatments (P > 0.05) in both the 14 and 28 day periods. At 28 d post weaning, feed intake (FI) was higher (P<0.05) for piglets fed diet 2 from sows fed diets with no probiotics. At 28 d postweaning, FI was higher (P<0.05) for piglets fed diets 2 and 3 from sows fed probiotics. F:G was higher for piglets fed diet 3 from sows fed probiotics. In conclusion, the combination of both antibiotics and probiotics used to supplement sow diets (during gestation and lactation) and young piglets diets during 14 and 28 days post-weaning resulted in positive effects on piglet growth performance.

Key Words: additive, sows, piglets

W149 Effects of ginger root powder on growth performance and antioxidant status of broiler chickens. G. F. Zhang[1], Z. B. Yang*[1], Y. Wang[2], W. R. Yang[1], X. Y. Zhao[3], and S. Z. Jiang[1], [1]*Shandong Agricultural University*, *Tai-an, Shandong, China*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre*, *Lethbridge, AB, Canada*, [3]*Tsinghua University*, *Beijing, China*.

A study using 144 of day-old AA broilers was conducted to assess the effects of dried ginger root (*Zingiber officinale*) that was processed to particle sizes of 8.4, 37, 74, 149 or 300 μm on growth performance, antioxidant status and serum metabolites of broiler chicks. The birds were housed in 24 wire cages in an environmentally controlled room with continuous overhead lighting, and were fed starter rations from d1 to 21 and finish rations from d22 to 42. Dietary treatments were non-ginger supplementation (Control) and ginger root processed to 5 particle sizes supplemented at the level of 0.5% (DM basis). Broilers were fed for *ad libitum* intake and had free access to water. Body weight and feed intake of chicks of each cage were measured weekly for determination of average daily gain (ADG), average daily feed intake (ADFI), and feed conversion rate (FCR). Blood samples were taken on d21 and 42 to determine the antioxidant status and serum metabolites. All broilers had similar ADG, DMI or FCR in each period or over the entire experimental period. However, supplementation of ginger powder increased (P<0.001) activities of total superoxide dismutase (TSOD) and glutathione peroxidase (GSHPx), but reduced (P<0.01) concentrations of malondialdehyde (MDA) and cholesterol in the serum of broilers at 21 and 42-day of ages. Concentration of total protein (TP) in the serum of ginger supplemented broilers tended (P=0.09) to be higher at 21-d and was higher (P<0.01) at 42-d of age compared to that of control broilers at the same ages. Reducing particle size of ginger powder linearly reduced (P<0.05) cholesterol (d21), linearly increased (P<0.05) GSHPx (d21), TSOD (d42) and TP (d21 & d42), but had no effect on MDA in the serum of ginger supplemented chickens. Supplementation of ginger at 0.5% level did not affect growth performance, but improved antioxidant status of broilers and the efficacy was enhanced as the particle sizes reducing from 300 to 8.4 μm.

Key Words: ginger root, broilers, antioxidant status

W150 Effects of long term dietary supplementation of betaine, CLA or both to mice on growth and viscera weight. L. González-Valero, J. M. Rodríguez-López, M. Lachica, and I. Fernández-Fígares*, *Spanish Research Council, CSIC*, *Granada, Spain*.

Betaine (BET) and CLA have the potential to alter growth and body composition in different animal models. Previous results in pigs have shown that BET and CLA have a synergistic effect on growth and carcass composition leading to leaner carcasses (Fernandez-Figares *et al*., 2008), although increased liver weight was found in BET+CLA fed pigs. The aim of the present study was to gain further insight on the possible adverse effects of BET or CLA using mice as a model in a sub-chronic study. Male ICR (CD-1) mice, weighing 14-18 g, were group housed (5 mice per cage, 4 cages per treatment) and *ad libitum* fed Teklad global 14% protein rodent diet containing either no added BET or CLA (control), 0.5% BET, 1% CLA, or 0.5% BET + 1% CLA for 90 days. Mice were slaughtered and viscera was removed and weighed. Feed intake was significantly higher in BET+CLA fed mice (P<0.001) compared to the other treatments. No differences in BW gain and gain:feed were found among treatments (P>0.05). Carcass weight of CLA fed mice was higher (P<0.05) than mice fed the control diet with no further benefit when BET was added to the same diet. Gastrointestinal tract weight of mice fed BET+CLA diet was lighter (P<0.05) than control mice. Furthermore, gastrointestinal tract weight relative to body weight was lighter (P<0.05) in mice fed BET and/or CLA supplemented diets relative to control mice. Spleen weight and spleen weight relative to body weight were higher (44 and 42%, respectively; P<0.05) in BET+CLA fed mice than in control mice. No changes (P>0.05) in liver, kidneys, cecum and total viscera weight or relative to body weight were observed. Splenomegaly observed when mice were fed BET+CLA diets deserves

further investigation. Fernandez-Figares, Conde-Aguilera, Nieto, Lachica, Aguilera. (2008). J. Anim. Sci. 86: 102-111.

Key Words: betaine and CLA, mice, growth viscera

W151 The effect of dietary laminarin and fucoidan in the diet of the weanling piglet on performance, selected faecal microbial populations and volatile fatty acid concentrations. P. McDonnell and J. V. O'Doherty*, *Lyons Research Farm, University College Dublin, Newcastle, Co Dublin, Ireland*.

A 2x2 factorial experiment (n = 12 replicates/treatment, 4 pigs/replicate) was performed to investigate the effects of laminarin and fucoidan, independently or in combination on post weaning piglet performance and selected microbial populations. At weaning the piglets (24 days of age, 6.4 kgs live weight) were assigned to one of four dietary treatments: (T1) basal diet, (T2) basal diet with 300 ppm laminarin, (T3) basal diet with 236 ppm fucoidan, (T4) basal diet with 300 ppm laminarin and 235 ppm fucoidan. Pigs offered diets supplemented with laminarin had an increased daily gain (P< 0.01) and gain to feed ratio (P<0.05) compared to unsupplemented laminarin diets during the experimental period (d 0-21). Pigs offered laminarin supplemented diets had an increased faecal dry matter and reduced diarrhoea (P< 0.05) during the critical d 7-14 period. Pigs offered diets containing laminarin had reduced faecal E.coli populations. There was a significant interaction (P<0.01) on faecal Lactobacilli populations between laminarin and fucoidan. Pigs offered the fucoidan diet had an increased Lactobacilli population compared to pigs offered the basal diet. However, there was no effect of fucoidan on faecal Lactobacilli populations when included with laminarin. Overall, the reduction in E.coli population and the increase in daily gain suggest that laminarin may provide a dietary means to improve gut health post weaning.

Key Words: piglets, laminarin, fucoidan

W152 *Acanthopanax senticosus* extract improved growth performance and antioxidative capacity in weaned piglets. X. Wu[1], F. Y. Yan[1], Y. L. Yin*[1], X. F. Kong[1], T. J. Li[1], R. L. Huang[1], and L. X. Chen[2], [1]*The Chinese Academy of Sciences, Changsha, China*, [2]*Guang An Biological Technique Company, China*.

This study was conducted to investigate the effect of *Acanthopanax senticosus* extract (ASE) on the growth performance and antioxidant capacity of weaned piglets. Dried AS herb was decocted in boiling distilled water (200 g/L) for 2 h. The decoction products were filtered and lypholized. The yield of extract was about 25% (w/w), with total polysaccharides, flavone and organic acids 2.94, 0.19 and 1.04%, respectively. Ninety-six Duroc×Landrace×Yorkshire piglets weaned at 21 days of age (BW=5.64±0.48 kg) were randomly assigned to one of 3 treatments with 4 replicates each and fed a basal diet (BD), BD+ASE (1 g/kg), and BD+antibiotics (10% bacitracin zinc 400 mg+15% carbadox 300 mg) for 14 days. Blood samples were collected on d 7 and 14. ADG in the ASE group (216.80 g/d) and antibiotics group (231.38 g/d) were 16.81 and 24.66% higher than the control group (P<0.01), and gain-feed ratio was improved by 18.18 and 21.39% (P<0.05), respectively. However, there was no difference in growth performance between the ASE and antibiotic group (P>0.05). Compared to the control group, both ASE and antibiotics increased Cu-Zn superoxide dismutase (SOD) activity on d 7 and 14 (P<0.05). SOD activity decreased from 147.96±15.88 to 125.68±14.26 in the antibiotics group (P<0.05), while it increased in the ASE group (from 132.37±7.64 to 135.44±12.68). Malondialdehyde in the ASE group significantly decreased by 20.00 and 30.46% (P<0.01) on d 7 and 14, respectively. Glutathione also had an increasing trend in the ASE group on d 7 and 14 (P=0.235 and 0.211, respectively). In addition, ASE influenced serum IgG on d 14 (P<0.05). These findings indicated that ASE could alleviate weaning stress by improving antioxidant enzymatic system effectively in piglets.

Key Words: *Acanthopanax senticosus* extract, antioxidative capacity, weaned piglets

W153 Weaned piglet responses to Escherichia coli K88+ oral challenge when receiving yeast fermentation products: growth performance and gastrointestinal measurements. E. Kiarie*[1], S. Bhandari[1], M. Scott[2], D. O. Krause[1], and C. M. Nyachoti[1], [1]*University of Manitoba, Winnipeg, MB, Canada*, [2]*Diamond V, Cedar Rapids, IA*.

Ninety weaned piglets (17 d of age; 5.2 ± 0.31 kg BW) were used to investigate the effects of in-feed and in-water yeast fermentation products (YFP) on the growth performance and gastrointestinal measurements upon E. coli K88$^+$ oral challenge. Pigs were randomly allotted to one of six diets with five replicate pens/diet and 3 pigs/pen. Treatments consisted of a negative control (NC, no in-feed or in-water additive), positive control (PC, 0.0055% carbadox), yeast culture (YC, in-feed, 0.2% Diamond V XPC Yeast Culture), and a yeast fermentation-based prototype (YFBP, in-water, 0.5, 1 or 2 g/head/d). Pigs were acclimatized to treatments for a 7-d period prior to oral challenge and BW and feed intake were measured. Pigs were orally inoculated with a 6 ml dose of 2 × 10^9 cfu/ml of *E. coli* K88$^+$. On d 3 and 7 post challenge, performance measures were recorded and GIT digesta and tissues were obtained. The BW, ADG, or G:F of NC pigs did not differ from those receiving additive treatments (PC, YC, YFBP) pre- or post-challenge. Pigs receiving additives (PC, YC, YFBP) had higher ADFI compared to NC pigs during the pre-challenge (P = 0.06) and post-challenge (P = 0.01) periods. PC pigs had a higher (P < 0.05) ADFI compared to YFP pigs (576 vs. 506 g/d) d 4 to 7 post challenge. Less digesta ammonia was observed in the ileum (2.4 vs. 3.1 mg/dL, P = 0.05) and colon (5.4 vs. 6.5 mg/dL, P = 0.04) of pigs receiving additives relative to NC pigs. Pigs fed YC had lower (P = 0.01) colonic ammonia compared to PC pigs (4.1 vs. 7.0 mg/dL) while pigs fed YFBP tended (P = 0.07) to show a linear reduction as the level increased (5.6, 5.9, and 4.4 mg/dL for 0.5 g, 1.0 g, and 2.0 g, respectively). In conclusion, pigs receiving YFP (YC, YFBP) had a healthier colonic environment during 7 d post-challenge period as suggested by reduce ammonia concentration.

Key Words: *E. coli* K88+, piglet performance, yeast culture

W154 Effect of multi-microbe probiotic product processed by high drying temperature and antibiotic on performance, nutrient digestibility, fecal and intestinal microflora and intestinal morphology of weanling pigs. J. Y. Choi[1], P. L. Shinde[1], Y. X. Yang[1], I. K. Kwon[1], C. S. Ra[1], W.-T. Cho[2], and B. J. Chae*[1], [1]*Kangwon National University, Chuncheon, Republic of Korea*, [2]*Genebiotech Co. Ltd., Seoul, Republic of Korea*.

In this study effect of multi-microbe probiotic product subjected to high temperature drying was investigated. The probiotic product was prepared by solid substrate fermentation and dried at 70 °C for 36 h. The product comprised of *L. acidophilus*, *B. subtilis*, *S. cerevisiae* and *A. oryzae* and the count of each microbe was less than 10^5 cfu/g. Weanling pigs

(n = 360, initial BW 5.84 ± 0.18 kg and 21 ± 2 d age) were randomly allotted to 5 treatments (4 replicates per treatment with 18 pigs in each) on the basis of BW. Effects of probiotic level (low, 0.3 or high, 0.6%), and antibiotic (chlortetracycline, 0 or 0.1%) on growth performance, nutrient digestibility, small intestinal morphology, fecal and intestinal microflora were investigated in a 2 × 2 factorial arrangement with a negative control diet (NC, diet without antibiotic and probiotics). Pigs fed high probiotic diet had greater ADG (342 vs 333 g, P < 0.05) and nutrient digestibility, lesser coliforms and *Clostridium* and more *Lactobacillus* in intestine and feces (d 14) than pigs fed low probiotic diet. Inclusion of antibiotic improved ADG (344 vs 331 g, P < 0.01), ADFI (521 vs 510 g, P < 0.05) and DM digestibility (d 14). Also, higher fecal *Lactobacillus* (d 28), greater villus height at jejunum and ileum were noticed in pigs fed high probiotic (P < 0.05) and antibiotic (P < 0.01) diets. Pigs fed NC diet showed the poorest (P < 0.05) performance and nutrient digestibility than pigs fed probiotic diets with or without added antibiotic. In addition, higher (P < 0.05) fecal and intestinal coliforms and *Clostridium* and less (P < 0.05) *Lactobacillus* were noted in pigs fed NC diets when compared with other treatment diets. These results suggest that the probiotic product was more effective at higher inclusion levels, while the addition of an antibiotic to high and low probiotic diets improved weanling pig performance; however, no interaction (probiotic level × antibiotic) effect was noticed on any of the measured parameters.

Key Words: piglet performance, intestinal morphology, multi-microbe probiotic product and antibiotic

W155 Effects of dietary supplementaion of talc on growth performance and meat quality in finishing pigs. H. D. Jang*[1], J. H. Lee[1], J. H. Jung[1], H. J. Jung[2], I. B. Chung[2], and I. H. Kim[1], [1]*Dankook University, Cheonan, Choongnam, Korea*, [2]*National Institute of Animal Science, RDA, Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of dietary supplementation of talc on growth performance and meat quality in finishing pigs. Fifty-six pigs (Landrace × Yorkshire × Duroc, 94.20 kg±1.28 kg average initial BW) were used in a 30 d growth assay. Dietary treatments included 1) CON (basal diet) and 2) Talc (basal diet + Talc 0.3%). The pigs were allotted into 4 pigs per pen with 7 replicate pens per treatment using a completely randomized design. There were no differences in final weight, ADG, ADFI and gain/feed during the whole period. All pigs were killed at the end of experiment, and the loin muscle were obtained for further meat quality evaluation. For meat color, redness was significantly increased in the talc treatment compared to CON treatment (P<0.05). However, yellowness was greater in CON treatment than talc treatment (P<0.05). There were no significant differences in other meat quality parameters (TBARS, water holding capacity, drip loss and pH) among treatments. For the sensory characteristics of meat, talc treatment significantly increased palatability compared to CON treatment (P<0.05). In conclusion, inclusion of talc in the diet can increase meat redness and palatability in finishing pigs.

Key Words: talc, finishing pigs, meat quality

W156 Effects of dietary wild-ginseng adventitious root meal on growth performance, blood characteristics and meat quality in broiler chicks. H. D. Jang*[1], E. J. Han[2], W. K. Jeon[3], K. Y. Paek[2], S. D. Lee[4], J. C. Park[4], and I. H. Kim[1], [1]*Dankook University, Cheonan, Choongnam, Korea*, [2]*Chungbuk University, Cheongju, Chungbuk, Korea*, [3]*Korea Institute of Oriental Medicine, Daejeon, Korea*, [4]*National Institute of Animal Science,RDA, Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of dietary wild-ginseng adventitious root meal on growth performance, blood characteristics, and meat quality characteristics in broiler chicks. Five hundred fifty two broilers (Arbor Acre broiler) with average initial body weight of 42.82±0.38g were used in a 35d growth trial. Dietary treatments included 1) CON (Basal diet), 2) WGR1 (Basal diet + 0.1% wild-ginseng adventitious root meal), 3) WGR2 (Basal diet + 0.2% wild-ginseng adventitious root meal) and 4) WGR3 (Basal diet + 0.3% wild-ginseng adventitious root meal). The broilers were allotted to four dietary treatments with 6 replicate pens and 26 broilers per pen in a completely randomized design. For the whole period, weight gain and feed intake were increased in the WGR1 treatment compared to the CON treatment (P<0.05). Total blood cholesterol concentration was higher in both WGR2 and WGR3 treatments compared to the CON treatment (P<0.05). CON treatment resulted in a higher IgG than WGR1, WGR2 and WGR3 treatments (P<0.05). On d35, chicks were slaughtered and carcass samples were obtained. All carcass parameters were not affected by treatment with the exception of meat pH. A higher pH value was found in CON and WGR3 treatments (P<0.05). TBARS was significantly increased in CON, WGR2 and WGR3 treatments compared to the WGR1 treatment (P<0.05). In conclusion, the 0.2% WGR treatment increased weight gain and feed intake in broilers.

Key Words: wild ginseng adventitious root meal, blood characteristics, broilers

W157 Effects of the Chinese herb extract supplementation on growth performance, blood characteristics and meat quality in growing-finishing pigs. T. X. Zhou*, J. S. Yoo, J. P. Wang, L. Yan, and I. H. Kim, *Dankook University, Cheonan, Choongnam, Korea*.

The effects of the Chinese herb extract (Taraxacum, Chinese Coptis, Forsythia and Glycyrrhiza) supplementation on growth performance, blood characteristics and meat quality in grow-finishing pigs were investigated in a 18-week feed trial. A total of 32 [(Landrace × Yorkshire) × Duroc] pigs with an initial body weight of 20 ± 2.6 kg were randomly assigned to four dietary treatments with 4 replications per treatment and 2 pigs per pen. A corn-soybean meal-based diet was formulated as a control diet and other treatment diets were supplemented with 0.5, 1 and 1.5 g/kg Chinese herb extract, respectively. After the feeding period, meat samples were collected from those pigs, which reached market body weight. During the feeding periods, grow performance was improved (Linear, P<0.05) by the supplementation of the herb extract. Immunoglobulin (IgG) was increased (Linear, P<0.05) by the herb extract addition at the end of the experiment. Pigs fed the herb extract at level of 1.5 g/kg had better (P<0.05) meat color, pH value and water holding capacity (WHC). In conclusion, the supplementation of the Chinese herb can improve the growth performance, IgG concentration and meat quality in growing-finishing pigs.

Key Words: herb extract, blood characteristics, growing-finishing pigs

W158 Effects of anion emission rock powder supplementation on growth performance, nutrient digestibility, blood characteristic and fecal gas emission of weaning pigs. J. H. Lee*, J. S. Yoo, H. D. Jang, and I. H. Kim, *Dankook University*, *Cheonan, Choongnam, Korea*.

A total of 96 weaning pigs (6.73 ± 0.52 kg, 21 d of age) were blocked by BW and then divided into one of four dietary treatments for five weeks to evaluate the effects of anion emission rock powder supplementation. Dietary treatments included 1) NC (corn-SBM diet), 2) PC (Phase I : NC + avilamycin 40ppm + apramycin 100ppm; Phase II : NC + BMD 25ppm + avilamycin 40ppm + tylosin 100ppm; Phase III : NC + BMD 25ppm + tylosin 100ppm), 3) AP1 (NC + 1/2 antibiotics + anion emission rock powder 0.3%) and 4) AP2 (NC + anion emission rock powder 0.6%). During the overall experimental period, ADG and G:F ratio were significantly lower in NC treatment than other treatments (P<0.05), and ADFI was higher in NC and AP2 treatments than PC treatment (P<0.05). DM digestibility was higher in the PC treatment than that of NC and AP2 treatments (P<0.05) at d 7, while at 21d, PC, AP1 and AP2 treatments were higher than the NC treatment (P<0.05). Nitrogen digestibility was increased by PC treatment at 7d, compared to NC and AP2 treatments (P<0.05). At 21d, NC treatment had the lowest nitrogen digestibility (P<0.05). There was no difference in blood IgG and lymphocyte concentration at 0, 7, 21 and 35d among the treatments. However, RBC concentration of PC treatment was higher than that of the NC treatment at 7d (P<0.05), and WBC of NC and PC treatments was higher than AP2 treatment at 35d (P<0.05). For the fecal total mercaptan concentration at 10d, NC treatment was higher than other treatments (P<0.05), and at 15d, AP1 and AP2 treatments was lower than NC and PC treatments (P<0.05). In conclusion, supplementation of anion emission rock powder in weanling pig dietd can reduce fecal odor gas emission without negative effects on growth performance.

Key Words: anion emission rock powder, odor gas emission, weaning pig

W159 Effects of delta-aminolevulinic acid and antibiotics on the growth performance, nutrient digestibility, hematological status, and immune responses of weanling pigs. J. P. Wang*[1], J. S. Yoo[1], J. H. Lee[1], R. Noble[2], S. H. Oh[2], and I. H. Kim[1], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*North Carolina A&T State University*, *Greensboro*.

Delta-aminolevulinic acid (ALA) is a non-protein amino acid that plays a rate limiting role in the process of heme biosynthesis. In this study, the effects of supplementation of the diet with ALA and antibiotics on growth performance, nutrient digestibility, hematological status, and immune responses in early weanling pigs were evaluated. A total of 144 weaned castrated male pigs (6.37 ± 0.52 kg, 21 d of age) were blocked by BW and litter and then divided into one of four dietary treatments. The treatments were arranged as a 2 × 2 factorial design with the inclusion of 2 levels of ALA (0 or 10 mg/kg) and antibiotics (0 or 40 mg/kg of apramycin and 100 mg/kg oxytetracycline). Supplementation of the diet with antibiotics resulted in a significant increase (P<0.05) in ADG during phase 2. In addition, an interactive effect between ALA and antibiotics was found to increase ADFI (P<0.05), whereas ADG and G:F were not affected by treatments in the overall phase. ALA significantly decreased the digestibility of DM and nitrogen (N) on d 21 (P<0.05) and DM digestibility on d 35 (P < 0.05). The serum hemoglobin (Hb) and hematocrit (HCT) values increased significantly in response to ALA supplementation (P<0.05). Despite this, the CD-8, B cell, and MHC-I were increased by the interactions between ALA and antibiotics (P<0.01). ALA was found to elevate the numbers of CD-2, CD-8, B-cell, MHC-I and MHC-II (P<0.05, P<0.05, P<0.01, P<0.01 and P<0.01, respectively). Furthermore, an interaction effect between ALA and antibiotics resulted in an increase of CD-8, B-cell, and MHC-I and -II cells (P < 0.01). Overall, the results of this study indicate that dietary supplementation with ALA had no effect on the growth performance of weanling pigs, but that it did reduce the DM and N digestibility. Furthermore, supplementation with ALA resulted in improved iron status and had beneficial effects on the immune responses.

Key Words: delta-aminolevulinic acid, immune status, weaning pig

W160 Utilization of delta-aminolevulinic acid for livestock: Blood characteristics and immune organ weights in broilers. L. Yan*, Y. J. Chen, H. J. Kim, J. P. Wang, and I. H. Kim, *Dankook University*, *Cheonan, Choongnam, Korea*.

A study was conducted to evaluate the effects of delta-aminolevulinic acid (ALA) on blood characteristics and immune organ weights in broilers. A total of 480, one-day-old broiler chicks were randomly assigned to one of four dietary treatments with six replicates of 20 chicks each. Treatments were a basal diet supplemented with 0, 5, 10 and 15 mg/kg ALA. The two-phase experimental diets were formulated to meet the NRC requirements for chicks and fed for 5 weeks. Growth performance was not affected by supplementation of ALA during any of the experimental periods. Blood cell counts (WBC, RBC and lymphocyte), serum total protein, albumin, iron concentrations, and total iron binding capacity (TIBC) were also not influenced by dietary treatments. Hemoglobin concentration (8.85, 9.17, 9.49 and 9.67 g/dL) tended to increase with increased ALA supplementation levels (linear effect; P<0.10). Dietary ALA addition did not influence liver weight. However, spleen (0.097, 0.122, 0.138 and 0.122 g/100g BW) and bursa of fabricius (0.190, 0.227, 0.270 and 0.294 g/100g BW) weights were increased with the increased ALA supplementation levels (linear effect; P<0.05). The current data indicate that supplementation of ALA in commercial broiler diets could partly improve hemoglobin concentrations and immune organ weights, without influencing growth performance and other blood characteristics of broilers.

Key Words: delta-aminolevulinic acid, blood characteristics, immunity

W161 Effects of supplementation with a combination of delta-aminolevulinic acid and chito-oligosaccharide supplementation on the growth performance, nutrient digestibility, blood parameters and appearance of diarrhea in weanling pigs. T. X. Zhou*[1], Y. J. Chen[1], J. H. Lee[1], C. Y. Lee[2], B. C. Park[3], and I. H. Kim[1], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*Regional Animal Industry Center, Jinju National University*, *Jinju, Gyeongnam, Korea*, [3]*CJ Feed Inc.*, *Inchon, Gyeonggi, Korea*.

This study was conducted to investigate the effects of supplementation with a combination of delta-aminolevulinic acid and chito-oligosaccharide (ACO) supplementation on the growth performance, nutrient digestibility, blood parameters and appearance of diarrhea in weanling pigs. A total of 144 pigs [(Landrace×Yorkshire)×Duroc] with an average initial body weight (BW) of 7.10±0.48 were randomly allotted into four dietary treatments, with 6 pens per treatment and five pigs per pen. A corn-soybean meal-based diet was formulated as a control diet and then supplemented with antibiotics (phase 1, 40 ppm avilamycin and 100 ppm OTC; phase 2, 40 ppm chlortetracycline), or with 1 or 2 g/kg

ACO, respectively. The experiment lasted 42 days and was divided into 3 phases, including phase 1 (d 0 to d 7), phase 2 (d 8 to d 21) and phase 3 (d 22 to d 42). Growth performance in the ACO group was improved in phase 2, 3 and for the overall period (P<0.05). ACO improved feed intake (P<0.05) and total tract apparent digestibilities (TTAD) for DM and N (P<0.05). However, lymphocyte concentration and appearance of diarrhea decreased (P<0.05) in response to supplementation of ACO. Taken together, the results of the current study indicated that dietary supplementation with ACO enhanced growth performance by increasing the apparent digestibility of nutrients and decreasing the incidence of diarrhea.

Key Words: delta-aminolevulinic acid, chito-oligosaccharide, blood parameters

W162 Effects of AROMEX-ME supplementation in high and low nutrient density diets on growth performance, nutrient digestibility, blood characteristic, carcass trait and fecal malodor emission in growing-finishing pigs. H. J. Kim*[1], J. P. Wang[1], L. Yan[1], H. J. Jung[2], I. B. Chung[2], and I. H. Kim[1], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*National Institute of Animal Science, RDA*, *Cheonan, Choongnam, Korea*.

This study was conducted to investigate the effects of AROMEX-ME supplementation in high and low nutrient density diets on growth performance, nutrient digestibility, blood characteristic and carcass trait in growing-finishing pigs. A total of 96 pigs (23.89 kg, average initial body weight) were used during 112 days. Dietary treatments included: 1) HNDD (high nutrient density diet), 2) HNAR (high nutrient density diet + 0.01% AROMEX-ME), 3) LNDD (low nutrient density diet) and 4) LNAR (low nutrient density diet + 0.01% AROMEX-ME). Each treatment had 6 replicates of 4 pigs per pen in a randomized complete block design. During 12 to 16 weeks, average daily gain and G/F ratio were higher (P<0.05) in HNAR group than others. Average daily feed intake was higher (P<0.05) in LNAR group than others. Dry matter, nitrogen and energy digestibility at 6 week were highest (P<0.05) in LNAR group than others. At 16 week, energy digestibility was lower (P<0.05) in HNAR group than others. White blood cell concentration was higher (P<0.05) in LNDD group than HNDD group at 6 week and was higher (P<0.05) in HNDD group than LNAR group at 18 weeks. Lymphocyte concentration of blood was higher (P<0.05) in HNDD group than HNAR group at 6 weeks. In sensory evaluation, marbling score was improved (P<0.05) in low nutrient density diet group than high nutrient density diet group. In meat color, yellowness (b*) was higher (P<0.05) in HNDD group than AROMEX group and drip loss at day 1 was higher (P<0.05) in HNDD group than LNDD group. Loin muscle area was highest (P<0.05) in HNAR group. Fecal malodor emission was reduced in LNDD and LNAR treatments (P < 0.05). In conclusion, AROMEX supplementation in high nutrient density diet maximizes growth performance in pigs and AROMEX supplementation in low nutrient density diet improves growth performance, nutrient digestibility, marbling score and reduces fecal malodor emission.

Key Words: AROMEX, malodor, pigs

W163 Effects of complex probiotics supplementation on growth performance, fecal gas emission and meat quality in finishing pigs. J. H. Jung*[1], H. J. Kim[1], S. M. Hong[1], C. Y. Lee[2], and B. C. Park[3], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*Jinju National University*, *Jinju, Gyeongnam, Korea*, [3]*CJ Feed Inc.*, *Inchon, Gyeonggi, Korea*.

This study was conducted to evaluate the effects of complex probiotics (Bacillus subtilis 1×10^7 cfu/g and Lactobacillus acidophilus 1×10^6 cfu/g) on growth performance, fecal gas emission and meat quality in finishing pigs. A total of sixty pigs [(Landrace×Yorkshire)×Duroc] (initial body weight 69.3kg) were used for a 56 day feeding trial. Dietary treatments included 1) CON (corn-soybean meal diet), 2) CM01 (CON + probiotics 0.1%) and 3) CM02 (CON + probiotics 0.2%). There were three dietary treatments with five replicate pens per treatment and four pigs per pen. From 0 to 28 days, gain:feed was higher in CM01 treatment than CON treatment (P<0.05). There were no significant differences in ADG and ADFI among the treatments (P>0.05). L* value (lightness) in CM01 and CM02 treatment was lower than CON treatment (P<0.05). Compared with CM02 treatment, a* value (redness) was lower than in CM01 and CON treatments (P<0.05). The b* value (yellowness) was lower in CM01 and CM02 treatments than CON treatment (P<0.05). There were no significant differences in sensory evaluation, drip loss, cooking loss, pH, TBARS and loin muscle area among the treatments (P>0.05). During 0 day of this experiment, ammonia gas emission in CM01 and CM02 treatments was lower than CON treatment (P<0.05). By 10 days of the experiment, fecal total mercaptan had decreased in CM01 and CM02 treatments compared to CON treatment (P<0.05). At 5 days of this experiment, there were no significant differences in fecal hydrogen sulfide, ammonia and total mercaptan (P>0.05). In conclusion, dietary complex probiotics increased meat color and decreased fecal noxious gas emission.

Key Words: probiotics, noxious gas emission, finishing pigs

W164 Effects of essential oils supplementation and difference stocking density on performance of growing-finishing pigs. J. H. Lee*[1], J. S. Yoo[2], H. D. Jang[1], J. C. Park[2], S. D. Lee[2], and I. H. Kim[1], [1]*Dankook University*, *Cheonan, Choongnam, Korea*, [2]*National Institute of Animal Science, RDA*, *Cheonan, Choongnam, Korea*.

A 2×3 factorial (CON vs. Essential oils, three regimens of stocking densities; 1.08, 0.81 and 0.65 m2/pig) arrangement was used with 96 pigs (45.64 kg). The diets were supplemented with 0.02% essential oils. The essential oils used in the experiment included thyme (23.0%), rosemary (12.0%), oregano (8.0%) extract, and carrier (57.0%). The experiment lasted for 84 days. Overall, ADG (0.793, 0.762, 0.655 kg) of pigs was decreased linearly with increased stocking density (P=0.042). ADG (0.703 kg) and ADFI (2.204 kg) were significantly improved by essential oil supplementation (P<0.05), as compared to the CON treatment (0.761, 2.173 kg, respectively). Both DM (71.38 vs. 74.37%) and N (70.55 vs. 73.27%) digestibilities were significantly increased by essential oil supplementation (P=0.01, P=0.03, respectively). Moreover, a significant linear decrease of increasing stocking density was found on DM (74.70, 72.51, 71.40%) and N (73.52, 72.45, 69.77%) digestibilities (P=0.01, 0.02, respectively). Blood sample were collected at the initial and final day, and the differences were calculated. WBC counts (Difference -7.55, -4.94, -0.23 10^3 /mm3) were linearly decreased by high stocking density (P=0.02). Cortisol concentration (Difference 0.53, 0.68, 1.35 μg/dl) were linearly increased by high stocking density (P=0.05). IgG concentration (Difference 177, 198, 307 mg/dl) responded quadratically to increasing stocking density (P=0.02). Difference of Lymphocyte percentage (Difference 3.09 vs. -4.08%), IgG (Difference 202.00 vs. 252.93 mg/dl) and norepinephrine (Difference -199.49 vs. 141.85 (pg/mL) were increased (P<0.05) in the essential oil treatment compared to non supplemented treatment. However, cortisol (Difference 1.19 vs.

0.52 μg/dl) was decreased (P<0.05) in essential oils treatment compared to non supplemented treatment. In conclusion, the data suggests that high stocking density exerted negative effects on growth performance, digestibility and blood characteristics which could be corrected by supplementation of essential oils.

Key Words: stocking density, essential oils, growing-finishing pigs

W165 Effects of yucca and *Bacillus subtilis* on nutrient digestibility, fecal noxious gas content and meat quality in finishing pigs. J. H. Lee*[1], H. J. Kim[1], S. M. Hong[1], S. H. Oh[2], R. Noble[2], and I. H. Kim[1], [1]*Dankook University, Cheonan, Choongnam, Korea,*, [2]*North Carolina A&T State University, Greensboro*.

This study was conducted to evaluate the effects of yucca and Bacillus subtilis on growth performance, apparent total tract digestibility (ATTD) of DM and N, fecal noxious gas content and meat quality in finishing pigs. Twenty pigs (81.54±1.33kg average initial body weight) were used in a 49d growth assay. Dietary treatments were: 1) CON (basal diet), 2) P1 (CON + protein coated *Bacillus subtilis* 0.3%), 3) P2 (CON + protein coated probiotics complex 0.3%), 4) Y1 (CON + (yucca extract + *Bacillus subtilis* 0.3%)) and 5) Y2 (CON + (yucca extract + protein coated probiotics complex 0.3%)). The pigs were allotted into one pig per pen using a completely randomized design. Through the whole experimental period, CON treatment showed the lowest dry matter digestibility among treatments (P<0.05). However, nitrogen digestibility was not significantly affected by treatments. For lean percent, P2 treatment was higher than CON treatment (P<0.05). L*-value of M. longissmus dorsi in CON treatment showed the lowest among treatments (P<0.05). The b*-value of M. longissmus dorsi muscle were decreased in P2, Y1 and Y2 treatments compared to CON treatment (P<0.05). Marbling score of sensory evaluation in P1 and P2 treatments were significantly higher than Y1, Y2 and CON treatments (P<0.05). Cooking loss of CON treatment was the lowest among treatments (P<0.05). Water holding capacity was higher in P2 and Y2 treatments than Y1 and CON treatments (P<0.05). Ammonia, acetic acid and total mercaptans concentration were not affected by dietary treatments (P<0.05). In conclusion, this experiment suggested that yucca and *Bacillus subtilis* supplementation could improve dry matter digestibility and meat quality in finishing pigs.

Key Words: probiotics complex, meat quality, ammonia

W166 Effect of Siberian Ginseng (*Acanthopanax senticosus*) and *Eucommia ulmoides* on growth performance and immune functions in broiler chickens. S. Y. Kang, Y. H. Ko, S. H. Sohn, Y. S. Moon, C. Y Lee, and I. Jang*, *Jinju National University, Jinju, Gyeongnam, Korea*.

The objective of this study was to investigate the effect of dietary inclusion of Siberian Ginseng (*Acanthopanax senticosus*) and *Eucommia ulmoides* in a broiler chicken diet on growth performance and immune functions. A total of two hundred 3-d old male broiler chickens (Ross 308) were assigned to five dietary treatments: (1) control diet (corn, wheat and soybean meal based), (2) control diet supplemented with Siberian Ginseng at 0.5% (low level; LSG), (3) control diet supplemented with Siberian Ginseng at 1.0% (high level; HSG), (4) control diet supplemented with *Eucommia ulmoides* at 0.5% (low level; LEU) and (5) control diet supplemented with *Eucommia ulmoides* at 1.0% (high level; HEU). The birds fed the diet supplemented with 1.0% Siberian Ginseng showed a significantly lower (P<0.05) feed conversion ratio than those fed control diet, whereas weight gain and feed intake were unaffected by dietary treatments. The organ weight of the bursa of Fabricius was significantly (P<0.05) higher in birds fed the diet supplemented with 1.0% *Eucommia ulmoides* (HEU) without change in weights of other organs such as the liver, spleen and thymus. In cytokine expressions, there was no significant dietary effect on the expression of interleukin-4 (IL-4), interleukin-6 (IL-6), interferon-γ (IFN-γ) and inducible nitric oxide synthases (iNOS) in the lymphocytes and bursa of Fabricius. In the thymus, however, the expression of IFN-γ and iNOS was higher (P<0.05) in birds fed the diets supplemented with Siberian Ginseng (LSG and HSG groups) compared with those fed the control diet, whereas gene expression was not changed by dietary inclusion of *Eucommia ulmoides*. Thymic IL-4 known as an anti-inflammatory gene was significantly (P<0.05) higher in birds fed the diet supplemented with *Eucommia ulmoides* (LEU and HEU groups). In conclusion, dietary inclusion of *Eucommia ulmoides* had a beneficial effect on the expression of anti-inflammatory cytokine without affecting growth performance of birds.

Key Words: broiler chickens, immune functions, cytokines

W167 Effects of dietary supplementation of Biacton™ on growth performance of pigs from weaning through finishing phases. K. Bregendahl and M. Z. Fan*, *University of Guelph, Guelph, Ontario, Canada*.

Biacton™, a probiotic product of highly concentrated live microbial culture of the beneficent bacterium Lactobacilli farciminis. L. farciminis, is manufactured in France as an alternative probiotic growth promoting product. The objective of this study was to examine and compare the efficacy of dietary supplementation (0.1-0.2%) of Biacton™ and a sub-therapeutical level of antibiotics, i.e., Lincomix-44 for weanling pigs and Tylan-10 for growing-finishing pigs, in improving growth performance, and carcass quality. A total of 180 purebred Yorkshire pigs, with an average BW of 5.6±0.1 kg were weaned at 16±2 d of age in five periods, each consisting of 36 pigs, were used. Dietary supplementation (0.2%) of Biacton™ was only effective (P<0.05) for improving growth rate and feed intake in weaning phase (5-10 kg) equivalent to the efficacy of a sub-therapeutical level of the antibiotics. Biacton™ supplementation had no effects (P>0.05) on growth performance, including growth rate, feed intake and feed utilization in post-weaned (10-20 kg), growing (20-50 kg) and finishing (50-110 kg) phases. Whereas the growth-promoting effects of a sub-therapeutical level of antibiotics were consistently observed (P<0.05) over these phases. Dietary supplementation of both Biacton™ and a sub-therapeutical level of antibiotics had no effects (P>0.05) on major carcass quality parameters such as hot carcass weight, dressing percentage, backfat thickness and carcass lean in pigs. Dietary supplementation (0.2%) of Biacton™ may improve growth performance for weanling pigs in the absence of antibiotics.

Key Words: antibiotics, probiotics, pigs

W168 Effects of dehydrated chicory root powder on growth, nutrient utilization and manure odor in weanling pigs. M. Z. Fan*, T. Archbold, Y. Shen, C. Yang, and T. C. Rideout, *University of Guelph, Guelph, Ontario, Canada*.

The objectives of this study were to determine the effect of dietary supplementation of dehydrated chicory root powder on growth performance, efficiency of dietary nutrient utilization and fecal excretion of

volatile sulfides in the weanling pig fed a corn and SBM-based diet. Six corn and SBM-based diets were formulated to contain six levels of dehydrated chicory root powder (diet 1, 0; diet 2, 0.20; diet 3, 0.40; diet 4, 0.60; diet 5, 0.80; and diet 6, 1.00%). A total of 36 weanling Yorkshire barrows (10-14 kg BW) were randomly assigned to the six experimental diets and fed according to a completely randomized block design. Orthogonal polynomial contrasts were conducted to examine treatment effects and Dunnett's tests were used to compare a treatment group with the control diet 1. Dietary supplementation of the chicory root powder had a quintic effect (P<0.05) on the average daily gain with the best responses in diets 2, 3 and 5. Supplementation of the chicory powder had a negative linear effect (P<0.05) on the apparent fecal dry matter digestibility with the lowest value observed in diet 5. Supplementation of the chicory powder had a negative linear effect (P<0.05) on the apparent fecal CP digestibility and efficiency of the apparent CP retention with the lowest values observed in diets 4 and 6. Supplementation of the chicory powder had a quartic effect (P<0.05) on the apparent fecal Ca digestibility and efficiency of apparent Ca retention and a quintic effect (P<0.05) on urinary Ca excretion with the highest retention efficiency in diet 2. Furthermore, supplementation of chicory root powder had a quartic effect (P<0.05) on efficiency of apparent P retention with the highest retention efficiency in diets 2 and 5. Chicory root powder supplementation did not change (P>0.05) the fecal content of total volatile sulfides. Taking together, dietary supplementation of dried chicory root powder within 0.20% improved efficiency of dietary Ca and P utilization without adversely affecting growth performance and efficiency of whole body N utilization in weanling pigs fed corn and SBM-based diets.

Key Words: chicory inulin, nutrient utilization, weanling pigs

W169 Different enzymatic activities of sixty-two isolated lactic acid bacteria of chicken digestive tract. H. R. Taheri*[1], H. Moravej[1], F. Tabandeh[2], M. Zaghari[1], and M. Shivazad[1], [1]*University of Tehran, Karaj, Tehran, Iran*, [2]*National Institute of Genetic Engineering and Biotechnology, Tehran, Iran*.

Lactic acid bacteria are used as a source of probiotics and one major reason for using probiotics is their enzymatic activities, but there is no data about different enzymatic activities of chicken origin bacterial strains. A total of 62 lactic acid bacteria were isolated from the digestive tract of broilers varying in age. These isolated bacteria were selected based on different aggregation times. The aggregation was a test that shows the adherence ability of lactic acid bacteria to mucosa. The aggregation time of bacterial strains was 15, 30, 45, 60, 75, 90, 115 and 120 min. They were then studied for amylase, protease, lipase and phytase activities. The medium culture used for detecting the amylase, lipase and phytase activities contained starch, olive oil and calcium phytate, respectively. The bacteria were spot-inoculated and then incubated for 48 h at 37°C. For examination of protease activity, the supernatant of an overnight culture of lactic acid bacteria were poured on discs that were placed on plates containing skim milk. Clear zone was measured with a caliper. The results were analyzed using the GLM procedure of SAS. No lipase activity was detected, but all of them showed almost similar proteolytic activities. However, they had different amylase and phytase activities (Table 1). The results of this study showed that there are only noticeable differences among the bacterial strains for amylase and phytase activities. Also it indicates that lipase and protease activities should not be used as a major screening test for probiotics.

Table1. Different enzymatic activities of 62 selected lactic acid bacteria

Halo zone (mm)	+++[1]	+	nd
Amylase	4	40	18
Phytase	5	52	5
Halo zone (mm)	14-16	12-14	10-12
Protease	21	35	6

+++, Halo zone was more than 3 mm that was noticeable compared to other strains; +, halo zone was just detected as less than one mm; nd = Not Detected

Key Words: enzymatic activity, lactic acid bacteria, probiotic

W170 Effects of sanguinarine on growth performance, serum biochemical indices and HSP70 of weaned piglets. X. H. Zhou, X. Wu, K. Yao, D. Zhou, R. L. Huang, and Y. L. Yin*, *Chinese Academy of Sciences*, *Changsha, China*.

This study was conducted to investigate the effects of *Sanguinarine* (SA) on the growth performance, serum biochemical indices, HSP70 and TNF-α in weaned piglets. One hundred and twenty Landrace×Yorkshire piglets weaned at 28 d with initial average weight 8.30±0.29 kg were randomly allotted to 3 treatments with 4 replicates each. Piglets were fed the following diets for 14 days: 1) NC (control diet without antibiotics), 2) PC (NC+100 ppm aureomycin), and 3) SA (NC+SA≥1.5%, 30 ppm). Six piglets from each treatment were selected randomly for serum samples for biochemical indices. Serum heat shock protein 70 (HSP70) and TNF-α was analyzed by ELISA. The results showed that ADFI and ADG of SA Group were significantly improved (P<0.05) compared to the NC. However, no difference was observed in ADFI, ADG and F/G between the PC and SA group (P>0.05). Compared to the NC, dietary supplementation with SA increased GLU level in serum significantly (P<0.05), but had no significant effects on levels of ALP, TP, LDH, ALT, AST and BU (P>0.05). Serum HSP70 significantly decreased in the PC and SA groups (P<0.05), which indicated that both antibiotics and SA alleviated weaning stress. Serum TNF-α tended to be high in the SA and antibiotics groups (P=0.118). In conclusion, SA improved growth performance and alleviated weaning stress, and didn't affect any serum biochemical parameters in weanling piglets. This study demonstrates the potential use of SA as a feed additive instead of antibiotics in weaned piglets.

Key Words: *Sanguinarine*, growth performance, eeaned piglet

W171 Effects of low doses of encapsulated cinnamaldehyde on the performance and antioxidant status of weaned piglets. C. Moynat, C. Ionescu*, and D. Bravo, *Pancosma*, *Geneva, Switzerland*.

Animal studies have demonstrated that at high levels (> 500 ppm), cinnamaldehyde (CIN) exhibits antioxidant properties, but the effect of low levels of CIN on performance and antioxidant status of animals is poorly described. The intent of the present study was to investigate the effect of low dietary supply of encapsulated CIN on piglets performance and antioxidant status. Ninety six weaned piglets (BW = 7.69 ± 0.80 kg) at 26 days of age were moved to pens for a period of 14 days. The animals were allotted based on sex and initial BW to 16 pens of 6 animals and to one of the 4 dietary treatments (4 pens per treatment): no additive (NC), 9, 18 and 35 ppm of encapsulated CIN (CIN9, CIN18, CIN35 respectively). CIN was encapsulated in modified starch using fluidized

bed technology. Animals had *ad libitum* access to water and feed. FI and ADG were measured at days 7 and 14. At day 7, blood samples of 8 piglets in each group were collected and analyzed on blood glutathione peroxidase (GSH-Px). Data were analyzed using GLM procedure of SAS. FI was increased by CIN18 ($P = 0.09$) during week 2 (506.5 vs. 454.6 g/d) and for the whole period (354.8 and 330.8 g/d with $P = 0.18$) and decreased by CIN35 ($P < 0.01$) during week 1 (206.9 vs. 160.8 g/d) and for the whole period (306.3 vs. 330.8 g/d with $P = 0.18$). ADG was increased by CIN18 during week 1 (+7.0%, $P > 0.1$) and week 2 (435.6 vs. 367.8 g/d with $P = 0.02$). ADG was decreased ($P < 0.01$) by CIN35 during week 1 (144.1 vs. 200.9 g/d) and increased ($P = 0.04$) during week 2 (427.4 vs. 367.8 g/d). For the whole period, ADG was improved ($P = 0.03$) by CIN18 (326.9 vs. 280.1 g/d) but not by CIN35 (+1.1%, $P > 0.1$). GSH-Px was numerically increased by CIN18 (+7.4%, 15.15 UI/mL) and by CIN35 (+ 7.2%, 15.13 UI/mL). This study suggested that the dose of CIN was essential to the response of piglets. Eighteen ppm of CIN improved performance and antioxidant status whereas 35 ppm seemed to decrease feed palatability, while sustaining ADG and improving antioxidant status.

Key Words: piglet, essential oil, antioxidant status

W172 Efficacy of a combination of essential oils in weaned pigs. I. Aragonés*[1], K. Wendler[2], E. McCartney[3], J. Sánchez[1], and M. I. Gracia[1], [1]*Imasde Agroalimentaria, S.L., Spain*, [2]*Delacon Biotechnik GmbH, Austria*, [3]*EU Pen&Tec Consulting S.C.P., Spain*.

A total of 280 pigs were sorted according to litter origin and sex and then allocated to 28 pens in 2 weaner rooms. A randomized complete block design was applied using two experimental treatments: T1-Control and T2-Fresta® F Conc. at 250 g/T of feed (phytogenic feed additive containing a mixture of essential oils as main active substances); each treatment group equivalent in terms of pen weights, sex distribution, and litter origin. Pelleted feeds were available *ad libitum* with no added growth promoter or veterinary antibiotics. Prestarter feeds were fed from 28-42 days and starter feeds from 42-70 days of age. Criteria investigated included growth, body weight, feed intake, feed efficiency and body uniformity and were analyzed using the GLM procedure of SAS. Mortality was considered normal and was unaffected by treatment (2.86 *vs* 2.14%; P = 0.660). Pigs fed on the supplemented diet weighed 6.0% more than Controls at 70 days of age (22.9 *vs* 24.3 kg bodyweight; P = 0.015). During the prestarter period, no significant differences were observed for any of the parameters studied. During the starter period, pigs of the supplemented group had a significantly higher daily gain (431.4 *vs* 473.7 g/d; P = 0.032), and tended towards a better feed conversion rate (1.57 *vs* 1.46 g feed/g gain; P = 0.069) than Controls. For the overall period, pigs fed the phytogenic feed additive grew 9.4% more (343.1 *vs* 375.2 g/d; P = 0.015) and had 7.1% better feed conversion rate (1.54 *vs* 1.43 g feed/g gain; P = 0.044) than Controls. No significant differences were found for feed intake. Pig′s body weight uniformity at the end of the trial was unaffected by treatment (85.9 *vs* 87.9%; P = 0.122), but this is not surprising as the pigs selected for the trial were very homogeneous at study start. We conclude that, under our experimental conditions, the dietary addition of a combination of essential oils (Fresta® F Conc.) at 250 g/T feed significantly improved growth and feed conversion rate in weaned pigs.

Key Words: essential oils, performance, weaned pigs

W173 Effects of yeast fermentation products on fecal consistency and gut microbial population in weaned piglets challenged with *Escherichia coli* K88+. S. K. Bhandari*[1], E. Kiarie[1], M. Scott[2], D. O. Krause[1], and C. M. Nyachoti[1], [1]*University of Manitoba, Winnipeg, Manitoba, Canada*, [2]*Diamond V, Cedar Rapids, IA*.

One hundred and two weaned piglets (17 d of age; 5.2 ± 0.31 kg BW) were used to evaluate two yeast fermentation products (YFP) as potential alternatives to antibiotics for controlling post-weaning diarrhea. Twelve pigs were euthanized at 20 d of age to generate baseline data. The remaining 90 pigs were assigned to one of six diets in a randomized complete block design with 5 replicate pens/diet and 3 pigs/pen. Treatments were: negative control (NC, no in-feed or in-water additives), positive control (PC, in-feed, 0.0055% carbadox), yeast culture (YC, in-feed, 0.2% Diamond V XPC Yeast Culture), and a yeast fermentation-based prototype (YFBP, in-water, 0.5, 1 or 2 g/head/d). Diets were formulated to meet NRC (1998) recommendations. After a 7-d adaptation period, pigs were orally inoculated with a 6 mL dose of 2 x 10^9 cfu/mL of ciprofloxacin-resistant *E. coli K88* $^+$(K88). Pigs were euthanized on d 3 (1 pig/pen) and d 7 (2 pigs/pen) post-challenge. Fecal consistency scores were determined daily. Microbial enumeration on ileal mucosa, digesta, and feces were performed on an EMB media with or without 0.05 µg ciprofloxacin/mL. On d 2 post-challenge, fecal consistency score of pigs fed PC, YC, and YFBP tended (P = 0.08) to be lower compared to NC pigs (0.88 vs. 1.3) suggesting less severe diarrhea. Fecal score did not differ between the NC pigs and those receiving additives d 4 to 7 post-challenge. A lower (P = 0.03) number of K88 were found in the ileal mucosal scrapings of PC pigs (3.2) compared to YFP pigs (4.3) d 7 post-challenge. Pigs fed YFBP tended (P = 0.14) to have less K88 in the ileal mucosa compared to pigs fed YC (3.9 vs. 5.3). Results suggest that YC and YFBP may help to reduce severity of diarrhea in weaned pigs shortly after K88 challenge.

Key Words: *E. coli K88* $^+$, weaned piglets, yeast fermentation

W174 Effects of *Pediococcus acidilactici* and *Saccharomyces cerevisiae boulardii* on the ileal microbiota of piglets two weeks after weaning. J.-P. Brousseau*[1,2], F. Beaudoin[1], D. Roy[1], and M. Lessard[2], [1]*Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada*, [2]*University Laval, Quebec, Quebec, Canada*.

Weaning is a stressful period for piglets. The transition from milk to a solid diet causes major changes in the intestinal microbiota. In North America, to minimize effects of weaning, low doses of antibiotics (Atb) are added to the food. But this practice has increasingly become the focus of concern, with a rising number of resistant bacteria to Atb. A lot of research is now in progress to develop new and more natural approaches to replace the Atb use as a growth promoter. Among the alternatives, probiotics (Pbt) arouse great interest. We have evaluated the effects of two Pbt, *Pediococcus acidilactici* MA18/5M (Pa) and *Saccharomyces cerevisiae boulardii* CNCM I-1079 (Scb). Gestating sows (6 per treatment), 28 days before parturition, were divided into five groups that received: 1) Pa, 2) Scb, 3) Pa+Scb, 4) Control (no Pbt) (Ctrl) and 5) Ctrl+Atb. One day after their birth, piglets (12 per treatment) received the same treatment as their mother (Pbt at 1×10^9 CFU/day). After weaning, a dose of 2×10^9 CFU/day was added to the feed of the pigs. The Terminal Restriction Fragment Length Polymorphism (T-RFLP) technique was used to evaluate the composition of the ileal microflora, two weeks post-weaning. Traditional plating on selective medium was used to quantify: *E. coli*, Lactobacilli, total coliform and the two Pbt. A treatment effect was found when comparing the counts of *E. coli* for Pa+Scb and Ctrl+Atb (P=0.034). From the T-RFLP profiles obtained, diversity indices were calculated for each treatment and

significant results were obtained for the Evenness and Shannon indices, respectively, when comparing Ctrl to Ctrl+Atb (P=0.006; P=0.008) and Ctrl to Pa (P=0.017; P=0.018). A major terminal restriction fragment (177 bp), was significantly different when comparing treatment Ctrl to Ctrl+Atb (P=0.006) and Ctrl to Pa (P=0.006). In conclusion, the administrations of Pa diminished the microbial diversity of the ileum, two weeks after weaning, in a comparable manner to the addition of Atb; while co-administration of Pa and Scb attenuated the reducing effect of Pa on the microbial diversity.

Key Words: probiotics, piglets, ileal microbiota

W175 Effects of acidifiers on growth performance and intestine health in weanling piglets. P. Li[1,2], H. J. Zhang[1], Y. Miao[3], S. G. Wu*[1], H. Y. Yue[1], and G. H. Qi[1], [1]*Feed Research Institute of Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*Institute of Animal Husbandry and Veterinary Science, Tianjin Academy of Agricultural Sciences, China*, [3]*Beijing General Station of Animal Husbandry and Veterinary, China*.

This research was conducted to study the effects of phosphoric acid and lactic acid acidifiers on growth performance and gut health in weanling piglets. Two hundred weanling piglets were allotted into five groups randomly: control group without acidifier, four groups with phosphoric acid or lactic acid acidifier at 0.1% or 0.3%, respectively. Feed intake, average daily body weight gain, feed efficiency, and rate of diarrhea in each group were recorded. Three piglets from every group were randomly selected and sacrificed at 28 d of experiment to determine the pH of the digestive tract, digestive enzyme activities, intestine morphology and microflora, serum immune and biochemical indexes. Results showed that acidifiers significantly increased average feed intake, daily weight gain, remarkably improved feed efficiency and decreased the diarrhea rate compared to the control group (P<0.05). Lactic acid acidifier addition of 0.3% showed the best growth performance among treatments. Acidifiers significantly decreased the pH value in stomach and duodenum, increased the activities of pepsin, trypsin in duodenum, and increased the ileum villi height (P<0.05). E.coli and salmonella counts were decreased, lactobacillus and bifidobacteria counts were increased in the cecum (P<0.05). Acidifiers significantly increased the content of serum immunoglobulin (Ig) A and G (P<0.05). Serum IgM content and the ratio of CD4+/CD8+ were not affected by acidifiers. Addition of acidifiers at 0.3% concentration significantly decreased serum uric nitrogen content (P<0.05). In conclusion, acidifiers improved growth performance and ameliorated gut health in the weanling piglets. The appropriate addition level of acidifier was 0.3% in this study. The acidifier of the lactic acid type exhibited superior effects compared to that of the phosphoric acid type.

Key Words: acidifier, weanling piglet, gut health

W176 Plant active compounds or extracts can be effective as antioxidants in vitro. C. Ionescu*[1], J. Seppey[2], D. Bravo[1], M. Grogg[2], X. Simonnet[2], N. Marcon[3], and A.-F. Grogg[3], [1]*Pancosma, Geneva, Switzerland*, [2]*Médiplant, Conthey, Switzerland*, [3]*HESSO, Sion, Switzerland*.

A selection of active compounds were investigated as free radical scavengers, antioxidants and phospholipase A2 (sPLA2) inhibitors. The free radical scavenging activity was checked by mean of DPPH test and the antioxidant activity by the Fe^{3+}/Fe^{2+} antioxidant test (FRAP). Carvacrol (CAR), cinnamaldehyde (CIN), eugenol (EUG), anethol (ANE), capsicum oleoresin type 1 (CAP1), capsicum oleoresin type 2 (CAP2), coffee row extract (COF1), coffee refined extract (COF2), hazelnut row extract (HAZ1), hazelnut refined extract (HAZ2), grape extract (GRA), olive extract (OLI) and sclareol (SCL) were screened. In DPPH test, EUG and GRA were the best products, with identical activities, based on the low concentrations needed to reach EC50 (4.2 and 4.7 µg/mL, P > 0.1). COF1, COF2, HAZ1 were less effective (respectively, 10.9, 19.1, 20.6, 27.1 µg/mL, P > 0.05). OLI, SCL and CAR (respectively, 48, 57 and 72 µg/mL) and CAP1, CAP2, CIN and ANE had poor activities (> 100 µg/mL). CIN and ANE had poor activities in FRAP (> $1.1x10^{11}$ µg/mL). EUG, the most efficient product, was not dose-dependent (0.004 µg/mL). GRA and HAZ2 had similar activities (3.1 and 4.8 µg/mL, P > 0.1), which were better than the activities of COF1, COF2 and HAZ1 (respectively, 11.4, 11.8, 20 µg/mL, P > 0.05). EUG was only different from CAP1, CAR and SCL (respectively, 307, 486 and 1455 µg/mL, P < 0.05). sPLA2 screening lead to IC50 values of 59, 140 and 456 µg/mL, for SCL, CAR and HAZ1, respectively. The other compounds inhibited sPLA2 with higher concentrations. EUG could be used in the digestive tract to reduce oxidation process because it has effective radical scavenging and antioxidant activities. sPLA2 inhibitors such as SCL could be used in different types of disease therapy aiming to reduce the oxidation process.

Key Words: essential oils, antioxidant, in vitro

W177 Effect of dietary acids on growth performance of weanling pigs-a cooperative study. J. E. Pettigrew*, O. Adeola, M. J. Azain, S. D. Carter, G. L. Cromwell, G. M. Hill, D. C. Mahan, and P. S. Miller, *NCCC-42 Committee on Swine Nutrition*.

An experiment involving 854 crossbred pigs (20 replicate pens of 4 to 8 pigs per pen) was conducted at 8 stations (blocks) to determine the effects of acids in the diets of weanling pigs and their inclusion levels on growth performance using diets and weaning ages typical of those used in US commercial pork industry. Basal diets supplemented with various types and levels of acid and constant levels of ME and standardized ileal digestible lysine were fed to pigs in 3 phases of 1, 1, and 2 wk, respectively. Treatment diets included 0% acid as a control, 0.1% or 0.2% phosphoric acid, 1% or 2% organic acid, and 0.1% phosphoric acid plus 1% organic acid with or without antibiotic. The organic acid consisted of 50% citric acid and 50% fumaric acid by weight. All but the latter diet contained antibiotic. Addition of acids to diets did not affect pig performance during any phase or the overall period. In phase 2, pigs in the non-antibiotic group had decreased ADG and ADFI as compared to those in the other treatment groups ($P<0.01$). Overall, ADG of pigs fed the non-antibiotic diet was lower ($P<0.05$) than that of pigs fed the others. Pigs fed the combination of acids without antibiotic had similar G:F as those fed the control, phosphoric acid, and a combination of acids with antibiotic, but a lower G:F ($P<0.05$) than those fed the organic acid. In summary, acids added to nursery diets did not improve pig performance, but including antibiotic in the acid-supplemented diets increased ADG and ADFI.

Table 1. Effects of dietary acids on ADG, ADFI, and G:F of pigs from d 0 to 28 after weaning

	Phosphoric acid			Organic acid[a]		Combination[b]		
	0%	0.1%	0.2%	1%	2%	0.1% + 1%		SEM
Antibiotic	+	+	+	+	+	+	-	
ADG, g*	359[c]	350[c]	358[c]	352[c]	348[c]	349[c]	320[d]	8
ADFI, g*	539[c]	522[c]	527[c]	528[c]	508[cd]	513[cd]	481[d]	12
G:F, g/kg*	669[cde]	662[e]	683[cd]	687[c]	685[c]	683[cd]	663[de]	7

[a]Citric:fumaric = 1:1 by weight, [b]phosphoric acid (0.1%) + organic acid (1%). *Means within a row with different superscripts differ ($P<0.05$).

Key Words: inorganic and organic acids, performance, nursery pigs

W178 Effects of feeding *Lathyrus sativus* on broiler performance. M. Eslami* and B. Ahmadipour, *Ramin Agricultur and Natural Resources University, Ahwaz, Khouzestan, Iran*.

Lathyrus sativus is a legume grain with 28-30 percent crude protein, which can be a suitable substitute for soybean meal in broiler diets. However, the use of this feed in poultry nutrition involves some limitations due to anti-nutritive factors. It is necessary to evaluate the effects of different levels of *Lathyrus sativus* in comparison with soybean meal, on broiler performance, final weight, daily weight gain, feed consumption, feed conversion rate, carcass characteristics and abdominal fat. A total of 240 chicks (day-old) were allotted randomly to four dietary treatments each in four replicates of 15 birds per pen in a completely randomized design. The experiment lasted for 42 d and the birds were fed four different levels (0, 10, 20 and 30 percent) of *Lathyrus sativus* instead of soybean meal. The results revealed that using *Lathyrus sativus* even up to 30 percent in broiler diets does not indicate any significant difference in final weight, daily weight gain, feed conversion rate, and carcass characteristics (P>0.05). At 30 percent usage of *Lathyrus sativus*, feed consumption was significantly reduced compared with the control diet (P<0.05). Increasing *Lathyrus sativus* level significantly increased abdominal fat (P<0.05). In conclusion, the present study demonstrated that *Lathyrus sativus* up to 30 percent could be used instead of soybean meal in broiler diets.

Key Words: *Lathyrus sativus*, broilers performance, feed conversion

W179 Effects of dietary Biomate (Artemisia, Acanthopanax and garlic) on performance in lactating sows. S.-M. Hong*[1], M.-J. Kim[1], M.-B. Cho[1], B.-U. Yang[1], M.-J. Kim[1], I.-H. Kim[1], and S.-H. Oh[2], [1]*Dankook University, Cheonan, Chungnam, South Korea*, [2]*North Carolina A&T State University, Greensboro*.

The objective of this experiment is to investigate the effects of dietary Biomate (Artemisia, Acanthopanax and garlic) on the performance of lactating sows. Artemisia, Acanthopanax and garlic are known as natural growth promoters and stimulate the secretion of growth hormones. They also improve feed conversion, daily weight gain, and backfat in lactating sows. A total of 15 lactating sows were used in this experiment. There were three treatments, which were control (basal diet; CON), basal diet + Biomate 0.1% (BM1), and basal diet + Biomate 0.2% (BM2). Sows were fed ab libitum for three weeks after farrowing. The number of piglets was equalized in each group of treatments within 24 to 48 hours after birth. Each treatment had three replications, and it was assumed that there is no parity effect. Litter weights of piglets, changes in backfat thickness, ADFI and return to estrus in sows were measured and analyzed using Duncan multiple range test in SAS. Loss of backfat thickness (mm) from farrowing to weaning were 1.50, 0.84 and -0.33 in CON, BM1, and BM2, respectively. Average daily feed intakes (kg) and litter weight gain (kg) were 8.13, 6.33, 6.74, and 4.69, 5.48, 4.02 in CON, BM1, and BM2, respectively. There was no significant difference among treatments, but BM1 showed higher performance compared to other treatment groups. Further studies will be needed to compare blood profiles in treatments.

Key Words: artemisia, acanthopanax, lactating sow

W180 Effects of dietary probiotics of endospores and complex enzyme supplementation on growth performance in pigs. M.-J. Kim*[1], B.-U. Yang[1], M.-B. Cho[1], M.-J. Kim[1], S.-M. Hong[1], I.-H. Kim[1], T. Barrios[2], and S.-H. Oh[2], [1]*Dankook University, Cheonan, Chungnam, South Korea*, [2]*North Carolina A&T State University, Greensboro*.

The current study was conducted to investigate the effects of dietary probiotics of endospores and complex enzyme supplementation on growth performance, ADG, ADFI and gain/feed in growing pigs. A total of 96 pigs were used in this experiment. Pigs were grouped by weight with 16 pigs per pen and 6 pens per treatment. Dietary treatments included: 1) CON (basal diet), 2) basal diet + 0.1% dietary probiotics of endospores and complex enzyme supplementation (Spe 1) and 3) basal diet + 0.2% dietary probiotics of endospores and complex enzyme supplementation (Spe 2). Pigs were weighed three times at the beginning, 3 weeks, and 5 weeks. Pigs in each pen were assumed that they were fed equally. Average daily gain and feed efficiency were calculated using their feed intake and gain in total. Each treatment had weight gains and feed efficiency similar to those fed the control diet and there were no significant differences among treatments. Although significant differences were not found among treatments, feed efficiency (gain:feed) was significantly improved (P < 0.05) in the low weight group (0.42) compared to high weight group (0.39). Therefore, it may be suggested that dietary probiotics of endospores and complex enzyme supplementation would be more effective in lower weight pigs.

Key Words: endospore, growth, pig

W181 Comparison of Bio-Mos® and carbadox on growth performance during the early nursery phases of weanling pigs. J. L. Pierce*, R. F. Gilliam, and C. A. Moran, *Alltech, Inc., Nicholasville, KY*.

The three week period following weaning is one of the most challenging of a piglets life. Antibiotics have been used for many years during these production phases to help control disease and promote growth. However, alternatives to antibiotics continue to be examined for numerous reasons. Therefore an experiment was conducted in a Midwest commercial research barn to evaluate the effectiveness of Bio-Mos as a replacement for carbadox during the first three weeks following weaning. A total of 540 pigs were blocked by sex, initial weight, pen location, and nursery room and randomly allotted to one of three dietary treatments; negative control, 50 g/t carbadox, or 1 kg/t Bio-Mos. From days 1-7 pigs were fed a commercial nursery containing 25% dried whey, 5% lactose, 6.5% SDPP, 6.0% select menhaden fish meal. Phase 2 diets were fed from days 8-14 and contained 20% dried whey, 2.0% lactose, 2.5% SDPP, and 4.0% select menhaden fish meal. Phase 3 diets were fed from days 15-21 and were comprised of diets containing 57.4% corn, 34.2% SBM, and 3.9% tallow. No dried whey, lactose, fish meal, or SDPP were fed after day 14. There were 3 dietary treatments with pen as the experimental unit. There were eighteen replicate pens per treatment with 180 pigs per treatment. The 3 diets were commercial nursery diets with 1, No additive; 2: carbadox (50g/t) and 3, Bio-Mos 1 kg/t. Data were analyzed as a randomized block split-plot design with means separation performed by the pdiff option of LSMEANS in SAS. Overall, pigs fed 1kg/t of Bio-Mos had a 9% improvement in ADG compared with pigs fed the Control diet (410 vs. 373 g/d, P< .02). Pigs fed Bio-Mos had a tendency toward an improvement in ADG compared to pigs fed carbadox (410 vs. 393 g/d). Pigs fed 1 kg/t of BioMos grew 20% more efficiently (F:G) than the Control-fed pigs (1.39 vs. 1.21 P< .01) and 6% more efficient than pigs fed carbadox (1.39 vs 1.31 P< .01). Based on these results, Bio-Mos is a valuable alternative to carbadox and was more effective at improving feed efficiency in this study.

Key Words: pig, MOS, antibiotic

W182 The effect of ractopamine supplemented for 14 or 28 days on growth performance of finishing pigs. E. T. Fialho*, L. V. C. Girão, M. G. Zangeronimo, N. O. Amaral, V. S. Cantarelli, R. C. Wolp, and P. B. Rodrigues, *University Federal of Lavras*, *Lavras, MG, Brazil*.

A total of 30 hybrid barrows and 30 gilts (TOPIGS; initial and final weight of 93.8±1.8 kg and 130.6±1.6 Kg) were used to evaluate the effects of ractopamine (Paylean®) supplementation for 14 or 28 day periods on late finishing pig performance. Pigs were blocked by weight and sex and randomly allotted to one of six treatments. There were two pigs (one barrow and one gilt) per pen and five pens/treatment. Pigs were fed corn soybean meal based diets formulated to meet NRC (1998) requirements, with 0.68% ileal digestible lysine. Treatments were arranged as a 3 × 2 factorial with main effects of Paylean® (0, 5 and 10 ppm) and period length (14 and 28 days). There were no Paylean® period interactions (P>0.39) observed. For the overall study, ADG and final weight were higher (P<0.05) for pigs fed Paylean®. Barrows had better ADG and final weight than gilts. However, gilts had better F:G than barrows. The Paylean® inclusion (5 to 10 ppm) as well as the period length (14 to 28 days) did not improve growth performance. In conclusion, diets containing 5 ppm Paylean® and fed for 14 or 28 days improved the performance of finishing pigs from 93 to 130 kg of body weight

Key Words: B-agonist, additive, performance

W183 Effects of natural clay enterosorbent on vulva sizes and reproductive organ weights of postweaning female pigs fed zearalenone contaminated diets. Z. B. Yang*[1], S. Z. Jiang[1], W. R. Yang[1], H. Zao[1], C. C. Chen[2], and F. Chi[3], [1]*Shandong Agricultural University*, *Taian, Shandong, PRC*, [2]*Chaoyang University Technology*, *Taichung, Taiwan, ROC*, [3]*Amlan International*, *Chicago, IL*.

A total of thirty-five postweanling gilts (L x Y x D) with an average of 12.36 ± 1.46 kg body weight were used in the study. The gilts were raised individually in metabolic cages and fed a corn-soybean meal-whey based diet with an addition of 0 or 1 ppm of zearalenone (ZEA, Fermentek, Israel) for 24 d with four levels of natural clay added in the feeds. The treatments were 1) control diet; 2) control + 0.25% clay; 3) control + 1 ppm ZEA; 4) control + 1 ppm ZEA + 0.125% clay; 5) control + 1 ppm ZEA + 0.25% clay; 6) control + 1 ppm ZEA + 0.5% clay; 7) control + 1 ppm ZEA + 1.0% clay. Pigs were weighed at the beginning and the end of trial. Feed intakes were recorded daily. Vulva length and width were measured at 3 days intervals. Vulva area was calculated as (L × W)/2. Pigs were killed at the end of trial, and reproductive organs were obtained and weighed. Pigs fed a diet with 1 ppm ZEA consumed more feed and gained more than pigs fed control feed (P<0.05) but showed no difference on feed efficiency (P>0.05). Overall gilts fed diets containing 1 ppm ZEA with or without natural clay had increased vulva size (length and width) and reproductive organ weights as compared to gilts fed control diets with or without natural clay (P<0.001); on the other hand, gilts fed natural clay in ZEA contaminated diets significantly reduced the vulva size (P<0.1) and reproductive organ weights (P<0.05). Treatment effects of ZEA and clay enterosorbent are shown in Table 1. Reproductive organ weights in pigs fed ZEA contaminated feeds were decreased linearly as dietary natural clay increased (P<0.05). However, reduction of vulva sizes was not correlated to dietary clay concentrations. In conclusion, ZEA clinical symptoms can be shown in postweanling gilts continuously fed a diet containing 1 ppm ZEA for 24 d, and feeding natural clay enterosorbent can significantly improve the clinical symptoms in the reproductive tract.

Table 1. Treatments effects on vulva size and reproductive organ weights

Treatment	Vulva Length, cm	Vulva Width, cm	Vulva Area, cm^2	Ovary + Uterus Wt., g
Control	2.10[a]	1.61[a]	1.69[a]	14.25[a]
Control + 0.25% clay	1.90[a]	1.45[a]	1.40[a]	13.67[a]
Control + 1 ppm ZEA (Test)	2.90[b]	2.39[b]	3.46[c]	52.00[c]
Test + 0.125% clay	2.30[a]	1.92[a]	2.25[b]	45.00[bc]
Test + 0.25% clay	2.58[ab]	2.16[ab]	2.80[bc]	33.67[bc]
Test + 0.5% clay	2.49[a]	1.99[a]	2.52[bc]	25.00[b]
Test + 1.0% clay	2.52[a]	1.90[a]	2.39[b]	19.00[a]

[abc]significant difference between treatments (P<0.05)

Key Words: zearalenone, natural clay enterosorbent, postweanling female pig vulva size

W184 Effects of natural clay enterosorbent on nutrient digestibility of postweaning female pigs fed zearalenone contaminated diets. Z. B. Yang*[1], S. Z. Jiang[1], W. R. Yang[1], H. Zao[1], C. C. Chen[2], and F. Chi[3], [1]*Shandong Agricultural University*, *Taian, Shandong, PRC*, [2]*Chaoyang University Technology*, *Taichung, Taiwan, ROC*, [3]*Amlan International*, *Chicago, IL*.

A total of twenty-one postweaning gilts (L × Y × D) with an average BW of 12.66±1.18 kg were used in the study. The gilts were raised individually in metabolic cages and fed a corn-soybean meal-whey based diet with an addition of 0 or 1 ppm of zearalenone (ZEA, Fermentek, Israel) for 21 d with various levels of natural clay added in the feeds. The treatments were 1) control diet; 2) control + 0.25% clay; 3) control + 1 ppm ZEA; 4) control + 1 ppm ZEA + 0.125% clay; 5) control + 1 ppm ZEA + 0.25% clay; 6) control + 1 ppm ZEA + 0.5% clay; 7) control + 1 ppm ZEA + 1.0% clay. Pigs were weighed at the beginning and the end of trial. Feed intakes were recorded daily. Total fecal and urine samples were collected daily and samples pooled weekly. Gross energy and nitrogen content were determined in the feed, fecal and urine samples; and digestible energy (DE), metabolizable energy (ME), digestible crude protein (DCP), and biological value (BV) were calculated. The BV was calculated as (RN/DN) x 100 where DN (digestible N) = ingested N - fecal N; RN (retained N) = DN - urinary N. Gilts fed the test diet (1 ppm ZEA without clay enterosorbent supplement) had significant reductions in DE and DCP as compared to the gilts fed the control diet. Dietary addition of natural clay enterosorbent in the test diet linearly improved the DE as the clay concentrations increased, and DCP followed a similar trend with higher clay inclusion having a better performance. Although treatment difference was observed in the ME value, the ME and BV were not different between gilts fed control (diet 1) and gilts fed the test diet (diet 3), suggesting little negative effects of dietary ZEA on ME and BV values. In conclusion, feeding low concentrations (1 mg/kg) of ZEA to young gilts for 21 days resulted in a reduction of DE and DCP, but the reduction was not found in ME and BV. Addition of clay enterosorbent could improve the reduced DE and DCP in young gilts.

Table 1. Treatment effects on digestible and metabolizable energy, digestible protein, and biological value

Treatment	DE, %	ME, %	DCP, %	BV, %
Control	83.69[a]	77.59[abc]	84.45[a]	77.08
Control + 0.25% clay	83.79[a]	77.80[ab]	85.47[a]	76.90
Control + 1 ppm ZEA (Test)	79.81[b]	75.68[c]	83.33[b]	77.99
Test + 0.125% clay	81.13[ab]	76.04[bc]	83.06[b]	78.03
Test + 0.25% clay	82.33[ab]	75.51[c]	82.98[b]	77.69
Test + 0.5% clay	83.75[a]	77.51[abc]	84.23[ab]	76.02
Test + 1.0% clay	84.02[a]	78.27[a]	84.33[ab]	77.97

[abc]Statistically different (P < 0.05)

Key Words: zearalenone, natural clay enterosorbent, nutrient availability

W185 Evaluation of the efficacy of a commercial purified phylosilicate to reduce the toxicity of zearalenone + deoxynivalenol in gilts. K. Bond[1], C. K. Maune[1], J. R. Stoltz[1], R. J. Malone[1], and D. Zaviezo*[2], [1]*Trilogy Analytical Laboratory*, *Washington, MO*, [2]*Special Nutrients*, *Miami, FL*.

An experiment was conducted to study the efficacy of a very low inclusion commercial purified phylosilicate (Myco-Ad A-Z) in preventing the deleterious effects of natural zearalenone (ZEA) plus deoxynivalenol (DON) contaminated feed in prepubertal gilts. Eighteen 19-day old recently weaned Yorkshire Cross gilts were individually housed and randomly distributed into 3 dietary treatments with 6 replications each. Pigs were fed a corn-soy diet containing or exceeding NRC recommended nutrients levels for 21 days. Treatments were: (1) control diet; (2) control + 1.2 ppm ZEA + 6 ppm DON; and (3) control + 1.2 ppm ZEA + 6 ppm + 1.0 kg/mt Myco-Ad A-Z. Highly contaminated corn was used to provide the ZEA + DON in treatments 2 and 3. Performance, relative liver and internal reproductive organs weights were evaluated at the end of the experiment, and vulva measurements (height x width) recorded at day 7, 9, 12, 14, 16, 19 and 21. Results indicated that gilts fed the ZEA + DON contaminated diet presented significant lower body weight gain, poorer feed conversion, heavier internal reproductive organs (94%) and lighter livers (23%) than gilts fed the control diet. The addition of Myco-Ad A-Z to the contaminated diet resulted in gilts with a statistically significant higher body weight gain (2220 vs 1040 g), better feed efficiency (5.53 vs12.82), lighter internal reproductive organs weight (17%) and heavier livers (8%) than those fed ZEA + DON. Starting on day 9 until the end of the experiment there was a significant increase in size of the vulva in gilts fed the contaminated diet compared to gilts fed the control and Myco-Ad A-Z diets (29.1 vs 16.5 and 18.6 at 21 days). These results indicate that Myco-Ad A-Z at 1.0 kg/mt was very effective in preventing both the toxic effects of DON and the estrogenic effects of ZEA in prepubertal gilts.

Key Words: Myco-Ad A-Z, zearalenone, deoxynivalenol

W186 Effects of dietary levels of tylosin on growth performance and efficiency of nutrient utilization in growing pigs. M. Z. Fan*[1], T. Archbold[1], K. Bregendahl[1], C. Yang[1], X. Yang[1], R. Bagg[2], G. Vessie[2], P. Dick[2], and D. Anderson[2], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Elanco Animal Health Canada Inc.*, *Guelph, Ontario, Canada*.

The objectives of this study were to examine effects of graded dietary levels of tylosin on growth performance and efficiency of utilization of dietary nutrients, including CP, calcium (Ca), and phosphorus (P) in growing pigs. Sixty Yorkshire barrows, with an average initial and final BW of 31 and 48 kg, were fed four diets for 15 blocks according to a randomized complete block design. The four diets were corn and SBM-based and formulated to contain four levels of tylosin at 0, 11, 22, and 44 ppm, respectively. Each experimental block consisted of a 12-d pre-adaptation to the control diet, 9-d adaptation and a 5-d collection of total urine excretion, and fecal samples. Orthogonal polynomial contrasts and Dunnett's tests were conducted to examine treatment effects. Tylosin supplementation improved ADG (P<0.05) at 11 ppm but not at the higher levels. Tylosin did not affect (P>0.05) feed intake and feed conversion efficiency. Tylosin supplementation did not affect (P>0.05) fecal content (mg H2S/g DM) of total volatile sulfides. The apparent DM digestibility values in the diets were not affected (P>0.05) by tylosin. Tylosin improved (P<0.05) the apparent CP digestibility at 11 ppm, but not at higher levels, yet did not affect (P>0.05) the efficiency of CP retention at any of the tested levels. Efficiency of Ca utilization was not improved (P<0.05) by tylosin. Dietary supplementation of tylosin had cubic effects (P<0.05) on the efficiency of P utilization at the digestive and post-absorptive levels. In conclusion, dietary supplementation of tylosin at 11 ppm may improve growth and efficiency of P utilization in growing pigs.

Key Words: growing pigs, nutrient utilization, tylosin

W187 Effect of the combined use of ractopamine and chromium picolinate on growth performance and carcass traits of finishing pigs. E. Toledo*, K. Gomezjurado, A. García-Rendón, G. Cárdenas, and A. Borbolla, *Departamento de Producción Animal: Cerdos, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México*, *Ciudad de México, Distrito Federal, México*.

An experiment was conducted to evaluate the dietary effects of ractopmaine plus chromium picolinate on growth performance and carcass traits of finishing pigs. One hundred and twenty seven mixed-sex pigs (64 pigs/treatment/4 replicates/treatment) were randomly assigned to two dietary treatments. Control (R) group used a ractopamine-formulated diet containing 5 ppm 1000 Kg-1 of the β-agonist. Experimental group (R+Cr) used the same diet and level of ractopamine plus 200 ppb of chromium using chromium picolinate as the source. Diets were fed ad libitum for 21 days before slaughtering. Initial and final weight ± SE, for R (84.16 ± 10.8 and 105.12 ± 12.7 Kg), and R+Cr (84.94 ± 9.2 and 104.43 ± 11.1) were not different (P > .05). However, growth data indicated that pigs fed the R-diet exhibited greater (P<0.05), ADG and decreased (P<0.05) FC than R+Cr pigs (1.00 vs. 0.93 Kg and 2.92 vs. 3.34, respectively). Meanwhile, ADFI was greater (P<0.05) in R+Cr (2.99 kg/d), than in R (2.88 Kg/d) pigs. At the end of the trial, 5 pigs per treatment were selected to evaluate dietary effects on carcass traits. Overall carcass traits (carcass weight, carcass length, 10th rib backfat) in R+Cr pigs differed (P>0.05), + 1.94%, + 1.4% and - 3.8%, respectively, when compared to the carcass of R pigs. Furthermore, the butcher in charge of quartering preferred the meat from R+Cr rather than R pigs. According to this study, there appeared to be a slight improvement when finishing pigs were supplemented with ractopamine and chromium.

Key Words: finishing pigs, ractopamine vs chromium, growth performance

W188 Early prediction tools for the selection of reproductive traits on spring born crossbred Angus heifers. R. A. Franco*[1], G. Scaglia[2], W. S. Swecker[3], and M. L. Wahlberg[1], [1]*Department of Animal and Poultry Sciences, Virgina Tech, Blacksburg,* [2]*Louisiana State University AgCenter-Iberia Station, Jeanerette,* [3]*Virginia-Marylan Regional College of Veterinary Medicine, Virginia Tech, Blacksburg*.

The objective of this study was to evaluate the efficacy of insulin like growth factor-1, leptin, insulin, thyroxine, triiodothyronine, glucose, lactate dehydrogenase, hip height (HH), frame score (FS), and body weight (BW) as predictors of pregnancy, calving and weaning of a live calf on spring born beef cattle. Thirty-six Angus crossbred heifers (BW=280.5±3.8 kg, mean age=308±2 d) were blocked by BW into six groups and randomly assigned to one of six paddocks. The experimental period covered six months from December 21, 2006 to the start of the breeding season in May 2007. Reproductive outcomes were computed up to breeding in 2008 (after first calving). Blood samples, BW, and HH measurements were collected once a month. Data were analyzed with the Proc logistic procedure from SAS. Hip height measured when heifers were yearlings was a significant explanatory variable for pregnancy, calving and weaning of a live calf (P=0.01; P=0.01; P=0.03, respectively). Heifers that were pregnant, calved and weaned a live calf had an average HH=119.4±0.6 cm whereas animals with negative outcomes on pregnancy had an average HH=116.8±0.8 cm in 2007. Pre breeding BW (yearling) was a significant explanatory variable for pregnancy after first calving in 2008 (P<0.002). Pregnant heifers (BW=335.2±5.7 kg) were 27.8 kg heavier as yearlings than non pregnant animals (BW=307.4±4.7 kg). No other variables studied were significant. The results from this study indicate that HH as yearlings and pre breeding BW were the more useful measurements for pregnancy prediction in the first and second year of the study, respectively.

Key Words: reproductive traits, body weight, hip height

W189 Endometrial gene expression of estradiol, progesterone, and oxytocin receptors in anestrous Bos indicus cows treated with progesterone. O. G. Sa Filho*, D. M. Guerra, and J. L. M. Vasconcelos, *FMVZ/UNESP, Botucatu, SP, Brazil*.

In anestrous cows, treatment with progesterone (P4) prior to ovulation prevents subsequent premature luteolysis. In Exp. 1 we evaluated the effects of follicular diameter on endometrial mRNA for receptors of estradiol (ER), P4 (PR), and oxytocin (OTR) in anestrous Nelore cows. Cows (30-60 DPP) had ovaries examined by ultrasound daily and were hysterectomised when follicles reached 7 (n=4), 8.5 (n=4), or 10 mm (n=4). An additional group (n=4) of cows had mean follicular diameter of 11.31±0.03 mm at 48 h after temporary weaning (TW). In Exp. 2 we evaluated the effects of treatment with P4 on endometrial mRNA for ER, PR, and OTR in anestrous Nelore cows. Cows (30-60 DPP) were randomly assigned as control (CTL; n=20) or to receive a CIDR containing 1.9 g of P4 (CIDR; n=20) from days -8 to -2 before GnRH injection on Day 0. All cows were submitted to 48 h TW from Day -2 to 0. Hysterectomies were performed at Days -8, -2, 0, and 5 (n=5/treatment/day point). In both experiments, endometrial tissue was dissected and samples were submitted to real-time RT-PCR. The mRNA abundance of target genes are presented relative to CYC-A. Data were analyzed by PROC MIXED of SAS. In Exp. 1, no effects of follicle size were found on PR-mRNA, ER-mRNA, and OTR-mRNA. In Exp. 2, PR-mRNA was not affected by day or treatment, whereas treatments affected (P<0.05) ER-mRNA at Days -2 (CTL: 6.8±1.6; CIDR: 2.5±1.6), 0 (CTL: 6.6±1.0; CIDR: 3.5±1.0), and 5 (CTL: 4.3±0.9; CIDR: 2.4±0.9), and OTR-mRNA at Days -2 (CTL: 14.3±1.2; CIDR: 2.5±1.2), 0 (CTL: 14.7±1.4; CIDR: 7.7±1.4), and 5 (CTL: 6.9±1.2; CIDR: 3.8±1.2). We conclude that in anestrous cows: 1) PR-mRNA, ER-mRNA, and OTR-mRNA were expressed in high concentrations, similar to those observed during the proestrus/estrus, and did not change as the dominant follicle developed; 2) treatment with P4 for 6 d caused a decrease in ER-mRNA and OTR-mRNA with no changes PR-mRNA. These responses may be related to the mechanisms underlying and preventing premature luteolysis by PR treatment in anestrous cattle.

Key Words: endometrium, receptors, premature luteolysis

W190 Controlling the onset of a new estrous cycle utilizing a persistent follicle. J. P. N. Martins*, R. Policelli, and J. R. Pursley, *Michigan State University, East Lansing*.

Ovsynch is most effective when initiated on d 6 or 7 of the estrous cycle. Thus, it is imperative that a pre-Ovsynch strategy be developed to allow for the greatest percent of cows possible to be at this stage of the estrous cycle when Ovsynch is initiated. We hypothesized that inserting a CIDR following $PGF_{2\alpha}$ would create a persistent follicle that could be time ovulated to control the onset of a new estrous cycle and thus control of the start of Ovsynch. The objectives of these studies were to determine: 1) if treatment with a 1.38 g CIDR insert would result in the creation of a persistent follicle with ovulatory capacity and 2) if pre-Ovsynch strategies that utilized the development of a persistent follicle would increase conception rates following Ovsynch. Lactating Holstein dairy cows were assigned randomly to control and treated groups in two studies. In Study 1 (n=496) and 2 (n=435), controls were treated with two injections of $PGF_{2\alpha}$ 14 d apart and 11 d prior to the 1st GnRH of Ovsynch (14/11). Cows in the treated groups received two injections of 25 mg $PGF_{2\alpha}$ 14 d apart with a CIDR inserted either 7 (P7;Study 1) or 5 (P5;Study 2) d respectively, following the 2nd $PGF_{2\alpha}$. Treated cows in both studies received 100 μg GnRH 7d following CIDR insertion then received the 1st injection of GnRH of Ovsynch 6 d later. All groups completed Ovsynch (G-7d-P-56h-G-16h AI). In Study 1, 97% of treated cows ovulated a follicle (20.37mm ± 0.3) to the GnRH at time of CIDR removal. Size of ovulatory follicle was greater (17.4mm ± 0.4 vs 14.5 ± 0.3; P=0.001) at 1st GnRH of Ovsynch but similar at final GnRH of Ovsynch (16.9mm ± 0.2 vs. 16.5 ± 0.2; P=0.09) in 14/11 vs. P7. Percent of cows with corpora lutea on d of 1st GnRH of Ovsynch was greater in P7 vs. 14/11, 98 vs. 89% (P=0.001). Conception rates were similar (41 vs. 38%; P=0.31), in 14/11 vs. P7. In Study 2, conception rates were similar between treatments (39 vs. 36%; P=0.24). In summary, pre-Ovsynch strategies that induced a persistent follicle to control the start of an estrous cycle did not positively impact conception rates in lactating dairy cows following Ovsynch.

Key Words: persistent follicle, Ovsynch, pre-synchrony

W191 Embryo transfer following treatment of cystic ovaries in cattle. C. E. Ferguson*[1], F. M. LeMieux[1], D. J. Kesler[2], and R. A. Godke[3], [1]*McNeese State University, Lake Charles, LA*, [2]*University of Illinois, Urbana*, [3]*Louisiana State University, Baton Rouge*.

Cystic ovaries occur at a rate of 6 to 19% in dairy and <10% in beef cattle. Although this incidence may represent a small part of a herd, it

can represent a loss in overall animal production. In an effort to reduce the time period from treatment to conception in cystic cattle, a protocol was developed using embryo transfer (ET) 7 d post-GnRH treatment. A total of 16 mature crossbred beef cows were induced to form follicular cysts (Cook et al., 1991). In this study, formation of a follicular cyst was defined as a follicular structure >24 mm existing for ≥ 7 d in absence of a corpus luteum. Within 10 to 28 d after cyst induction 8 of the 16 cows developed follicular cysts. Once determined to be cystic, each female was randomly allotted to either a GnRH treatment or a control group. The treatment group (n = 3) received an injection of 100 μg GnRH im (Cystorelin) while the control animals (n = 3) received sham injection im. In the treatment group, females received two d-7, grade-1 IVF-derived blastocysts in the uterine horn ipsilateral to the luteinized follicular cyst. In the control group, females similarly received two d-7 grade-1 IVF-produced blastocysts (no luteinized cysts present). At time of ET, 4 of 6 females (2 in treatment and 2 in control group) had luminal fluid in the uterine horns, with the uteri of these animals resembling that of a female in either proestrus or estrus. At 30 d post-GnRH treatment, 1 female in the GnRH-treated group (one female without uterine fluid at time of ET) was pregnant. Unfortunately, this female aborted after d 45 of pregnancy. In conclusion, the development of ET 7 days following GnRH-treatment of follicular cysts could reduce the time from treatment to conception (0 vs 30 to 60 d). Possibly, pre-transfer progestin treatment following GnRH treatment would produce a more receptive uterine environment for an embryo at transfer.

Key Words: cystic ovaries, embryo transfer, pregnancy

W192 GnRH affects emergence of a new follicular wave in cows with cystic ovaries. E. Dirandeh, H. Kohram*, T. Saberifar, and A. Zare Shahneh, *University of Tehran*, *Iran*.

The objective of this study was to evaluate the effect of GnRH on follicular wave emergence in cows with cystic ovaries. The estrous cycles of 15 cows were synchronized with two intra-muscular injections of prostaglandin F2Î± given 11 days apart. The cows were randomly assigned to one of three treatments. Control cows (n=five) received no injection, whereas GnRH cows (n=five) received a GnRH injection on day six of the estrous cycle (day of injection=day 0). In cows with cystic ovaries (n=five), diagnosis of a cyst was based on the palpation per rectum of an abnormally large (≥20 mm) follicle and no corpus luteum then these cows received a GnRH injection. The ovaries scanned by daily ultrasonography from four days before (day -4) the day of GnRH treatment (day 0) until four days after GnRH treatment (d 4). Daily ultrasonography confirmed the presence of a cyst for at least 10 days in the ovary of the cystic cows then these cows received a GnRH injection (day 0). All follicles were classified as small (4-6mm), or large (≥7 mm) follicles. Data were analyzed using the GLM procedure of SAS. Results showed In controls, the number of small follicles tended to decline until day two of the experiment (Figure 1). Following GnRH injection (day 0) in groups GnRH and cystic cows, the number of small follicles increased until day two. The number of large follicles in control group did not decrease, however, this class of follicles decreased (P<0.05) until day two in the GnRH and cystic cows. An increase in the number of small follicles two days following GnRH injection showed that GnRH treatment could promote the emergence of a new follicular wave in cystic cattle similar to the normal cyclic cattle.

Key Words: GnRH, follicular wave, cystic ovaries

W193 Immediate and carryover effects of Gram-negative or Gram-positive toxin-induced mastitis on follicular functions in cows. Y. Lavon*[1], G. Leitner[2], R. Meidan[1], U. Moallem[3], E. Klipper[1], and D. Wolfenson[1], [1]*The Hebrew University*, *Rehovot, Israel*, [2]*The Veterinary Institute*, *Bet-Dagan, Israel*, [3]*Agricultural Research Org*, *Bet-Dagan, Israel*.

This study compared immediate and carryover effects of clinical mastitis induced by Gram (-) or Gram (+) toxin on follicular functions. Uninfected cyclic lactating Holstein cows were synchronized and monitored by ultrasound. On d 5.5 of the cycle, cows were treated with $PGF_{2\alpha}$ and 36 h later, a dose of Gram (-) (LPS, n=8) or Gram (+) peptidoglycan (PTG, n=10) toxin or saline (n=9) was injected into the udder. Seven h later, follicular fluids and granulosa cells were aspirated from the preovulatory follicles and GnRH injected. This (cycle 1; immediate effect) was repeated 3 times (excluding injection of toxins) to induce three 7-d cycles (cycles 2, 3 and 4; carryover effect). Gene expression and steroids were determined by RT-PCR and RIA. Data were analyzed by ANOVA, means ±SE presented. LPS and PTG transiently increased body temperatures, TNF_{α} concentrations, and somatic cells count. Follicles size was similar in all groups. PTG decreased the number of follicles developed (P<0.05). Follicular estradiol (949±77 ng/ml) and androstenedione in control cows remained stable during the 4 cycles. LPS reduced in 1/3 of the treated cows in cycle 1, the level of estradiol (149±18 ng/ml) and androstenedione, and mRNA for LHr reached about 30% of controls (P<0.05; immediate effect). Later, the concentrations in all LPS cows were restored to control levels (cycles 2, 3, 4). In contrast, 30 to 50% of PTG cows exhibited low follicular estradiol (123±100 ng/ml) and androstenedione level, low circulating estradiol (2.2 vs. 6.2 pg/ml in controls), and low mRNA for LHr; all lasted 4 cycles (immediate and carryover effects; P<0.05). LPS-induced mastitis caused an immediate/short-term (typical for G- clinical events) impairment of follicular functioning, whereas the G+, PTG toxin exhibited both immediate and carryover disruptive effects on follicular theca and granulosa cells of the preovulatory follicle.

Key Words: mastitis, follicle, estradiol

W194 Do progesterone changes during early lactation in Holsteins, Jerseys and their crosses affect subsequent reproductive performance? S. M. Sheer*, K. L. Brown, B. G. Cassell, and F. C. Gwazdauskas, *Virginia Tech*, *Blacksburg*.

One hundred and forty-seven first lactation cows were sampled to determine if plasma progesterone differed between breeds and affected subsequent reproductive performance. Thirty-five cows were Holstein-Jerseys (HJ) crosses, 42 were Jersey-Holsteins (JH) crosses, 45 were Holsteins (HH), and 25 were Jerseys (JJ). Blood samples were collected weekly postpartum for a 10 wk period. Statistical models (MIXED) evaluated breed, profile of progesterone, season (cool – November to May; hot – June to October), and breed by season interaction on days open, the slope of change in progesterone plasma prior to 30 d postpartum and number of services per conception (S/C). Days open were significantly affected by profile and breed. The days open for HH were longest (152.6 ± 4.5 d), not different for HJ (132.4 ± 4.5 d) and JH (128.2 ± 4.1 d), and JJ (140.5 ± 5.2 d) was different from all except HJ. Cows with a short profile had 33 to 60 fewer days open than the other groups. There was a breed by season interaction for days open (P < 0.05). Slope was affected by breed, profile, and breed by season interaction (P < 0.05). The HH group had a slope of 0.196 ± 0.023, HJ had a 0.160 ± 0.022 slope, JH had a 0.157 ± 0.020 slope, whereas the JJ slope was 0.229 ± 0.026. The JJ slope was steeper than the HJ and

JH slopes. Profile of progesterone affected slope. Cows with a delayed profile had a slope of 0.0024 ± 0.014, suggesting that there was no increase in progesterone during the early postpartum period. The breed by season interaction showed a greater slope for JJ in summer and a lower slope in winter than other breed combinations. Number of S/C was affected by breed, season and the breed by season interaction ($P < 0.05$). Holsteins had 2.3 ± .1 S/C which was higher than HJ (2.0 ± .1), JH (1.9 ± 0.1) and JJ (2.1 ± 0.1). S/C were higher in the cool season (2.3 ± 0.05) compared to the hot season (1.9 ± 0.06). Cool season had higher S/C in all breeds except HJ. Breed differences were evident in measures of reproductive efficiency.

Key Words: reproduction, progesterone, crossbreds

W195 Pregnancy success and luteal function of lactating Holstein cows after hCG on day 5 after insemination. E. Urzua[1], C. G. Gutierrez[1], A. Garza[2], C. Corona[3], G. Mapes[3], and J. Hernandez-Ceron*[1], [1]*Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, México*, [2]*Beta San Gabriel S.A. de C.V., Torreón, México*, [3]*Intervet Schering Plough Animal Health, México*.

Low serum progesterone concentration after breeding is being associated with pregnancy losses. Human chorionic gonadotropin (hCG) treatment on day 5 after estrus induces ovulation of the first-wave dominant follicle and formation of an accessory corpus luteum. Here, we tested whether an injection of hCG on day 5 after artificial insemination (AI) increases conception rate and plasma progesterone in lactating dairy cows. Nine hundred eighty-nine multiparous Holstein cows were used. Cows were inseminated at fixed timed after an Ov-synch protocol or after natural estrus. Five days AI, cows were randomly assigned to either a treated (hCG; n =482) or a control (n = 507) group; animals in the treated group were given 3,500 UI im of hCG. Pregnancy diagnoses were performed on day 30 and 60 post-AI by ultrasonography and rectal palpation respectively. Blood samples were taken on days 5, 11 and 15 from fifteen cows from each group for progesterone quantification. Conception rates were higher for hCG-treated cows on day 30 (47.5 > 35.5%), and 60 (41.1 > 31.6%) after AI. Pregnancy losses were similar between groups. The number of previous inseminations affected the response to the hCG treatment. First insemination cows improved conception rate when treated with hCG both on day 30 (55.9% > 41.0%) and 60 (45.2% > 33.1%). However, this effect was not observed in cows of two or more inseminations ($P>0.20$). Progesterone concentrations were higher ($P<0.05$) in cows treated with hCG than in control cows. It is concluded that hCG on day 5 after AI increases conception rate and plasma progesterone in first service lactating dairy cows.

Key Words: hCG, fertility, dairy cows

W196 Plasma LH concentrations and CL function in Holstein cows given porcine LH, GnRH, or estradiol benzoate. M. G. Colazo*[1], T. O. Ree[2], A. G. A. Lamont[3], J. P. Kastelic[4], R. J. Mapletoft[5], and D. J. Ambrose[1,3], [1]*Alberta Agriculture and Rural Development, Edmonton, AB, Canada*, [2]*Lakeland College, Vermilion, AB, Canada*, [3]*University of Alberta, Edmonton, AB, Canada*, [4]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [5]*University of Saskatchewan, Saskatoon, SK, Canada*.

We compared LH concentrations and CL function in nonlactating Holstein cows following treatment with estradiol benzoate (EB), porcine LH (pLH), GnRH, or no treatment during proestrus. Cows (n=28) were given a 1.9 g progesterone (P4) intravaginal device (CIDR) for 5 d and 500 μg cloprostenol (PG) at CIDR removal. On d 6 after estrus, cows were treated with 2 PG 12 h apart and allocated randomly to 1 of 5 groups to receive im: 1 mg EB, 20 h after first PG, 12.5 or 25 mg pLH or 100 μg GnRH 36 h after PG, or no treatment (Control). Ovulation (d 0), follicles and CL diameter were assessed by transrectal ultrasonography. Plasma concentrations of LH were determined for 8 h (except in Control cows) from treatment, and plasma P4 was determined once daily from d 0 to 12. Mean (±SEM) plasma LH (ng/mL) was greater ($P<0.05$) in cows treated with 25 mg pLH (5.0±0.5) than in those given 12.5 mg pLH (2.7±0.5); it was intermediate in those given GnRH (3.8±0.5) or EB (4.1±0.5). Preovulatory follicle diameter (POFD; mm) was largest ($P<0.05$) in Control cows (15.6±0.8, 13.7±1.0, 15.2±0.8, 14.3±1.0 and 18.4±0.9, mm, for EB, 12.5 pLH, 25 pLH, GnRH and Control, respectively). On d 12, CL diameter (mm) was largest in Control (25.1±1.2) cows, intermediate in pLH (22.8±1.3 and 22.7±0.9 for 12.5 and 25 mg) and EB (22.5±1.0) cows, and smallest in GnRH cows (20.4±1.2). However, CL area did not differ among treatments. The POFD was correlated to CL diameter ($P<0.01$, $r=0.6$) but not to CL area ($P=0.15$, $r=0.33$). Nothing was significantly correlated with plasma P4. Mean plasma P4 in cows given either 25 mg pLH or GnRH did not differ from that in Control cows, but 12.5 mg pLH or EB resulted in lower plasma P4 after ovulation. In summary, cows given 25 mg pLH had greater LH concentrations; Control cows had larger POFD and CL diameter, but P4 concentrations did not differ from cows given 25 mg pLH or GnRH.

Key Words: LH, CL function, progesterone

W197 Prostaglandin (PG) E1 or E2 (PGE1, PGE2) luteal implants prevent luteoysis in cows. C. W. Weems*[1], Y. S. Weems[1], R. C. Vann[2], S. P. Ford[3], D. A. Neuendorff[4], A. W. Lewis[4], T. A. Welsh[5], T. M. Nett[6], P. J. Bridges[7], and R. D. Randel[4], [1]*University of Hawaii, Honolulu*, [2]*Mississippi State University, Raymond*, [3]*University of Wyoming, Laramie*, [4]*Texas AgriLife Res., Overton*, [5]*Texas A&M University, College Station*, [6]*Colorado State University, Fort Collins*, [7]*University of Kentucky, Lexington*.

Loss of progesterone secretion at the end of the estrous cycle is via uterine PGF2∝ secretion; however, uterine PGF2∝ is not decreased during early pregnancy in ewes to prevent luteolysis as the embryo imparts resistance to PGF2∝-induced luteolysis via the two-fold increase in PGE1 and PGE2 in the endometrium during early pregnancy. Infusion of PGE1 or PGE2 every 4 hr intrauterine prevents spontaneous or an estradiol-17β or an IUD-induced premature luteolysis in ewes (C W. Weems, Y. S. Weems, R. D. Randel, The Vet. J. 171:206-228, 2006). Estradiol-17β or PGE2 infused every 8 hr did not prevent luteolysis, but estradiol-17β+PGE2 inhibited luteolysis in heifers (L.P. Reynolds, D. Robertson, S. P. Ford, J. Reprod. Fertil. 69:703–709, 1983). The objective of this experiment was to determine whether intraluteal implants of PGE1 or PGE2 prevent luteolysis in Brahman or Angus cows. Cows received intraluteal implants of Dow Corning 360 elastomer containing Vehicle, PGE1, or PGE2 from D-13-D-19 post-estrus via a flank laparotomy. Corpora lutea (CL) were recovered on D-19 and weighed. D-13 Angus CL weights served as preluteolytic controls. Daily venous progesterone concentrations are being analyzed. D-19 CL weights were analyzed by a Factorial Design for ANOVA. D-19 CL weights of Vehicle-treated Brahman or Angus cows were lower ($P<0.05$) than those treated with PGE1 or PGE2 from D-13-D-19. D-13 Angus CL weights were higher ($P<0.05$) than Vehicle-treated Angus cows on D-19, but weights of D-13 CL were similar ($P>0.05$) to D-13-D-19 PGE1 or PGE2-treated

Angus CL. It is concluded that PGE1 or PGE2 alone prevents luteolysis regardless of breed.

Key Words: prostaglandins, cows, corpus luteum

W198 The effect of a shortened dry period on follicular dynamic in early lactation Holstein cows. S. Safa[1], A. Heravi Moussavi*[1], M. Danesh Mesgaran[1], and A. Soleimani[1,2], [1]*Department of Animal Science, Ferdowsi University of Mashhad, Iran*, [2]*Islamic Azad University-Kashmar Branch, Iran*.

The study was designed to test the effect of dry period length on follicular dynamics in early lactation cows. Cows were randomly assigned in 1 of 2 treatments: 1) traditional 60 d dry period (n=14) and 2) a shortened 20 d dry period (n= 13). Holstein cows were blocked in pairs based on their previous 305 d milk, parity and expected calving dates. All cows were fed by routine ration of farm (total mixed diet) twice a day at 0800 and 1400 h and had at all time free access to water. To monitor follicular parameters, ultrasound measurements of follicular activity were made on alternate days from 10-35 day postpartum (PP) to determine the characteristics and fate of the 1st follicular wave, using a 7.5 MHz rectal transducer. Dominant follicle development was characterized by follicular mapping of recorded ultrasound images. A dominant follicle was defined as a follicle that was >10 mm in diameter in the absence of other large (>9 mm) growing follicles. The data were analyzed using the GLM procedure of SAS for a completely randomized design. The number of follicles (5 to 10 mm) present on d 10 (p=0.12; 4.14±0.44 and 3.08±0.48, respectively) and 14 PP (p=0.11; 5.21±0.47 and 4.08±0.51, respectively), number of days until detection of a follicle ≥ 10mm in diameter (p=0.24; 11.43±0.82 and 12.85±0.85 d, respectively), diameter of the first dominant follicle on d 14 PP (p=0.25; 13.57±0.73 and 12.29±0.79 mm, respectively), maximum diameter of the first dominant follicle (p=0.38; 15.32±0.66 and 14.46±0.69 mm, respectively), and days to first ovulation (p=0.62; 29.31±2.89 and 27.18±3.14 d, respectively) were all similar among the groups. Results of this study showed that the reduced dry period length had no apparent effect on follicular parameters and days postpartum to first ovulation.

Key Words: dairy cows, dry period, follicular dynamic

W199 Characteristic of the largest follicle of the waves emerged after treatment with GnRH during estrous cycle of Iranian Holstein cows. E. Dirandeh and H. Kohram*, *University of Tehran, Karaj, Tehran, Iran*.

This study was done to consider the effect of GnRH on largest follicle of the waves in Iranian Holstein cows. The estrous cycles of 10 cows were synchronized with 2 im injections of Prostaglandin $F_{2\alpha}$ given 11 d apart. The cows were randomly assigned to 1 of 2 groups. In control group of animals no injection of GnRH was performed. GnRH administered on Day 6 of the estrous cycle (estrus = Day 0). The diameter of the largest follicle was also recorded. Ovarian follicular development was monitored daily by transrectal ultrasonography with a real-time linear scanning ultrasound diagnostic system. Ultrasonography was performed once daily from the day that second $PGF_{2\alpha}$ inject until the day of next estrous. The follicular wave during which growth phase the treatment was administered was designated as wave 1. Any follicular wave induced by treatment was designated as wave A. The follicular wave emerging after the induced wave (GnRH treated cows) or the follicular wave emerging after 7–8 days after the emergence of wave 1 (control cows) was designated as wave 2 was designated as wave 2. Comparisons of waves 1, A, and 2 detected in GnRH-treated cows were made by one-way RM ANOVA. Results are reported as least square means ± SEM. There was no significant effect (P>0.05) of wave, group, or a wave*group interaction for the parameter of largest follicles of waves 1 in both GnRH-treated and control cows. There was no significant effect (P>0.05) of wave for the parameters above for waves 1 in GnRH-treated cows (Table 1). The ovulatory follicle in control group grew larger (14.0 ± 1.8 vs. 12.6 ± 1.1 mm, P<0.05), and maintained for a longer period of time (P<0.05) than in GnRH-treated cows (9.50 ± 0.6 vs. 5.8 ± 0.4). The results suggested that administration of GnRH on day 6 of estrous cycle induce ovulation and the ovulatory follicle in GnRH-treated cows was older than that in control cows.

Key Words: ultrasonography, GnRH, follicle

W200 Subclinical mastitis effects on steroid concentrations and gene expression in theca cells of preovulatory follicles in cows. Y. Lavon*[1], G. Leitner[2], R. Meidan[1], E. Klipper[1], and D. Wolfenson[1], [1]*The Hebrew University, Rehovot, Israel*, [2]*The Veterinary Institute, Bet-Dagan, Israel*.

We have recently observed that subclinical mastitis (SCM) lowered steroid concentrations and gene expression in granulosa cells of preovulatory follicles in about 1/3 of the infected cows. To complement these studies, we examined the effect of SCM on follicular steroid levels and gene expression in the other follicular steroidogenic cell – the theca cells. Cyclic lactating Holstein cows (n=20) were diagnosed for mastitis by somatic cell counts and bacteriological examinations. On day 6 of the estrous cycle, synchronized cows were treated with $PGF_{2\alpha}$ and 42 h later, the cows were slaughtered and their ovaries were collected. Follicular fluids and theca cells were obtained from preovulatory follicles. Gene expression and steroids were determined by RT-PCR and RIA. Data were analyzed by ANOVA and means ± SE presented. One third of SCM cows (n=4) exhibited low estradiol concentrations in the follicular fluid, whereas the remaining 2/3 (n=8) cows, and uninfected cows (n=8), exhibited normal concentrations (269±71 vs. 815±127 and 870±62 ng/ml, respectively, P<0.01). The SCM cows with low estradiol also exhibited low follicular androstenedione concentrations (32±12 vs. 109±31 and 130±30, respectively, P<0.05), and estradiol to progesterone ratios (6.4±1.3 vs. 14.8±2.4 and 13.3±1.4, respectively, P<0.05). Accordingly, mRNA expression in theca cells, for LH receptor, cytochrome P450 side chain cleavage, and cytochrome P450 17α-hydroxylase were lower in SCM cows with low estradiol than in SCM cows with normal estradiol levels, and uninfected cows (P<0.05). However, 3βHSD and StAR mRNA were not affected by SCM. Results show that low gene expression in theca cells is associated with low preovulatory steroid concentrations. The resulting low estradiol level in 1/3 of the SCM cows could be associated with delayed preovulatory LH surge and ovulation, as documented in our earlier studies. These mechanisms may explain mastitis-induced low fertility in dairy cows.

Key Words: mastitis, estradiol, theca cells

W201 Effect of dry period lengths on complete blood count in early lactating Holstein cows. A. Soleimani*[1,2], A. Heravi Moussavi[1], M. Danesh Mesgaran[1], A. Golian[1], and S. Safa[1], [1]*Department of Animal Science, Ferdowsi University of Mashhad, Iran*, [2]*Islamic Azad*

University-Kashmar Branch, *Iran*.

The study was designed to test the effect of reducing dry period length on complete blood count and differential white blood cell count in early lactating cows. Cows were randomly assigned in 1 of 2 treatments: 1) traditional 60 d dry period (n=14) and 2) a shortened 35 d dry period (n=15). Holstein cows were blocked in pairs based on their previous 305 d milk, parity and expected calving dates. All cows were fed by routine ration of farm (total mixed diet). Using vacutainer tubes, blood samples were collected weekly from -7 to 50 day relative to calving via venipuncture of coccygeal vessels before the morning feeding to monitor complete blood count (CBC). The blood samples were kept in room temperature until analyzing for CBC by a hematology analyzer. The data were analyzed using the Mixed procedure of SAS for a completely randomized design with repeated measures. The white blood cells (P=0.64; 12277 ± 1798 and 13468 ± 1733 /µl, respectively), red blood cells (P=0.58; 5283037 ± 104596 and 5363237 ± 100280 /µl, respectively), platelet (P=0.13; 250271 ± 16913 and 286354 ± 16122 /µl, respectively), hemoglobin (P=0.91; 8.09± 0.15 and 8.11± 0.14 g/dl, respectively), hematocrit (P=0.70; 27.97 ± 0.5 and 28.24 ± 0.5%, respectively), and also number of neutrophils (P=0.52; 3445.3 ± 198 and 3622.6 ± 188, respectively), lymphocytes (P=0.59; 7703.9 ± 1609 and 8920.2 ± 1547, respectively), monocytes (P=0.82; 685.6 ± 100 and 716.5 ± 96.4, respectively) and eosinophils (P=0.52; 173.8 ± 23 and 152.8 ± 22, respectively) were all similar among the groups. Red blood cell, hemoglobin and hematocrit were decreased and platelet were increased over the time (P<0.05). Result of this study showed that the reduced dry period length had no effect on cell blood count and differential white blood cell count.

Key Words: dairy cow, dry period, complete blood count

W202 Evaluation of sperm motility in stored semen collected from boars fed a diet supplemented with organic selenium. S. Speight, M. Estienne*, A. Harper, and R. Crawford, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

The objective was to compare sperm motility during storage for semen from boars fed diets supplemented with organic or inorganic sources of selenium. At weaning, boars were assigned to one of three treatments: I. basal diets with no supplemental selenium (controls), II. basal diets supplemented with 0.3 ppm organic selenium (Sel-Plex; Alltech, Inc., Nicholasville, KY), and III. basal diets supplemented with 0.3 ppm sodium selenite (n = 10 boars/treatment). At sexual maturity, ejaculates were collected, processed and stored at 18° C in Beltsville Thawing Solution and Androhep-Lite (Minitube of America, Inc., Verona, WI) (3×10^9 sperm/85 mL semen and extender) and sperm motility assessed daily for 10 d using a computer-assisted sperm analysis system (Hamilton Thorne Research, Beverly, MA). Data were analyzed using repeated measures ANOVA and individual ejaculate was the experimental unit. There were no effects of day x extender or day x treatment x extender (P > 0.1), thus data were pooled between extenders. Effects of treatment x day were detected for percent motile spermatozoa (P < 0.01), path velocity (smoothed cell path; VAP) (P = 0.06), amplitude of lateral head displacement corresponding to the mean width of the head oscillation as the sperm swam (ALH; P = 0.02), frequency with which the sperm track crossed the sperm path (BCF; P = 0.04), straightness (P = 0.01) and percent static spermatozoa (P = 0.009). In general, values were indicative of an enhanced ability of sperm cells from Sel-Plex-fed boars to maintain good motion characteristics during storage. For example, VAP (µm/s) was greater (P < 0.03; SE = 2.5) for sperm from boars fed Sel-Plex (77.5) after 3 d of storage compared to control (66.5) or selenite (65.5) boars. After 10 d of storage, VAP was greater (P < 0.01; SE = 2.5) for sperm from boars fed Sel-Plex (77.2) compared to selenite-fed boars (57.2). Sperm VAP from control boars (65.2) was not different (P > 0.16) from either the Sel-Plex- or the selenite-fed boars. Results indicate that dietary organic selenium supplementation may help ameliorate the negative effects of semen storage on sperm motility.

Key Words: boar, selenium, semen

W203 Effect of melatonin on in vitro manipulated rat oocytes and embryos. S. Nandi*[1,2], V. Girish Kumar[2], and F. C . Gwazdauskas[3], [1]*National Institute of Animal Nutrition and Physiology*, *Bangalore, India*, [2]*Karnataka Veterinary Animal and Fishery Sciences University*, *Bangalore, India*, [3]*Department of Dairy Science, Virginia Polytechni Institute and State University*, *Blacksburg*.

Melatonin, N-acetyl-5 methoxytryptamine, acts as a powerful agent against reactive oxygen species (ROS) and a potent apoptosis blocker. The aim of the present study was to investigate the effect of different concentrations of melatonin on the development of rat oocytes and embryos in vitro. In experiment 1, control (38.5°C) and heat stressed (39°C during maturation) and chemically stimulated (glycolytic stimulator dinitrophenol, DNP:10 µM and glycolytic inhibitor hexametaphosphate, HMP:100 µM) oocytes were matured in vitro in 9 different concentrations (0, 1, 5, 10, 25, 50, 100, 500 and 1,000 µM) of melatonin. The maturation rates were recorded after 24 hrs of culture. The oocytes were fertilized in vitro and the resultant embryos were further cultured for the production of morulae/blastocysts. Supplementation of melatonin at 10 µM concentration in the oocyte culture medium resulted in a significantly higher (P < 0.05) maturation rate (control: 90.3%, heat stressed: 84%, DNP: 86% and HMP: 78%) and morula/blastocyst yield (control: 25.3%, heat stressed: 16%, DNP: 20% and HMP: 18%) compared to control (without melatonin). Based on result of experiment 1, in vivo produced embryos were divided into 2 groups: control and heat stressed (39°C during first 2 d of culture). The heat stressed embryos were cultured in medium supplemented with 10 µM melatonin. Supplementation of melatonin in the embryo culture medium resulted in comparable morula/blastocyst yield in control and heat stressed embryo groups. Melatonin also decreased the death (assessed by trypan blue staining) of oocytes and surrounding cumulus cells and also decreased the developmental block, asynchronous development and degeneration of embryos from 5 to 100 µM concentrations However, melatonin decreased the oocyte development at the 1,000 µM concentration. In conclusion, enriching the culture medium with 10 µM melatonin improved the development of in vitro manipulated rat oocytes.

Key Words: melatonin, oocyte, rat

W204 17β-estradiol and spontaneous myometrial contractions in ovariectomized rats. O. Yildiz-Gulay*[1], A. Bulbul[2], M. S. Gulay[1], K. Altunbas[3], and O. Ozden-Akkaya[3], [1]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Department of Physiology*, *Burdur, Turkey*, [2]*Afyonkarahisar Kocatepe University, Faculty of Veterinary Medicine, Department of Physiology*, *Afyonkarahisar, Turkey*, [3]*Afyonkarahisar Kocatepe University, Faculty of Veterinary Medicine, Department of Histology and Embryology*, *Afyonkarahisar, Turkey*.

The aim of this study was to evaluate the effect of injecting different doses and time intervals of 17β-estradiol on spontaneous myometrial contractions of ovariectomized rats. Three to 6 months old 71 female

Sprague Dawley rats, weighing 270±20 g, were used in the current study. The ovariectomized rats were randomly assigned to one control (Ov) and three experimental (17β-estradiol injected) groups of 18 rats each. Rats in the Ov group received daily sesame oil (0.2 ml, IM), whereas each rat in the three experimental groups was treated with daily IM injections of 25, 50 and 100 μg estradiol in sesame oil, respectively. Each group was further divided in 3 subgroups: 6 rats in each group were sacrificed by cervical dislocation at 18, 90 and 162 hr. In order to determine endogenous nitric oxide (NO) activity, L-arginine solution was used. Sodium nitroprusside was used for evaluation of the exogenous NO pathway. In addition, L-NNA (nitro-N-arginine) treatment was applied in order to determine the effect of endogenous NO at receptor level. Immunohistochemical evaluation was performed to determine cGMP-PK1 expression from the uterus samples. In the current study, 17β-estradiol treatments increased spontaneous myometrial contraction in dose and time dependent manner. Treatments also inhibited L-Arginin-NOS-NO-cGMP-PK1 pathway. However, our results indicated that 17β-estradiol did not show its effect through cGMP-PK1.

Key Words: 17β-estradiol, nitric oxide, myometrium

W205 Stability of reference genes in mouse liver after immunity stimulation. X. L. Dong, J. Q. Wang*, D. P. Bu, H. Y. Wei, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Real-time quantitative PCR (qPCR) is the technique of choice for detection and quantification of mRNA expression in cells or tissues. Suitable reference genes are used for normalization of mRNA across different samples for an exact comparison of mRNA transcription level. The purpose of the present study was to evaluate the expression stability of six reference genes *B2M*, *ACTB*, *GAPDH*, *SDHA*, *HPRT1* and *ARBP* using qPCR in mouse liver after immunity stimulation. Twenty four Kunming white mice were divided into four groups. They were injected with different vaccines as following isotonic Na chloride, Lipase + isotonic Na chloride, Immunostimulating Complexes (ISCOM), Lipase + ISCOM at 4 days after parturition. It was found that the specific antibody titer in serum increased significantly ($P<0.05$) at 8 days after parturition. The stability of these reference genes was investigated using geNorm application. The range of expression stability in the analyzed genes was (from the most stable to the least stable): *ACTB/GAPDH*, *SDHA*, *ARBP*, *HPRT1* and *B2M*. Results from the present study suggest that *ACTB* and *GAPDH* genes were relatively more stable than other tested genes. Based on our study we recommend that *ACTB* and *GAPDH* are better suited reference genes for normalization of mRNA across different samples while studying genes expression in mouse liver after specific treatments.

Key Words: quantitative real-time PCR, immunity stimulation, geNorm program

W206 Detection of alternative splicing form of PRL mRNA in the chicken anterior pituitary gland. N. Kansaku*[1], T. Sasanami[2], T. Ohkubo[3], G. Hiyama[1,4], and D. Zadworny[4], [1]*Azabu University*, *Sagamihara, Janap*, [2]*Shizuoka University*, *Shizuoka, Japan*, [3]*Kagawa University*, *Miki-cho, Japan*, [4]*McGill University*, *Montreal, QC, Canada*.

Prolactin (PRL) and Growth hormone (GH) belong to the same hormone gene family and are mainly produced in the anterior pituitary gland. The expression and presence of alternative splicing forms of GH mRNA were reported in several mammalian species including humans, where an exon skip splicing form of GH mRNA was detected using RT-PCR. However, it is unknown whether similar alternative splicing forms of PRL mRNA exist in mammals or birds. Accordingly, this study aimed to examine the possibility of presence of alternative splicing forms of PRL in the anterior pituitary gland of chickens. Total RNA was extracted from anterior pituitary gland and One micro gram of RNA was reverse transcribed using random hexamers . One-tenth of the reaction mixes were used for subsequent thermocycling. Amplification was conducted for 35 cycles using antisense primers which contained 2 bases of skipped exon sequence at the 3'-end (E3S, E4S, E3-4S) and sense primer (complimentary to 5' untranslated region) and polymerase with and without exonuclease activity individually. After PCR, products were separated by electrophoresis and the size of products was identified. Polymerase with exonuclease activity produced the expected size of amplicon for normal PRL cDNA, whereas exon3, exon4, exon3-4 skipped PCR products were amplified from the PCR using non-exonuclease activity polymerase. Although the relative amounts of normal PRL mRNA to the exon skipping forms requires further investigation, the results of this study may indicate the presence of small molecular weight isoforms of PRL in the anterior pituitary gland. In conclusion, expression of alternative splicing forms of PRL mRNA may result in truncated proteins which may provide novel roles and/or functions to PRL. Since exon 3 of chicken PRL gene contains the region encoding the putative glycosylation site and Cys which play important roles in formation of disulphide bond structure and globular structure, PRL isoforms lacking exon 3 or exon 4 coding region may have different physiological activity or function in the chicken.

Key Words: prolactin, splicing, exon

W207 Culture of chicken germline stem cells. J. N. Petitte*, J. Angerman-Stewart, R. Wysocki, and P. E. Mozdziak, *Department of Poultry Science, North Carolina State University*, *Raleigh*.

Germline stem cells are those cells that give rise to haploid gametes. In the unincubated chick embryo, 25 to 35 germline stem cells or primordial germ cells (PGCs) can be detected before gastrulation. Upon gastrulation, PGCs are found in the anterior germinal crescent. At 55 h of incubation, the PGCs enter the blood and circulate throughout the embryo. From 55 to 72 h of incubation, the PGCs leave the circulation and migrate to the gonadal ridge. In previous work, when FACS-purified PGCs from blood or the gonadal ridge are injected into the unincubated embryo, they retain their ability to migrate to the gonadal ridge, and they can develop into functional gametes in the adult bird. Further studies have been hampered by the low number of PGCs/embryo. The purpose of this study was to establish cultures of chicken germline stem cells from PGCs. Individual embryonic blood samples were obtained from stage 15 embryos, and they were seeded onto inactivated STO feeder layers . PGCs were cultured in KO-DMEM, 7.5% FBS, 2.5% chick serum, 20% BRL-conditioned media, essential and nonessential amino acids, and nucleosides. In some cases, hSCF, mLIF, and bFGF were added. Six lines of germ line stem cells were established from White Leghorn and Barred Plymouth Rock embryos. The ability of each line to migrate to the gonadal ridge was tested by labeling the cells with PKH-26 before injection into the subgerminal cavity of the unincubated embryo or into the vasculature of a stage 17 to 18 embryo. After 3.5 days of incubation the embryonic gonad was removed and the presence of PKH-labeled germline stem cells was examined. Germ line stem cells were also injected into embryos, incubated to hatch, and raised to sexual maturity. No somatic cell chimerism was observed. Roosters were test

mated to determine germ line transmission. The frequency of germ line chimeras ranged from 13 to 100%. Three lines always gave rise to germ line chimeras. The frequency of germ line transmission varied between lines and ranged from 0 to 41%. The results of this study confirm that cell lines of germ line stem cells can be established from chicken PGCs and can only give rise to fully functional gametes.

Key Words: stem cells, avian, primordial germ cells

Production, Management and the Environment: General

W208 Biodegradation of genetically modified seeds and plant tissues during composting with manure. T. Reuter*[1], T. W. Alexander[1], K. Stanford[2], and T. A. McAllister[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*, [2]*Alberta Agriculture and Rural Development, Lethbridge, AB, Canada*.

The increasing global market volume of genetically modified (GM) crops amplifies the potential for environmental impact and/or non-conformance with legislation. Methods proposed for disposal of crop residues should be assessed to prevent unintended distribution of GM materials. Composting is an inexpensive and location-independent option. To determine the effectiveness of composting for disposal of GM plant material, seed viability tests and molecular techniques were used to assess degradation during the composting process. Replicate samples of corn seeds, alfalfa leaves, and GM canola seeds, meal and pellets in sealed nylon bags were implanted into duplicate feedlot manure compost piles and collected periodically during 230 days of composting. The compost piles (25 m × 5 m × 2.4 m; L × W × H) each had initial weight of approximately 85,000 kg. Canola and corn seeds lost germination capacity after 7 days of composting at temperatures exceeding 50°C. Using PCR, plant-specific DNA fragments (882 bp) could be detected in meal and pellets, and in manure samples from random sites in the pile for up to 56 days, whereas those fragments in seeds and leaves were detectable for up to 230 days. Real-time PCR revealed small (<200 bp) plant- and GM-specific fragments in decreasing quantities up to 230 days in all samples. Southern blotting assessment of genomic DNA extracted from canola seeds verified differences in the persistence of intact Rubisco-, 16S- and GM-specific genes during composting. Composting GM and non-GM plant materials with manure resulted in inactivation of germination, and efficient, though not complete, DNA degradation. This study indicates that dissemination of viable GM seed or functional transgenes would be highly unlikely following composting of GM plant material.

Key Words: compost, genetically modified, viability

W209 Arrangements of *Acacia decurrens, Acacia melanoxylon* and *Alnus acuminata* as silvopasture systems in a high tropic ecosystem. A. Conde*[1], L. L. Betancourt[1], C. J. Jaramillo[1], A. Umaña[1], D. Barrera[1], and D. R. Chamorro[2], [1]*Universidad de La Salle, Bogotá, Colombia*, [2]*Corpoica, Bogotá, Colombia*.

The objective of this study was to evaluate dasometric measures during establishment period and initial effects on soil and the availability and quality of grass in silvopasture arrangements: live fences and tree dispersed in pasture in high tropic in Colombia. Three species of trees were planted in a hill pasture with *Pennisetum clandestinum* near to Sopo, Colombia (73° 57′ O, 4° 54′ N), 2580 meters mean altitude, 14 °C, mean rainfall 693 mm/yr, in two arrangements: A) Single row of two meters spaced trees like live fence and B) Dispersed Trees in pasture 10 x 5 m each line with one specie. Dasometric measures were: average height, basal diameter and diameter at 40 cm height, Three treatment were imposed: 1) *Acacia decurrens* (Ad) 2) *Acacia melanoxylon* (Am) and 3) *Alnus acuminata* (Aa) in a randomized complete block design with 6 replicates. Changes on soil and availability of forage and its quality was measured. Best growth were achievement for Ad and Am compared with Aa ($p<0.05$). In all dasometric measures were not differences between Ad and Am but *Alnus acuminata* showed lower means values than acacias ($p<0.05$). Pastures with trees did not show differences in chemical characteristic in soil compared with pastures without trees. Availability of forage was higher in pastures with trees dispersed 10x5 (720 g of dry matter/m^2) compared with pastures without trees (649 g of dry matter/m^2). Carbohydrates and protein fractions in grass did not report differences with or without tree into the pastures ($p>0.05$). Based in dasometric measures Acacia decurrens and Acacia melanoxylon had faster growth and best performance than the native *Alnus acuminata* in the reported ecosystem. The long term effects of planting tress in nutrient quality of grass (protein a carbohydrate fractions) and soil characteristics may become cumulative and need further research.

Key Words: silvopastoral systems, carbohydrate fractions, protein fractions

W210 Influence of *Acacia mangium* on soil chemical characteristics in a silvopastoral system in northwestern Venezuela. T. Clavero* and R. Razz, *Centro de Transferencia de Tecnologia en Pastos y Forrajes, Universidad del Zulia, Maracaibo, Estado Zulia, Venezuela*.

Acacia mangium (L.) Willd is an important multipurpose tree of tradicional agroforestry system in tropical semi-arid regions. Understanding the changes in soil properties in silvopastoral system is important in regulating the interactions between trees and understorey pastures. In this study, the influence of *Acacia mangium* on soil chemical characteristics under *Brachiaria humidicola* pastures in northwestern Venezuela was studied. The trees were seven years old at the time of the study. Transects extending from the tree trunk to open grass areas were established, and two soil depths (0-15 and 15-30 cm) samples were taken at 25 and 150% of the average canopy radius (4.5 ± 0.30 m) at five sites. A randomized block design was used with five replications. Soil analyses showed no significant differences ($p\geq 0.05$) in Na, Ca, K and ph under tree canopy compare to open pastures. Higher levels of soil C, N, P, Mg ($p\leq 0.05$) were found under *Acacia mangium* canopies as compared to open grass areas. Soil organic carbon content was higher by 38% in silvopastures than in adjacent open pastures. Soil organic carbon and N were maximum in 0-15 cm (0.88% and 150 mg/soil kg, respectively) and declined with the depth of soil. Total and mineral P contents were nearly uniform across the depths. Net mineralization rates were higher in silvopastoral system due to greater input of soil organic matter associated with higher soil biological activity from decomposition of litter and dead tree-roots. It was concluded that the incorporation of *Acacia mangium* in *Brachiaria humidicola* pastures improved soil chemical conditions.

Key Words: *Acacia mangium*, *Brachiaria humidicola*, silvopastoral

W211 Discrimination and classification of the new co-products from bio-energy production using infrared spectroscopy with multivariate techniques-AHCA and PCA: Comparison among blend DDGS, wheat DDGS and corn DDGS and between wheat and wheat DDGS, and corn and corn DDGS. D. Damiran and P. Yu*, *College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada*.

Dramatic increase in bio-ethanol production has resulted in different types of new co-products: wheat dried distillers grains with solubles (DDGS), corn DDGS, and blend DDGS. There is an urgent need to quickly understand molecular structural profile in these co-products. The objective of this study was to investigate molecular structural features of the new co-products from Bio-energy product using infrared spectroscopy with two multivariate spectral analysis techniques as a novel approach: agglomerative hierarchical cluster (AHCA) and principal component analyses (PCA) and compared among blend DDGS, wheat DDGS and corn DDGS, wheat and wheat DDGS, and Corn and Corn DDGS. The results show that by application of these two multivariate techniques of AHCA (Distance method: Euclidean; Cluster method: Ward's algorithm) and PCA with the infrared spectroscopy, it makes possible to quickly discriminate and classify the inherent molecular structural features among the different types of DDGS and between wheat and wheat DDGS and between Corn and Corn DDGS with a great efficiency, in the fingerprint region of protein amide I and II ca. 1720-1484 cm-1. The DDGS and feedstock inherent structures can be grouped in separate ellipses. The first principal component explained > 90% of the total variance. Information from this study may provide a further insight as to why DDGS exhibit different biodegradation behaviours and nutrient availability in animals.

Key Words: classification and discrimination of molecular spectra, co-products from bio-energy production, DDGS

W212 Biochemical profile of Maguey silage. G. Álvarez-Fuentes*, J. C. García-López, J. M. Pinos-Rodríguez, Y. Jasso-Pineda, and F. M. Tristán-Patiño, *Universidad Autónoma de San Luis Potosí, San Luis Potosí, SLP, México*.

With the aim of characterize silage maguey alone and mixed; pH, hemolytic activity of maguey saponins, humidity percentage, dry matter, color and smell was measured of silage maguey alone and mixed with alfalfa and mezquite pod. Five maguey silages were elaborated in micro silos in glass bottles 10 cm diameter wide and 25 cm high, each treatment with five replicas: Maguey 100% (E1); Maguey 90% and mezquite pod 10% (E2); Maguey 50% and alfalfa 50% (E3); Maguey 40% and alfalfa 60% (E4); Maguey 33.3%, alfalfa 33.3% and mezquite pod 33.3% (E5). The first four maguey silages had higher humidity levels; E1 90.2%, E2 82%, E3 81.2%, E4 82.7% and E5 58.4%, there were statistically different ($P<0.05$), E1 and E5 were different to the rest of treatments. There were no differences ($P>0.05$) for pH 3.9, 3.7, 3.7, 3.6 y 3.7 values for each treatment, respectively. Regarding quality such as color there were green to light green; and the smell was like lactic acid, characteristic of good silage procedure. There was a decrease in the hemolytic activity of saponins observed in the first hours of fermentation and disappear through the time. It is concluded that silages made of maguey are not affected by high humidity content, and that maguey can be used combined with other forage with not optimum characteristics for silage.

Key Words: silage, maguey, saponins

W213 Copper and zinc accumulation in dairy production systems. T. Downing*, K. Stiglbauer, M. Gamroth, and J. Hart, *Oregon State University, Corvallis*.

Dairy farmers often use either $CuSO^4$ or $ZnSO^4$ solutions in footbaths to control diseases of the hoof. Solutions are frequently changed before each milking requiring significant quantities of Cu and/or Zn a year. Used solutions are dumped into the dairy manure handling system and applied to fields in their liquid manure system. The objectives for this project were to survey 30 dairy farms in Oregon to estimate the amount of $CuSO^4$ and $ZnSO^4$ used in footbaths, measure mineral concentrations in soils on the farm, access the concentration of Cu and Zn in the manure system and measure minerals in the forage produced on the dairy. Footbath practices were recorded for each dairy. Soils samples were collected from two major fields at 15 cm deep and analyzed for Cu and Zn. Forages grown on the farm were sampled and analyzed for Cu and Zn and manure was collected directly from milk cows and from the liquid manure storage system. Forages, soils and manure were all analyzed at Agri-Check Labs, Umatilla, OR. Footbath usage by farm ranged from no usage to continuous usage. Soil Cu concentrations ranged from .7 to 34.7 ppm and averaged 5.7±6.6. Soils Zn concentrations ranged from .6 to 41.8 ppm averaging 10.1±9.3. Copper concentrations in forages ranged from 1 to 10 ppm averaging 3.4±2.1 and Zn ranged from 3 to 51 ppm averaging 13.8±10.3. Manure Cu concentrations directly from milk cows were very consistent typically at 10 ppm with Cu concentrations in the manure storage ranging from 2 to 58 ppm averaging 10.3±12.02 ppm. The use of $CuSO^4$ and $ZnSO^4$ in footbaths on dairies in Oregon continue to a common practice. Over 75% of dairy soils tested are considered high (>2ppm) in Cu concentration and 38%were extremely high (>5ppm). Using $CuSO^4$ and $ZnSO^4$ in footbaths is creating potential long term environmental and cropping challenges on many Oregon dairies.

Key Words: footbaths, copper sulfate, zinc sulfate

W214 Growth performance, carcass yield and economical evaluation of two genotypes of quails under two housing systems. D. Cardoso-Jiménez[1], R. Rojo-Rubio[1], A. Z. M. Salem*[1,2], S. Rebollar-Rebollar[1], J.L. Martínez-Benítez[1], and J. Hernández-Martínez[1], [1]*Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Toluca-Tejupilco, Estado de México, México*, [2]*Department of Animal Production, Faculty of Agriculture (El-Shatby), Alexandria University, Alexandria, Egypt*.

Two genotypes of quails (*Coturnix coturnix japonica*) of Japanese (JAP) and *Coturnix coturnix japonica* variety Jumbo (JUM)) were evaluated for growth performance and carcass yield as well as the economic efficiency, reared in floor (F) or cage (C) housing systems. Eighty four quails (~58g) of each genotype of one week of age (both sexes) were used during the 19 days of the experimental period reared in the two housing systems. Quails were randomly assigned in two groups of bifactorial experimental design (2 genotype x 2 housing systems, of 42 chicks for each group). At the end of the experimental period, all animals of each group were slaughtered (7 repetitions of each) for the carcass yield measurements. Feed intake (DMI) was increased in all quails groups except in JAP reared in F versus C system ($P=0.001$). Overall, DMI was increased ($P=0.032$) in quails reared under C versus F system. ADG was improved ($P=0.011$) in JUM of the F system than the other quails groups, although the final BW was not affected ($P=0.477$) under the two rearing systems, as an overall mean. Overall, the Average daily gain (e.g. ADG) was higher (7.52 vs. 4.7; $P=0.0117$) in JUM versus JAP birds. Consequently, Feed conversion ratio (e.g. FCR) was improved (3.35 vs. 3.8; $P=0.0001$) in JUM versus JAP quails reared in both hous-

ing systems. Carcass yield were not affected (P=0.327) neither by the genotype nor the housing system during the experiment, although and C system was cheaper than F system for the both genotypes. Reared quails in cages were more profitable and comfortable for quails that appeared a better animal growth performance (e.g. final BW, ADG and FCR), while best improvement in bird growth performance was in JUM versus JAP under the two housing systems.

Key Words: quails, housing systems, growth performance

W215 The effects of management and environmental factors on broiler breeder performance in Iran. H. Hosain*[1], M. Moradi Sharbabak[2], A. Noshari[1], M. Zaghari[2], and M. B. Zandi[2], [1]*Tehran Azad University, Karaj, Tehran, Iran*, [2]*University of Tehran, Karaj, Tehran, Iran*, [3]*Young Researchers Cloob, Sanandaj, Kurdistan, Tehran*.

In order to study the effect of management and environmental factors on coob strain data from 40 herds of broiler breeder under different environmental condition of Iran were analyzed. The chicken traits were measured including the persistency of peak production and total chicken production. The management and environmental factors such as the percentage of uniformity in body weight (age of 20 weeks), age and weight at the end of uniformity stage, the same and to be difference in age (all-in all-out), altitude, to be separate hen and cockle in growing period or to be joint, the number of birds in unit area and the feeder and watering area were investigated. The GLM procedure of SAS software (2002) was used for analyses. The results showed that management factors such as the percentage of body weight uniformity, age and weight at the end of uniformity stage, all-in all-out, feeding area have significant effects (P<0.01) on performance traits of broiler breeder. Altitude from sea level as a environmental factor has significant effect on chicken production (P<0.01) and the production persistency (P<0.05) too. The number of birds per unit area has significant effect (P<0.01) on performance traits. Moreover under growing period if hens were with cockle the performance traits were higher (P<0.1).

Key Words: environmental factors, altitude, Coobstrain

W216 Effects of stocking rate of weaned to finishing pigs on bermudagrass ground cover. S. Pietrosemoli*[1], J. T. Green[2], and R. Vibart[3], [1]*Animal Science Department, North Carolina State University, Raleigh*, [2]*Crop Science Department, North Carolina State University, Raleigh*, [3]*AgResearch Limited, Grasslands Research Centre, New Zealand*.

Management of outdoor pig operations presents environmental issues such as the deterioration of vegetative ground cover, soil disturbance, and high nutrient loads. Vegetative ground cover ensures that nutrients from swine excreta are held within the soil and plants and kept from leaching or flowing to surface waters. At the Center for Environmental Farming Systems in Goldsboro, NC, 60 purebred Yorkshire female and castrated pigs (18.4 and 118.5 kg initial and final BW, respectively) were used to evaluate the effects of stocking rate (SR) on soil and vegetation disturbance. The trial was conducted for 91 d during summer 2008 in a mature (> 10 years) bermudagrass (*Cynodon dactylon*) pasture. Five hogs were randomly assigned to each of twelve paddocks sized to equal SR of 37, 74, 111, and 148 head/ha. Wallows, shade, feeders and nipple waterers were provided at fixed locations within each paddock. Animals had *ad libitum* access to concentrate feed. Ground cover was assessed every 14 d using a step-point technique with transect lines evenly spaced across the plots. The experimental design was a randomized complete block, with three field replicates. Data were log (log[x+10]) and square root ([x+10]1/2) transformed for percent bermudagrass cover (BGC), vegetation cover (VC), and bare soil (BS). Percent BGC and VC decreased linearly ($P \leq 0.001$; 87.4, 78.8, 73.8, 60.4%; and 92.6, 84.8, 79.9, 67.6%, respectively) whereas percent BS increased linearly with increasing SR ($P \leq 0.001$; 7.4, 15.2, 20.0 and 32.4%). Daily gain was not influenced by SR (avg: 0.89±0.02 kg/d). Results suggest that to maintain vegetative ground cover above 80% with continuous access to pasture, stocking rate must be kept below 74 hogs/ha during the finishing phase. In addition, based on observations from this trial, it may be possible to alter vegetative ground cover using a more mobile setting of drinking water, shade and feeders.

Key Words: outdoor pig production, stocking rate, ground cover

W217 Suckling effect on the survival of crossbreed goats kids at weaning. L. F. D. Medeiros[1], D. H. Vieira[2], C. A. Oliveira[1], D. F. Guerson[1], G. M. Fagundes[1], J. P. F. Silveira[3], R. S. B. Pinheiro[3], V. L. Tierzo[3], and J. L. C. B. Reis*[4], [1]*Rural Federal university of Rio de Janeiro, Seropedica, RJ, Brazil*, [2]*Center of Creation of Animals of Laboratory, Rio de Janeiro, RJ, Brazil*, [3]*São Paulo State University, Botucatu, SP, Brazil*, [4]*University of Agrarian Sciences, University of Marília, Marília, SP, Brazil*.

Seventy crossbreed (½ Boer + ½ Nondescript breed) goats kids were randomly assigned, from 15 to 90th days of age, in three treatment groups: T1 – kids suckling continuously (n=26), the kids stay with there mothers during the day; T2 – kids suckling twice a day (n=23), the kids were set with there mothers for suckling during twenty minutes, in the morning and afternoon; T3 – kids suckling once a day (n=21), the kids suckling only in the morning, during forty minutes. From 8th days of age the kids stay all night in the shelter separate of there mothers, where received a balanced supplement and water. After 15th days of age the kids had access to the pasture. The survival rate at weaning was 94.36%, with no significant treatment effect (P>0.05). Also there was no significant difference (P>0.05) based on birth type and sex by the survival to weaning.

Key Words: goats, management, mortality

W218 The effect of Clarifly™ larvacide in purchased grains on fly populations on dairy farms in northern Vermont. E. E. Osmanski*[1], R. E. Butzler[2], C. S. Ballard[2], and C. S. Mooney[2], [1]*The University of Vermont, Burlington*, [2]*William H. Miner Agricultural Research Institute, Chazy, NY*.

Reducing fly populations on dairy farms can increase cow comfort and reduce the spread of disease pathogens. The objective of this experiment was to determine the effect of inclusion of diflubenzuron larvicide (Clarifly™) in purchased grains on fly populations on dairy farms. Twelve dairy farms were assigned to 6 blocks by herd size, geographic location and lactating herd housing. On treated dairy farms, Clarifly™ was added to all purchased grains to achieve an intake of 0.10 mg diflubenzuron/kg BW/d. Control dairy farms were permitted to use all other fly control methods. Each dairy was visited once in each of 10 14-day periods from June to November 2008. Fly populations in lactating herd housing were quantified with fly speck count on 3 × 5 notecards (n = 3 per period) and collection of flies on a sticky trap during walk on predetermined path (n = 1 per period). In calf housing, fly populations

were measured using fly speck notecards (n = 3 per period) and on-calf counts (n ≤ 10 per period). Data were analyzed as a randomized block design with main effects of random block, treatment, period, and treatment by period interaction in MIXED procedure of SAS. Period effects ($P < 0.01$) reflected normal seasonal changes in fly population. With treatment, fly speck counts decreased in the lactating herd housing when compared to control (58 vs. 132 per card, $P < 0.02$) but an interaction of treatment and period ($P = 0.07$) increased difference in summer and removed difference after hard frost. Also, total flies collected in lactating herd housing were decreased with treatment ($P < 0.01$). In calf housing, treatment did not decrease fly populations as measured by fly specks count (200 per card) or flies per side of calf (6.0 flies). The inclusion of Clarifly™ in purchased grains decreased fly populations evident in lactating herd housing but not in calf housing. The lack of effect of Clarifly™ in calf housing is likely related to limited intake of purchased grain during first weeks of life.

Key Words: fly control, dairy cattle

W219 Black soldier fly larvae grown on cow manure. M. Chahine*[1], M. E. de Haro Marti[2], S. St Hilaire[3], O. Pozo[1], and R. E. Sheffield[4], [1]*University of Idaho, Twin Falls*, [2]*University of Idaho, Gooding*, [3]*Idaho State University, Pocatello*, [4]*Louisiana State University, Baton Rouge*.

The objective of the study was to examine the feasibility of growing black soldier fly larvae on a dairy farm to decrease the volume of manure generated. The study was conducted on a 3000 cows dairy in southern Idaho. Small scale containers using 640-gallon water tanks were designed so that fresh manure and black soldier fly eggs could be layered. Small ramps that allowed the larvae to migrate when ready to pupate were built in the containers. At the top of each ramp a hole was designed through which prepupae fell into buckets. Other containers used in the study included containers purchased from ESRI International LLC (lab Container) as well as a recycle bin. Prior to initiation of the study, a former structure of manure separator was modified to give shadowed conditions and some wind protection to the larvae. Study was started on June 11 2008. Approximately 1,763,100 eggs were distributed into the three previously mentioned containers. On June 27, the larvae were fed fish offal to stimulate their growth. On July 4 2008, the harvest of the first prepupae started in small amounts. A week later, there was an intensive period of two weeks with 88% of the harvest migrating during this period. Afterward, the harvest decreased dramatically. The shape of the recycle bin container made the migration difficult to accomplish and it was removed from the study. The total harvested quantity from all containers and the floor was 13,238 g, equivalent to around 93,990 prepupae. This value represents only 5.3% of the original population. The large proportion of losses was distributed between immature and dead larvae within the containers. Black soldier larvae reduced manure by 40 percent on a dry matter basis even in less than ideal conditions. The best behavior and development of the larvae occurred when the maximum environmental temperature exceeded 30°C. For better results, it would be important to design a facility that provides stronger protection against rain, wind and low temperature. Even during summer, the wide differences in temperatures between day and night could present challenges for growing black soldier larvae outside without heating in high desert climates.

Key Words: manure, black soldier fly

Ruminant Nutrition: Dairy Calves

W220 The influence of parity, sex and twining on birth weight of Holstein calves. M. H. Fathi Nasri* and H. Farhangfar, *Department of Animal Science, The University of Birjand, Iran*.

The birth weight of calves is one of the factors affect the calf growth especially before weaning. In this study the effects of dam parity, sex and twining factors on calf birth weight were evaluated. The birth weight records of 1654 calves born in a large dairy herd during 6 years were analyzed using the SAS Proc GLM according to the following model: $Yijk = \mu + Pi + Sj + Wk + eijk$ where Yijk = the dependent variable, μ = overall mean, Pi = the fixed effect of parity (i = 1 to 9), Sj = the fixed effect of sex (j = 1, 2), Wk = the fixed effect of twining (k = 1, 2), and eijk = random residual. Least square means (LSM) are reported and significance is declared at $P < 0.05$. The effect of parity (Table 1) on calves birth weight was significant. Also the calf sex and twining effects on calves birth weight were significant, so that the male calves were 3.4 kg heavier than females (42.1 vs. 38.7 kg, respectively) and twins calves were 7.8 kg lighter than single birth calves (32.7 vs. 40.5 kg, respectively). As the birth weight is used as a criterion for genetic selection of candidate replacement calves, these environmental factors are needed to be taken into account in the statistical selection models.

Table 1. The birth weight of calves at different parities

Parity	1	2	3	4	5	6	7	8	≥9
Number	124	349	370	270	197	140	78	59	34
LSM	37.8^{c}	38.7^{c}	39.4^{b}	40.0^{b}	41.3^{ab}	41.9^{a}	41.4^{a}	41.4^{a}	41.5^{ab}
SD	0.60	0.44	0.40	0.43	0.49	0.54	0.69	0.80	0.98

Means in the same row of Tables with no common letters differ.

Key Words: calf, birth weight, parity

W221 Influence of altering conventional milk replacer feeding rate and protein source on pre- and post-weaning performance and health of dairy calves. D. Carlson*[1], S. Hayes[1], B. Ziegler[2], R. Larson[2], M. Raeth-Knight[3], G. Golombeski[3], J. Linn[3], D. Ziegler[4], and H. Chester-Jones[4], [1]*Milk Products, LLC, Chilton, WI*, [2]*Hubbard Feeds Inc., Mankato, MN*, [3]*University of Minnesota, St. Paul*, [4]*University of Minnesota, Southern Research and Outreach Center, Waseca*.

Holstein heifer calves (n = 125; 2 to 4 d of age) were assigned randomly to 1 of 4 medicated milk replacer (MR; 20% protein, 20% fat) programs to evaluate the effect of feeding rate and protein source on pre-weaning (d 1 to 42) and post-weaning (d 43 to 56) performance and health. Calves were housed in individual calf pens within a naturally-ventilated barn with curtain sidewalls. Treatments (Trt) were: 1) all-milk (AM) protein MR fed at 0.57 kg/d (powder weight) in 2 daily feedings for d 1 to 35 and 0.28 kg/d 1X daily from d 36 to 42 (AMCON); 2) AM protein MR fed as Trt 1 from d 1 to 14, stepped down (SD) to 0.45 kg/d fed in 2 daily feedings from d 15 to 35, then 0.23 kg/d fed 1X daily from d 36 to 42 (AMSD); 3) Animal plasma (APL) and milk protein MR with additives fed as in Trt 2 (APLSD); 4) Wheat (W), APL, and milk protein MR with additives fed as in Trt 2 (WAPLSD). All MR were reconstituted with water to achieve a 12.5% solids solution. Calves were fed an 18% CP (as-fed) texturized calf starter and had access to fresh water. Average daily gain (ADG) was not affected by MR protein source from d 1 to 14; likewise, neither MR protein source nor feeding rate affected ADG from d 15 to 42 or d 43 to 56. Calf starter dry matter intake (DMI) was similar from d 1 to 14, but greater ($P < 0.05$) from d 1 to 42 for AMSD (0.41 kg/d), APLSD (0.38 kg/d), and WAPLSD (0.36 kg/d) compared with AMCON (0.29 kg/d). Total MR DMI was greater ($P < 0.05$) for AMCON (21.1 kg) compared with AMSD (18.5 kg), APLSD (18.4

kg) and WAPLSD (18.3 kg). Total health costs did not differ among groups. Under the conditions of this study, decreasing feeding rate of a conventional milk replacer at d 14 resulted in similar performance due to greater calf starter intake.

Key Words: dairy calves, milk replacer, protein source

W222 Effect of milk replacer carbohydrate source on performance and health of dairy calves. J. K. Bernard*[1] and A. F. Kertz[2], [1]*University of Georgia*, *Tifton*, [2]*ANDHIL LLC*, *St. Louis, MO*.

Fifty-one Holstein calves (23 male and 28 female) were used in an 8 wk randomized block design trial to determine the effect of milk replacer carbohydrate source on performance and health. After receiving colostrum for 2-d, calves were randomly assigned to one of four experimental milk replacers. Experimental milk replacers were formulated to contain 20% protein and 20% fat (as fed basis) using different sources of carbohydrate (MSC Speciality Nutrition, Carpentersville, IL). Carbohydrate sources in the milk replacers were: 33% lactose whey (A), 25% lactose whey + 20% corn syrup solids (B), 33% lactose whey + 10% corn syrup solids (C), or 25% lactose whey + 10% corn syrup solids + 10% dextrose (D). Experimental milk replacers were reconstituted to 12% solids and fed at a rate of 0.45 kg/d divided into two equal feedings during wk 1-5. During wk 6 the amount of milk replacer was reduced by 50% and fed once daily. Calves were weaned at the end of wk 6. Starter grain was offered for ad libitum consumption throughout the trial. Body weights and measurements were recorded every 2 wk. Intake of milk replacer was lower ($P = 0.03$) for D versus B or C: 3.55, 3.57, 3.56, and 3.52 kg/d for A, B, C, and D, respectively. Starter intake was similar among treatments; 0.26, 0.34, 0.36, and 0.29 kg/d for A, B, C, and D, respectively. Calves receiving experimental milk replacer C and D had numerically higher ($P = 0.18$) rate of BW gain during wk 0 through 6 than A: 307, 376, 443, and 481 g/d for A, B, C, and D, respectively. Calves fed C gained more ($P = 0.01$) wither height than those fed A or D: 6.0, 7.1, 8.4, and 5.8 cm for A, B, C, and D, respectively. No differences were observed in hearth girth or body length among treatments. Average scour score was higher ($P = 0.02$) for B and D compared with A: 1.65, 2.15, 1.75, and 2.01 for A, B, C, and D, respectively. The results of this trial indicate that corn syrup solids can be used to replace a portion of lactose whey in milk replacers, but the combination of lactose whey, corn syrup solids and dextrose is not advantageous.

Key Words: milk replacer, carbohydrate, dairy calve

W223 Impact of glycerol in milk replacer on dairy calf performance. M. Raeth-Knight*[1], J. Linn[1], R. Larson[2], and J. Salzer[1], [1]*University of Minnesota*, *St. Paul*, [2]*Hubbard Feeds*, *Mankato, MN*.

The objective of our study was to evaluate the impact of adding glycerol to milk replacer (MR), as a partial replacement for lactose, on calf performance and health. Following birth, thirty-four Holstein or Holstein crossbred calves were blocked by sex and breed and randomly assigned to 1 of 2 MR treatments for 70 d. Treatments were MR without glycerol supplementation (CON) or MR with glycerol added at 35% of the total DM (G). Calves were born November to December of 2007 and were individually housed in outdoor hutches. Colostrum was fed twice daily the first 2 d following birth. Calves assigned to the CON treatment were offered a 20% protein: 20% fat MR (42.7% lactose) at 0.32 kg MR DM twice daily from 3 to 36 d of age and then once daily from d 37 to weaning at d 42. A 30% protein: 30% fat MR (23.2% lactose) was fed to calves on the G treatment. Calves were offered 0.22 kg MR DM and 0.11 kg glycerol (DM basis) twice daily d 3 to 36 and then once daily d 37 until weaning at d 42. The CON and G MR were mixed with water to contain 15.2% solids and glycerol was added to the G MR after being reconstituted with water. Starter (18% CP) and water were offered ad libitum starting d 3. Feed intake was recorded daily. Body weight was recorded at birth and 14, 28, 42, 56 and 70 d of age. Hip height was measured at birth and d 70. Fecal scores were observed daily and blood samples were taken on d 21 and 56. There was no difference in MR, starter or total DM intake across treatments. Calves consumed 0.59 kg/d MR and 1.06 kg/d starter DM pre-weaning and 3.10 kg/d starter DM post-weaning. Average daily gain was also similar with calves gaining 0.59 and 1.01 kg/d pre- and post-weaning, respectively. There was no difference in stature growth with calves gaining 15.2 cm in hip height d 1 to 70. Blood glucose concentration was 10.4 mg/dl higher for CON compared to G calves on d 21 however not different at d 42. Fecal scores indicated no impact of MR treatments on fecal consistency with an average score of 1.1 pre-weaning across treatments. Under the conditions of this study, glycerol replaced approximately 46% of lactose in MR without negatively impacting calf growth or health.

Key Words: milk replacer, glycerol, dairy calves

W224 Effect of group penning on dairy calf performance. D. Carr* and A. Chestnut, *Vigortone Ag Products*, *Hiawatha, IA*.

Two trials were conducted to evaluate the effect of group vs individually fed calves on pre-weaning growth and starter intake. In trial 1, Holstein bull calves from a single source were gathered weekly and assigned to either group or individual pens after being stratified by age and weight. A total of 25 calves were distributed among 5 pens (13.4m^2) for the group penned treatment (GP) and 23 calves were allotted to individual pens (3.3m^2) for the individual penned treatment (IP). A 22% protein 20% fat milk replacer was fed to all calves and an 18% protein calf starter feed was provided ad libitum to all calves. The GP calves received 1400 g milk replacer mixed in 9.5 l water twice daily from a teat bar with five teats connected to a shared compartment. The IP calves were bucket fed 280 g milk replacer in 1.9 l water twice daily. Milk replacer feedings were reduced from twice daily to once daily during wk 5 and calves were weaned at the end of wk 5. Data was analyzed using AOV with means separated by LS. In trial 2 the same protocol was followed with the following changes. Group pens (20.1m^2) consisted of 6 calves in each of 6 pens and IP calves were divided between those that were bucket fed (n=12) or bottle fed (n=15) with teats similar to those used by GP calves. A 23% protein 15% fat milk replacer was fed to all calves. In trial 1, GP calves gained more weight than IP calves by 2 wks (4.4 vs 3.0 kg, $P<0.10$) and by 5 wk (19.0 vs 14.4 kg, $P<0.01$). Starter intake tended to be greater for GP than IP calves at 2 wk (0.7 vs 0.4 kg, $P<0.10$) but not at 5 wk (12.5 vs 9.6 kg, $P>0.10$). In trial 2, weight gains of IP calves fed by bucket vs bottle were similar ($P>0.50$). At 2 wk GP calves gained more than IP calves (7.2 vs 5.7 kg, $P<0.05$) but displayed similar gains by 5 wk (21.6 vs 22.7 kg, respectively). Starter intakes were similar ($P>0.10$) for GP and IP calves at 2 wk (2.0 vs 1.7 kg, respectively) and at 5 wk (16.8 vs 15.5 kg, respectively). Group penning calves has the potential to reduce labor without reducing performance.

Key Words: calves, group, penning

W225 Relationship between immunoglobulin G intake and serum immunoglobulin G concentrations in calves fed titrated levels of immunoglobulin G in colostrum replacers. J. M. Campbell*[1], J. C. Gawthrop[2], A. W. Riad[2], L. E. Russell[1], S. K. Hayes[1], J. D. Quigley[1], and J. D. Crenshaw[1], [1]*APC, Inc.*, *Ankeny, IA*, [2]*CalfCare*, *North Manchester, IN*.

The impact of increasing the mass of immunoglobulin G (IgG) concentration in a single feeding of a colostrum replacer (CR) containing IgG derived from bovine serum fractions on serum IgG and the ability to achieve adequate passive transfer in calves was determined in two experiments. In experiment 1, forty-five heifer or bull calves were randomly assigned to receive a CR containing 130, 150, 170, or 190 g of IgG. In experiment 2, sixty heifer or bull calves were randomly assigned to receive a CR containing 125, 150, 175, 200, or 225 g of IgG. For both experiments, care was taken to equalize sex among treatments. All CR were blended, individually packaged, and irradiated prior to feeding calves. Colostrum replacers were reconstituted in warm water, mixed using a hand blender to a constant solids concentration of 20.9%, and fed with an esophageal feeder. Colostrum replacers were fed in one feeding at 1 h of age. Acquisition of passive immunity was assessed by measuring 24-h serum IgG levels, serum protein levels, determining apparent efficiency of absorption (AEA) of IgG, and assessing the ability to prevent failure of passive transfer (FPT). In experiment 1, increasing mass of IgG intake from 130 to 190 g of IgG resulted in a linear increase ($P < 0.05$) in 24-h serum IgG and a linear decrease in percent FPT. No differences were noted in serum total protein or AEA. In experiment 2, increasing IgG intake from 125 to 225 g of IgG resulted in a linear increase ($P < 0.05$) in 24-h serum IgG and serum total protein, and a linear decrease in AEA and percent FPT. Collectively, these studies indicate that increasing mass of IgG in CR derived from bovine serum fractions fed in the one feeding improves subsequent serum IgG and passive transfer in calves.

Key Words: calves, immunoglobulin, colostrum replacer

W226 Effects of protein sources in calf milk replacers on growth and fecal score of dairy calves. S. Y. Luan[1], J. Q. Wang*[1], D. P. Bu[1], H. T. Zhang[1], Z. F. Zhou[1], and A. F. Kertz[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, P. R. China*, [2]*ANDHIL LLC*, *St. Louis, MO*.

The objective of this study was to evaluate soybean and milk protein sources in milk replacer on pre- and post-weaning growth of female Holstein dairy calves. Forty-eight calves (housing outdoors in individual hutches at Mengniu Australia International Dairy Farm) were blocked by BW and assigned randomly within block to one of two milk replacer treatments: milk replacer containing soy protein (MR-S, $3.07/kg) or milk protein (MR-M, $4.31/kg). Milk replacers contained soybean protein (soy protein concentrate to provide 50% of total protein) or milk protein (whey protein). Calves were fed 500g/d DM divided into two equal feedings mixed into 2 liters water per feeding, from d-4 to 10, and then reduced to 400 g/d from d-11 until weaning. Milk replacers contained 22% CP and 18% fat. Body weight, wither height, heart girth and blood samples were measured and collected at birth, and then on d 11, 18, 25, 32, 39, at weaning, 46, 53, and 60. Calf starter (CS, $0.55/kg) and water were offered for ad libitum consumption from d-4, and CS feed refusals were measured daily. No hay was fed. Fecal scores were recorded daily. Weaning criterion was based on a minimum daily starter intake of ≥900 g for 2 consecutive days. Body weight, wither height, heart girth, dry matter intake from both milk replacer and calf starter, and gain to feed ratio were not different between treatments. And all of the selected blood metabolites (BUN, GLU, NEFA and BHBA) were also not different from birth to 60d. Fecal scores between birth and 14 d were significantly higher($P<0.05$) for calves fed MR-S versus MR-M, but did not differ for d 15 to 28, 29 to weaning, and weaning to 60 d old. Feed cost(including milk replacer and starter) per calf was significantly greater ($P<0.01$) for calves fed MR-M. Under conditions of this study, compared with the milk protein milk replacer, the calves fed MR-S achieved the same level of body growth and reduced feed cost by 26%.

Key Words: calves, soybean protein, milk protein

W227 Effects of combining hydrolyzed wheat gluten and spray dried plasma in calf milk replacer (CMR) on calf performance. D. Wood*, J. Sowinski, and R. Blome, *Animix*, *Juneau, WI.*

There are considerable published data and wide scale use of plasma in CMR. Hydrolyzed wheat gluten protein (WGP) is widely used as a milk protein replacement, particularly in the sizable EU. There are no data examining a combination of these two protein sources in CMR. The objective of this study was to evaluate if supplying functional proteins in spray dried bovine plasma (SDBP) can improve effectiveness of using WGP in CMR. Auction sourced Holstein bull calves (n=120; app. 1 wk of age) were shipped to the facility and randomly placed in individual raised, slatted stalls. Calves were randomly assigned to receive either a CMR (22% CP, 20% fat) containing 6% WGP and 5% SDBP providing 24.5% and 17.7% of total CP respectively (W/P; n=60), or 2.) 22:20 all-milk formula (Control; n=60). Both formulas contained oxytetracycline / neomycin and mannanoligosaccharides. Content of LYS was 2.19% and 1.93% in W/P and control, respectively. A starter grain (17% CP, 4% fat) was introduced day 14. Individual calf BW was determined at placement, on d 15, 29 and 43. Initial BW were 47.3 and 48.1 kg for W/P and control respectively ($P < 0.18$). Calves fed the all milk formula grew faster ($P<0.05$) from d 0 - 15 than calves fed W/P (0.23 vs. 0.18 kg/d). This trend was reversed during the second period when W/P fed calves grew faster ($P<0.059$) than control calves (0.86 vs. 0.90). Over the entire experimental period (0-43 d) there was no significant treatment effect on daily gain (0.64 and 0.65 kg/d for control and W/P fed calves, respectively). Twenty-five percent fewer calves fed the W/P diet required treatment for health problems week one ($P<0.32$) while 35% more W/P calves were treated week five ($P<0.12$). There was a trend for reduced incidence of grain refusal by 24% in W/P fed calves ($P<0.16$). Mortality/cull was 6 and 4 for W/P and control, respectively. In conclusion, a combination of WGP and SDBP can effectively replace up to 42% of the milk protein in CMR fed to young calves.

Key Words: calf, plasma, wheat gluten protein

W228 Hydrolyzed proteins from animal origin can replace dried skim milk from milk replacer formula. M. Terré*[1], E. Borda[2], F. Boe[1], and A. Bach[1,3], [1]*IRTA-Unitat de Remugants*, *Barcelona, Spain*, [2]*Bioinerica, S.A.*, *Barcelona, Spain*, [3]*ICREA*, *Barcelona, Spain*.

Nowadays, the increasing price of protein from milk origin leads the industry to investigate new ingredients for milk replacers (MR). Palbio calves RD and Palbio calves SD (Bioiberca S.A., Spain) are two products obtained from the enzymatic hydrolysis of porcine intestinal mucosa, which comply with European legislation concerning animal by-products manufacturing and non-ruminant and ruminant feeding regulations. Forty-five Holstein male calves (13.8 ± 6.20 d old and

42.1 ± 5.34 kg of BW) were arranged in 3 groups to study the effect of replacing part of dried skim milk from MR by Palbio calves RD or Palbio calves SD. The three groups were: calves fed a MR based on dried skim milk (CT), calves fed a MR containing 5.5% of Palbio calves SD (PSD) and calves fed a MR containing 14.5% of Palbio calves RD (PRD). Calves were fed an isonitrogenous MR (23.4% CP) at 12.5% DM at the rates of 4 l/d from 1-7 d, 6 l/d from 8-28 d, 4 l/d from 29-35 d and 2 l/d from 36 to weaning day (42 d). Calf starter was offered ad libitum until the end of the study (42 d). Individual calf MR and starter consumption were recorded daily, and calves were weighed weekly. Fecal scores and medical treatments were recorded daily. Performance data were analyzed with an ANOVA with repeated measures, and medical treatments and liquid feces with a logistic regression. Comparisons with $P \leq 0.05$ were considered as significant. None of the performance parameters measured (BW, ADG, starter and milk replacer intake, gain to feed ratio) was affected by MR formula. There were no differences in the weekly number of days that calves were not medically treated (6.7, 6.6 and 6.4 d in CT, PSD and PRD calves, respectively) and the weekly number of days with no liquid feces (6.6, 6.5 and 6.1 d in CT, PSD and PRD calves, respectively). It is possible to replace part of dried skim milk from MR formula by hydrolyzed protein without impairing calf growth and calf starter intake, and without increasing the number of days with liquid feces.

Key Words: calves, milk replacer, Palbio

W229 The effect of feeding alfalfa hay at different ages on pre- and post-weaning performance of Holstein calves. A. Ahangarani*, M. H. Fathi Nasri, H. Farhangfar, and A. Omidi, *Department of Animal Science, The University of Birjand, Iran*.

Thirty Holstein calves (15 males and 15 females) were used to evaluate the effects of feeding alfalfa hay at different ages on pre- and post-weaning performance and weaning age. Following 2 d of colostrum and transition milk feeding, calves were allocated in a completely randomized design to 3 treatments, including 1) feeding starter from beginning 2) feeding starter and alfalfa hay from beginning and 3) feeding starter from beginning and alfalfa hay from 21 d age. Calves were fed whole milk at 10% of the initial daily body weight and had free access to starter, alfalfa hay and water. The weaning criterion was defined as the calf's age at a daily intake of 0.80 kg of solid feed(s) for 2 days, consecutively. Increased solid feeds (starter and alfalfa hay) DMI was observed ($P < 0.05$) for calves fed treatment 2 during the pre-weaning (322.1, 606.3 and 393.0 g/d for treatments 1, 2 and 3, respectively), the post-weaning (1975.0, 2592.5 and 2176.0 g/d for treatments 1, 2 and 3, respectively) and over the entire experiment period (751.7, 1269.7 and 894.9 g/d for treatments 1, 2 and 3, respectively). Weaning age in treatment 2 was attained earlier ($P < 0.05$) than two other treatments (59.3, 47.7 and 54.9 d for treatments 1, 2 and 3, respectively). Average daily gain (ADG) of calves in treatment 2 was significantly ($P < 0.05$) higher than calves in two other treatments during the pre-weaning (432, 517 and 476 g/d for treatments 1, 2 and 3, respectively) but not carry over into the post-weaning phase or over the entire experiment period. Feed efficiency ratio (ratio of ADG to DMI) was not different between treatments during the pre-weaning, the post-weaning and over the entire experiment period. These findings revealed that adding the alfalfa hay to diet in lower ages, increased DMI and decreased the weaning age of calves.

Key Words: calf, weaning age, alfalfa hay

W230 Effects of supplementing a mix of nucleotides to dairy calves prior to weaning on respiratory afflictions and immune response during the postweaning period. A. Bach*[1,2], A. Ferrer[2], D. Martínez-Puig[3], and J. Ahedo[4], [1]*ICREA, Barcelona, Spain*, [2]*IRTA-Ruminant Production, Caldes de Montbui, Spain*, [3]*Bioiberica, Barcelona, Spain*, [4]*Rancho Las Nieves, Mallén, Spain*.

Seventy-eight dairy replacement calves (initial age = 18±6.3 d and BW = 43±6.1 kg) were fed a 2 L of milk replacer (MR) twice daily via a bottle at 0730 and 1630 until 45 d of life, and then a daily dose of 2 L of MR at 0730 for an additional week. At 37 d of age half of the calves received a daily dose of 3 g of a mix of nucleotides (Nucleoforce, Bioiberica, Spain) supplemented through the morning feeding of MR until weaning time (52 d). After weaning, calves were moved from individual hutches into pens holding 8 animals until reaching 111±2.1 d (when the study was completed). Animal performance was monitored from 52 until 111 d of life. Respiratory afflictions were monitored daily from 37 to 111 d of life. Blood samples from half of the animals randomly chosen from each treatment group were obtained by venipuncture of the jugular vein at the age of 37 and 52 d. Incidence of respiratory afflictions was analyzed using mixed-effects logistic regression analysis, and the number of respiratory cases using a mixed-effects Poisson regression analysis. Body weight gain and blood determinations were analyzed using a mixed-effects ANOVA. The incidence of animals affected by respiratory problems tended ($P = 0.06$) to be lower in calves that received Nucleoforce (27±0.45%) than in the unsupplemented animals (48.7±0.51%). Also, the total number of respiratory cases was a numerically ($P = 0.13$) 55% lower in the supplemented than in the unsupplemented calves. Average daily gain was not affected by Nucleoforce supplementation, with supplemented calves gaining 1,169 g/d and the unsupplemented ones 1,152 g/d. Blood plateletcrit was lower ($P<0.05$) in supplemented than in control calves (22.9 vs 21.5±0.45%, respectively). Similarly, mean platelet volume was also lower ($P< 0.05$) in supplemented than in control calves (7.9 vs 10.3±0.01 fL, respectively). It could be concluded that 3 g/d of Nucleoforce tended to be effective in providing animals with an adequate immune response to reduce the incidence of respiratory upsets during transition from liquid to solid feeds.

Key Words: nucleotides, immune, pneumonia

W231 The effect of vanilla flavoured calf starter on performance of Holstein calves. M. H. Fathi Nasri*, A. Riasi, A. Arab, M. Kamalalavi, V. Vosoughi, and H. Farhangfar, *Department of Animal Science, The University of Birjand, Iran*.

Twenty one male Holstein calves were used to evaluate the effects of vanilla flavour added to starter on preweaning and postweaning calf performance. Following 2 d of colostrum and transition milk feeding, calves were assigned in a completely randomized design to 2 treatments including 1) unflavoured starter and 2) flavoured starter (containing 0.2% vanilla, DM basis). Calves were fed whole milk at 10% of the initial body weight daily and had free access to starter and water. The weaning criterion was defined as the calf age at a daily intake of 0.80 kg of starter for 2 days, consecutively. Increased starter DMI was observed for calves fed flavoured starter during the preweaning period. This effect did not carry over into the postweaning phase, but this increase was observed over the entire experiment for calves fed flavoured starter from 3 d age to weaning (Table 1). Weaning age was attained 2 to 3 d earlier ($P < 0.03$) when flavoured starter was fed (60.3 and 57.7 d for calves fed unflavoured and flavoured starter, respectively). Average daily gain (ADG) over the preweaning phase was significantly ($P < 0.01$) higher for calves fed flavoured starter. No differences in ADG were observed

postweaning or over the entire experiment due to treatment. Calves fed flavoured starter were more efficient in converting diet DM to gain than calves fed unflavoured starter during the preweaning phase. These findings demonstrate that supplementing starter with vanilla as a flavour agent is advantageous to calf performance.

Table 1

	Diet [1]			
Item	UF starter	F starter	SEM [2]	P
Starter DMI (kg)				
Preweaning	0.40	0.44	0.010	0.03
Postweaning	2.12	2.25	0.121	NS[3]
Overall	1.05	1.25	0.082	0.02
ADG (kg)				
Preweaning	0.33	0.40	0.02	0.01
Postweaning	0.86	0.92	0.03	NS
Overall	0.44	0.47	0.02	NS
Feed efficiency [4]				
Preweaning	0.38	0.43	0.02	0.04
Postweaning	0.40	0.41	0.02	NS
Overall	0.34	0.31	0.02	NS

[1]UF, unflavoured and F, flavoured starter, [2]SEM – standard error of the means, [3]NS- non significant, [4]Ratio of ADG (kg) to DMI (starter and milk) (kg)

Key Words: calf, vanilla, weaning age

W232 Flavor effects on feed intake and performance of calves. C. Montoro*[1], I. Ipharraguerre[2], and A. Bach[1,3], [1]*IRTA-Ruminant Production, Caldes de Montbui, Spain*, [2]*LUCTA S.A., Barcelona, Spain*, [3]*ICREA, Barcelona, Spain*.

An experiment was conducted to determine whether calves can be encouraged to increase consumption of dry feed by association of oronasal cues (flavor) elicited by the milk replacer (MR) with those produced by the starter. Forty-three calves (initial BW=51.3±0.63 kg, age=23±1.2 d) participated in this study. All calves were weaned 6 wk after the beginning of the study, which was continued until 2 wk after weaning. Twenty-two calves received a MR treated with a novel flavor and the other 21 calves consumed the same MR but unflavored. Until the preweaning week (wk 4) all calves were fed the same unflavored starter. During the preweaning week (wk 5), within each MR group, half of the calves were fed a pelleted starter treated with the same flavor used in the MR, whereas the remaining calves were offered the same starter but unflavored following a 2x2 factorial design. Starter and MR consumption was registered daily, and BW was determined weekly. Overall, starter intake (as a percentage of BW) was not affected by flavor addition. However, the increase of starter consumption expressed as the percentage of starter intake with respect to average consumption the week before preweaning, was numerically greater when the flavored starter was offered (regardless of the MR treatment). Furthermore, when calves were classified in 4 groups according to the preweaning level of starter consumption, calves in the lowest consumption category consumed (as a % of BW) more ($P < 0.05$) dry feed when fed the flavored starter compared with the unflavored control. As a result, feeding the flavored starter numerically reduced the coefficient of variation of BW gain from 34.4 to 13.7% from preweaning to the end of the study. Results suggest that flavoring calf starters may improve feed intake of calves with a poor drive to consume dry feed, potentially reducing thereby variability in BW gain.

Key Words: aroma, palatability, choice

W233 Development of an animal model to evaluate oro-sensorial preferences in weaned calves. C. Montoro*[1], F. Boe[1], I. Ipharraguerre[2], and A. Bach[1,3], [1]*IRTA-Ruminant Production, Caldes de Montbui, Spain*, [2]*Lucta S.A., Barcelona, Spain*, [3]*ICREA, Barcelona, Spain*.

A series of experiments were conducted to develop an animal model to evaluate oro-sensorial preferences in weaned calves. First, the feeding pattern of 35 calves (65±0.7 d of age) was monitored over 24 h every 60 min to define the optimum moment to conduct the assays. Results indicated that the best time to initiate a preference test would be around 0800. This is because at that time calves showed moderate hunger, allowing thereby detecting differences in oro-sensorial preferences that otherwise would be blunted by excessive or deficient feed consumption. Subsequently, a double-choice model involving 30 naive calves (65±0.7 d of age) was used to assess the capacity of animals to discern between a control diet and the same diet sweetened with 10% sucrose. Feed intake was monitored every 30 min during 6 h. The diet supplemented with 10% sugar was preferred when compared with the unsweetened control ($P<0.001$). The model was able to detect differences in oro-sensorial preferences when 10 calves were randomly removed from the dataset, and even when only the first 30 min of feed consumption were considered in the analysis. In a subsequent experiment, the model was evaluated using 30 calves (65±0.9 d of age) and novel feeds. All calves were simultaneously offered a choice of ground corn or barley, and feed consumption was registered over 6 h every 30 min. Using this model allowed to find significant differences when intake data from only the first 3 h were considered. Randomly removing 10 animals from the dataset did not change the statistical power of the model, but in this case using data from the first 5 h was required because of the low feed consumption during the initial hours of the study. It is concluded that a double-choice model consisting on offering 2 options of feed ad libitum to a minimum of 20 naive weaned calves while measuring feed consumption every 30 min for 6 h represents an effective approach to evaluate oro-sensorial preferences in calves.

Key Words: palatability, taste, model

Ruminant Nutrition: Dairy Heifers

W234 Pre- and post weaning performance and health of heifer calves fed different levels of bovine spray dried animal plasma in a traditional milk replacer program. S. Hayes*[1], D. Carlson[2], D. Ziegler[3], M. Raeth-Knight[4], G. Golombeski[4], B. Ziegler[5], R. Larson[5], J. Linn[4], and H. Chester-Jones[3], [1]*APC, Inc., Ankeny, IA*, [2]*Milk Products, Chilton, WI*, [3]*University of Minnesota Southern Research and Outreach Center, Waseca*, [4]*University of Minnesota, St. Paul*, [5]*Hubbard Feeds, Inc., Mankato, MN*.

Holstein heifer calves (n = 120; 2 to 4 d of age; 40.4 kg ± 0.68 kg) were randomly assigned to 1 of 4 different milk replacers (MR; 20% protein, 20% fat) in November 2007 to develop feeding programs that targeted the use of spray-dried animal plasma (SDP) in MR. Calves were

housed in 2.29 x 1.17 m individual calf pens within a frame-steel curtain side-wall naturally ventilated barn. Treatments (Trt) were:- 1) All-milk (AM) protein medicated MR fed at 0.284 kg in 1.99 L water (12.5% solids) 2X daily for the first 35 d and 1X daily from d 36 to weaning at 42 d (CON); 2) Medicated MR with 4% inclusion of SDP fed as in Trt 1 (SDP4); 3) Medicated MR with 8% inclusion of SDP fed as in Trt 1 (SDP8); 4) Same as Trt 3 with additional amino acids (SDP8AA). Calves were fed an 18% CP (as-fed) texturized calf starter and had access to fresh water. Total DMI from MR averaged 22.9 kg. Average daily gain (ADG) pre-weaning (0.56 kg/d), ADG post weaning (0.99 kg), total d 1 to 56 (0.67 kg/d) and hip height gain (9.9 cm) were not affected ($P > 0.05$) by MR program. Pre-weaning and total calf starter dry matter intake were 21 and 12.2% greater ($P < 0.05$), respectively, for SDP8AA calves vs. those fed the other MR programs. Calves fed SDP8 had 4.2% greater feed efficiency ($P < 0.04$) than those fed SDP8AA but similar to calves on other MR programs. There were no Trt differences in health parameters. Under the conditions of this study, inclusion of 4 or 8% SDP in a 20:20 milk replacer resulted in similar calf performance and health to those fed an all-milk protein milk replacer. The addition of amino acids to milk replacer formulated with 8% SDP increased starter intake but not calf growth.

Key Words: dairy calves, milk replacer, animal plasma level

W235 Performance and health of post weaned Holstein heifer calves from 9 to 25 weeks of age fed grain mixes containing varying levels of bovine spray dried plasma protein during the initial transition to group pens. H. Chester-Jones*[1], S. Hayes[2], R. Larson[3], B. Ziegler[3], D. Ziegler[1], M. Raeth-Knight[4], G. Golombeski[4], and J. Linn[4], [1]*University of Minnesota Southern Research and Outreach Center*, *Waseca*, [2]*APC, Inc.*, *Ankeny, IA*, [3]*Hubbard Feeds, Inc.*, *Mankato, MN*, [4]*University of Minnesota*, *St. Paul*.

Ninety-six heifer calves (85.1 ± 1.56 kg BW) were used in a 112-d study to evaluate feed intake and performance from 9 to 25 wk of age. Heifers were randomly assigned to 1 of 4 diets among 4 replicated pens/treatment (6 heifers/pen). Treatments were:-1) 16% CP pelleted grain mix fed free-choice (FC) d 1 to 7 and limit-fed (LF) 2.72 kg/d d 8 to 28 with FC hay (CON); 2) 16% CP pelleted grain mix containing 5.5 g/kg spray-dried plasma protein fed as described for CON (SDP2); 3) 16% CP pelleted grain mix containing 11 g/kg spray-dried plasma protein fed as described for CON (SDP3); 4) 16% CP pelleted grain mix containing 16.5 g/kg spray-dried plasma protein fed as described for CON (SDP4). From d 29 to 112 heifers were fed a common diet of 16% CP whole corn and pellet mix at 2.72 kg/d d 29 to 56 and 2.27 kg/d d 57 to 112 with FC hay. Daily gain d 1 to 28 was higher ($P < 0.05$) for heifers fed CON and SDP2 vs. those fed SDP4 with SDP3 heifers being intermediate. Total DMI d 1 to 28 was higher ($P = 0.04$) for CON heifers than the other heifer groups due to higher ($P = 0.03$) hay intake but this was not reflected in feed/gain differences. There were no heifer performance differences d 29 to 112 and overall d 1 to 112. Overall daily gain, DMI and feed/gain averaged 1.08, 4.29 and 4.07 kg, respectively. Under the conditions of this study, offering a complete pellet grain mix that contained spray-dried plasma protein (5.5, 11, or 16.5 g/kg) did not enhance heifer performance during the initial 28 d transition period to group pens when compared to a grain mix without supplemental plasma protein. There were no overall effects on heifer performance and health from the diets fed.

Key Words: dairy heifers, grain mixes, performance

W236 Performance of post weaned Holstein heifer calves fed limit or free-choice pelleted grain mixes with two differing fiber levels along with free-choice hay. D. Ziegler*[1], R. Larson[2], B. Ziegler[2], M. Raeth-Knight[3], G. Golombeski[3], H. Chester-Jones[1], and J. Linn[3], [1]*University of Minnesota Southern Research and Outreach Center*, *Waseca*, [2]*Hubbard Feeds, Inc.*, *Mankato, MN*, [3]*University of Minnesota*, *St. Paul*.

Ninety-six heifer calves (85.5 ± 1.73 kg BW) were used in a 112-d study to evaluate feed intake and performance from 9 to 25 wk of-age. Heifers were randomly assigned to 1 of 4 diets among 4 replicated pens/treatment (6 heifers/pen). Treatments (Trt) were:- 1) 16% CP (as-fed) grain mix (66.25% cracked corn, 32.5% pellet, 1.25% tallow) fed at 2.72 kg/d for 28 d and 2.27 kg/d from d 29 to 112 with free-choice (FC) hay (CON); 2) 16% CP high fiber (19.9% ADF; 37.8% NDF, DM basis) pelleted grain mix limit-fed as CON with FC hay (LFHF); 3) High fiber pelleted grain mix as in Trt 2 fed FC with FC hay for 84 d and then switched to CON with FC hay from d 85 to 112 (FCHF); 4) Medium fiber (11.1% ADF; 32.5% NDF, DM basis) pelleted grain mix fed for 84 d as Trt 3 and switched to CON d 85 to 112 (FCMF). Daily gain d 1 to 84 was the highest ($P < 0.05$) for heifers fed FCHF (1.16 kg/d) vs. other heifers groups (0.95 kg/d), which were similar. Grain and hay intake d 1 to 84 averaged 2.18, 1.73; 2.18, 1.64; 3.96, 0.64; 3.64 and 0.59 kg for heifers fed CON, LFHF, FCHF and FCMF diets, respectively. Overall 112 d average daily gain (1.10 kg) and hip height gain (22.1 cm) were the highest ($P < 0.05$) for FCHF heifers with the other heifer groups being similar (av. 0.93 kg and 18.9 cm). Total DMI expressed as a percentage of body weight was the lowest ($P < 0.05$) for CON and LFHF heifers d 1 to 84 and FCHF heifers d 85 to 112. There were no overall differences in feed/gain. Under the conditions of this study, feeding FC hay with FCHF pellet mix resulted in gain and growth advantages when compared to heifers fed FCMF, LFHF or CON for 84 days without excessive body condition. This advantage was maintained from d 85 to 112 when heifers were on a common diet.

Key Words: dairy heifers, grain mixes, fiber levels

W237 Correlation between future production performance and hepatic gene expression in postpubertal Holstein dairy heifers. J. Doelman*, N. G. Purdie, H. Cao, N. A. Karrow, and J. P. Cant, *University of Guelph*, *Guelph, ON, Canada*.

As the metabolic hub in the ruminant animal, the liver is essential in the assimilation and distribution of nutrients. The objective of this study was to assess the correlation between liver gene expression and both milk yield and milk component production in yearling heifers. One-hundred postpubertal Holstein heifers between 9 and 13 months of age were randomly assigned to a fed or a 24-hour feed withdrawal treatment under a randomized block design. Liver biopsies were taken to obtain RNA for microarray analysis and quantitative RT-PCR analysis. A cDNA microarray consisting of 8800 oligonucleotide inserts was used to identify hepatic transcript profiles. Array elements were selected from a database of bovine ESTs. A reference design was employed to compare Cy-5 labelled RNA from liver to Cy-3 labelled RNA from reference standard (derived from bovine liver, spleen and placenta). Gene Spring analysis software was used for LOWESS normalization procedures and statistical analysis (ANOVA, $P = 0.05$). Sixty-two differentially expressed genes were found using Benjamini and Hochberg's False Discovery Rate ($P = 0.05$). Validation of microarray results was performed on 24 genes using qRT-PCR. Correlation analysis was conducted using those genes identified as differentially expressed by microarray. This analysis revealed moderate positive correlations between 305 DIM milk yield and Apolipoprotein A-IV, Cadherin 2 and Retinoid X Receptor

γ (correlation value 0.27- 0.36) for both the fed and fasted treatments. Similar correlations between 305 DIM milk yield and Fructose 1,6 Bisphosphate, Fatty Acid Binding Protein, Glutathione S-transferase A1, and Aldehyde Dehydrogenase 1 Family (0.22- 0.43) were found in the fasted condition alone; comparable correlations in the fed state include Apolipoprotein A1, Homer 3 Homolog, and Centrosomal Protein 250kDa (0.24- 0.38). Moderate positive correlations were also noted between 305DIM protein yield and Apolipoprotein A1, Cadherin 2 and Retinoid X Receptor γ (0.24- 0.34) for both treatments.

Key Words: heifer, gene expression, correlation

W238 High protein level in the diet to dairy heifers from 10 to 22 months of age reduced milk yield in first lactation. M. Vestergaard*, M. B. Petersen, and K. Sejrsen, *Faculty of Agricultural Sciences, Aarhus University, Tjele, Denmark*.

Many Danish dairy farmers use one total mixed ration (TMR) based on a mixture of grass- and corn silage to all heifers. Thus, the heifers above one year of age receive a surplus of protein compared to the Danish recommendations. Our hypothesis was that high (H, +15% of N) compared to the recommended (N) protein level would not affect growth rate (ADG), reproduction and energy-corrected milk yield (ECM). A total of 145 heifers; 51 Red Danish (RD), 57 Holstein (HF) and 37 Jersey (DJ) loose-housed in pens of 6 or 8 started the experiment at 10.5 mo of age. Heifers were double-weighed at birth, and at 10.5, 15 and 22 mo. ADG from birth to 10.5 mo was 810 (RD and HF) and 580 g/d (DJ). TMR was based on whole-crop maize or -barley silage, barley straw and soybean meal. Within a pen, N-and H-heifers had free access to N-TMR and H-TMR, respectively, via transponder-controlled access to the feeding troughs. Crude protein (CP) content was 101-105 and 116-120 g/kg DM for N- and H-TMR, respectively. The fill value of TMRs allowed for an ADG of 750 g/d from 10 to 15 mo and 900 g/d from 15 to 22 mo (e.g., RD and HF). Data was analyzed with a mixed model including treatment, breed, their interaction, and blocks as fixed and animal as random factors and with days or weeks as repeated measures. There was no difference in ADG from 10 to 22 mo (RD and HF: 840±16; DJ: 630±18 g/d), percent pregnant at first service (55%), age (26.4±0.5 mo) and BW at calving (HF: 630, RD: 610, and DJ: 440 kg), and calving ease between N- and H-heifers. The cow-dataset included 105 animals. Days to first service, inseminations per pregnancy (2.5±0.2) and days open (96±6 d) were not different, but a chi-square test revealed lower pregnancy percentage at first service ($P \leq 0.05$) in N- compared to H-heifers. Milk yield was recorded at each milking and milk composition was analyzed twice weekly. ECM to 120 d of lactation was lower in H- compared to N-heifers (25.1 vs. 26.5 kg/d, $P \leq 0.05$), the difference being highest in DJ (2.2 kg) and lowest in HF (0.7 kg). The milk yield effect is surprising and warrants further investigation.

Key Words: replacement heifers, protein, performance

W239 Effects of limit feeding and ionophore supplementation on replacement heifer growth, rumen function and manure excretion. K. A. Kruse*, N. M. Esser, P. C. Hoffman, and D. K. Combs, *University of Wisconsin, Madison*.

Ninety-six Holstein heifers (400 ± 6 kg, 15.2 ± .1 mo) including 9 heifers fit with ruminal cannulae were assigned one of three dietary treatments for 180 ± 8 days in a pen replicated randomized complete block design. Treatment diets included: control (C100) fed ad libitum, (L85) fed at 85% of C100 intake, and (L80+I) fed at 80% of C100 intake containing 325 mg/hd/d of Lasalocid. Diets were formulated to provide isonitrogenous and isocaloric intakes and balanced according to NRC requirements. Treatment diets were fed as a TMR (1x/d) and heifers were evaluated for growth, rumen function, and manure excretion parameters. Heifers fed L85 and L80+I consumed less DM, CP, and NDF when compared to heifers fed C100. Heifers fed C100 had lower ADG and higher feed to gain ratios, and tended to excrete more DM. Heifers fed L80+I retained more N compared to heifers fed L85. No differences were found in pH and NH_3-N between limit and control fed heifers. Lower rumen fill was observed 7-14d post trial in heifers fed L85 and L80+I. Limit feeding increased growth, feed efficiency, tended to decrease DM excretion and reduced rumen fill potential 7-14d post trial. Ionophore supplementation appeared effective in replacing dietary DM and CP in limit feeding programs.

Table 1.

Item	C100	L85	L80+I	SEM	Treatment	C vs L	L80+I vs L85
DMI, kg/d	10.3	8.5	8.1	0.2	0.0001	0.0001	0.18
CP intake, kg/d	1.4	1.3	1.2	0.03	0.02	0.03	0.05
NDF intake, kg/d	5.1	3.1	2.9	0.1	0.0001	0.0001	0.25
ADG, kg/d	0.81	0.96	0.89	0.03	0.03	0.01	0.2
Feed:gain, kg/kg	5.9	4.1	4.2	0.2	0.0001	0.0001	0.74
DM excretion, kg/d	4.3	3.9	3.2	0.4	0.19	0.15	0.24
Apparent N retention[1], g/d	77.1	84.1	96.8	8.7	0.04	0.3	0.04

[1] Does not account for potential N volatilization.

Key Words: limit feeding, growth, heifers

W240 Effect of feeding method on the behavior and growth of dairy heifers. A. M. Greter*[1], K. E. Leslie[2], G. J. Mason[3], B. W. McBride[3], and T. J. DeVries[1], [1]*Department of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada*, [2]*Department of Population Medicine, Ontario Veterinary College, Guelph, ON, Canada*, [3]*Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*.

Provision of a TMR to growing heifers promotes a balanced nutrient intake across the day. Alternatively, top-dressed (TD) feeding results in the rapid consumption of concentrate after feeding and increased feed sorting across the day. The objective of this study was to determine the long-term effects of feeding method on the growth, feeding, and sorting behavior of dairy heifers. Thirty-two Holstein heifers (146.2 ± 21.9 d of age; mean ± SD) were divided into 8 groups of 4 and exposed to 1 of 2 dietary treatments for 13 weeks using a completely randomized design. The treatment rations contained 65% grass/alfalfa haylage and 35% textured concentrate (on a DM basis) fed either as a: 1) TMR or 2) TD ration. Group DMI were recorded daily. Feeding behavior was recorded using time-lapse video for 7 d during weeks 1, 5, 9, and 13. Fresh feed and orts were sampled each day of the recording weeks and were subjected to particle size analysis. The particle size separator contained 3 screens (19, 8, and 1.18 mm) and a bottom pan, resulting in 4 fractions (long, medium, short, and fine). Sorting activity for each fraction was calculated as the actual intake expressed as a percentage of the predicted intake. To determine if sorting occurred, each fraction was tested for a difference from 100%. Animals were fecal scored for consistency of stool twice weekly using a scale from 1 (liquid) to 4 (normal). Neither DMI (7.5 kg/d) nor ADG (1.3 kg/d) differed between treatments. Sorting against long particles was greater for the TD ration compared to the TMR (96.0 vs. 98.9%; SE=0.4; *P*=0.002). Daily feeding

time did not differ between treatments (201.0 min/d), but heifers did spend more time at the bunk in the 2 h following feed delivery on the TD ration (50.1 vs. 32.0 min/d; SE=1.3, *P*<0.001). Fecal scores were lower for heifers on the TD ration (2.7 vs. 3.4; SE=0.1; *P*=0.003). Lower fecal scores may reflect altered rumen fermentation on the TD ration from lower effective fiber intake, as result of greater sorting against long particles, and consumption of a large portion of concentrate following feed delivery.

Key Words: heifers, sorting, feeding behavior

W241 Wheat grain eases metabolic transitions in periparturient heifers. F. Ehsanbakhsh, H. Amanlou, D. Zahmatkesh, and A. Nikkhah*, *Zanjan University*, *Zanjan, Iran*.

Wheat grain possesses reasonably synchronous starch and protein fermentation rates, low cation-anion difference, and high palatability. Such prepartal diet properties can reduce the risk of postpartum hepatic lipidosis, hypocalcemia, and subacute rumen acidosis. We determined the effects of feeding WG to prepartum heifers on periparturient metabolic, health, and productive criteria. Fifteen Holstein heifers at 31 ± 6 days prepartum were blocked based on expected calving date and assigned to three treatments. The treatments were totally mixed rations containing either 1) a conventional blend of barley grain and wheat bran (BGW), 2) 10% wheat grain (WG10), or 3) 18% WG (WG18) (DM basis). Prepartum diets contained no anionic salts. Cows were monitored until 21-day postpartum and fed a same early lactation diet. The prepartal WG tended to linearly increase DMI (10.1, 10.6, 10.7 kg/d, P=0.09), reduced urine pH at 7-day prepartum (7.0, 6.7, 6.6; P<0.001), and elevated (P<0.05) blood calcium and glucose at 7-day prepartum (40 vs. 52, 53 mg/dl; 7.5 vs. 8.6 and 9.1 mg/dl) and at 3-day postpartum (30 vs. 39 and 40 mg/dl; 7.5 vs. 8.0 and 8.8 mg/dl). Milk fat (0.98 vs. 1.03 and 1.14 kg/d, P<0.01) and protein (0.89 vs. 1.02 and 1.02, P<0.05) yields increased during 21-day postpartum in heifers receiving prepartal WG10 and WG18 instead of BGW. The prepartal apparent dry matter (59.9 vs. 54.3%, P=0.09) and crude protein (67.7 vs. 60.3%, P=0.05) total tract digestibilities were greater for WG10 than for BGW. Blood albumin, globulins, total proteins and urea were similar among groups. Feeding WG did not affect body condition score, calving difficulty, calf weight and health, placenta weight, and the time interval between calving and placenta expulsion. In conclusion, prepartal WG provision concurrently improved energy and calcium states in transition heifers without compromising parturition status and calf health. These data support our previous findings in mature cows and suggest that novel feeding strategies using most suitable ingredients ease the periparturient metabolic transition even without anionic salts in the diet.

Key Words: wheat, preparturient, heifer

Ruminant Nutrition: Fat Supplementation

W242 Effect of dietary lipids on selected strains of ruminal bacteria. R. B. Potu*[1], A. A. AbuGhazaleh[1], K. L. Jones[1], R. L. Atkinson[1], D. Hastings[1], J. D. Haddock[1], and S. Ibrahim[2], [1]*Southern Illinois University*, *Carbondale*, [2]*North Carolina A&T University*, *Greensboro*.

Previous studies have shown that fish oil (FO) promotes vaccenic acid (VA) accumulation in the rumen by inhibiting the last step of biohydrogenation. The objective of this study was to compare the effects of different lipid sources on DNA concentration of bacteria involved in biohydrogenation. Four continuous culture fermenters were used in a 4 x 4 Latin square design with four periods of 10 d each. Treatment diets (50% alfalfa pellets, 50% concentrate) were fed (45 g/d DM basis) in three equal portions during the day. The diets were 1) control (CON), 2) control + saturated fat (rumofat; SAT), 3) control + soybean oil (SBO), and 4) control + fish oil (FO). Lipid supplements were added at 3% of diet DM. Samples collected at 3 h post feeding on d 10 were used for fatty acids and quantitative PCR analysis. The concentrations (g/100g fatty acids) of VA were similar between the SBO (10.50) and FO (12.72); both were higher (P < 0.10) than the levels for CON (6.71) and SAT (3.64). Concentrations of C18:0 were lowest (P < 0.10) for FO (4.82) compared with the other treatment diets (SAT- 45.46, SBO- 21.14, and CON- 14.61). The concentration of conjugated linoleic acid (cis-9, trans-11 CLA) was highest (P < 0.10) with SBO (0.41) in comparison with the other treatment diets (SAT- 0.04, FO- 0.10, and CON- 0.11). DNA concentrations for total bacteria, *Anaerovibrio lipolytica*, and *Succinivibrio dextrinosolven*s were similar (P > 0.10) for all diets. The concentrations of *Butyrivibrio fibrisolvens* (0.06196 ng/45ng total DNA) and *Ruminococcus albus* (0.00196 ng/45ng total DNA) were lowest (P < 0.10) with FO but were similar among the other treatment diets (SAT- 0.1042; 0.005416, SBO- 0.1212; 0.00571, and CON- 0.1263; 0.00517). In conclusion, SBO and rumofat had no effects on bacterial DNA concentrations tested in this study and FO effects on biohydrogenation may be due in part to its effect on *Butyrivibrio fibrisolvens* and *Ruminococcus albus*.

Key Words: fish oil, trans FA, bacteria

W243 Effects of docosahexaenoic acid and linoleic acid on rumen trans-vacceinc acid and microbe populations. D. Li, J. Q. Wang*, D. P. Bu, K. L. Liu, and P. Yu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

The objective of this study was to determine the influence of dietary refined docosahexaenoic acid and free linoleic acid supplementation on the population of *Anaerovibrio lipolytica, Fibrobacter succinogenes, Ruminococcus flavefaciens, Megasphaera elsdenii* strain YJ-4, *Butyrivibrio fibrisolvens* A38, *Butyrivibrio hungatei* JK684, and *Butyrivibrio hungatei* Su6 in ruminal fluid and the concentration of trans vaccenic acid (TVA) in rumen from lactating cows fed high forage diets (forage to concentrate ratio 60:40). Four lactating cows with ruminal, duodenal and ileal cannulas were randomly assigned into a 4 × 4 Latin square with 21-d periods. These diets included basal diet (control), basal diet with 2.73% refined free linoleic acid (RFLA), 2.73% refined free linoleic acid plus 0.50% refined docosahexaenoic acid (RFLDA), or 0.50% refined docosahexaenoic acid (RFDA) on a DM basis. Rumen samples were obtained via the fistula at 0, 4, 6, 8, 10 and 12 h after morning feeding on the 15th d of each period, respectively. TVA was measured with gas chromatography. DNA was extracted and shift in the microbial populations were monitored by real-time PCR using specific primers. The data were statistically analyzed using the PROC MIXED models of SAS (SAS Institute, 2002). The TVA contents in RFLA, RFLDA and RFDA treatments increased by 3.5-, 5.4- and 1.0-fold compared

with the control. *A. lipolytica, F. succinogenes, B. hungatei* JK684 and *B. hungatei* Su6 decreased ($P<0.05$) with DHA and LA addition, while *M. elsdenii* YJ-4 and *B. fibrisolvens* A38 increased ($P<0.05$). DHA and LA addition did not change *R. flavefaciens* population. The study indicated that PUFA addition or a combination of refined linoleic acid and DHA led changes to ruminal bacteria populations. TVA accumulation in rumen was partly due to DHA and LA inhibition on *A. lipolytica*, *F. succinogene* and *B. hungatei*, and increase of *B. fibrisolvens* A38 and *M. elsdenii* to some extent.

Key Words: docosahexaenoic acid, linoleic acid, trans vaccenic acid

W244 Effect of coconut oil on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech Biotechnology, Nicholasville, KY*.

The feeding of coconut oil has reduced methane emissions but effects of this oil on ruminal N metabolism deserve further attention. Effects of coconut oil (CO) were investigated in single-flow rumen-simulating fermenter cultures. Cultures were fed diets formulated in CPM (version 3.08) with four levels of CO (0, 1.67, 3.34, and 5.0% DM). Twelve cultures were used in a completely randomized design with 4 dietary treatments and 3 replications per treatment. Cultures were fed 12.5 g as fed of experimental diets twice daily for 6 days. Fermentation samples were collected from all cultures prior to morning feeding during the last 3 days of experiment. Composite effluent samples from each fermenter were used for DM and NDF disappearance and volatile fatty acid (VFA) analyses. Methane concentration was estimated from VFA concentrations based on a theoretical fermentation balance (Wolin. 1960. J. Dairy Sci. 43:1452). Nitrogen flow measures were estimated by using purine to N ratios for effluent and bacteria. Data were analyzed for effects of treatment using GLM procedure of SAS and linear effects were determined by orthogonal contrasts. Increasing levels of CO resulted in a linear increase in culture pH ($P<0.01$), molar proportions of acetate ($P<0.0001$), and butyrate ($P<0.05$), while decreasing propionate ($P<0.0001$), isoacids ($P<0.05$), and total VFA ($P<0.01$). Methane concentration (mmoles/L) and production (mmoles/d) decreased with more CO in culture diets ($P<0.0001$). Culture ammonia concentration was higher in 1.67 and 3.34% oil cultures than in cultures fed control or 5% oil diets ($P<0.001$). Digestion of true DM and NDF decreased as oil level increased (linear effect; $P<0.01$). N flow measures were also affected by oil with linear decreases in protein degraded ($P<0.05$) and bacterial N yield ($P<0.0001$) as CO increased. Coconut oil at 1.67 to 5% of dietary DM shifted ruminal fermentation in a manner that resulted in lower methane concentration and production but negatively affected digestion and N flow.

Key Words: coconut oil, methane, ruminal metabolism

W245 Effects of different rates of continuous abomasal or pulse ruminal infusions of either free or protected nicotinic acid on plasma NEFA concentrations. J. Pescara*, J. Pires, and R. Grummer, *University of Wisconsin, Madison*.

Five non-lactating feed-restricted Holstein cows were used in a 5x5 Latin square to test the effects of different rates of nicotinic acid (NA) infusion on plasma NEFA concentration. From d 1 to 5 of each period, cows were fed at 30% of energy requirements to increase plasma NEFA concentration; 9 d were allowed between periods. Treatments were continuous abomasal infusion of free NA beginning at feed restriction and continuing for 108 h at a rate of 0, 0.5, 1 or 3 mg/h per kg BW or protected NA (as Niashure; Balchem Corp.; New Hampton, NY) administered into the rumen every 6 h a rate of 0.5 mg/h per kg BW starting at 48 h before feed restriction and continuing through feed restriction. Blood samples were collected every 6 h starting immediately prior to feeding and lasting for 108 h. After termination of NA infusions, blood samples were collected hourly for 12 h. During period 1 and 4, the cow receiving 3 mg NA/h per kg BW had to be euthanized after 72 h of continuous infusion. Evidence suggested that death was due to NA toxicity. Plasma NEFA concentrations started at approximately 70 μEq/L prior to feed restriction, and at 108 h of continuous infusion were 509, 587, 442, 850 and 108 μEq/L for cows that received 0, 0.5 (Niashure), 0.5 (Free), 1 or 3 mg NA/h per kg BW, respectively. Cows receiving 3 mg NA/h per kg BW had lower plasma NEFA than all other cows ($P < 0.05$). Greater plasma NEFA concentration was observed for cows receiving 1 than cows receiving 0.5 mg (Niashure) NA/h per kg BW ($P < 0.05$). After termination of infusion, an increase in plasma NEFA concentration was observed for cows receiving 1 or 3 mg NA/h per kg BW compared to cows receiving the other treatments ($P < 0.01$); plasma NEFA concentration peaked at approximately 1900 μEq/L or 1360 μEq/L at 4 or 5 h after termination of infusions, respectively. It is unlikely there is a dose of NA that can suppress plasma NEFA and avoid a dramatic increase in NEFA following termination of treatment.

Key Words: nicotinic acid, NEFA, dairy cow

W246 Effects of infusing volatile fatty acids intraruminally on rumen and milk odd and branched-chain fatty acids. E. A. French* and L. E. Armentano, *University of Wisconsin, Madison*.

Our objective was to determine if the presence of VFA precursors increased odd and branched-chain fatty acids (OBCFA) in either rumen microbes or milk. Four midlactation cows were assigned to a 4×4 Latin square design with 2 d periods. Infusion treatments were acetate (A), propionate (P), 3-methylbutyrate (3B), and 2-methylbutyrate (2B). Infusions began 5.5 h before feeding (time=0 h) at 17.4 mmol of VFA/min for 18 h. Infusions were well above any attainable physiological level for 3B and 2B. Fatty acid analysis was performed on solid (S) and liquid (L) phase rumen samples collected at 18 h, and daily milk fat composites (M) from d 1 and 2 of each period. Intakes were determined at 23 h. VFA, blood NEFA, and blood glucose were measured at 18 h. Pre-planned, single df contrasts were made for 3B v. 2B, P v. 2B, and A v. P for intakes and blood measurements. Surprisingly, the greatest differences in OBCFA were the increases in L *iso* C15:0 and C17:0 for 2B. Infusing 3B increased *iso* C15:0 in both S and M. Propionate increased M C15:0 and C17:0. Both gluconeogenic compounds, P and 2B, had similar and greater M C15:0 compared to A and 3B. Intakes were 23, 23, 16, and 18 kg DM for A, P, 3B, and 2B ($P \neq 2B$, $P < 0.05$). Rumen L concentrations of the infused VFA were 115.2, 49.6, 62.6, and 62.0 m*M* for A, P, 3B, and 2B. Both 3B and 2B had similar decreases in energy intake and balance; however, 2B maintained blood NEFA (121, 102, 172, and 78 mmol/L for A, P, 3B, and 2B; $3B \neq 2B$, $P < 0.10$) and glucose (56.3, 64.3, 31.9, and 59.1 mg/dL for A, P, 3B and 2B; A, P, $2B \neq 3B$, $P < 0.05$). Rumen and milk OBCFA responses were minimal considering the large amounts of VFA infused.

Tablt 1. Treatment effects on rumen and milk OBCFA (g/100 g total fatty acids)

Site	Treatment	*i* C15:0	*ai* C15:0	C15:0	*i* C17:0	*ai* C17:0	C17:0
L	2B	1.47	.29	.30	.06	.08	1.18
	3B	.27	.10	.27	.01	.06	.76
	A	.29	.16	.32	.02	.05	.66
	P	.23	.09	.32	.02	.05	.49
S	2B	.20^{b}	.49	.49	.17	.17	.55^{ab}
	3B	.34^{a}	.41	.53	.16	.13	.57^{a}
	A	.25^{ab}	.41	.50	.14	.12	.47^{b}
	P	.22^{b}	.43	.58	.15	.13	.52^{ab}
M	2B	.14^{b}	.34	.94^{ab}	.15	.30	.53^{ab}
	3B	.16^{a}	.32	.78^{b}	.15	.29	.51^{ab}
	A	.14^{b}	.32	.80^{b}	.13	.28	.48^{b}
	P	.15^{ab}	.33	1.06^{a}	.14	.28	.55^{a}

$^{a-b}$Means within a column and sampling site not sharing a common superscript differ (P<.05)

Key Words: odd and branched-chain fatty acids, rumen fermentation

W247 Effects of *trans*-monounsaturated and omega-6 fatty acids on performance of periparturient Holstein cows. C. Caldari-Torres*, M. C. Perdomo, C. A. Risco, C. R. Staples, and L. Badinga, *University of Florida*, *Gainesville*.

Fat supplementation has become a common practice in the dairy industry due to the inability of high-producing dairy cows to maintain a positive energy balance during the transition to lactation. The objective of this study was to examine the effects of *trans*-monounsaturated fatty acid (*t*FA) and omega-6 fatty acids (n-6 FA) on performance of periparturient Holstein cows (n = 28). Treatments were the following: 1) Rumen-bypass fat (RBF, 91.4% saturated fat, 1.8% of DM), 2) Ca salts of *t*FA (57.5% *trans* isomers of C18:1, 1.5% of DM), and 3) Ca salts of fatty acids made from safflower oil (n-6, 63% C18:2, 1.5% of DM). Dietary treatments were initiated approximately 28 d before calculated calving dates and continued through d 50 postpartum. Dry matter intake (DMI, as a % of BW) decreased (P < 0.001) from 1.77 ± 0.1% at wk 3 prepartum to 0.87 ± 0.1% on day of calving and then increased to 3.10 ± 0.1% at wk 7 postpartum. Cows fed an RBF-enriched diet had greater (P = 0.03) DMI (2.35 ± 0.09%) than those fed the *t*FA (1.99 ± 0.10%)-supplemented diet. The average BW decreased (P < 0.001) from 750 ± 14 kg at wk 3 prepartum to 628 ± 14 kg at wk 5 postpartum and did not differ among dietary treatments. Although overall milk production did not differ among dietary treatments, cows fed the n-6 FA-enriched diet produced less (P = 0.04) fat-corrected milk (FCM; 29.3 ± 2.1 kg/d) than those receiving the RBF (36.5 ± 1.8 kg/d) or *t*FA (34.4 ± 1.5 kg/d) supplements. Milk fat percentage decreased (P < 0.001) from 4.8 ± 0.2% at wk 1 to 2.6 ± 0.2% at wk 7 of lactation. Cows fed n-6 FA-enriched diet had lower (P = 0.002) milk fat content (2.8 ± 0.2%) than those receiving isolipid RBF (3.6 ± 0.2%) or *t*FA (3.8 ± 0.2%)-supplemented diets. Results indicate that peripartum *t*FA supplementation may increase feed efficiency for milk production. Whether or not the decrease in milk fat content in cows fed n-6 FA-supplemented diet reflects an increase in endogenous CLA production warrants further investigation.

Key Words: fat, performance, dairy cow

W248 Effects of *trans*-monounsaturated and omega-6 fatty acids on uterine health and reproductive efficiency of transition Holstein cows. C. Caldari-Torres*, M. C. Perdomo, C. R. Staples, C. A. Risco, and L. Badinga, *University of Florida*, *Gainesville*.

Modern dairy cows experience varying degrees of immunological dysfunction from approximately 3 wk before calving to 3 wk after calving, which may have practical implications for health and reproductive management. The objective of this study was to determine the effects of *trans*-monounsaturated (*t*FA) and omega-6 fatty acids (n-6 FA) on uterine health and reproductive efficiency of early postpartum Holstein cows (n = 28). Treatments consisted of 1) Rumen-Bypass Fat (RBF, 91.4% saturated fat, 1.5% of DM), 2) Ca salts of *t*FA (57.5% trans C18:1, 1.8% of DM), and 3) Ca salts of fatty acids made from safflower oil (n-6, 63% C18:2, 1.8% of DM). Dietary treatments were initiated approximately 28 d before expected calving dates and continued through d 50 postpartum. Cows fed the n-6 FA-supplemented diet tended (P = 0.07) to have higher rectal temperatures at d 12 postpartum (39.1°C) than those fed isocaloric RBF (38.8°C) or *t*FA (38.9°C)-supplemented diets. Incidences of postpartum metritis (Metricheck score = 3 in the first 21 DIM) were 90, 60 and 62%, respectively, for cows fed RBF-, *t*FA- and n-6FA-supplemented diets. Corresponding values for subclinical endometritis (uterine cytology with ≥ 10% neutrophils at 40 DIM) were 30, 0, and 0%. By 50 DIM, accumulated progesterone concentration was higher (P < 0.05) in cows supplemented with n-6 FA than those receiving isolipid *t*FA or RBF-supplemented diets. First-service conception rates were 30, 50, and 71%, respectively, for the RBF, *t*FA and n-6 FA groups. Corresponding values for days open were 130, 113 and 101 d. Results provide preliminary trends that peripartum fat supplementation may improve uterine health and reproductive responses in postpartum dairy cows. Studies with larger numbers of animals are needed to fully document the beneficial effect of fat supplementation on postpartum health and reproductive efficiency in cattle.

Key Words: fat, reproduction, dairy cow

W249 The long-term effect of supplementation with fish oil or microalgae on the performance of grazing dairy cows. P. Vahmani*[1], E. Gnemmi[2], K. Glover[2], and A. Fredeen[2], [1]*Dalhousie University*, *Halifax, NS, Canada*, [2]*Nova Scotia Agricultural College*, *Truro, NS, Canada*.

The effect of long-term supplementation with rumen protected fish oil (PFO) or rumen protected microalgae (PMA) on milk yield and composition of dairy cows grazing a mixed sward was evaluated. Twenty four pre-partal Holstein cows were blocked by parity and predicted calving date and assigned randomly within block to receive one of three treatments: 1) control (no supplement), 2) PFO (300 g/d) or 3) PMA (300 g/d) for 120 days beginning 30 days before calving. Cows were housed in tie stalls and fed TMR plus one of the treatments twice daily from the start of study until 30±5 days after calving, then they grazed pasture under rotational management for the rest of study. Grazing cows were fed a concentrate according to milk yield plus one of the treatments after morning and afternoon milkings. The basal diets were formulated to be isocaloric, isonitrogenous and isolipidic and to meet nutritional requirements. Pasture dry matter intake was estimated by the net energy balance method. Cows were milked twice daily and milk samples were taken at 7, 30, 60 and 90 DIM for compositional analysis. Analysis of variance was conducted using a completely randomized block design with repeated measures. No significant treatment effects (P>0.05) were observed except in milk fat yield, which was significantly lower (P= 0.04) when cows were fed PFO and tended to be lower (P= 0.07) when

cows were fed PMA compared with control. However milk fat yield was similar (P = 0.65) among the cows fed PMA or PFO. This study suggests that PFO and PMA may reduce milk fat yield due to nonsignificant reductions in both milk yield and fat percentage and this effect may be slightly less with PMA.

Table 1. Effect of PFO or PMA on the performance of grazing dairy cows

	Control	PFO	PMA	SEM
DMI, kg/d	24.41	21.57	23.51	1.67
Milk, kg/d	36.42	33.57	34.26	1.82
Milk fat, %	4.67	4.11	4.13	0.24
Milk fat, kg/d	1.70[a]	1.35[b]	1.41[ab]	0.10
Milk protein, %	2.98	2.99	3.01	0.06
Milk protein, kg/d	1.09	1.00	1.02	0.06
Milk lactose, %	4.46	4.57	4.55	0.04
Milk lactose, kg/d	1.63	1.54	1.56	0.09

[ab] Least square means within a row not sharing a common superscript differ (p<0.05).

Key Words: grazing, fish oil, microalgae

W250 Effect of feeding rapeseeds on lactation performance in dairy cows and oxidative stability of milk and butter. O. Y. Tsisaryk*, *Lviv National University of Veterinary Medicine and Biotechnologies, Lviv, Ukraine*.

Twelve multiparous Ukrainian Red Milk cows were divided into 2 groups (on 6 heads) – C (no rapeseeds) and R (2.6% fat from rapeseeds). Diets were composed of 45% (dry basis) concentrate mix, 22% corn silage, 15% hay and 18% haylage. Ground full-fat rapeseeds replaced a part of concentrate mix in the canola diets. Diets were isonitrogenic. Ether extract and NEL increased from 3.4% and 1.42 Mcal/kg for the control diet, to 5.8% and 1.47 Mcal/kg for the fat supplemented diet, respectively. Groups were fed identical diets (control) for 3 weeks preparatory period of (PP) and C and R diets for 6 weeks of trial period (TP). Compared to the control cows, the treated cows had similar dry matter intake and milk production. Feeding canola seeds increased fat content and yield, contents and yield of fat were 3.91% and 798 g/day (C) and 3.22% and 651 g/day (R) in PP and 4.09% and 774 g/day (C) and 3.78% and 708 g/day (R) in TP respectively. Addition of supplemental fat did not affect milk protein and lactose percentage or milk component yields. After 3 weeks of feeding rapeseeds experimental cows had higher total plasma lipids (3.33 vs. 1.7 g/L, p <0.05), NEFA (123.0 vs. 112.0 μmol/L, p < 0.05), but no differences in plasma TAG, total cholesterol, HDL- and LDL-cholesterol. After 6 weeks of trial period, the difference in plasma lipid metabolites was not significant between groups. R cows had higher activity of plasma and erythrocyte GSH-Px (p < 0.05) and lower plasma concentration of hydroperoxides and MDA (p < 0.01) during all trial period. The sensibility to oxidation of milk and butter was analyzed. Pasteurized milk with the addition of copper (0.1 mg/kg) from R cows had lower content of TBA-activity products (p < 0.05) after 6 days storage at 4°C. Rapeseeds diet butter exhibited no changes in oxidative stability during 35 days storage under 4°C, but at +102°C it had lower peroxide value and TBA-test after 48 hours. Penetrometer readings indicated that R butter was softer at 4°C. Feeding dairy cows full-fat ground canola seeds had positive effect on milk fat yield and had not harmfull effect on the oxidative sensibility on milk and butter.

Key Words: cows, rapeseeds, milk

W251 Performance and metabolic measures of lactating dairy cows fed diets supplemented with either mostly saturated or more unsaturated fatty acids. J. K. Bernard*[1] and A. F. Kertz[2], [1]*The University of Georgia, Tifton*, [2]*ANDHIL LLC, St. Louis, MO*.

A 10-wk lactation trial was conducted during the late summer and early fall of 2006 using 45 late lactation cows (199.7 ± 66.3 DIM and 32.0 ± 5.2 kg milk/d) to determine the effect of feeding supplemental mostly (85%) saturated (SAT) or more (50%) unsaturated (UNS) fatty acids on performance and metabolic concentrations. Cows were fed a control diet during the first 2 wk of the trial without any supplemental fat. At the end of wk 2, cows were blocked by parity and randomly assigned to one of 3 treatments. Treatments included no supplemental fat (control), or the equivalent of 1 kg/d of mostly saturated or more unsaturated fatty acids. DMI, milk yield, milk fat percentage and milk protein percentage were similar among treatments and averaged 23.8 kg/d, 32.5 kg/d, 3.47%, and 3.23%, respectively. The BW and BCS was similar for all treatments throughout the trial. Concentrations of total cholesterol ($P < 0.01$), HDL ($P < 0.01$), and LDL ($P = 0.02$) were higher for cows fed diets supplemented with UNS compared with either control or SAT. Triglyceride and BUN concentrations were similar among treatments. Concentrations of NEFA were higher ($P = 0.02$) for UNS whereas insulin concentrations were higher ($P = 0.05$) for SAT than either control or UNS. Internal body temperature of cows was measured every 5 min using a vaginal probe. There were no differences among treatments but there was an interaction of treatment and time of day ($P = 0.06$) during wk 4 related to higher body temperatures for cows fed UNS at 0500 through 0530 compared with control and SAT and again at 0930 through 1030 compared with SAT. Respiration rates were similar among treatments during week 4, but were higher ($P = 0.06$) for cows fed UNS during week 8 than control or SAT. These results indicate that supplemental SAT or UNS did not alter intake or performance of late lactation cows that have been through heat stress; however, feeding UNS did increase cholesterol and NEFA concentrations along with lowered insulin and tended to keep body temperature higher than either control or SAT-supplemented diets.

Key Words: supplemental fat, blood metabolites, heat stress

W252 Effects of duodenal infusion of linolenic acid on nutrient digestion, milk production, and milk composition in dairy cows. . Khas-Erdene[1], D. P. Bu[1], J. Q. Wang*[1], Q. S. Liu[1], L. Wang[1], H. Y. Wei[1], L. Y. Zhou[1], and J. K. Drackley[2], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, P. R. China*, [2]*Department of Animal Sciences, University of Illinois, Urbana*.

Our objective was to determine the effects of duodenal infusion of a high C18:3 free fatty acid mixture on nutrient digestion, milk production, and milk composition. Four multiparous Chinese Holstein cows (BW = 556 ± 19 kg, DIM = 93 ± 9 d) fitted with duodenal cannulas were administered 2 treatments in a crossover design. Treatments were homogenized aqueous mixtures of α-linolenic acid (LNA; 82.4% *cis*-9, *cis*-12, *cis*-15 18:3; 14.7% *cis*-9, *cis*-12 18:2; 2.8% *cis*-9 18:1) or control containing only the emulsifying ingredients. The control infusate consisted of 15 g/d of xanthan gum, 5 g/d sodium alginate, and 25 g/d of Tween 80 in 10 L of water. Each period lasted 5 wk, during period 1, 2 cows received each amount (0, 40, 80, 120, and 160 g/d) of LNA for 1 wk each, and the other 2 cows received only the carrier infusate. In period 2, the procdures were repeated so that the other 2 cows received the LNA infusate, and the cows that previously received LNA received the control infusate. Measurements were made during the last 3 d of

each infusion amount. Data were analyzed statistically by using PROC MIXED of SAS. Dry matter intake (17.3 kg/d) and total tract apparent digestibilities of DM (63.1%), OM (66.1%), CP (66.9%), and ADF (53.3%) were not affected by LNA infusions. Milk production tended (P = 0.08) to decrease as LNA infusion increased (18.5, 17.2 16.9, 15.9, and 16.3 kg/d for 0, 40, 80, 120, and 160 g/d of LNA, respectively) but production of 4% FCM (17.3 kg/d) was not changed. Milk fat content increased linearly with LNA infusion (4.01, 4.12, 3.96, 4.32, 4.41%). Milk protein content (3.31%) was not changed by LNA infusion, whereas milk lactose content (4.67, 4.60, 4.68, 4.59, 4.57%) and milk lactose yield (0.85, 0.79, 0.79, 0.73, 0.74 kg/d) were lower for LNA vs. control and decreased quadratically as LNA infusion increased. Increasing the amount of LNA supplied to the small intestine of dairy cows had no effect on DMI and nutrient digestibility, but increased milk fat percentage. Infusion of LNA did not affect milk protein or fat yield, but decreased milk lactose content and yield.

Key Words: linolenic acid, nutrient digestion, milk composition

W253 Effects of feeding different rumen-protected fat supplements on the fatty acid composition of milk. A. R. Sewell*, M. L. Eastridge, P. N. Gott, B. Mathew, and D. L. Palmquist, *The Ohio State University, Columbus*.

Specialty fat supplements to target specific functions in dairy cattle, including fatty acid (FA) composition of milk, continues to be of interest. Five lactating Holstein cows (153 ± 74 DIM; 690 kg BW), used in a 5 x 5 Latin square design, were fed: 1) Control with no supplemental fat; 2) 2.5% Veggielac (VEG; Double Pass LLC, Tualatin, OR; canola as a source of 18:1, 35.0% FA); 3) 2.5% Prequel (PRQ; Virtus Nutrition, Corcoran, CA; calcium salt of soybean fatty acids as source of 18:2, 90.2% FA); 4) 2.5% Omegain (OMG; Double Pass LLC, Tualatin, OR; linseed as a source of 18:3, 36.1% FA); and 5) 5.0% OMG. Diets contained 34.8% corn silage, 15.8% alfalfa hay, and 49.4% concentrate. All diets were formulated to contain similar concentrations of CP, nonfiber carbohydrates, and NDF. Cows were milked twice daily, and diets were mixed once daily and fed twice daily for ad libitum intake. Each of the 5 periods were for 2 wk. Dry matter intake and milk yield were recorded daily. Two milk samples were taken for 4 consecutive milkings during wk 2 of each period, one set with preservative for analysis of fat, protein, and urea nitrogen and the other set without a preservative for FA analysis were composited by cow based on milk yield. Due to illnesses unrelated to dietary treatments, 2 cows within different periods were removed from the data anlaysis. Performance and milk composition were similar among treatments: DMI, 24.0 kg/d; milk, 34.4 kg/d; milk fat, 2.89%; milk protein, 3.06%; and MUN, 15.6 mg/dl. Feeding supplemental fat reduced ($P < 0.05$) unsaturated FA in milk, and PRQ resulted in the highest level of unsaturated FA in milk ($P < 0.05$). The PRQ resulted in the highest level of 18:1 *t*-11 (5.73 versus 2.31% of FA). Both the VEG and OMG tended ($P < 0.10$) to increase total 18:1*c* in milk, and compared to PRQ, they increased 18:0 ($P < 0.01$). The PRQ increased ($P < 0.01$) 18:2 *c*-9 *t*-11 (1.53 versus 0.65%) and total 18:2 (7.19 versus 5.30% of FA). The OMG resulted in the highest level of 18:3 n-3 ($P < 0.05$), and the level increased ($P < 0.01$) with level of OMG fed. Feeding these fat supplements altered some of the targeted FA in milk.

Key Words: canola oil, soybean oil, linseed oil

W254 Fatty acids profile of milk fat from cows with different forage and lipids levels in the diet. M. A. Oliveira[1], M. M. Ladeira[2], I. G. Pereira[3], B. N. Faria[1], and R. B. Reis*[1], [1]*Veterinary School, Federal University of Minas Gerais, Brazil*, [2]*Animal Science Department, Federal University of Lavras, Brazil*, [3]*Animal Science Department, Federal University of Jequitinhonha and Mucury Valley, Brazil*.

The objective of this study was to evaluate the effects of forage to concentrate ratio (60:40 or 40:60) and lipids levels (2.8 or 5.5% of dry matter) in the diet on milk yield and fatty acids profile in the milk fat of dairy cows. Eight Holstein cows ranging from 58 to 67 days in milk, averaging 28 ± 4 kg milk/day were distributed in a Latin Square design 4x4, in a 2x2 factorial arrangement. Forage and lipid sources were corn silage and whole extruded soybeans, respectively. The treatments were high forage and low lipids (HFLL), high forage and high lipids (HFHL), low forage and low lipids (LFLL) and low forage and high lipids (LFHL). Main effects of forage, lipid and their interaction were tested by analysis of variance using Proc Mixed (SAS, 1999). The increase of lipids levels in a high and a low forage diets decreased short chain fatty acids concentrations ($C_{4:0}$ to $C_{12:0}$) ($P<0.05$). Conjugated linoleic acid (CLA) content (*Cis*-9 *trans*-11 $C_{18:2}$) increased from 3.72 to 4.85 mg/g milk fat (30.5%, $P<0.01$), when lipid levels were increased in high forage diets. Similarly, the inclusion of lipids in low forage diets increased the CLA in 28%, from 4.60 to 5.89 mg/g milk fat ($P<0.01$). The increasing in dietary lipid levels resulted in higher *Trans*-11 $C_{18:1}$ fatty acid concentration ($P=0.01$). Fatty acid *Trans*-10 $C_{18:1}$ tended to increase with the increasing dietary lipid levels, indicating increased contribution of intermediate fatty acids from rumen biohydrogenation to the mammary glands. The CLA *Trans*-10 *cis* 12 increased for diets with high lipid levels regardless of forage to concentrate ratio. Increasing lipid and decreasing forage levels in the diet increased CLA content of milk fat.

Key Words: conjugated linoleic acid, extruded soybean

W255 Milk fatty acid composition of dairy cows fed whole flaxseed or/and Ca-salts of flaxseed oil. C. Côrtes*[1], D. C. da Silva[1,2], R. Kazama[1,2], N. Gagnon[1], C. Benchaar[1], G. T. d. Santos[2,3], L. M. Zeoula[2,3], and H. V. Petit[1], [1]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [2]*Universidade Estadual de Maringa, Parana, Brazil*, [3]*CNPq, Brazil*.

The objective of this study was to examine the effects of dietary whole flaxseed and Ca-salts of flaxseed oil on milk fatty acid (FA) composition. Four primiparous Holstein cows (BW = 602 kg; DIM = 64 d) fitted with ruminal cannulae were used in a 4 x 4 Latin square. Each experimental period consisted of 21 d of adaptation and 7 d of data collection. Cows were milked and fed twice a day. Four total mixed rations were formulated: no flaxseed product (CO), 5% (DM basis) whole flaxseed (WF), 2% Ca-salts of flaxseed oil (CF), and a mixture of 2.5% whole flaxseed and 1% Ca-salts of flaxseed oil (MF). Results were analyzed using the GLM procedure of SAS. Tukey-Kramer multiple-comparison test was applied to separate means. Significance was declared at $P < 0.05$. Feeding flax products led to the lowest 16:0 concentration (% of total FA). Cows fed CF had higher concentrations of *trans*9-18:1, *trans*11-18:1 and *cis*6-18:1 than those fed CO and WF. Feeding flax products increased *cis*9-18:1 concentration. Concentration of *cistrans*11-18:2 was higher for CF than for WF and concentration of *cis*9,12,15-18:3 was higher for CF and MF than for CO. In general, feeding CF resulted in the highest concentrations of *cis*9,*trans*11-18:2, *cis*9,12,15-18:3, and long-chain FA in milk fat and n-3 FA concentration tended to increase. Supplementation with flaxseed products, mainly Ca-salts, decreased the n-6 to n-3 ratio in milk fat, which may improve the nutritive value of milk fat.

Table 1. Fatty acids concentrations (% of total FA)

	CO	WF	CF	MF	SE	P-value
16:0	32.1[a]	29.0[b]	26.4[b]	27.4[b]	0.43	0.01
*trans*9-18:1	0.28[b]	0.33[b]	0.41[a]	0.37[a]	0.01	0.01
*trans*11-18:1	0.91[b]	0.94[b]	1.65[a]	1.26[ab]	0.08	0.02
*cis*6-18:1	0.73[d]	1.08[c]	1.98[a]	1.44[b]	0.04	0.001
*cis*9-18:1	14.8[b]	16.7[a]	17.6[a]	16.7[a]	0.14	0.003
*cis*9,*trans*11-18:2	0.43[ab]	0.42[b]	0.67[a]	0.53[ab]	0.04	0.05
*cis*9,12,15-18:3	0.59[b]	0.84[ab]	1.03[a]	0.95[a]	0.05	0.02
Long-chain FA	31.9[c]	36.5[b]	41.1[a]	38.4[b]	0.37	0.002
n-3	0.88	1.16	1.39	1.32	0.08	0.07
n-6:n-3	3.48[a]	2.61[b]	2.19[b]	2.27[b]	0.10	0.01

Key Words: dairy cows, flaxseed, milk fatty acids

W256 The effect of nonstructural carbohydrate and addition of full fat roasted canola seed on milk fatty acid composition in lactating cows. M. Sari, A. A. Naserian*, and R. Valizadeh, *Ferdowsi Universuty of Mashhad, Mashhad, Iran*.

The objective of this study was to examine the effects of modifying the dietary profile of neutral detergent-soluble carbohydrate (NDSC), addition of full fat roasted canola seed (RCS) as a source of polyunsaturated fatty acid, and possible interactions on milk fatty acid composition in lactating cows. Twelve lactating Holstein cows (BW=596±29 kg, DIM=85±14) were used in a 4×4 Latin squares design. Treatments were in a 2×2 factorial arrangement, and periods were 21 d. The first 15 d were used for diet adaptation. The cows were fed individually four experimental diets as TMR ad libitum. The diets, which contain 15% barley (S), 10% dry citrus pulp (NDSF), with or without addition of 6% ground RCS, were formulated to meet NRC (2001) recommendations. Diets contained 17.5% CP, constant forage to concentrate ratio (45:55). Cows were milked three times a day and samples were collected at each milking over the last three d of each treatment period. Pooled milk samples were analyzed for milk fatty acid composition. Data were analyzed using the GLM procedure of SAS (2001). The inclusion of RCS reduced proportion of short- and medium chain fatty acids in milk fat (C10:0-C17:0, (P<0.01)). Partial replacement of barley with citrus pulp significantly increased C10:0 and decreased C14:1 cis-9, C15:0, and C17:0 (P<0.05). Interaction (P<0.05) between NDSC profile and RCS were detected for trans-11 C18:1, with increase in trans-11 C18:1 for cows consumed NDSF+RCS (P<0.05). The CLA content increased by 30.1% in milk fat of cows fed the S+RCS diet and by 33.3% in milk fat of cows fed the NDSF+RCS diet (P<0.05). Milk fat contents of cis-9, cis-12 C18:2, C18:3 n3, and C20:0 were increased by RCS addition (P<0.01), but were not affected by NDSC profile. Results of this study showed that there were only minor differences in fatty acid composition of milk fat related to NDSC profile. Adding RCS to dairy cow diets can improve the nutritive value of milk fat.

Key Words: milk fatty acids, nonstructural carbohydrates, roasted canola seed

W257 Effect of coconut oil and lauric acid on ruminal protozoa and milk production and composition in dairy cows. A. Faciola*[1] and G. Broderick[2], [1]*University of Wisconsin, Madison*, [2]*U. S. Dairy Forage Research Center, Madison, WI.*

Ruminal protozoa (RP) are major contributors to bacterial protein turnover in the rumen; therefore, reducing RP may improve N utilization. In our previous studies, lauric acid (LA), a 12 carbon saturated fatty acid, found in fats such as coconut oil (CO), sharply decreased RP. However, despite reducing RP, LA has also consistently reduced DMI and milk yield. In this trial, we tested CO as a practical defaunating agent and assessed the effects of partial defaunation on N utilization, fermentation patterns, nutrient digestibility, milk production and composition. Thirty Holstein cows (6 fitted with ruminal cannulae) were blocked by DIM into 10 blocks of three cows and randomly assigned within blocks to 3 dietary treatments in a 3 X 3 replicated Latin square with 21 days of adaptation and 7 days of sampling. The basal diet contained (DM basis) 50% alfalfa silage, 10% corn silage, 17% high-moisture corn, 5% soybean meal, 10% dry molasses, 4% ground corn, vitamin and mineral premix, 16% CP and 29% NDF. Diets A and C provided the same amount of fat: A) 3% Megalac and C) 3% CO. Diets B and C provided the same amount of LA (287g/d). Data were analyzed using proc mixed in SAS. Results are reported in the table. DMI was similar among treatments; however, both CO and LA were effective in reducing RP. LA reduced yields of milk, 3.5% FCM, and milk components and CO reduced MUN.

Table 1.

Item	Megalac	LA	CO	SEM	P>F
DMI, kg/d	22.5	22.2	22.9	0.6	0.18
Milk yield, kg/d	35.6[a]	34.1[b]	35.9[a]	1.7	<0.01
Fat, %	4.19	3.95	4.05	0.14	0.21
Fat yield, kg/d	1.49[a]	1.32[b]	1.42[a]	0.06	<0.01
Protein, %	2.98	3.03	3.01	0.07	0.32
Protein yield, kg/d	1.06[a]	1.00[b]	1.04[ab]	0.03	0.03
Lactose, %	4.93[a]	4.82[b]	4.77b	0.05	<0.01
Lactose yield, kg/d	1.76[a]	1.61[b]	1.68[b]	0.07	<0.01
SNF yield, kg/d	3.15[a]	2.92[c]	3.05[b]	0.11	<0.01
MUN, mg/dL	11.3[a]	11.1[a]	10.4[b]	0.4	<0.01
Protozoa, x 106 cells/ml	5.71[a]	3.45[b]	3.29[b]	0.21	<0.01

[a,b,c]LSM with different superscriptions differ (P<0.05)

Key Words: coconut oil, protozoa, dairy cows

W258 Evaluation of camelina meal as a protein and omega-3 source for lactating dairy cattle. B. Hatch*, K. Boydston, P. Rezamand, and M. A. McGuire, *University of Idaho, Moscow*.

Camelina (*camelina sativa*) is a dry land winter oil crop and its meal is similar in nutrient content to canola meal with a greater concentration of alpha-linolenic (41.3%). In order to identify the optimum feeding rate of camelina meal, lactating primiparous cattle (*n*=18) were randomly assigned to a treatment sequence in a 4x4 Latin square design. The four diets were designed for inclusion of camelina meal in place of canola at 0, 3, 6, and 9% diet DM. Animals were fed individually using Calan gates with intakes recorded daily. Each period lasted 16 d with milk production measured during the final 2 d of each period. Data were analyzed using the MIXED procedure in SAS. Milk yield was unaffected by inclusion of camelina meal (27.8, 28.5, 27.7, and 27.1 ± 1.7 kg/d for the 0, 3, 6, and 9% diets, respectively). Dry matter intake (19.7, 18.9, 19.2, and 17.9 ± 0.8 kg/d for the 0, 3, 6, and 9% diets, respectively) was reduced for cows fed 9% camelina meal compared with cows fed diets containing up to 6% camelina meal. There was a linear reduction (P <0.05) in milk fat concentration from 0 to 9% diets; however, significance (P <0.05) was only detected when cows were fed a diet containing 9% camelina meal (3.01% milk fat) as compared with the 0% diet (3.51% milk fat). Neither milk protein concentration (2.92, 2.91, 2.94, and 2.95 ± 0.08%

for the 0, 3, 6, and 9% diets, respectively) nor protein yield (0.81, 0.83, 0.81, and 0.79 ± 0.52 kg/d for the 0, 3, 6, and 9% diets, respectively) was affected by feeding camelina meal. Milk concentrations of alpha-linolenic acid was linearly enhanced as the feeding rate of camelina increased from 0 to 9% (0.45, 0.51, 0.68, 0.81 ± 0.04% of total lipid for 0, 3, 6, and 9% diets, respectively; P <0.001). Overall, inclusion of camelina meal up to 6% of diet DM supported production of milk and milk components similar to canola meal.

Key Words: camelina, milk fat, dairy cattle

W259 Assessment of whole Nutrasaff safflower seed as a fat supplement to lactating Holstein dairy cows. C. M. Dschaak*[1], J.-S. Eun[1], A. J. Young[1], and J. W. Bergman[2], [1]*Utah State University*, *Logan*, [2]*Safflower Technologies International*, *Sidney, MT*.

A lactating dairy trial was conducted to determine lactational performance of dairy cows and their milk fat production when fed whole Nutrasaff safflower seed (NSS; Safflower Technologies International, Sidney, MT) at varying levels. The NSS is a new variety of safflower seed containing high fat and low fiber. Fifteen Holstein dairy cows in midlactation (DIM = 118 ± 39) were assigned randomly to 3 balanced 5 × 5 Latin squares. Each period lasted 21 d with 14 d of treatment adaptation and 7 d of data collection. The animals were fed diets containing approximately 56% forage (69% alfalfa hay and 31% corn silage) and 44% concentrate mix supplemented with 0 (control), 1, 2, 3, or 4% whole NSS. Data were analyzed using the MIXED procedure of SAS. Intake of DM did not differ due to NSS inclusion. Digestibility of DM (P = 0.12) tended to increase when NSS was supplemented at 1, 2, or 3%, whereas N and fiber digestibilities were not affected. Milk yield was similar among treatments (average 33.7 kg/d). Milk fat percentage decreased with increasing NSS inclusion, while milk protein and lactose concentrations did not differ among treatments. Milk fat concentration was greatly affected when NSS was included at 4% with an 11% reduction. Feeding NSS at 1, 2, or 3% resulted in a similar milk fat concentration, and these diets also had similar milk fat percentage compared with the control diet. Milk urea N concentration decreased by NSS inclusion regardless of level of NSS inclusion, implying that NSS supplementation improved dietary N use for milk production. *Cis*-9, *trans*-11 conjugated linoleic acid (CLA) linearly increased as the NSS inclusion increased. This study clearly demonstrated that supplementing NSS in dairy diets can be a promising means of fat supplementation to lactating dairy cows without negative impact on lactational performance if added at maximum of 3% dietary DM. The increased *cis*-9, *trans*-11 CLA concentration by the addition of NSS can enhance milk quality because of its potentially beneficial health effects.

Key Words: Nutrasaff safflower seed, milk fatty acids, lactating dairy cows

W260 Effects of protected fat supplements on total tract digestion and plasma metabolites of early lactation Holstein cows. M. Ganjkhanlou*[1], K. Reza Yazdi[1], G. R. Ghorbani[2], M. Dehghan Banadaky[1], H. Morraveg[1], W. Z. Yang[3], and A. Zali[1], [1]*University of Tehran*, *Karaj-Tehran, Iran*, [2]*Isfahan University of Technology*, *Isfahan, Iran*, [3]*Lethbridge Research Centre*, *Lethbridge, AB, Canada*.

This study was conducted to evaluate the digestibilities of commercial fat supplements in early lactation cows. Twelve (nine multiparous and three primiparous) Holstein cows (26 ± 4 day in milk) were used in a replicated 3 × 3 Latin square design with 21-d experimental period and three treatments: control (no fat supplementation), and supplemented with 30 g/kg prilled protected fat (Energizer-10) or 35 g/kg Ca salt of protected fat (Magnapac). Cows were fed ad libitum a total mixed ration consisting of 200 g/kg corn silage, 200 g/kg alfalfa hay and 600 g/kg concentrate mix. Each period had 14 days of adaptation and 7 days for sampling. Ether extract digestibility was increased by 7% and 8% with supplementation of rumen protected fat in multiparous and primiparous cows respectively, but total tract digestibilities of DM, OM, CP, NFC, ADF, or NDF(66%, 69%, 68%, 86%, 50%, 55%; 63%, 68%, 72%, 86%, 42%, 53% respectively for multiparous and primriparous) were not affected (p>0.05) by fat supplements in all cows. Mean apparent digestibility of fat were not influenced by source of fat supplemented and the TMR containing Ca salt of protected fat had similar digestibility of fat than did TMR containing prilled fat. Plasma urea; glucose; triglyceride; LDL and plasma HDL were unaffected by supplemental fat (P > 0.05). Total cholesterol and NEFA in plasma was greater (p<0.05) in cows fed inert fat than in cows fed the control diet in multiparous and primiparous cows (256.71, 258.79 vs 220.56 mg/dl and 267.32 ,268.33 vs 249.33 mg/dl and 0.47, 0.48 vs 0.45 mmol/l and 0.40, 0.44 vs 0.36 mmol/l respectively). These results indicate that supplementation of early lactating diet with rumen protected fat increased ether extract digestibility but without altering digestibilities of DM; OM; CP; NFC; ADF; or NDF.

Key Words: rumen protected fat, inert fat, digestibility

W261 Effect of lipids source and supplementation frequency on ingestive behavior of beef heifers grazing tropical grass. M. Cristina Araújo Santana[1], T. Teresinha Berchielli[1], R. Andrade Reis[1], A. Vaz Pires[2], G. Fiorentini[1], P. Henrique de Moura Dian[1], J. Cesar Martinez*[1], and M. Antonio Alvares Balsalobre[3], [1]*São Paulo State University*, *Jaboticabal,São Paulo, Brazil*, [2]*São Paulo University*, *Piracicaba, São Paulo, Brazil*, [3]*Bellman*, *Mirassol, São Paulo, Brazil*.

The objective of this trial was to evaluate the effect of different sources of lipids and frequency of supplementation of beef heifers grazing palisade grass (*Brachiaria brizantha* cv. Marandu) pasture. Twelve heifers, 270 kg average initial body weight (BW) were distributed in six palisade grass paddocks of two hectares each. The sources of lipids were soybean oil, soybean seed or Megalac-E. Supplementation (0.75% of BW) was offered at 8:00 am daily or on 3 alternate days of each week (Monday, Wednesday and Friday). Heifers were submitted to visual observation for ingestive behavior evaluation every 15 minutes from 8:00 AM to 5:00 PM (total time). The times expended in grazing, in the consumption of the supplements, drinking water, standing and lying were determined. The experiment was analyzed using Mixed Procedure of SAS (2000). There was no effect of source, supplementation frequency and interaction between source and frequency (P > 0.05). Treatments did not affect (P > 0.05) the time expended in grazing, consumption of the supplements, remaining lying or standing, drinking water or other activities (Table 1). It was concluded that lipid source and supplementation frequency did not affect the ingestive behavior of heifers grazing palisade grass pasture, suggesting producers should consider using the less expensive lipid source delivered on alternate days.

Table 1. Ingestive behavior (% of the Total Time) of heifers supplied with different sources of lipids and frequency

		Source				
		MEG[1]	SO[2]	SS[3]	Mean[4]	Pr(t)
Daily	Grazing	43.5	51.7	55.1	50.1	0.1
	E. suppl.	3.9	4.8	6.7	5.2	0.9
	Stand	18.4	15.7	13.0	15.7	0.2
	Lay down	20.6	17.8	16.8	18.4	0.3
	D. water	2.6	2.3	2.6	2.5	0.6
3x/Week	Grazing	53.6	44.	48.9	49.0	0.1
	E. suppl.	3.4	3.2	6.5	4.4	0.9
	Stand	13.8	19.4	18.8	17.3	0.2
	Lay down	16.2	25.0	20.5	20.5	0.3
	D. water	2.7	1.9	1.0	1.9	0.6

[1] Megalac-E; [2, 3] Soybean oil and seeds; [4] Mean;

Key Words: tropical pastures, beef cattle, energy supplementation

W262 Degree of dietary fatty acid saturation affects plasma glucose kinetics in growing beef steers. S. E. Cartiff*, V. Fellner, and J. H. Eisemann, *North Carolina State University*, *Raleigh*.

The objective was to determine the effect of type of fatty acid on insulin sensitivity in growing steers. Steers (n=12, initial BW=336.3 kg, SEM=7.7) were adapted to a basal diet that was 70% concentrate mix and 30% orchardgrass hay and contained 13.1% CP and 2.7 Mcal ME/kg DM. Steers were fed a daily amount of 0.26 Mcal ME per kg $BW^{.75}$. The basal diet contained no added fat. After 3 wks steers were transitioned to one of 2 treatment (Trt) diets (n=6 per diet) containing added Ca salts of fatty acids (FA; Virtus Nutrition) at 4% of DM using a source of fat that was enriched in omega-3 fatty acids (StrataG) or a source of fat without omega-3 fatty acids and a greater percentage of C16:0 and C18:1 (EnergII). Three i.v. glucose tolerance tests (IVGTT; 0.9 g glucose/kg $BW^{.75}$) were conducted; one while on the basal diet, and two while on treatment diets at time 1(T1; d3 Trt), and time 2(T2; d38 Trt). Three i.v. insulin tolerance tests (IVITT; 0.45 IU insulin/kg $BW^{.75}$) were conducted the day after each IVGTT. Blood samples were taken at 30, 15, and 5 min before and 2.5, 5, 10, 15, 20, 30, 40, 50, 60, 75, 90, 120, and 150 min after infusion. Variables were analyzed for effect of time, diet, and diet*time. Measurements of glucose kinetics on the basal diet were used as covariates. For IVGTT, peak glucose tended to be greater (p=0.06) at T2 (12.4mM) than TI (12.0mM). There was a diet by time interaction (p<0.05) for area under the response curve (AUC). The AUC (mM glucose*50min) at T1 was less (p=0.02) for EnergII (126.2) than StrataG (151.8), AUC at T2 tended to be greater (p=0.07) for EnergII (165.9) than StrataG (146.0). For IVITT, minimum glucose value was less (p=0.02) on StrataG (1.5mM) than EnergII (1.8mM); AUC (mM glucose*150min) was less (P=0.001) for EnergII (203.1) than StrataG (263.6). Results show that the amount of time steers were on diets affected glucose kinetics, and response to insulin was greater in steers supplemented with omega-3 FA compared to more saturated FA.

Key Words: fatty acid, insulin sensitivity

W263 Seminal characteristics in beef bulls supplemented with rumen bypass fat. H. O. Patino*[1], M. M. H. Ramirez[3], J. C. C. Angel[1], K. C. Swanson[2], and R. M. Gregory[3], [1]*Dep. Zootecnia, UFRGS*, *Porto Alegre, RS, Brazil*, [2]*Dept. Animal and Poultry Science, University of Guelph*, *Guelph, ON, Canada*, [3]*Faculdade Veterinaria, UFRGS*, *Porto Alegre, RS, Brazil*.

Twenty Hereford, Angus, Brangus and Braford mature bulls (950 kg average body weight) were used in a completely randomized design to evaluate the effect of bypass fat supplementation on fresh semen characteristics. Bulls were fed diets with similar levels of crude protein and metabolizable energy consisting of green forage and concentrate supplemented with rumen bypass fat (BF) or energy supplement (ES). For 75 days bulls in the BF treatment received Megalac-E® (200 g/day) and bulls in the ES treatment received Cassava meal (750 g/day). Bulls were naturally stimulated by androgenic cows and semen samples were collected with an artificial vagina every 15 days. There were no differences due to treatment on seminal volume (6.38 ml/ejaculate), concentration (983,000/ml) and mass motility of spermatozoa (3.6 ; p>0.05). Semen of bulls supplemented with rumen bypass fat had a 10% increase in individual motility (83.2 vs 75.8%) and a 11% increase in vigor (3.62 vs 3.26) in relationship to semen of bulls supplemented with cassava meal (p<0.05). Energy supplementation in the form of rumen bypass fat resulted in greater individual motility and vigor of spermatozoa in semen from bulls.

Key Words: bypass fat, semen, cassava meal

Ruminant Nutrition: Metabolism

W264 Malate and fumarate enhanced CLA production and reduced methane emission by rumen microbes when incubated with linoleic acid. G. L. Jin*[1], X. Z. Li[2], C. G. Yan[2], R. J. Long[3], and M. K. Song[1], [1]*Department of Animal Science, Chungbuk National University*, *Cheong-ju, Chungbuk, Korea*, [2]*Animal Science department of Agricultrue college, Yanbian University*, *Yanji, Jilin, China*, [3]*International Centre for Tibetan Plateau Ecosystem Management, Lanzhou University*, *Lanzhou, Gansu, China*.

An in vitro study was conducted to investigate the effect of malate or fumarate on production of conjugated linoleic acid (CLA) and methane (CH4) by rumen microbes when incubated with linoleic acid (C18:2). Sixty mg of C18:2 (LA), or C18:2 (60mg) with 24mM malic acid (M-LA) or C18:2 (60mg) with 24mM fumaric acid (F-LA) was added to the 150mL culture solution consisting of 75 ml rumen fluid and 75ml artificial saliva. Culture solution was also prepared without any supplements (Control). Two grams of feed (70% concentrate and 30% ground alfalfa hay, DM) were added to the culture solution. The incubation was made anaerobically in a shaking incubator up to 12 hours at 39 C. Malate (M-LA) or fumarate (F-LA) increased pH (P<0.0001) and total VFA (P<0.032) in culture solution from 3h compared to other treatments. The F-LA increased proportion of C3 from 3h incubation (P<0.001-0.0015) compared to other treatments while M-LA increased (P<0.001) its proportion at 6h and 12h incubation times compared to control and LA. Increased (P<0.0007) total gas production was observed from M-LA or F-LA at 12h but was not influenced by LA. Total CH4 production for 12h incubation was greatly reduced (P<0.0001) by all the supplements and its production from M-LA or F-LA was smaller than that from LA. Malate or fumarate with C18:2 also increased concentrations of c9,t11-CLA (P<0.039 - 0.001) and t10,c12-CLA at 1h (P<0.013), 3h (P<0.036) and 12h (P<0.025) incubation times compared to LA. It

may be concluded that malate and fumarate as propionate precursors act as alternative electron sinks, and are competing with CH4 generation and bio-hydrogenation of C18:2 in the utilization of metabolic H2. The increased CLA concentration at early (1h) incubation stage was accompanied by the reduced propionate proportion.

Key Words: propionate precursors, methane, CLA

W265 Phosphate inhibits in vitro ruminal acetoclastic methanogenesis of maize-rich substrates with lactating Holstein dairy cow rumen liquor. H. J. Yang*[1], D. F. Zhang[1], Y. C. Cao[1], Y. H. Jiang[1], and J. Q. Wang[2], [1]*Department of Animal Nutrition and Feed Science, College of Animal Science and Technology*, *Beijing, P.R. China*, [2]*State key Laboratory of Animal Nutrition, Beijing Institute of Animal Science, China Academy of Agricultural Sciences*, *Beijing , P.R. China*.

An in vitro cumulative gas production trial was conducted with mixed rumen microorganisms from cannulated lactating Holstein dairy cow. 25 ml mixed populations of ruminal microbes collected from cannulated cows were incubated together with 50 ml anaerobic modified Menke's basal medium at 39°C for 48 h under a 100% Nitrogen gas phase in 100 ml volume glass bottles preweighted inside with 0.1 g grounded Chinese wildrye grass hay and 0.4 g maize meal. Modified mediums with phosphate addition level of 10, 20, 50, and 100 mM were compared for its in vitro kinetic gas production, volatile fatty acids and methane productions. The control cultures containing citrate buffer instead of phosphate buffer were incubated simultaneously together with treated incubations. Phosphate additions significantly decreased total gas production (GP, ml/g DM) as well as the rate to reach maximum digestion (RmaxG, ml/h) ($P<0.05$). Increasing phosphate inclusion in the cultures decreased the total volatile fatty acids (VFA) production ($P<0.05$), and rumen fermentation shifted from an initially acetate dominated production towards a propionate production as demonstrated by the ratio of non-glucogenic to glucogenic acids (NGR) ($P<0.05$). Although increased phosphate inclusion in the culture fluids did not shift CH_4 proportion in end-product gases, net fractional CH_4 production (ml/g DM), compared to the control, were significantly reduced from those measured in 10, 20, 50, 100 mM phosphate buffers by 6.2%, 11.8%, 18.57%, and 26.2% respectively ($P<0.05$). Therefore, rumen microorganism is indeed sensitive to increased phosphate addition. Methanogen in rumen may be mostly acetotrophic, and phosphate addition inhibits ruminal methanogenesis at the expense of the overall fermentation efficiency of starch-rich substrates. Phosphate level in ration should not be neglected with cares of CH_4 production in ruminant when designing strategies of ruminal methanogenesis inhibition.

Key Words: phosphate buffer, methanogenesis, in vitro cumulative gas production

W266 The effect of concentrate to forage ratios on methanogenes bacteria population in rumen fluid of Holstein steers determined by real-time PCR. A. R. Vakili*[1], M. Danesh Mesgaran[1], A. Heravi Moussavi[1], D. R. Y´ñez Ruiz[3], and C. J. Newbold[2], [1]*Dept. of Animal Science, Ferdowsi University of Mashhad*, *Mashhad, Iran*, [2]*Institute of Biological, Environmental and Rural Sciences, Aberystwyth University*, *Aberystwyth, UK*, [3]*Unidad de Nutrición Animal Estación Experimental del Zaidín (CSIC) Profesor Albareda*, *Spain*.

The objective of the present experiment was to investigate the effect of concentrate to forage ratios on the population of methanogenes bacteria in the rumen fluid of Holstein steers (300±15 kg, body weight) fitted with rumen canolae. Animals were fed experimental diets (7 kg of DM/d) differing in their concentrate (155 g CP/kg DM; 30% maize, 34% barley, 8% soybean meal, 5% sugar beet pulp, 10% wheat bran, 12% cottonseed meal, 0.3% CaCo3, 0.5% mineral and vitamin premix, 0.2% salt) to alfalfa (155 g CP/kg DM) ratios [60:40 (T1), 70:30 (T2), 80:20 (T3), and 90:10 (T4)] in a 4×4 Latin square design (28-day periods). Steers fed the experimental diets as a total mixed ration at 0800 and 2000h. The samples of rumen fluid were taken before the morning feeding and 4 h post feeding. DNA was extracted from the samples using the QIAamp® DNA stool mini kit (Qiagen Ltd, Crawley, West Sussex, UK). Methanogenes bacteria rDNA concentrations were measured by real time PCR relative to total bacteria amplification (ΔΔCt). The 16s rRNA gene-targeted primer sets used in the present study were forward: TTCGGTGGATCDCARAGRGC and reverse: GBARGTCGWAWCCGTAGAATCC. Cycling conditions were 95°C for 10 min, forty five cycles of 94°C for 10s, 55°C for 20s and 72°C for 15s; fluorescence readings were taken after each extension step. Data were analyzed using the GLM procedure of SAS (Y = Mean + Treatment + Animal + Period + Time + Time × Treatment + Animal × Time + residual) and the means compared by the Tukey test ($P<0.05$). The results of the present study demonstrated that increasing the inclusion of concentrate in diets caused a change in the population of methanogenes bacteria in the free rumen fluid taken before and 4 h after the morning feeding [T1= 93 and 84, T2= 60 and 45, T3= 36 and 75, T4= 45 and 81, SEM = 25 and 17 ($\times 10^{-5}$) methanogenes bacteria relative to total bactria, respectively].

Key Words: rumen, PCR, methanogenes

W267 Microbial growth, methane production and fermentation of a high-concentrate diet in Rusitec fermenters as affected by dilution rate and concentrate retention time. M. E. Martínez, M. J. Ranilla*, S. Ramos, M. L. Tejido, C. Saro, and M. D. Carro, *Departamento de Producción Animal, Universidad de León*, *León, Spain*.

Increasing dilution rate (DL) and solids retention time (RT) in ruminal fermenters usually result in significant changes in pH values, making difficult to separate the relative effects of each factor. This study was therefore conducted to investigate the effects of two DL (LDL: 3.78%/h; HDL: 5.42%/h) and two concentrate RT (CRT; T24: 24 h; T48: 48 h) on microbial growth, methane production and fermentation of a 30:70 alfalfa hay:concentrate diet in Rusitec fermenters maintained at similar pH values. Forage RT was 48 h in all fermenters. Differences among treatments were declared at $P < 0.05$. Increasing DL and CRT increased degradability of diet dry matter and neutral detergent fiber (NDF), DL effects being more pronounced in T48 fermenters than in T24 ones. Methane production was not affected by DL, but it was greater in T48 compared to T24 fermenters which was consistent with the greater NDF degradation in T48 fermenters. Increasing DL augmented volatile fatty acid (VFA) production and molar proportions of propionate, isovalerate and valerate. Greater VFA production and molar proportions of acetate and butyrate, and lower propionate, valerate and isovalerate proportions were observed in T48 fermenters compared to T24 ones. Ammonia-N production was greater at HDL compared to LDL which would indicate enhanced deaminative activity, but it was not affected by CRT. Microbial growth was not affected by DL, but was greater in T48 compared to T24 fermenters. Efficiency of microbial growth was augmented by lowering DL and increasing CRT. Fibrolytic activities in ruminal fluid were greater in HDL than in LDL fermenters, but were not affected by CRT. There were DL x CRT interactions for diet apparent disappearance, molar proportions of propionate, butyrate, isovalerate,

and acetate:propionate ratio, indicating that effects of DL on these variables were influenced by CRT.

Key Words: dilution rate, retention time, RUSITEC

W268 Effect of diets supplemented by sucrose and/or starch on *Ruminococcus albus* populations in the rumen fluid of Holstein steers determined by real time-PCR. F. Rezaii, M. Danesh Mesgaran*, A. Vakili, A. Heravi Moussavi, and S. Ghovvati, *Dpt. of Animal Science (Exellence Center for Animal Science), Ferdowsi University of Mashhad, Iran*.

The objective of this work was to investigate the effect of diets containing different types of non-fiber carbohydrates (NFC) on *Ruminococcus albus* populations in the rumen fluid of Holstein steers as determined by real-time polymerase chain reaction (RT-PCR). Four steers (body weight= 280±15 kg) were assigned to a 4 X 4 Latin square with 21 days in each period. A basal diet (BD) was formulated containing alfalfa hay, barley grain, soybean meal and sugar beet pulp (400, 290, 190 and 50 g/Kg DM, respectively). Sucrose (Su) and/or starch (St) or a 1:1 mixture of sucrose and starch (Su+St) was added to the basal diet at the rate of 70 g/Kg DM. Diets were offered at 2-2.5 times maintenance requirements (7 Kg DM/d). Rumen fluid samples were collected before and 4 h after the morning feeding on the last day of each period. Samples were stored in liquid nitrogen until used for *Ruminococcus albus* quantitation by qPCR. DNA was extracted from the samples using the QIAamp® DNA stool mini kit (Qiagen Ltd, Crawley, West Sussex, UK). *Ruminococcus albus* rDNA concentrations were measured by RT-PCR relative to total bacteria amplification. The 16s rRNA gene-targeted primer sets used in the present study were forward: CCCTAAAAGCAGTCTTAGTTCG and reverse: CCTCCTTGCGGTTAGAACA. Cycling conditions were 95°C for 5 min, forty cycles of 95°C for 15 s, 60°C for 15 s and 72°C for 30 s. Data were expressed relative to quantification of the total bacterial population, and analyzed statistically using mixed procedure of SAS (2003). model was: Y = Mean + Treatment + Animal + Period + residual and the means compared by the Tukey test ($P < 0.05$). Present experiment results indicated that the source of NFC added to the basal diet did not cause a significant change in the ruminal *Ruminococcus albus* population relative to the total bacterial population before and 4 h after the morning feeding (BD= 0.0048 and 0.0175, Su= 0.0125 and 0.0242, St= 0.0062 and 0.0107, SuSt= 0.0093 and 0.0178, SEM= 0.0068 and 0.0130, respectively).

Key Words: non-fiber carbohydrate, *Ruminococcus albus*, real-time PCR

W269 Synergistic fibrolysis by cellulolytic *Ruminococcus flavefaciens, Fibrobacter succinogenes,* and non-cellulolytic *Prevotella ruminicola* and *Prevotella bryantii*: study in semi-defined cultures. J. Chiquette* and K. Lauzon, *Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*.

The objective was to investigate the occurrence of synergistic fibrolysis when cellulolytic bacteria are co-cultured with non-cellulolytics in a semi-defined medium in vitro. Cellulolytic bacteria were: *Fibrobacter succinogenes* GC5 and *Ruminococcus flavefaciens* NJ and the non-cellulolytics were: *Prevotella bryantii* 25A and *Prevotella ruminicola* 19189. Avicel, timothy hay and alfalfa hay were used as substrates to measure dry matter (DM) disappearance with time. Cellulolytic bacteria were grown at 37°C for 72 h in basal medium containing 1% (w/v) Avicel (NJ) or 0.3% cellulose filter paper (GC5). After 5 passages in Avicel or cellulose filter paper, fiber was removed and the bacterial pellet was recovered and suspended in an anaerobic dilution solution which OD_{660} was adjusted to 0.5. Non-cellulolytic bacteria were grown in basal medium containing 0.5% (w/v) cellobiose as a sole carbon source until the end of the log phase (12h). The bacterial pellet was treated as mentioned previously. The OD-adjusted inocula were added in monocultures (0.2 ml) or in cocultures (0.2 ml each for cellulolytics and non-cellulolytics) to tubes containing 10 ml of basal medium with 100 mg of each fiber substrate. After 3 days of incubation, a greater ($P \leq 0.001$) disappearance of Avicel was observed when *flavefaciens* was cocultured with *ruminicola* (11.0%) or *bryantii* (10.5%) compared with the monoculture of *flavefaciens* (6.7%). No synergy was recorded in the cocultures with timothy hay or alfalfa hay. Oppositely, after 3 days of incubation, a greater ($P \leq 0.01$) disappearance of alfalfa hay DM was observed when *succinogenes* was cocultured with *ruminicola* (12%) or *bryantii* ($P \leq 0.08$) (9.9%), compared with the monoculture of *succinogenes* (3.1%). No synergy was observed with timothy hay. All of these synergistic effects were observed after 3 days of incubation but not after 7 days. The presence of *ruminicola* and *bryantii* seem to accelerate fiber digestion by the cellulolytic species *succinogenes* and *flavefaciens*. The synergistic effect is substrate dependent.

Key Words: fiber digestion, rumen bacteria, synergism

W270 Role of inulin as a modifier in rumen fermentation. H. D. Umucalilar[1], N. Gulsen[1], A. Hayirli*[2], and M. S. Alatas[1], [1]*Department of Animal Nutrition and Nutritional Disorders, Faculty of Veterinary Medicine, Selçuk University, Konya, Turkey*, [2]*Department of Animal Nutrition and Nutritional Disorders, Faculty of Veterinary Medicine, Atatürk University, Erzurum, Turkey*.

Few studies dealing with inulin fermentation by rumen microbes are available, although its prebiotic effects in the hindgut of humans, nonruminant farm animals and pet animals have been extensively investigated. The objective of this *in vitro* experiment was to examine the effects of inulin (0, 2 and 4%) (Frutafit® TEX, Sensus, The Netherlands) at different forage:concentrate ratio (F:C, 20:80, 40:60 and 60:40) on rumen fermentation variables. Ruminal fluids were collected from two Holstein steers and incubated with the mixtures for 48 hours. Rumen variable data were subjected to 2-way ANOVA using the MIXED Procedure. Ruminal fluid pH (from 6.71 to 6.77) and NH_3-N concentration (from 11.72 to 15.71 mmol/L) increased linearly, whereas lactate concentration (from 28.11 to 26.29 mmol/L) decreased quadratically as the forage proportion increased ($P < 0.0001$ for all). Inulin did not affect ruminal fluid pH and concentrations of NH_3-N and lactate. Increasing F:C ratio was associated with a linear increase in the proportion of acetate from 53.39 to 55.41% ($P < 0.0001$), no change in the proportion of propionate, a linear decrease in the proportion of butyrate from 19.74 to 17.59% ($P < 0.002$). Total VFA concentration quadratically decreased with increasing the forage proportion ($P < 0.006$). Inulin had no effect on VFA proportions. There was no F:C ratio by inulin level interaction effect on rumen variables, except for total VFA concentration. Increasing inulin level increased total VFA concentration at high concentrate, whereas decrease it at low concentrate ($P < 0.02$). Total gas production linearly decreased from 41.14 to 33.74 mL with increasing the forage proportion ($P < 0.0001$), whereas it linearly increased from 36.76 to 38.25 mL with increasing inulin level ($P < 0.005$). However, there was no interaction effect on gas production. In conclusion, our data do not support that inulin may play a modifier role in rumen fermentation.

Key Words: inulin, rumen fermentation, gas production

W271 Role of lactulose as a modifier in rumen fermentation. N. Gulsen[1], H. D. Umucalilar[1], A. Hayirli*[2], and O. B. Citil[1], [1]*Department of Animal Nutrition and Nutritional Disorders, Faculty of Veterinary Medicine, Selçuk University, Konya, Turkey*, [2]*Department of Animal Nutrition and Nutritional Disorders, Faculty of Veterinary Medicine, Atatürk University, Erzurum, Turkey*.

Lactulose is a prebiotic and resistant to acidic hydrolysis and enzymatic digestion, but fermented to volatile fatty acids (VFA) by the colonic bacteria in humans and monogastric animals. This *in vitro* experiment was conducted to examine the effects of lactulose at 0, 2, and 4% (667 mg/ml, Osmolak® Solüsyon, Biofarma Ílaç Sanayi ve Ticaret A. S., Ístanbul, Turkey) on ruminal fermentation of the mixtures (230 mg) differing in forage:concentrate ratio (F:C; 20:80, 40:60 and 60:40). Ruminal fluids collected from two Holstein steers were incubated with the mixtures for 48 hours. Data were analyzed using 2-way ANOVA. Increasing F:C ratio caused a linear increase in ruminal fluid pH (from 6.71 to 6.76; $P < 0.0001$), a linear decrease in NH_3N concentration (from 15.84 to 11.77 mmol/L; $P < 0.0001$), and a quadratic increase in lactate concentration (from 25.51 to 26.91 mmol/L; $P < 0.04$), but did not affect total VFA concentration. There were also linear increases in acetate (from 53.89 to 55.69%; $P < 0.0002$) and valerate (from 3.05 to 3.25%; $P < 0.003$) proportions and a linear decrease in butyrate (from 19.74 to 17.32% ($P < 0.0001$) proportion. There were no main effect of lactulose and F:C ratio by lactulose level interaction effect on fermentation pattern. Increasing forage portion linearly decreased cumulative gas production from 41.14 to 33.54 mL ($P < 0.0001$), whereas increasing lactulose level did not alter cumulative gas production. In conclusion, lactulose failed to alter fermentation pattern of the basal mixtures consisting of different F:C ratios, suggesting that fermentation modifying role of lactulose in the ruminant animal is negligible.

Key Words: lactulose, rumen fermentation, gas production

W272 Lactic acid modulates DM degradation kinetics of barley grain in the rumen and decreases the risk of acidosis in dairy cows. S. Iqbal, Q. Zebeli*, A. Mazzolari, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada*.

The aim of this study was to evaluate the effects of barley grain treated with lactic acid (LA) on *in vivo* diurnal fermentation patterns and *in situ* DM degradation kinetics in the rumen of dairy cows. In the *in vivo* trial, 8 rumen-fistulated Holstein cows (~200 DIM) were fed once daily a TMR containing rolled barley grain (27% in DM) steeped for 48h in equal quantity of water (CTR) or with 0.5% LA (v/v; TRT) in a crossover design with two 21-d periods. Rumen fluid samples were collected at the last day of each period at 0, 2, 4, 6, 8, 10, and 12h post-feeding, and analyzed for pH and VFA concentration. The *in situ* trial consisted in ruminal incubation (n = 6 cows) of dublicate samples of 3 different substrates (CTR, TRT at 0.5% or 1.0% LA; v/v) for 0, 2, 4, 8, 12, 24, 48, and 72h. Data were analyzed statistically by PROC MIXED of SAS using a model for repeated measures. Degradation kinetics parameters were estimated by fitting the *in situ* data using NLIN PROC of SAS. Results of *in vivo* fermentation patterns showed an interaction between diet and hour of measurement for total VFA and pH of the ruminal fluid (P<0.05). The analysis indicated lower concentration of VFA particularly at 2 (P=0.03) and 4h (P=0.01) post-feeding for cows fed the TRT-diet compared to control group. Interestingly, the group of cows fed the TRT-diet had higher pH readings at 10 (P=0.02) and 12h (P=0.04) post-feeding. The latter effect was associated with a shorter duration time in which ruminal pH was below 5.8 for the TRT-diet (2.4h) compared to the CRT diet (3.9h; P=0.04). The *in situ* data indicated a lower (P=0.05) fractional DM degradation rate (kd=12.3%/h) and effective degradability (ED=81.5%) for barley grain treated with 0.5% LA compared to other two substrates (kd=18.6 and 21.2%/h and ED =82.4 and 83.6% for control- and 1.0% LA-substrates, respectively). In conclusion, treating barley grain with 0.5% LA modulated *in vivo* diurnal rumen fermentation patterns and *in situ* DM degradation kinetics suggesting a potential role for the LA-treatment of barley grain to decrease the risk of rumen acidosis in dairy cows.

Key Words: dairy cow, lactic acid, rumen fermentation

W273 Effect of condensed tannins and maceration on in vitro ruminal degradation of protein in legume hay. G. A. Broderick* and J. H. Grabber, *U.S. Dairy Forage Research Center, Madison, WI*.

Protein in alfalfa hay and most forages is extensively degraded in the rumen. Condensed tannins in birdsfoot trefoil (BFT) and polyphenol oxidase in red clover act differently to reduce protein degradation. Maceration (extensive mechanical conditioning) increases field-drying rate and decreases proteolysis in the swath, which may further reduce degradation. Alfalfa (ALF), low tannin BFT (LTBFT, 0.6% tannin), high tannin BFT (HTBFT; 1.5% tannin), and red clover (RC) were cut and conditioned using either rolling (ROLL) or maceration (MAC), field-dried and harvested as hay. Hay was ground (2 mm screen), analyzed for chemical composition and incubated with ruminal inocula in the Michaelis-Menten inhibitor in vitro method to quantify degradation (Broderick and Clayton, Brit. J. Nutr. 67:27-42, 1992). Extent of degradation was estimated from net release of ammonia N plus amino N determined using an assay that detects only free AA or one that detects both AA and small peptides. Results were analyzed by proc mixed in SAS; LS means are in the table. Quantifying peptide release increased ($P < 0.01$) degradation rate from 0.31 to 0.35/h. There was no effect of forage source or conditioning on CP. However, RC had lower NDF and NPN, higher NDIN, lower degradation rate and greater estimated escape. MAC gave a small increase in NDF but had large effects on NPN, NDIN, degradation rate and escape. Tannin slightly reduced NPN and increased ADIN but had little effect on degradation. Results indicated that maceration reduced protein degradation and that greater amounts of protein in RC hay would escape the rumen.

Table 1.

	Forage source					Conditioning		
Item	ALF	LTBFT	HTBFT	RC	P > F	ROLL	MAC	P > F
Composition								
CP, % of DM	23.9	23.3	22.6	22.8	0.07	23.4	22.8	0.18
NDF, % of DM	43.1^{a}	41.1^{ab}	42.4^{a}	39.6^{b}	0.02	40.1	43.0	0.04
NPN, % of N	26.4^{a}	27.4^{a}	24.2^{b}	19.6^{c}	<0.01	29.6	19.2	<0.01
NDIN, % of N	12.1^{b}	13.9^{b}	14.5^{b}	25.9^{a}	<0.01	11.4	21.9	<0.01
ADIN, % of N	2.6^{c}	3.0^{bc}	4.0^{a}	3.4^{b}	<0.01	3.2	3.2	0.67
Protein degradability								
Rate, /h	0.36^{a}	0.34^{a}	0.34^{a}	0.27^{b}	<0.01	0.40	0.26	<0.01
Est. escape, %	10.9^{c}	10.7^{c}	12.3^{b}	20.3^{a}	<0.01	6.7	20.5	<0.01

$^{a-c}$Forage sources with different superscripts differ (P < 0.05).

Key Words: tannins, forage conditioning, protein degradability

W274 Shift in in vitro microbial fermentation in response to condensed tannin supplementation in mixed ruminal cultures. C. M. Dschaak, J.-S. Eun*, Y.-M. Kim, F. H. Bhushan, and A. J. Young, *Utah State University, Logan*.

This study investigated the dose response of quebracho condensed tannins (CT) supplemented to high concentrate, lactating dairy TMR diet on ruminal pH, fermentation, and methane production in mixed ruminal cultures. A dual-flow continuous culture system consisting of 4 fermentors at liquid dilution rate of 10%/h was used in a 4 × 4 Latin square design. The diet used in the study consisted of 33% alfalfa hay, 7% corn silage, 40% rolled barley grain, and 20% concentrate mix. Water-soluble quebracho extract (QE) was used as the source of CT (99% solubility; Chemtan Company Inc., Exeter, NH). The 4 treatments were 1) control = TMR without QE; 2) TMR with 2% QE (LCT); 3) TMR with 4% QE (MCT); and 4) TMR with 6% QE (HCT). Filtered ruminal contents were allowed 5 d of adaptation to the treatments followed by 3 d of data collection. Data were analyzed using the MIXED procedure of SAS. Although ruminal pH linearly ($P < 0.01$) decreased with increasing CT supplementation, actual difference between control and HCT was only less than 0.1 (average pH 6.26). Methane production linearly ($P < 0.01$) increased in response to increasing CT, whereas ammonia-N concentration linearly ($P < 0.01$) decreased. Total VFA linearly ($P = 0.02$) increased by increasing CT supplementation. While molar proportion of acetate linearly ($P < 0.01$) increased, propionate proportion tended to decrease linearly ($P = 0.07$), resulting in increased acetate to propionate ratio ($P = 0.02$) when CT supplementation increased. The increased acetate to propionate ratio corresponded to the increased methane production. The supplementation of CT resulted in accelerated microbial production, as was seen in increased VFA and methane production and decreased ammonia-N. Supplementing CT to barley based-high concentrate dairy TMR had no negative impact on in vitro microbial fermentation, but sizably shifted its fermentation patterns due possible to the stimulation of cellulolytic bacteria.

Key Words: condensed tannins, continuous culture, methane production

W275 Deglycosylation of steroidal saponin to sapogenin by mixed rumen microbes and their enzymes. Y. Wang* and T. A. McAllister, *Agriculture & Agri-Food Canada Research Centre, Lethbridge, AB, Canada*.

Inconsistent effects of steroidal saponins on ruminal fermentation may arise from rumen microbes adapting to and/or deactivating saponins by deglycosylation. It is not known whether this process is intra- or extracellular in nature. To study this further, ruminal fluid (RF) was collected from two heifers that were non-adapted or saponin-adapted (i.e., fed powdered *Yucca schidigera* (YS) for 14 d). The RF was centrifuged at 20,000 × *g* (yielding clarified RF, cRF) or at 500 × *g* (whole RF, wRF), and incubated for 4 h with saponins extracted from YS. Four of 8 replicates were assayed directly (measuring soluble saponin + deglycosylated, insoluble sapogenin); the other four were centrifuged (12,000 × *g*; 20 min) and supernatant was assayed (measuring saponin only). Added YS saponins were all accounted for in directly assayed wRF and cRF (99.1 and 100.6%, respectively), whereas saponin recovery was greatly reduced ($P < 0.001$) in centrifuged wRF compared with centrifuged cRF (58.5 vs. 98.7%). Saponin recoveries did not differ between adapted (59.2 and 99.0%) and non-adapted cattle (57.3 and 99.3%). In Exp. 2, wRF prepared from non-adapted RF was centrifuged at 20,000 × *g*. Half of the supernatant was used as a source of mixed extracellular enzymes (ECE). The remainder was autoclaved, added back to the bacterial pellet, and the re-suspension was sonicated, yielding a source of mixed cell-bound enzymes (CBE). The ECE and CBE fractions were incubated with YS saponins for 24 h at 39°C. Subsamples were assayed directly, for saponin + sapogenin, and after centrifugation, for soluble saponin. In ECE, >92% of the added saponin was detected in supernatant fraction (i.e., as saponin), whereas in CBE, <30% was detected in supernatant, and >70% in the sapogenin fraction. These findings clearly demonstrate that mixed rumen bacteria deglycosylate steroidal saponin to sapogenin, irrespective of prior exposure to YS, but they were unable to degrade the sapogenin core structure. Deglycosylation activity was attributable primarily to cell-bound enzymes.

Key Words: steroidal saponin, mixed rumen bacteria, enzymes

W276 Starch fermentation kinetics in rumen fluid and synthesis of end products. J. W. Cone*[1] and P. M. Becker[2], [1]*Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands*, [2]*Animal Sciences Group of Wur, Lelystad, the Netherlands*.

In this study, fermentation kinetics in rumen fluid of 16 starchy feedstuffs, differing in starch content, were correlated with the amount of synthesized volatile fatty acids (VFA-s) and microbial mass (MM). The fermentation kinetics were determined using a gas production technique (GPT). Rumen fluid was collected from two non-lactating rumen cannulated cows, receiving 1 kg of standard compound feed (150 g/kg starch) in the morning and ad libitum hay in the morning and the afternoon. After 0, 4, 8 and 12 h of incubation, individual and total VFA-s were determined. Gas production profiles were modeled and the incubation time at which the proportional rate of gas production was maximal (tRmax) was determined. This is the time point at which MM is maximal and the substrate is to be exhausted. At tRmax VFA-s were determined as well as the purin content as a measure of the MM. Gas productions were corrected for blank gas productions, buffered rumen fluid without sample, and VFA and MM were corrected for contents at 0 h incubation. At all incubation times, there proved to be a rather good relationship between gas production and synthesis of total VFA ($r2 = 0.88$), acetic acid ($r2 = 0.88$), propionic acid ($r2 = 0.79$) and butyric acid ($r2 = 0.84$). The relationship between gas production at all incubation times and the non-glucogenic:glucogenic ratio (NGGR) was rather poor ($r2 = 0.34$). However, for each incubation period separately, there was a linear relationship between gas production and NGGR ($r2 = 0.77$), which was also the case at tRmax. There proved to be a linear relationship between tRmax for the different samples and the amount of synthesized MM ($r2 = 0.58$). A fast fermentation caused a high amount of MM. At tRmax there was a linear relationship between NGGR and synthesized MM. It was concluded that both the NGGR and amount of MM are largely determined by the rate of starch fermentation.

Key Words: gas production technique, rumen fermentation, starch

W277 Empirical prediction of oxygen consumption by portal-drained viscera in ruminants: Meta-analysis approach. C. Loncke*[1], I. Ortigues-Marty[1], S. Amblard[1], J. Vernet[1], S. Léger[2], H. Lapierre[3], D. Sauvant[4], and P. Nozière[1], [1]*Institut National de la Recherche Agronomique - UR 1213, Theix, France*, [2]*Université de Clermont Ferrand II - Laboratoire de Mathématiques, Aubière, France*, [3]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [4]*Institut National*

de la Recherche Agronomique - AgroParisTech - UMR 791, Paris, France.

In Ruminant nutrition, the evolution of feed evaluation systems towards nutrient-based systems is an important challenge. Net portal appearance of volatile fatty acids, glucose, β-hydroxybutyrate, lactate and α-amino N can be estimated with response equations based on ration intake and composition (Loncke et al., 2008, Renc. Rech. Rum. 15:285; Loncke et al., 2009, J. Anim. Sci. 87:253-268) characterized according to INRA Feed Tables for Ruminants and derived from a meta-analysis (Sauvant et al., 2008, Animal 2:1203-1214) on the FLORA (FLux of nutrients through Organs and tissues in Ruminant Animals) database (Vernet and Ortigues-Marty, 2006, Reprod. Nutr. Dev. 5:527-546). The present objective was to extend the meta-analysis to oxygen (O_2) consumption by portal-drained viscera (PDV) in relation with changes in intake and dietary composition. Data on PDV O_2 consumption in sheep and cattle (n = 38) were selected from FLORA database. Animals of the publications consumed on average 20.2 ± 7.2 g DM/kg BW/d with an average proportion of 25.6 ± 31.7 g concentrate/100 g DM. The best adjustment was obtained with a variance covariance model, common to both sheep and cattle, that included only DMI as predictor and a within experiment effect (R^2 = 0.78; RMSE = 0.4 mmol/kg BW/d; P < 0.001). Adding other parameters such as diet composition (ME, NDF and CP concentration) did not improve significantly the equation. The model showed that an increase of 1g DMI/kg BW/d induces a predicted increase of 0.081 ± 0.013 mmol/kg BW/d of O_2 consumption by the PDV, independently of the nature of diet. It is coherent with the two known factors of variation of PDV O_2 consumption, i.e. physical (digesta mass) and chemical (nutrients) components (Han et al., 2002, J. Anim. Sci. 80:1362-1374).

Key Words: meta-analysis, portal-drained viscera, oxygen consumption

W278 Plasma acetate, glucose and leucine turnover rates and whole body protein synthesis in growing lambs. H. Sano, K. Chiba, A. Saito, K. Shibuya, and M. Al-Mamun*, *Iwate University, Morioka, Iwate, Japan*.

The aim of the present experiment was to determine plasma acetate, glucose and leucine metabolism and whole body protein synthesis in growing lambs. The experiment was performed using crossbred (Corriedale x Suffolk) growing lambs (n=7; 3 male and 4 female) at 2 growth stage; 2 month old (2M, 18±3 kg of initial BW) and 6 month old (6M, 25±6). The lambs were offered mixed hay (metabolizable energy (ME) 1.79 kcal/g) and concentrates (ME 2.62 kcal/g) 33 g/kg$^{0.75}$/d each once a day at 14:00 for a period of 21 day with ad libitum water access. The animals were kept in individual pens for the first 14 day preliminary period in an animal shed and then moved to a controlled environmental house at a temperature of 23±1°C. Three isotope dilution methods using [1-^{13}C]Na-acetate, [U-^{13}C]glucose and [1-^{13}C]leucine were performed simultaneously as a primed continuous infusion for 4 h on the 21st day of the experimental period for each growth stage. Turnover rates of plasma acetate, glucose and leucine were determined from the isotopic enrichments of [1-^{13}C]Na acetate, [U-^{13}C]glucose and [1-^{13}C]leucine and α-[1-^{13}C]keto isocaproic acid (α-KIC), respectively using GC/MS. Whole body protein synthesis was determined using nitrogen balance test and leucine turnover rate calculated from α-KIC. Plasma concentration of NEFA was numerically lower (P = 0.13) in 6M than 2M. Plasma acetate concentration was higher (P = 0.01) and turnover rate was numerically higher (P = 0.15) in 6M than 2M. Plasma glucose concentration was lower (P = 0.05) and turnover rate tended to be lower (P = 0.10) in 6M than 2M. Plasma concentration of α-KIC tended to be lower (P = 0.10) and turnover rate of leucine remained comparable (P = 0.83) between age groups. The present findings laid an idea that the higher plasma acetate and lower plasma glucose metabolism might be attributed to increased microbial activity with the development of rumen. However, protein metabolism was not influenced with the development.

Key Words: nutrients metabolism, stable isotope, growing lambs

W279 Mammary cell signaling responses to abomasal starch and casein infusions in lactating dairy cows. A. G. Rius*[1], J. Escobar[2], O. Becvar[3], D. Kirovski[4], and M. D. Hanigan[1], [1]*Dept. of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg*, [2]*Dept. of Animal Science, Virginia Polytechnic Institute and State University, Blacksburg*, [3]*College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg*, [4]*Faculty of Veterinary Medicine, University of Belgrade, Belgrade, Serbia*.

The objective of this study was to evaluate the effects of abomasal infusions of starch and casein on cell signaling pathways in the mammary gland of lactating cows. We hypothesized that abomasal infusions of starch or casein could activate independently the mammalian target of rapamycin (mTOR) cell signaling cascade. Six primiparous, mid-lactation, ruminally cannulated Holstein cows were randomly assigned to casein (C) and starch (S) treatments using a 2 x 2 factorial arrangement of treatments. The design was a replicated incomplete 4x4 Latin-square. All animals received the same basal diet (17.6% CP and 1.58 Mcal NEL/kg DM) throughout the study. Cows were restricted to 70% of ad libitum intake and abomasally infused for 36 h with S (3 kg/d), C (1.3 kg/d), the combination (3kg/d S + 1.3kg/d C), or water using peristaltic pumps. Blood samples were collected during the last 8 h of treatment. At the end of the infusion, biopsy samples were collected and western blot analysis of signaling proteins was conducted. The main effects of S, C, or the interaction of both was analyzed using the Proc Mixed procedure of SAS. Casein increased plasma concentration of Phe (P < 0.01), Leu (P < 0.01), Ile (P < 0.01), and Met (P < 0.01). However, S decreased concentration of Lys (P < 0.01), Val (P < 0.01), and His (P < 0.01). Starch increased (P < 0.05) the phosphorylation of mTOR and ribosomal protein S6. There was a positive interaction between S and C infusion for the phosphorylation of protein kinase B (P < 0.01) and a negative interaction for the unphosphorylated form of mTOR (P < 0.01). Thus, the mTOR pathway in the mammary gland can be regulated by amino acids and energy substrates.

Key Words: amino acids, cell signaling, mammary gland

W280 Meta-analysis for the prediction of net portal absorption of amino acid nitrogen in ruminants. R. Martineau*[1], D. Sauvant[2], D. R. Ouellet[1], J. Vernet[3], I. Ortigues-Marty[3], and H. Lapierre[3], [1]*Agriculture and Agri-Food Canada, Stn Lennoxville, Sherbrooke, QC, Canada*, [2]*AgroParisTech INRA, Paris, France*, [3]*UHR INRA Clermont-Ferrand, Theix, St-Genès Champanelle, France*.

The objective of this meta-analysis was to determine a prediction equation for net portal absorption of amino acid-N (NPA-AAN) based on diet intake and composition. Selection of publications was based on availability of NPA-AAN (as α-amino-N or individual AAN), N intake (NI), BW, and feeding treatments. Some treatments were excluded because of fasting, use of metabolism modifiers, infusion in the gut or abnormal feeding conditions. The final database included 65 publica-

tions (203 treatments). Cattle treatments were aggregated (beef, n=68; dairy, n=22) and the meta-analysis was conducted on a total of 87 experiments (sheep, n=47; cattle, n=40). The diet characteristics were estimated using nutrient composition of feed ingredients from NRC (2001) tables, correcting only for N and NDF when reported. Fluxes of α-amino-N were multiplied by 1.396 to convert to fluxes of total AAN assuming that only the α-N is detected by the α-amino-N analysis. Daily NPA-AAN and NI averaged 0.216 ±0.125 and 0.465 ±0.199 g/kg BW, respectively. Linear and quadratic relationships between NPA-AAN and NI were tested inter- and intra-experiments, treating experiment as a fixed effect. In addition, other potential covariates were tested: DMI (%BW), forage:concentrate, TDN_{1X}, NDF and CP (%DM), NE_L (Mcal/kg), RDP and RUP (%CP), and digestible NFC (%NFC). The best fit was a linear model (R^2=0.916; RMSE=0.042) that included NI (P<0.001), NDF (P<0.001), and species (P=0.004). No outliers were detected on 191 observations in the post-model analysis. The overall equation was [coefficient (±SE)]: NPA-AAN = 0.120 (0.034) + 0.464 (0.040) NI – 0.0032 (0.0007) NDF with a species effect on the intercept: Δ = – 0.071 for cattle and 0.071 for sheep. There was no species × covariate interaction indicating that the variations of NPA-AAN were independent of species. Our results show that the magnitude of NPA-AAN was highest in sheep suggesting that they absorbed more AAN than cattle at similar NI and NDF. This indicates that sheep could transfer N ingested to NPA-AAN with a higher efficiency than cattle, likely due to a higher urea recycling into the rumen.

Key Words: amino acids, portal absorption, ruminants

W281 Acute fasting-induced changes in motilin, luteinizing hormone and metabolites in goat wethers. O. Gazal[1], B. Kouakou*[2], W. Mboko[1], S. Bialka[1], and J. H. Lee[2], [1]*St. Cloud State University, St. Cloud, MN*, [2]*Fort Valley State University, Fort Valley, GA*.

In monogastrics the secretion of motilin, a peptide hormone produced by cells in the gastrointestinal tract of many mammals, increases during fasting. Similarly, the secretion of luteinizing hormone (LH) is suppressed by fasting in monogastrics and other animals. Although different mechanisms of undernutrition-induced suppression of gonadotropin secretion have been proposed, the possible role of motilin in this process remains unclear. In this study, we tested the hypothesis that acute fasting induced changes in plasma motilin secretion in wethers and that changes in plasma motilin and LH secretion are correlated. Six wethers in high body conditions were fed ad-libitum and then fasted for 48 hours. Blood samples were obtained from an indwelling catheter for 4 hours at 10 minute intervals during each feeding regimen. Results indicate that motilin is secreted in a pulsatile manner and that fasting tended to increase plasma motilin secretion (P=.06). Acute fasting induced a paradoxical increase in plasma LH (P<.001). Fasting caused a significant decrease in plasma glucose (P<.02) but increased plasma urea nitrogen (P<.0001) and beta-hydroxybutyrate (P<.001). However, there was no effect of acute fasting on plasma non-esterified fatty acids (P=0.8). Plasma motilin levels were negatively correlated with plasma LH in the fed state (P<.001) but this correlation was not significant in the fasted state. These results indicate that the suppressive effect of acute fasting on LH secretion in goats may be dependent upon testosterone and body condition. Furthermore, fasting for 48 hours may be insufficient to cause a significant increase in plasma motilin in ruminants.

Key Words: goats, acute fasting, motilin

W282 Effect of diet and the $SGLT_1$ inhibitor phlorizin on net intestinal glucose absorption in Holstein steers. A. L. Ballou*, S. W. El-Kadi, and D. L. Harmon, *University of Kentucky, Lexington*.

Previous studies have shown that adult ruminants have a limited capacity for small-intestinal glucose absorption. This is thought to be the result of very low activity by the sodium glucose co-transporter, $SGLT_1$. However, attempts to induce increases in $SGLT_1$ have not been successful in cattle. We hypothesized that if $SGLT_1$ is the primary pathway of transcellular absorption then we should be able to decrease net glucose absorption by phlorizin infusion and this response may differ depending on diet. The objective of this study was to determine net glucose absorption in steers fed forage or grain-based diets in the absence and presence of phlorizin. Steers (n=3) were fed two isocaloric diets, high-forage and high-concentrate, at 1.5xNE_m over two periods of 14 days each. On d 14 of each period, repeated samplings were taken, representing two periods with two different abomasal infusions. For the first infusion, glucose was infused abomasally at a rate of 20g/h for four hours. The second four-hour infusion consisted of glucose infused at 20g/h with the addition of phlorizin at 400μmol/h. Para-aminohippuric acid was infused continuously into a mesenteric vein and six samples of portal venous and mesenteric arterial blood were collected over three hours of each infusion. Steers fed high-concentrate had higher ($P < 0.03$) portal blood flow, net glucose absorption ($P < 0.01$) and net portal glucose recovery ($P < 0.01$) of infused glucose (76 vs. 38%) than steers fed high-forage. Phlorizin infusion did not affect ($P > 0.05$) portal blood flow, net glucose absorption or net portal glucose recovery. These results show that while diet affects net glucose absorption, $SGLT_1$ may not be the primary mechanism through which this occurs.

Key Words: glucose, ruminant nutrition, $SGLT_1$

W283 Plasma concentration of glucose-dependent insulinotropic polypeptide is negatively correlated with respiratory quotient in lactating dairy cows. A. E. Relling*[1], L. A. Crompton[2], S. C. Loerch[1], and C. K. Reynolds[2], [1]*The Ohio State University, Wooster*, [2]*University of Reading, Reading, UK*.

In dairy cows, an increase in plasma concentration of GIP was associated with an increase in ME intake (MEI), but the role of GIP in energy partitioning of dairy cattle is not certain. The objective of our study was to examine the relationship between plasma GIP concentrations and energy metabolism. Four mid-lactation, primiparous, rumen-fistulated Holstein-Friesian cows were fed a control diet of 50% forage and 50% concentrate (DM basis) in a 4 X 4 Latin square design with 4-wk periods. The four treatments were: 1) a control diet fed at 1000 and 1600 h; the control diet plus one dose (1.75 kg DM basis at 0955 h) into the rumen of supplemental vegetable proteins (Amino Green, SCA, NuTec) and fed: 2) once (1000 h); 3) twice (1000 and 1600 h); or 4) 4 times (1000, 1600, 2200 and 0400 h). Measurements of respiratory exchange and energy balance were obtained over 4 d during the last week of each period while cows were housed in open-circuit respiration chambers. Blood was collected from the jugular vein every 30 min for 12 h using indwelling catheters and starting at 0800 h on d 20 of each period. Plasma GIP concentration was measured in samples pooled over each 5 consecutive blood samplings. Data were analyzed as repeated measures using mixed models testing random effects of animal and period and fixed effect of treatments, time and their interaction. The relationships between plasma GIP and MEI, heat production (HP), respiratory quotient (RQ) and milk yield (MY) were analyzed using linear correlation procedures, with MEI as partial variant. There was no effect (P> 0.2) of treatment on DMI (18.6 kg/d) and MY (27.6 kg/d). Plasma GIP

increased over time during the day ($P < 0.01$), but it did not change due to treatment ($P > 0.7$). Plasma GIP concentration was not correlated with MEI or HP ($P > 0.4$), but was positively correlated with MY ($r^2 = 0.42$, $P < 0.11$) and negatively correlated with RQ ($r^2 = -0.72$, $P < 0.01$). The correlations between GIP and RQ or milk yield do not imply causality, but suggest there may be a role for GIP, or associated factors, in the regulation of energy metabolism in dairy cows.

Key Words: GIP, energy partitioning, RQ

W284 Gluconeogenesis and carbon recycling in beef steers is modulated by energy-substrate supply. B. J. Bequette*[1], J. Sumner-Thomson[1], J. A. Moorefield[1], D. Hucht[2], M. Niland[2], and R. L. Baldwin VI[2], [1]*Department of Animal and Avian Sciences, University of Maryland, College Park*, [2]*Bovine Genomic Laboratory, Animal and Nutrition Resources Institute USDA-ARS, Beltsville, MD*.

To identify important rate-controlling sequences in regulation of gluconeogenesis by macronutrient supply, 19 beef steers (272.5 ± 17.6 kg initial BW) were fed a forage-based diet and infused per abomasum with either water (Control, n = 4), Casein (n = 5) or Starch (n = 5), or fed Na-propionate (n = 5) for 42 d. Treatments were administered on an equal energy basis (40 kcal/kg metabolic BW). On day 42, [U-^{13}C] glucose (1.25 g/h) was continuously infused into a jugular vein for 12 h. Over the last 5 h of tracer infusion, plasma glucose isotopic enrichment was determined by gas chromatography-mass spectrometry followed by ^{13}C-mass isotopomer distribution analysis. Data were analyzed by ANOVA and differences between Control and nutrient infusion treatments were assessed using Dunnett's *t*-Test. Steers receiving nutrient infusion gained more weight (3.6 to 5.2%, $P < 0.05$) over the 42-d experiment compared to Control. Apparent glucose production (g/kg empty BW/d) was greater (25 to 30%, $P < 0.05$) for steers receiving Starch, Casein, and Na-propionate compared to Control. Steers receiving Casein tended ($P < 0.10$) to have greater (40%) rates of glucose recycling (g/d) compared to Control. Steers receiving Starch and Na-propionate had greater (26 to 31%, $P < 0.05$) rates of gluconeogenesis plus glucose absorption. Despite different substrate compositions of the treatments, gluco-control was maintained and this involved different mechanisms. For example, steers receiving Casein increased glucose recycling whereas steers receiving Starch and Na-propionate had increased gluconeogenesis and/or glucose absorption.

Key Words: steer, gluconoegenesis, stable isotope

W285 First-pass glucose uptake (FPU) in the intestine of kids fed casein- or soy protein-based milk diets. U. Schönhusen, A. Flöter, P. Junghans, C. C. Metges, and H. M. Hammon*, *Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*.

Soy protein alters the intestinal morphology with consequences for absorptive function. Supplementation of soy protein with indispensable amino acids (AA) seems to ameliorate mucosal growth retardation and stimulates the glucose transport capacity in the mucosa. We investigated effects of feeding soy protein with or without AA supplementation on FPU in the intestine. Goat kids (14 d of age) were fed milk diets, in which 50% of the crude protein was either casein (CA), soy protein isolate (SP) or soy protein isolate with supplementation of those AA known to be lower concentrated in soy protein than in casein (SPA) for 43 d (n=8/group). A single bolus dose of D-[U-$^{13}C_6$]glucose (10 mg/kg BW) was given with the morning diet, and simultaneously, a bolus D-[6,6-$^2H_2$]glucose (5 mg/kg BW) was injected into a jugular vein. Blood samples were collected between -30 and +420 min relative to the tracer administration to measure plasma glucose enrichments, resulting in separate pools for D-[6,6-$^2H_2$]glucose and D-[U-$^{13}C_6$] glucose, respectively. FPU was calculated from the rate of appearance of differentially labeled glucose tracer in plasma. Glucose oxidation was calculated from $^{13}CO_2$ enrichment in blood. In addition, plasma concentrations of glucose, insulin, and glucagon were measured. Data were evaluated by using the Mixed Model and GLM procedures of SAS. Before feed intake, plasma glucose concentration tended to be higher ($P < 0.1$) in CA than SPA, whereas insulin was higher ($P < 0.05$) in CA than SP and SPA, and glucagon was higher ($P < 0.05$) in CA than SPA. Plasma glucose and insulin concentrations increased ($P < 0.05$) during first hour after feeding, whereas plasma glucagon increased immediately after feeding and after 1 h of feeding. The [6,6-$^2H_2$]glucose pool size tended to be higher ($P < 0.1$) in CA than SPA. FPU and glucose oxidation were not affected by diet. Feeding milk diets with soy protein isolate seems to impair glucose status in kids, but has no effect on FPU and glucose oxidation.

Key Words: goat kids, soy feeding, glucose uptake

W286 Plasma leptin, feed intake and body fat reserves in ruminants. An updated overview. E. González-García*[1], N. Debus[1], Y. Chilliard[2], and F. Bocquier[1], [1]*INRA, Montpellier, France*, [2]*INRA, Theix, St-Genes-Champanelle, France*.

We aimed to update knowledge on relationship between plasma leptin (PL), feed intake (FI) and body fat reserves (BF) in ruminants. A literature review was done, using papers published (n = 31; 1998-2008) in international scientific journals. Studies were done under controlled conditions in dairy (3) or beef (9), goats (1) or sheep (22). Database contained gender, physiological status, breed, age, feeding level and body fatness. Underfeeding decreased PL, basically in fat individuals, while refeeding increased it. The PL depended on physiological status, also being higher in fat vs. leans whereas it decreased during nutritional restriction, following BCS. PL was related to adipose cell size and was modulated by short-term energy intake (EI) in interaction with long-term regulations (i.e. nutritional history). Rather than type of energy, amount of EI and BF are regulators of PL. The PL was positively related to BW changes, feeding level, plasma glucose, β-OH-butyrate, IGF-I and insulin, and negatively related to plasma NEFA. During nutritional restriction, insulin did not correlate with PL. Metabolic effects of PL are thought to be mediated via neuronal systems that possess PL receptors rather than via peripheral effects. There is evidence for a dissociation of PL effects on appetite and neuroendocrine function. Hence, FI and BW increased under long photoperiod and were associated with increases in PL, which was also modulated by daylength. The last have a physiological significance for body fat deposition, which naturally occurs during long days when feed is abundant. The breed had a small effect although PL differences were probably related to breed differences in body composition. Carcass fat can be estimated using PL with the same accuracy than using ultrasound fat thickness. There are positive phenotypic correlations between PL and ultrasound backfat thickness and marbling score, fat depth between 12-13 rib, kidney, pelvic, and heart fat, lean meat yield, and yield grade. Performance (ADG, DMI, and gain:feed) and PL were poorly correlated. There are opportunities to use PL information for optimizing ruminant feeding efficiency and carcass quality.

Key Words: body reserves, leptin, ruminants

W287 Variation of basal expression of a sodium-dependent phosphate transporter between sections of cattle small intestine. A. P. Foote*[1], B. D. Lambert[1,2], and J. A. Brady[2], [1]*Tarleton State University, Stephenville, TX*, [2]*Texas AgriLife Research, Stephenville*.

Phosphorus (P) nutrition in cattle is increasingly becoming an important topic with the growing concern over the role of production animals in surface water pollution. Excess P in the diet of dairy and beef cattle is excreted in the manure and can be washed into surface water causing increased algal growth and eutrophication. P transporters have been characterized in other species and homologous genes have been found to be expressed in bovine cell cultures. However, no other information is available regarding the active transport of phosphate in cattle. The objective of this study was to determine the patterns of expression of a known phosphate transporter, NaPi-IIb, in four sections of the small intestine of cattle. RNA was isolated from the duodenal, proximal jejunal, distal jejunal, and ileal mucosa of 20 harvested cattle. Relative amounts of NaPi-IIb mRNA expressed were determined using real-time RT-PCR. Expression of NaPi-IIb was highest in the two distal sections ($P < 0.0001$) and almost absent in the proximal sections. Expression did not differ between the two proximal sections ($P = 0.67$) or the two distal sections ($P = 0.3$). The data suggest that a sodium-dependent secondary active P transport system is not responsible for P absorption in the proximal portion of the bovine small intestine while it does contribute to the P absorbed in the distal sections of the bovine small intestine.

Key Words: phosphorus absorption, gene expression, NaPi-IIb

W288 Insulin and essential amino acids have significant but independent effects on protein synthesis signaling in bovine mammary epithelial cells in-vitro. A. L. Bell*, J. A. D. R. N. Appuhamy, J. Escobar, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg*.

A better understanding of the regulation of milk protein synthesis could help improve the nitrogen efficiency of dairy cows. Protein synthesis responds to signals from hormones, energy substrate, and amino acid supply through several signaling proteins such as protein kinase B (Akt), mammalian target of rapamycin (mTOR), p70 ribosomal protein S6 kinase 1 (S6K1) and ribosomal protein S6 (rpS6) . This study investigated the effects of essential amino acids (EAA) and insulin on phosphorylation status (PS) of these signaling proteins using Mac-T bovine mammary epithelial (BME) cells. Cells were deprived of EAA and insulin overnight and then cultured with complete or EAA-deprived DMEM/F12 with and without 1 μg/ml of insulin (2x2 factorial design). After 1 h incubation, BME were lysed in the presence of protease and phosphatase inhibitors. Cell lysates were analyzed by Western immunoblotting with antibodies against phosphorylated mTOR (Ser^{2448}), Akt (Ser^{209}), rpS6 ($Ser^{235/236}$), and S6K1 (Thr389). Membranes were stripped and reprobed for the total form of each protein. The ratio of phosphorylated:total constitutes the PS of each signaling protein. Both EAA and insulin had significant effects on mTOR, S6K1, and S6 ($P<0.05$). EAA deprivation reduced PS by 55%, 47%, and 54%, respectively, and insulin deprivation reduced PS by 27%, 42%, and 46%, respectively. Akt PS was not affected by EAA status and markedly increased by insulin addition ($P<0.05$). There were no significant interactions between insulin and EAA on PS for any of the signaling proteins. Insulin and EAA appear to exert independent effects on cell signaling pathways in BME cells. If the same is true for intact mammary tissue, milk protein synthesis should be regulated independently by AA supply and insulin status.

Key Words: amino acid, cellular signaling, insulin

W289 Evaluation of the effects of ozonated water on the microbial ecology of the rumen *in vitro* and digestion of corn and alfalfa hay *in situ*. K. L. Neuhold*, S. K. Williams, K. K. Nightingale, and S. L. Archibeque, *Colorado State University, Department of Animal Sciences, Fort Collins*.

The overall goal of this work was to evaluate the effects of ozone treated water on the microbial ecology of the bovine rumen and the subsequent effect on Enterohemmorhagic *Escherichia coli* serotype O157:H7, and *Salmonella* Typhimurium populations *in vitro* and digestibility parameters *in vitro* and *in situ*. To accomplish the objective, rumen contents were collected from three fistulated beef steers consuming a high concentrate diet and provided with control water (non chlorinated well water; 0.05 ppm ozone) or ozone treated water (0.30 ppm ozone) in a cross-over design for at least 15 d. On d 16 ruminal samples were obtained 2-h post feeding. Following rumen fluid collection, we simulated the rumen environment, *in vitro* and evaluated two treatments; 1) Control water; and 2) Ozonated water. The supplemented rumen contents were then inoculated with rifampicin resistant *Escherichia coli* O157:H7, or *Salmonella* Typhimurium. To determine the effect of treatments on the total bacterial population after inoculation, samples were removed at 0, 1, 4, 8, 12, 24 and 48 h post inoculation for analyses. *In vitro* bags were prepared with corn and alfalfa samples and placed in the steers at 0, 2, 6, 12, 24, 48 and 72 h. There was no effect of water treatment on enumerations of *Escherichia coli* O157:H7, or *Salmonella* Typhimurium populations *in vitro*. However, ozone treated water did increase ($P = 0.027$) *in vitro* dry matter digestibility of ground corn. Water treatment had no effect on *in situ* DM disappearance of corn ($P = 0.64$) or alfalfa hay ($P = 0.27$). These data indicate that while ozonated water may have little effect on pathogen viability, ozonated water may improve the digestibility of corn grain in the ruminal contents of finishing beef steers.

Key Words: ozone, pathogen, digestibility

Ruminant Nutrition: Vitamins and Minerals

W290 The influence of feeding chelated trace minerals on dairy cattle performance and colostrum quality. A. Formigoni[1], S. Emanuele*[2], C. Sniffen[3], G. Biagi[1], and M. Fustini[1], [1]*DIMORFIPA-University of Bologna, Bologna, Italy*, [2]*Balchem, New Hampton, NY*, [3]*Fencrest LLC, Plymouth, NH*.

Dairy cow diets are often formulated to exceed NRC 2001 guidelines for Zn and Cu by up to 50%. Trial objective was to determine the effect of chelated trace elements (KeyShure® Zn, Cu and Mn) on dairy cattle performance and colostrum quality when diets were formulated to NRC 2001 guidelines for Zn and Cu. The experiment was conducted at the Pasetto farm, Verona, Italy. There were 2 treatments and 2 pens per treatment with 148 animals per treatment. Experimental period started at dry-off and continued through 150 DIM. Average dry period length was 60 ±11.5 days. The dry cow and lactation diets consisted of a 1-group TMR and were fed ad libitum once daily. The mineral premix for the dry period and lactation control diets contained 100% of the Zn, Mn and Cu as inorganic sulfates. The mineral premix for the dry period KeyShure®

diet contained 50% of the Zn, Mn and Cu as chelated minerals and 50% as inorganic sulfates. Lactation period premix for the KeyShure® diet contained 25% of the Zn, Mn and Cu as chelated minerals and 75% as inorganic sulfates. The dry cow and lactation diets contained 36 ppm Zn, 16 ppm Cu and 43 ppm Mn and 53 ppm Zn, 10 ppm Cu and 31 ppm Mn respectively. Colostrum quality was measured by analysis for total immunoglobulin content. Statistical analysis was performed with STATISTICA 7.0 (STATSOFT, INC. 2004,). Milk records and BCS were analysed with ANOVA for repeated measures; other data were analysed with CHI- SQUARE test. There was no effect of treatment on colostrum yield. Immunoglobulin concentration was greater for the KeyShure® diet (68 g/l) versus the control diet (57 g/l) (p=0.001). There was no effect of treatment on milk yield. Milk fat % was increased on the KeyShure® diet during the first 150 DIM compared to the control diet (4.03% vs. 3.86%) (p=0.001). There was no effect of treatment on milk protein. Days to 1st estrus were reduced (p=0.10) in the cows receiving chelated minerals versus the control diet (56 versus 63 days).

Key Words: chelated minerals, zinc, copper

W291 Effect of zinc from zinc sulfate on trace mineral concentrations of milk in Varamini ewes. A. Zali and M. Ganjkhanlou*, *University of Tehran*, *Tehran, Iran*.

This study was conducted to evaluate the effect of feeding supplemental zinc (zinc sulfate) in different levels (15, 30, or 45 mg/kg) on mineral concentrations in milk of ewes. Thirty lactating Varaminni ewes were assigned to three experimental groups according to their live body weights, milk production and lambs sex in a completely randomized design. Ewes were fed a basal diet containing alfalfa, wheat straw, cottonseed meal, barley grain, wheat bran, cracked corn, and vitamin-mineral supplements at 3.2% of body weight (BW) to meet NRC requirements for protein, energy, macro minerals, and micro minerals, excluding zinc. The basal diet contained 15 mg/kg Zn and zinc sulfate was added to the basal diet to supply 30 or 45 mg/kg of dietary zinc. Daily milk yielded was recorded at 7 days intervals, and samples of the milk were taken once per week for determination of milk composition and trace mineral concentration. Concentrations of Zn, Cu, Mn and Fe in milk were determined. Dry matter intake (DMI), milk yield and milk compositions were not affected by supplemental zinc ($P > 0.05$). But zinc concentrations in milk were affected by supplemental zinc ($P < 0.05$). Other mineral concentrations were not affected by supplemental zinc ($P > 0.05$). It suggests that supplementation of ewes diet with zinc sulfate could be an effective way to increase zinc concentration in milk when zinc concentration of basal diets is limited for ewes in lactation period. Abbreviation: BW, body weight; DMI, dry matter intake

Key Words: supplemental zinc, zinc sulfate, Varamini ewes

W292 Mineral status of semi-confined dairy cattle from Marcos Castellanos, Michoacán. E. Aguillón Trejo, E. Cruz Hernández, M. Huerta Bravo*, and R. Améndola Massiotti, *Universidad Autónoma Chapingo*, *Chapingo, México, México*.

The objective was to measure the mineral status of semi-confined dairy cattle from nine farms of Marcos Castellanos, Michoacán, and México. Samples from soil (n= 42), feeds (n= 58), blood of dairy cows and calves (n= 116) and drinking water (31) were taken. Contents of calcium, phosphorous, magnesium, sodium, potassium, copper, iron, zinc and selenium were measured in all samples. Additionally, manganese was measured in feeds and soil. Spectrofluorometry, colorimetry and atomic absorption spectroscopy were used for selenium, phosphorus, and the rest of minerals, respectively. Copper and iron were not detected in water. The effects of farm, animal type and their interaction on the mineral content in blood serum were evaluated, as well as the effect of farm on the mineral content of feeds, soil and drinking water. Data sets were analyzed using GLM procedures. Contents of P, Fe, Zn and Se in blood serum from cattle were different ($P < .05$) among farms. Calves had higher ($P < .05$) levels of P and Zn in serum than cows; while that of Se was lower ($P < .05$). An interaction among animal type and farm was observed for serum contents of P, K, Fe, Zn, and Se ($P < .05$). Differences in mineral status of cows and calves among farms were related. Contents of all minerals in soils (excepting sodium) differed among farms ($P < .05$). Water sources differed ($P < .05$) for Ca, P, Mg, Na, and K. Feeds differed in all minerals ($P < .05$), except K and Fe that were highly variable. Serum of cattle was deficient in zinc (100%) and copper (70%). These deficiencies, confirmed by means of clinical signs, are related to low concentrations of the elements in water, forages, and the soils where forages are grown. Concentrates used by farmers are also low in these minerals. It is recommended to increase Zn and Cu in the supplementary feed or to use a palatable mineral supplement rich in these elements. *This study was carried out as part of EULACIAS INCO-dev Project, EU sixth Framework Programme, Contract No. 032387.*

Key Words: copper, zinc, minerals

W293 Total mixed ration mineral content in California dairy farms. A. R. Castillo*[1], N. Silva del Rio[1], and N. St-Pierre[2], [1]*University of California*, *Tulare*, [2]*The Ohio State University*, *Columbus*.

Forty commercial dairy farms in Merced County (CA) were selected to evaluate the mineral composition of total mix rations (TMR) for lactating cows accordingly to NRC requirements. Duplicated samples of the total mixed rations (TMR) were collected on two non-consecutive days, and analyzed with wet chemistry for Ca, P, Mg, Cl, K, Na, S, Cu, Fe, Mn, Se, and Zn. Dietary mineral content per farm was calculated according to TMR mineral content weighted by the proportion of animals in each production group. Milk production was estimated based on Dairy Herd Improvement (DHI) records and when not available, on bulk tank milk data. Milk production ranged from 20.6 to 43.5 kg/cow per day. The mineral content in the TMR were classified as: < 80%, 80% to 120%, >120% to 200% and >200% of NRC 2001 requirements for lactating cows. The higher near value for milk production was used to determine NRC mineral requirements. Results are presented in Table 1. Dietary Ca and Se content were below 80% of the NRC requirements in 2.5% of the dairies and in 7.5% for Cu. However, the dietary mineral content per farm was 120% or more of the NRC requirements in 57.5% and in 100% of the dairies, depending on the mineral. This study indicates that there is opportunity to adjust dietary macrominerals and trace minerals in lactating dairy cow diets in California.

Table 1. Proportions of California dairies (n=40) fed different percentages of NRC requirements in the total mix ration.

	% of NRC		Requirements	
mineral	<80	80 to 120	120 to 200	>200
Ca1	2.5	40	57.5	--
P	--	37.5	62.5	--
Mg	--	--	82.5	17.5
Cl	--	2.5	32.5	65
K	--	7.5	85	7.5
Na	--	15	37.5	47.5
S	--	25	75	--
Cu	7.5	27.5	47.5	17.5
Fe	--	--	--	100
Mn	--	--	--	100
Se	2.5	15	77.5	5
Zn	--	17.5	65	17.5

1 The higher near value for milk production was used to determine NRC requirements

Key Words: TMR mineral content, mineral requirement, dairy cow

W294 Effects of supplementation of beef cattle ration with rare earth elements on fermentation and digestion in batch culture. W. Z. Yang* and M. L. He, *Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Rare earth elements (REE) have been used as feed additives for many years in China and recently shown to improve growth performance of pigs in Europe. A study was conducted to investigate the effects of adding a mixture of REE in diet varied ratios of forage to concentrate (F:C) on fermentation and DM digestion in batch culture. The experiment was a complete randomized block design with 2 x 4 factorial arrangement of treatments. The treatments were high F:C (55:45) or low F:C (10:90) diet combined each with 4 dosages of REE: control (0 mg), low (400 mg), medium (800 mg) and high REE (1200 mg/kg diet, DM basis). The mixture of REE contains 38% of $LaCI_36H_2O$, 52% of $CeCI_36H_2O$ and 10% chlorides of other light REE. There were no interaction between F:C and REE. Fermentation pH linearly (P<0.05) decreased from 6.22 to 6.17 with increasing dosages of REE, which was consistent with linearly increasing concentrations of total VFA (from 25.3 to 34.6 m*M*), acetate (from 8.9 to 12.8 m*M*) and propionate (from 8.2 to 11.3 m*M*). However, the molar proportion of acetate, propionate and butyrate was not affected by REE. Gas production (ml/g of OM) was not affected at 4, 8, 14 and 24 h of incubation, but was quadratically changed (P<0.04) at 48 h of incubation for the highest with medium REE (398) and for the lowest with control (310). Similarly, digestibility of DM was also quadratically changed (P<0.04) ranging from 62.3, 62.8, 65.2 and 63.3% for control, low, medium and high REE, respectively, at 48 h of incubation. As expected, with decreasing dietary F:C, mean fermentation pH slightly reduced (P<0.01) from 6.23 to 6.15, which was consistent with linearly increase of concentration of total VFA from 29.8 to 33.6 m*M* (P<0.10). The results indicate that adding mixture of REE in beef diet increased feed fermentation with a dose-dependent manner but not associated with dietary forage proportion. The overall effects of REE on rumen fermentation and digestion are apparently limited.

Key Words: rare earth elements, fermentation, batch culture

W295 The effects of trace mineral source, water quality, and choline supplementation on performance and carcass characteristics of steers. J. S. Schutz*[1], J. L. Seabrook[1], K. L. Neuhold[1], J. J. Wagner[1], M. de Veth[2], and T. E. Engle[1], [1]*Colorado State University*, *Fort Collins*, [2]*Balchem Corporation*, *New Hampton, NY*.

Two hundred and eighty eight steers (316.0 ± 13.8 kg) were utilized to determine the effects of trace mineral source, water quality, and choline supplementation on performance and carcass characteristics. Upon entry into the feedlot, cattle were processed, randomly assigned to trace mineral and water treatments (2 × 2 factorial), and housed in 9 head pens. Trace mineral treatments consisted of: 1) control, 15 mg Cu/kg DM, 20 mg Mn/kg DM, and 45 mg Zn/kg DM supplemental trace minerals in inorganic form and 2) organic, iso-concentrations to the inorganic trace minerals composed of 50% organic and 50% inorganic trace mineral. Water treatments consisted of: 1) a blend of reverse osmosis and well water (1072.4 mg SO4/L) and 2) well water (2377.5 mg SO4/L). Standard receiving and finishing diets were fed twice daily. Twenty nine days prior to harvest, 4 pens per trace mineral and water treatment were supplemented with 20 g of protected choline/h/d and the remaining 4 pens served as the controls (0 g of supplemental choline). Steers were weighed on d 0, 28 and then at approximately 56 d increments until the experiment was terminated. There were no trace mineral source x time, trace mineral source x water quality, or trace mineral source x water quality x time interactions for BW, ADG, DMI, G/F, or F/G. Initial and final body weights, ADG, DMI, F/G and G/F were similar across trace mineral and water treatments. Choline supplementation for only the last 29 d on feed did not impact performance. Morbidity, mortality, and percent repulls were similar across trace mineral and water treatments. Steers receiving organic trace mineral had an improved USDA yield grade compared to steers receiving inorganic trace minerals (2.61 vs 2.82, respectively, P<0.03). Steers consuming well water tended (P < 0.08) to have greater longissimus muscle area (REA) and lower (P < 0.08) calculated YG than steers consuming RO water. Other carcass characteristics parameters were not affected by water quality, trace mineral source, or choline supplementation.

Key Words: steer, trace mineral, choline

W296 Effects of rumen protected choline on productive performance and blood metabolites of Holstein lactating cows. M. Dehghan-Banadaky*, F. Fatehi, and T. Ghasemi, *University of Tehran, Department of Animal Sci.*, *Karaj, Iran*.

Fifty four Holstein cows in early lactation (90±11 days in milk, milk production 34±3.3 kg/day) were used to evaluating the effects of feeding ruminally protected choline on milk yield and composition and blood metabolites for 40 days (10 days for adaptation, 30 days for data collection), between November to December of 2007. Cows were used in a complete block design with 2 blocks (parity, monoparous and multiparous), two treatments (choline supplement and control) and 27 replicates (cows). Cows in first group fed total mixed ration (TMR) with 100 gr Col24 (contain 24% rumen protected choline, SODA) /head/day as mixed to diet and cows in second group fed same TMR without choline additive (control). Cows fed ad libitum (10% refusal from previous day) and milked 3 times per day. Daily milk production recorded and milk samples taken for milk composition analysis as weekly also group dry matter intakes were measured daily. Blood samples were taken from jugular on day 38 (2 h after morning meal) for plasma metabolites analysis. Col24 significantly increased milk production of cows (32.98 vs. 31.63 kg/day) but did not affect milk composition and feed intake. Col24 supplement did not change concentration of non esterified fatty

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

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

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

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

Key Words: vitamin E, soybean oil, milk fat

Ruminant Nutrition: Experimental Methods

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

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

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

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

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

Key Words: NDF digestion, analysis, fiber

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

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

Table 1. Lignin composition (%) and slopes

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

Key Words: dioxane, grass, legume

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

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

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

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

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

Key Words: wheat straw, byproduct fiber, beef

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

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

Key Words: redox potential, in vivo, in vitro

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

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

Key Words: urease, isolation, culture-independent

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

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

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

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

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

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

Key Words: rumination, feeding behavior, dairy cow

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

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

Key Words: BHBA, meter, ketone

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

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

Key Words: internal fat technique, ultrasound, carcass

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

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

Key Words: Lys, Met, simulation modeling

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

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

Table 1. Precision and accuracy statistics for CNCPS predictions

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

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

Key Words: CNCPS, nitrogen, modeling

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

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

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

Key Words: animal stress, meat pH, road transportation

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

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

Key Words: goat, sheep, carcass

W313 Growth performance and carcass characteristics of goat kids fed diets containing sericea lespedeza. S. Solaiman*, J. Thomas, N. Gurung, Y. Dupree, and C. Drake, *Tuskegee University, Tuskegee, AL*.

Twenty four Kiko cross intact buck kids (BW = 27.9 ± 2.2 kg) were stratified by BW and randomly assigned to four experimental groups (n = 6) and fed diets containing different levels of sericea lespedeza (SL). Animals were offered 30% of the diet bermudagrass hay (BGH), 30% SL/ alfalfa (ALF), and 40% concentrate in a 60: 40 forage: concentrate ration. Treatments were, A) 0% SL (control), B) 10% SL, C) 20% SL, and D) 30% SL where SL replaced ALF. Ground SL was mixed with the concentrate portion of the diet and offered to animals once a day. The mix and BGH were fed separately and intake was adjusted every 4th day to secure a 5 to 10% refusal. Feeds offered and refused were recorded daily and feed composite samples were collected every 3 wk for 12 wk performance period. Body weights were measured every 4 wk, and fecal eggs counted at wk 4 and wk 8 of the study. Blood was collected at wk 1 and wk 12 for complete analysis. After 12 wk goats were harvested and carcass measurements were recorded. There was no difference in initial BW of goats; however, ADG was higher (quadratic, P= 0.01) for goats consuming either 30% ALF or 30% SL diets. Average daily feed intake increased (linear, P = 0.03) as SL increased in the diets; however, G:F (quadratic, P = 0.002), scrotal circumference (quadratic, P = 0.07) and height (quadratic, P = 0.01) were reduced for goats consuming SL diets B and C. White blood cells decreased (linear, P = 0.05), lymphocytes % increased (linear, P = 0.05), serum alanine aminotransferase increased (linear, P = 0.0002) and serum amylase decreased (linear, P = 0.01) as the level of SL increased in the diets. Replacing SL for ALF did not affect carcass characteristics except adjusted fat that decreased (linear, P = 0.02) with increasing SL in the diets. There was no effect of added SL on fecal egg counts. Feeding SL alone (diet D) did not affect ADG and G:F; however, addition of SL in combination with ALF (diets B and C) adversely affected the growth performance and gain efficiency in growing goats.

Key Words: goats, growth performance, sericea lespedeza

W314 Effects of level of barley and corn in concentrate diet fed to Boer kids on growth, meat quality and muscle fatty acid composition. M.-E. Brassard*[1], R. Gervais[1], C. Gariépy[2], P. Y. Chouinard[1], and D. Cinq-Mars[1], [1]*Université Laval, Québec, QC, Canada*, [2]*Food Research and Development Centre, Saint-Hyacinthe, QC, Canada*.

The objective of this study was to investigate the effects of substituting barley grain with corn on growth performance, meat quality, and muscle fatty acid composition of goat kids. Twenty-four Boer males (26.5 ± 1.4 kg) were blocked by body weight and allotted randomly within block to one of three experimental diets. Treatments consisted in varying ratios of corn to barley of the concentrate: 0:100; 50:50; and 0:100. All diets were formulated with 70% concentrate (cereal, soybean meal, and vitamin and mineral premix) and 30% grass hay (DM basis). When all kids reached an average live weight of 43.0 ± 0.9 kg, fifteen kids (n = 5 kids/ treatment; randomly selected) were slaughtered and carcasses weighed. The *longissimus dorsi* was collected 96 h post-mortem from the left side of the carcass. Dietary treatments had no impact on dry matter intake, gain:feed ratio, number of days required to attain slaughter weight, carcass weight and carcass yield ($P \geq 0.22$). There were no differences in Warner-Bratzler shear force values, ultimate pH, ribeye area, cooking loss, moisture, crude protein and fat content ($P \geq 0.12$) among treatments. Saturated and unsaturated fatty acid contents of *longissimus dorsi* fat were unaffected by treatments ($P \geq 0.33$). Total *trans* fatty acids content in meat fat averaged 1.01 ± 0.07%, and were also not affected by the grain source in the diet. Levels of n-3 ($P < 0.01$), and n-6 fatty acids ($P < 0.01$) increased linearly, whereas n-6/n-3 ratio linearly decreased ($P < 0.01$) as corn inclusion in the diets increased. Results revealed that, in the conditions of this experiment, meat fat from kids presented low concentrations of total *trans* fatty acids compared to those generally observed in meat fat from other ruminants. Concentrations of n-3 and n-6 fatty acids in kid meat can be enhanced and n-6/n-3 ratio decreased by including corn to a concentrate-based diet without deteriorating animal performance or meat quality when compared with barley.

Key Words: goat kid, meat quality, fatty acids

W315 Comparative postweaning growth among four groups of percentage Dorper and Katahdin wethers. W. R. Getz*, W. Kimble II, J. Mack, and T. Harris, *Georgia Small Ruminant Research and Extension Center, Fort Valley State University, Fort Valley, GA*.

During the summer and fall of 2005-2007, 96 percentage Dorper, percentage Katahdin, Dorper x Katahdin composite, and crossbred Dorset, Hampshire or Suffolk-sired conventional wethers were evaluated for postweaning growth while on perennial warm-season pastures. Our purpose was to determine if breeding of the lambs was a significant factor in rate of growth in this hot, humid climatic environment. The lambs were weighed at 28-d intervals over an 84-d period. They were supplemented at the rate of 1% of their body weight as needed. Mean values for average weight gain each day were as follows: Dorper crosses (90.7 ± 7.7 g); Katahdin crosses (98.9 ± 9.4 g); composite (73.7 ± 6.4 g); conventional crossbred (105.7 ± 13.9 g). Analysis of variance indicated that breed was a significant ($P \leq 0.04$) source of variation in postweaning daily gain in this population. The composite group appeared to grow slower than other breed groups. This result was not expected and may reflect factors that will be investigated as more data become available. None of the breed groups grew particularly well in absolute terms. This may be a reflection of the climatic forces in southern Georgia.

Key Words: sheep, breeds, crossbreeding

W316 Body composition of growing meat and lactating dairy goats. A. T. Ngwa[1], L. J. Dawson[1,2], R. Puchala[1], G. D. Detweiler[1], R. C. Merkel*[1], Z. Wang[1], K. Tesfai[1], T. Sahlu[1], C. L. Ferrell[3], and A. L. Goetsch[1], [1]*American Institute for Goat Research, Langston University, Langston, OK*, [2]*College of Veterinary Medicine, Oklahoma State University, Stillwater*, [3]*USDA, ARS, US Meat Animal Research Center, Clay Center, NE*.

Growing 3/4 Boer x 1/4 Spanish (B) and Spanish (S) wethers were used to determine influences of diet and breed, and multiparous Alpine does were used to determine how stage of lactation and dietary forage level affect body composition. Growing goats were fed 50% concentrate pelleted diet (C) or one based on grass hay (H) free-choice. Six wethers of each breed were harvested at 0 wk and six of each diet-breed combination were harvested at 14 and 28 wk. Empty body concentration of protein was 18.3, 17.5, 18.3, and 19.7% (SE = 0.29) and of fat was 24.0, 23.4, 10.8, and 10.3% for B:C, S:C, B:H, and S:H, respectively (SE = 0.59). Energy in accreted tissue was 17.0, 18.7, 16.3, and 6.4 MJ/kg for C:wk 1-14, C:wk 15-28, H:wk 1-14, and H:wk 15-28, respectively (SE = 1.39). Initial measures with lactating goats were on six does a few days after kidding (0 mo). Eighteen does were fed a 40% forage diet (40F) and 18 received a diet with 60% forage (60F) for 2, 4, or 6 mo of lactation. Fat in the carcass (13.8, 13.1, 16.5, 11.2, 11.5, and 14.4%), noncarcass

tissues (18.6, 24.2, 33.3, 14.3, 16.5, and 24.5%), and empty body (16.5, 18.7, 25.2, 12.9, 14.1, and 19.5% for 40F-2 mo, 40F-4 mo, 40F-6 mo, 60F-2 mo, 60F-4 mo, and 60F-6 mo, respectively) were affected by stage of lactation and diet ($P < 0.06$). Based on daily change in tissue mass (-141, 56, and 90 g/d; SE = 21.4) and energy (-2.31, 1.11, and 2.90 MJ/d for 1-2, 3-4, and 5-6 mo, respectively; SE = 0.66), energy concentration in tissue mobilized or accreted was 16, 20, and 32 MJ/kg at 1-2, 3-4, and 5-6 mo, respectively. In conclusion, other than with a prolonged limited nutritional plane, an average energy concentration in accreted tissue of growing meat goats is 17.3 MJ/kg. The concentration of energy in tissue mobilized or accreted by dairy goats varies with stage of lactation.

Key Words: goat, body composition, diet

W317 Carcass traits of finishing lambs fed crude glycerin derived from biodiesel agro industry. J. F. Lage[1], P. V. R. Paulino*[1], L. G. R. Pereira[2], M. S. Duarte[1], J. P. I. S. Monnerat[1], E. Detmann[1], N. K. P. Souza[1], M. L. Chizzotti[1], and S. C. Valadares Filho[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*EMBRAPA – Semi–Árido*, *Petrolina, PE, Brazil*.

This trial aimed to evaluate the effect of feeding crude glycerin, derived from biodiesel agro industry, on hot carcass weight (HCW), dressing percentage (DP), backfat thickness (BT), rib eye area (REA), compacity index (CI) and carcass length (CL) of Santa Inês lambs. Thirty intact male lambs (20 kg initial body weight) were randomly assigned to 5 treatments, consisting of increasing crude glycerin levels in the diet: 0, 3, 6, 9 and 12% of diet DM. Six lambs per treatment were used, being individually fed. The diets were isonitrogenous and formulated to meet the requirements for maintenance and gain of 0.3 kg/d. The animals were slaughtered as the BW reached 35 kg, and the carcasses were cooled during 24 h at 0°C. After cooling, measurements of BT, REA, CI and CL were taken. DP was calculated using HCW. REA and BT were measured at the carcass in the region between 12-13th rib and CI was calculated as the ratio of cold carcass weight/carcass length. Data were analyzed using the GLM procedure of SAS and the effects of treatments (linear and quadratic) were considered significant at $P < 0.05$. Glycerin level did not affect BT (mean value of 0.92 mm), REA (mean value of 11.81 cm^2) and CL (mean value of 59.9 cm). However, feeding glycerin decreased linearly HCW, DP and CI, fitting the following regression equations: HWC = 15.7867 – 0.22694 x % of crude glycerin in the diet (linear, $P = 0.0026$); DP = 45.6227 – 0.22061 x % of crude glycerin in the diet (linear, $P = 0.0033$) and CI = 0.2503 – 0.00296 x % of crude glycerin in the diet (linear, $P = 0.0019$). Adding glycerin to finishing lambs diets can have a negative impact on HCW, DP and CI, but not on BT, REA and CL.

Key Words: byproduct, glycerol, sheep

W318 Effects of calcium salts of fatty acids on finishing lamb feedlot performance and carcass characteristics. J. L. Seabrook*, R. K. Peel, and T. E. Engle, *Colorado State University*, *Fort Collins*.

The objective of this study was to investigate the effects of replacing dietary carbohydrate with calcium salts of fatty acids (CSFA) on finishing lamb (n = 60, BW 41.6 ± 1.4 kg) performance and carcass characteristics. Upon arrival, lambs were weighed on two consecutive days and randomly assigned to one of four treatments: 1) Control (CNTL) 0% TDN CSFA; 2) Diet 5 (D5) 5% TDN CFSA; Diet 10 (D10) 10% CSFA; Diet 15 (D15) 15% TDN CSFA. Lambs were housed 3 to a pen and pair-fed one of four dietary treatments (75% concentrate, 25% corn silage) for 59 d. Diets were formulated to be isoenergetic (TDN) and isonitrogenous (DIP and UIP) by adjusted inclusion of flaked corn and pellet. Intake was controlled to balance TDN across treatments; all treatments met NRC requirements. Lambs were weighed every two weeks and performance, ADG, DMI and gain to feed (G:F) ratio was measured. On d 61, lambs were transported and slaughtered at a commercial abattoir. Hot carcass weight was determined at the time of slaughter, and longissimus dorsi (LD) muscle area and BF carcass measurements were determined after 48 h at a 0°C chill. Treatment was a significant ($P < 0.05$) source of variation for overall average daily gain: Lambs receiving CNTL and D5 treatments had similar overall ADG. Lambs receiving D10 and D15 had lower ADG compared to those receiving CTRL or D5. Overall ADG was higher ($P < 0.05$) for lambs receiving D10 than D15. There was a significant ($P < 0.05$) treatment effect for overall GF efficiency. Lambs receiving CNTL and D5 treatments had greater ($P < 0.05$) G:F than lambs receiving D10 and D15. Furthermore, lambs receiving D10 had a greater ($P < 0.05$) G:F than lambs receiving D15. Lambs receiving CNTL, D5 and D10 treatments had heavier ($P < 0.05$) HCW and larger ($P < 0.05$) LD areas than lambs receiving D15. Backfat depth was similar for lambs receiving CNTL, D5 and D10. Control lambs had greater ($P < 0.05$) BF than treatment D15. Data indicate that dietary carbohydrates can be replaced with CSFA at a rate of up to 5% of TDN without significant effects to finishing lamb performance.

Key Words: calcium salt, bypass fat, lamb finishing

W319 Physical and chemical qualities of meat of confined lambs receiving different concentrate:forage ratios in diet. R. S. B. Pinheiro, A. M. Jorge*, E. N. de Andrade, C. de L. Francisco, A. Polizel Neto, and J. P. F. da Silveira, *São Paulo State University*, *Botucatu, SP, Brazil*.

The objective of this study was to evaluate meat quality of lambs in confinement which received diets with different concentrate contents. 18 non-castrated ½ Ile de France ½ Santa Inês lambs were used, with initial weight of approximately 15 kg, arranged into two allotments, represented by Treatment 1 (T1) animals that received forage:concentrate ratio of 35:65 in diet and Treatment 2 (T2) lambs that received forage:concentrate ratio of 65:35 until reaching 32 kg of body weight in confinement, a pre-established weight for animals at slaughter. The forage used in the diets was the corn silage and concentrate: ground corn, wheat bran, soybean bran, salt, dicalcium phosphate, limestone, urea and mineral supplement (Zn 1.6 ppm; Cu 6.3 ppm; Mn 1.5 ppm; Fe 1.1 ppm; Co 10 ppm; I 27 ppm; Na 62 ppm and Se 22 ppm). Lambs from treatments 1 and 2 presented similar values for pH, shear force, cooking losses and meat water retention capacity, with average values of 5.7, 1.03 kgf/cm2, 35.2% and 59.3%, respectively. Forage:concentrate ratio did not influence the centesimal quality of meat of lambs fed with more concentrate or more forage diets for humidity, crude protein, ether extract and mineral matter, with average values of 74.0%, 19.3%, 5.47%, 1.17% and 19.31%, respectively. This fact can be explained as the diets used in this experiment have similar proportions of protein (T1 = 15.99% and T2 = 15.97 CP) and energy (T1 = 2.57 and T2 = 2.63 Kcal/kg DM). We conclude that lambs terminated in confinement receiving different concentrate contents in diet resulted in similar meat quality; therefore, diet choice depends on the cost of the ingredients of diet at the moment of confinement.

Key Words: feeding, meat tenderness, sheep

W320 Effect of shed type and supplementation on fatty acid profile in lamb tissues. M. A. Brown*[1], Y. S. Peng[2], and J. P. Wu[2], [1]*USDA-ARS, Grazinglands Research Laboratory, El Reno, OK*, [2]*Gansu Agricultural University, Lanzhou, Gansu, PRC*.

Meat from Small Tail Han sheep is an important dietary component of people in western China. Five-mo-old Small Tail Han ewe lambs (n = 40) were used to study the effect of supplementation [control (C), C+ sunflower seed (160 g/d) and C+ protected fat (30g/d and 60g/d)] and shelter type (conventional vs. greenhouse shed) on fatty acid (FA) composition in different tissues (*longissimus lumborum* muscle, subcutaneous back fat and kidney fat) in a winter feeding trial. Temperatures ranged from -12 to 6°C in conventional sheds and -3 to 20°C in greenhouse sheds. Five lambs were assigned to each of 8 treatment combinations (shed type x supplement). Mixed model linear models included shed type, supplement, shed type x supplement, lamb in shed type and supplement (random), tissue (repeated), tissue x shed type, tissue x supplement, tissue x supplement x shed type, and a random subunit residual. Sunflower seed supplementation appeared to increase concentrations of conjugated linoleic acid (CLA, 18:2^{c9t11}) ($P < 0.05$) in three tissues independent of shelter type. Total polyunsaturated FA in muscle and kidney fat were greater than those in back fat ($P < 0.05$ and $P < 0.10$), and muscle was greater than kidney fat and back fat in ratio of polyunsaturated to saturated (P:S) FA ($P < 0.01$). Averaged over tissue and shelter, sunflower supplemented lambs were greater than lambs fed other supplements for P:S ($P < 0.01$). However, the sunflower seed appeared to increase the ratio of omega-6 to omega-3 FA ($P < 0.05$) in all tissues, and to a greater extent in muscle ($P = 0.10$). In this study, protected fat supplementation did not substantially change the FA profile of lamb tissues. Generally, FA composition of lamb tissues was not affected by shelter treatment but there was some indication that tissue differences in oleic acid, CLA (18:2^{t10c12}), and short-chained FA depended on shed type ($P < 0.10$). Results imply that supplementation with sunflower seed may change FA profile of different lipids in lambs and their nutritional value, but shed type may have only a minor influence on FA composition of lipids in muscle fat, kidney fat, and back fat.

Key Words: lamb, fatty acid, sunflower seed

W321 Fatty acid profile from the longissimus muscle of grazing Merino lambs with or without winter supplementation in Northern Patagonia. L. Villar*[1], E. Pavan[2], C. Giraudo[1], and F. Santini[3], [1]*INTA-EEA Bariloche, Bariloche, Rio Negro, Argentina*, [2]*INTA-EEA Balcarce, Balcarce, Buenos Aires, Argentina*, [3]*INTA-CIA Castelar, Hurlingham, Buenos Aires, Argentina*.

The objective of this experiment was to study the effects of winter supplementation on longissimus muscle (LM) fatty acid (FA) profile of heavy Merino lambs raised at the Hills and Plateaus of Northern Patagonia. Forty six male lambs (8 mo) were randomly divided in two groups: one group was not supplemented during the study (CTRL), whereas the other one (SPPL) received 200 g alfalfa pellet and 150 g oat grain daily from June 15th to September 9th (95 d). Each group had free access to a 70 ha plot of shrub grass steppes (70° 03′ W and 41° 05′ S); groups switched plots every 15 d. When treatment mean LW reached 35 kg, 12 lambs from the group were randomly selected and slaughtered, and a sample from the LM was taken for FA evaluation. Samples were stored at -20 °C until FA profile was determined by GLC. Data were analyzed by ANOVA using GLM procedure of SAS. Winter supplementation did not affect ($P > 0.05$) total FA concentration in the LM (1.74 ± 0.12%) or the proportion of the highly atherogenic FA C14:0 (3.10 ± 0.26%) and C16:0 (26.6 ± 0.57%). Docosahexaenoic acid (C22:6 n-3) proportion was similar ($P > 0.05$) in both groups (0.34 ± 0.02%). Conjugated linoleic acid (CLA) cis-9, trans-11 proportion was decreased ($P = 0.03$; SEM = 0.02) from 0.35% of total FA in CTRL to 0.28% in SPPL, and C18:1 trans-11 proportion was decreased ($P = 0.02$; SEM = 0.11) from 2.57% in CRTL to 2.12% in SPPL. Taking CRTL values as a reference, SPPL reduced total n-3 PUFA proportion ($P = 0.05$; SEM = 0.42) from 6.62% to 5.30%, C18:3 n-3 ($P = 0.05$; SEM = 0.25) from 3.78% to 2.99%, and C22:5 n-3 ($P = 0.03$; SEM = 0.07) from 1.24% to 0.98%. The ratio n-6: n-3 was increased ($P < 0.001$; SEM = 0.07) by SPPL from 2.20 in CTRL to 3.06 in SPPL. These results suggest that a small level of supplementation can affect LM FA composition without changing total FA content.

Key Words: CLA, fatty acids, longissimus muscle

W322 Influence of feed deprivation time on physiological responses and microbial loads in meat goats. M. Vanguru, J. H. Lee, G. Kannan*, T. H. Terrill, and B. Kouakou, *Fort Valley State University, Fort Valley, GA*.

Previous findings have indicated that diet and feed deprivation time prior to slaughter influence fecal shedding of bacteria in goats. This experiment was conducted to determine the effects of preslaughter feed deprivation time on skin and carcass microbial loads and physiological responses in goats. Thirty-two Spanish × Kiko goats (BW = 18.8 ± 0.82 kg) were randomly assigned to one of 4 feed deprivation times (FDT; 0, 9, 18, or 27 h) before slaughter. Blood samples were collected to analyze for metabolites prior to slaughter. Immediately after slaughter and evisceration, the pH values of rumen liquor and cecal digesta were determined. Rumen and rectal contents were collected and transported to the laboratory for culture and determination of microbial loads. Initial pH of Longissimus muscle (LM) was determined at 15 min postmortem on each carcass. Swab samples were collected from skin and carcass of each animal to assess the bacterial loads. FDT did not influence glucose, plasma urea nitrogen, and non-esterified fatty acid concentrations, and creatine kinase activities. The 27-h FDT group had higher ($P < 0.05$) rumen pH than 0 or 9 h FDT groups. However, the microbial counts of rumen and fecal contents were not influenced by FDT. FDT had no effect on the initial pH (6.87) of LM. Both skin and carcass microbial counts were not affected by FDT. The E. coli, total coliform, and aerobic plate counts on skin were 1.13, 1.49, and 3.78 $\log_{10}$CFU/cm^2, respectively, and those on carcasses were 1.51, 1.65, and 3.11 $\log_{10}$CFU/cm^2, respectively. The results indicate that pre-slaughter FDT alone up to 27 h may not significantly affect blood metabolites and skin and carcass microbial loads in goats.

Key Words: goats, feed deprivation, carcass contamination

W323 Chemical composition, in vitro degradability, and consumption of *Calliandra calothyrsus* and tropical grass hay mixtures by goats and sheep. A. A. Rodriguez*, G. Castro, V. Rivera, E. Valencia, and P. Randel, *University of Puerto Rico*.

The chemical composition, in vitro degradability, and intake of *Calliandra calothyrsus* (CC) mixed tropical grass hay (TGH) was determined. Leaves of CC were manually harvested, sundried, and mixed with TGH at five different proportions: 100:0, 75:25, 50:50, 25:75 and 0:100 w/w. Triplicate samples from each combination were analyzed to determined CP, NDF, ADF, lignin, P and Ca content. In vitro degradability as % of DM (IVDMD) and NDF degradability as % of total cell-wall content

(NDFD) were determined after 48 h of incubation. To determine forage consumption two identical 2 by 2 Latin square experiments were conducted using four castrated mature native goats (BW 43.18 kg) and four crossbred lambs (BW 30.10 kg) as experimental units. In each experiment animals were assigned to two diets; 100% TGH and TGH mixed with CC in 50:50 proportion. Both experiments consisted of a 7 days diet adjustment period and 5 d of data collection. Crude protein, lignin, P, and Ca content increased ($P < 0.05$) as percentage of CC increased in the mixtures. DMD and NDFD also increased as proportion of CC was increased, but cell wall components (NDF and ADF content) decreased. Forage consumption was lower ($P < 0.05$) in animals fed with TGH:CC mixture than with TGH alone (757 vs 594 g/d and 1293 vs 1028 g/d for sheep and goats, respectively). Consumption of CC by goats and sheep constituted 37% and 28% of the total legume offered and 26% and 20% of total forage intake, respectively. In summary, chemical composition, IVDMD, and NDFD was improved as percentage of CC increased in TGH:CC mixtures, however, inclusion of CC at 50% of the total forage offered in tropical grass hay based diets decreased forage dry matter intake in goats and sheep.

Key Words: Calliandra Calothyrsus, chemical composition, intake

W324 The use of glycerin in lamb and ewe diets. M. Terré*[1], P. Casado[2], M. Salas[1], and A. Bach[1,3], [1]*IRTA-Unitat de Remugants, Barcelona, Spain*, [2]*General de Piensos de Soria S.A., Soria, Spain*, [3]*ICREA, Barcelona, Spain*.

Thirty-nine Ripollesa weaned lambs (40 ± 3.9 d old and 15 ± 1.3 kg of BW) were arranged in 3 groups to study three different diets that included 0%, 5% or 10% glycerin in the concentrate. Lambs were fed the treatment concentrate (18.2% CP, 4.36 Mcal of GE/kg DM) and straw ad libitum until the slaughter weight (24 ± 1.1 kg). Animals were grouped in groups of 5 or 4 lambs, weighed weekly, and concentrate and straw intake and water consumption measured weekly. Blood samples to determine glucose and insulin concentrations were obtained at 2 and 4 wk of the study, and carcass weight was recorded at the slaughterhouse. In a second experiment, 35 Ripollesa ewes were arranged in 3 groups to study three different diets that included 0%, 3% or 5% glycerin in the concentrate diet. Ewes were grouped in 6 groups of 6 or 5 ewes and were fed 1.32 kg DM of a concentrate (14.2% CP, 4.32 Mcal of GE/kg DM) and straw ad libitum. Straw intake was measured daily, and water consumption weekly. Body condition score was recorded before and after parturition, and 1 wk before weaning their lambs. Blood samples were obtained every 2 wk to determine glucose, insulin, NEFA and β-hydroxybutyrate. Rumen samples were obtained 2 wk after all ewes lambed to determine rumen pH. None of the parameters measured in lambs and ewes were affected by the glycerin content of the concentrate. Assuming an energy content of glycerin of 3.47 Mcal of ME/kg, it can be included as an ingredient in lamb and ewe diets without impairing the growth of lambs, without reducing concentrate or straw intake, and without affecting blood metabolites.

Key Words: lambs, ewes, glycerin

W325 Methane emission by goats consuming condensed tannin-containing forage at different frequencies. R. Puchala*[1], G. Animut[1], A. L. Goetsch[1], T. Sahlu[1], V. H. Varel[2], and J. Wells[2], [1]*American Institute for Goat Research, Langston University, Langston, OK*, [2]*USDA, ARS, US Meat Animal Research Center, Clay Center, NE*.

Twenty-four yearling Boer x Spanish wethers (33.5 ± 0.36 kg BW) were used in a 32-d experiment to assess effects of frequency of feeding condensed tannin (CT)-containing fresh sericea lespedeza (SL; *Lespedeza cuneata*) on ruminal methane (CH_4) emission. Fresh SL (15.3% CT) was fed free-choice every day (1SL), other day (2SL), fourth day (4SL), and eighth day (8SL), with ad libitum consumption of fresh alfalfa (0.2% CT) on other days. Measures occurred on the last 8 d of the experiment. Ruminal fluid for microbial assays was collected 1 d after SL feeding and at the end of the longest interval (short and long interval samples, respectively). Data were analyzed using mixed model procedures of SAS (Version 8.2, 2001, SAS Inst. Inc., Cary, NC, USA). Average daily DMI (0.94, 0.96, 1.01, and 0.95 kg, respectively; SEM = 0.057) was similar among treatments, and average daily heat production was less ($P < 0.05$) for 1SL and 2SL vs. 4 SL and 8SL (444, 452, 531, and 530 kJ/kg $BW^{0.75}$). Average daily CH_4 emission differed among all treatments ($P < 0.05$; 9.7, 11.6, 15.5, and 18.3 g/d, respectively), but emission on days when SL was fed did not differ (9.7, 10.2, 10.7, and 10.7 g/d for 1SL, 2SL, 4SL, and 8SL, respectively; SEM = 0.64). The number of protozoa in the short interval sample was similar among treatments (5.2, 5.3, 5.7, and 6.5 x 10^5/mL; SEM = 0.98), whereas the number in the long interval sample differed among treatments ($P < 0.05$; 6.5, 10.4, 18.4, and 20.5 x 10^5/mL for 1SL, 2SL, 4SL, and 8SL, respectively; SEM = 1.84). In vitro CH_4 emission (3-wk incubation for methanogens) was similar among treatments for the short interval sample (18.2, 18.2, 19.7, and 20.0 mL; SE = 1.45) but less ($P < 0.05$) for 1SL and 2SL vs. 4SL and 8SL in the long interval sample (20.5, 20.3, 26.3, and 29.5 mL, respectively). In conclusion, greatest effects of CT of SL occurred with daily feeding, although there were carryover effects with 2SL. The influence of SL CT on CH_4 emission was immediate with no or minimal time for adaptation, and the effect appeared attributable to activity of methanogenic bacteria and protozoa.

Key Words: goat, condensed tannin, methane

W326 The effects of feeding fresh citrus pulp to Merino wethers on wool growth and animal performance. Y. T. E. Fung, J. L. Sparkes, I. van Ekris, A. V. Chaves*, and R. D. Bush, *Faculty of Veterinary Science, The University of Sydney, Sydney, NSW, Australia*.

Two studies were conducted to determine the effects of replacing lupins with fresh citrus pulp in Merino wethers diets: (i) an *in vitro* study which measured ruminal fermentation; and (ii) an *in vivo* study in which 18 mature Merino wethers were fed dietary treatments ($n = 3$) over 56 d to evaluate effects on performance (i.e. DMI, ADG and wool growth). In both the *in vitro* and *in vivo* studies, the control treatment consisted (in diet DM) of alfalfa hay (69.9%), lupins (30.1%) and phosphate (0.3%), while the citrus pulp treatments ($n = 2$; replacing lupins on 20% and 30% DM basis, respectively) consisted of alfalfa hay (61.7 and 63.3%), lupins (18.5 and 6.3%), phosphate (0.34 and 0.33%) and fresh citrus pulp (19.5 and 30.1%). Data were analyzed using the MIXED model of SAS and orthogonal polynomial contrasts were used to determine linear (L) and quadratic (Q) responses to level of citrus pulp. In the *in vitro* study, gas production, net total VFA production as well as *in vitro* dry matter digestibility (IVDMD) were not significantly different among the dietary treatments ($P > 0.05$). Ammonia production in citrus pulp treatments were 2-fold lower compared to the control (L, $P < 0.01$). The addition of citrus pulp to the diet increased the molar proportions of acetic acid and decreased that of butyric, branched-chain VFA (BCVFA), and valeric acids (all L, $P < 0.01$) compared to the control diet. In the *in vivo*

study, DMI, ADG and feed conversion were similar among treatments (P > 0.52). Wool production parameters including clean fleece weight, yield, staple length and strength were not different between diets (P > 0.30). Hence, fresh citrus pulp can be included up to 30% on a DM basis replacing lupins without detrimental effects on wool production and animal performance.

Key Words: in vitro, sheep, wool

W327 Voluntary intake of silage from corn hybrids harvested at two physiological stages. J. P. F. Silveira[1], R. Belintani*[2], V. L. Tierzo[1], D. H. Vieira[3], T. F. Silveira[5], P. R. L. Meirelles[1], L. F. D. Medeiros[4], and C. Costa[1], [1]*São Paulo State University*, *Botucatu, SP, Brazil*, [2]*University of Agrarian Sciences - University of Marília*, *Marília, SP, Brazil*, [3]*Center of Creation of Animals of Laboratory*, *Rio de Janeiro, RJ, Brazil*, [4]*Rural Federal university of Rio de Janeiro*, *Seropedica, RJ, Brazil*, [5]*Agricultural Municipal school Adolfo Alves Rezende*, *Campina Verde, MG, Brazil*.

The increase in dry matter content due to postponing the harvesting date, as well as the corn hybrid chosen, may influence the voluntary intake by ruminants. Therefore, the objective of this experiment was to evaluate the effects of corn hybrid, harvesting stage and their possible interaction on the voluntary intake by sheep. Twenty four ewe lambs (average age, 3 mo; average initial weight of 25 kg) were used. The experiment followed a 2 x 2 factorial (two hybrids, dent and flint; and two harvesting stages, mealy and black layer), with three replicates, organized in a completely randomized design. The mean voluntary intake of dry matter varied from 620 to 750 g/ewe/d. The intake of silage from the flint hybrid was higher than the intake of silage from the dent hybrid (P < 0.05). Increasing the grain physiological maturity reduced the intake of silage from the dent hybrid, but showed no effect on the intake of silage from the flint hybrid. A hybrid x stage interaction was observed, and the highest intake was observed for the flint hybrid at the black layer stage. In conclusion, harvesting for silage should be done at the mealy and black layer stages for the dent and flint hybrids, respectively, as these combinations produced higher intakes.

Key Words: corn hybrids, dry matter intake, forage conservation

W328 Effect of corn hybrid and ensiling process on voluntary intake of lambs. J. P. F. Silveira[1], R. Belintani*[2], V. L. Tierzo[1], P. R. L. Meirelles[1], D. H. Vieira[3], P. Persichetti Junior[1], C. Costa[1], L. F. D. Medeiros[4], and T. F. Silveira[5], [1]*São Paulo State University*, *Botucatu, SP, Brazil*, [2]*University of Agrarian Sciences - University of Marília*, *Marília, SP, Brazil*, [3]*Center of Creation of Animals of Laboratory*, *Rio de Janeiro, RJ, Brazil*, [4]*Rural Federal university of Rio de Janeiro*, *Seropedica, RJ, Brazil*, [5]*Agricultural Municipal school Adolfo Alves Rezende*, *Campina Verde, MG, Brazil*.

The processing of the corn mass ensilage, as well as the hybrid chosen can interfere on voluntary intake of the ruminant animals. Therefore, this study aimed to evaluate the effects of the hybrid, processing and the possible interaction on the voluntary intake for lambs. Twenty-four Santa Inês lambs having an average age of three mo and an average initial weight of 25 kg were used. The experimental design was completely randomized, in a 2 x 2 factorial scheme (two hybrid, dent and flint; and two processing, smashed and no smashed) with three replicates. The average daily intake varied from 1.17 to 1.31 g/hd/d. The silage intake of the flint hybrid was larger than the dent hybrid. The processing reduced the voluntary intake of the hybrid dent silage, but not the intake of the hybrid flint silage. There was an interaction, hybrid x processing, in that intake was less for the processed dent corn hybrid. The flint corn hybrid was associated with increased intake and processing did not impact intake.

Key Words: harvesting date, dent, sheep

W329 Chemical composition, in vitro degradability, intake and digestibility of pigeon-pea (Cajanus cajan var. guerrero) and guinea-grass hay by goats. A. A. Rodríguez*, D. Carmona, L. Gonz´lez, E. Valencia, and P. Randel, *Univertsity of Puerto Rico*, *Mayaguez, PR*.

The chemical composition, in vitro degradability, intake and digestibility of pigeon-pea (Cajanus cajan var. Guerrero; PP) mixed guinea-grass (GG) harvested at 45 d of growth was determined. Pigeon-pea was harvested at 105 d of growth and mixed with GG (at five different proportions: 100:0, 75:25, 50:50, 25:75 and 0:100 w/w. Triplicate samples from each combination were analyzed to determine CP, NDF, ADF, and lignin. In vitro dry matter (IVDMD) and crude protein degradability (CPD) as % of DM, and NDF degradability as % of total cell-wall content (NDFD) were determined after 48 h of incubation. To determine forage consumption and digestibility a 2 by 2 Latin square experiment was conducted using castrated mature native goats (43.18 kg BW) as experimental units. Animals were assigned to two diets: 100% GG and GG mixed with PP in a 60:40 proportion. The experiment consisted of a 7-d diet-adjustment period and 5 d of data collection. Crude protein increased (P < 0.05) as percentage of PP increased in the mixtures, however NDF, ADF decreased (P < 0.05). Lignin was similar for all PP-GG mixtures. CPD also increased (P < 0.05) as proportion of PP was increased. IVDMD was similar in mixtures containing 100:0, 25:75 and 0:100 PP:GG, but higher than those mixed in a 50:50 and 75:25 PP:GG proportion. NDFD was higher (P < 0.05) in the 0:100 and 25:75 PP:GG mixtures than in the 100:0, 75:25 and 50:50 proportions. Forage intake and digestibility was lower (P < 0.05) in animals fed with PP:GG mixture than with TGH alone (1213 vs 968 g/d and 64.64 vs 58.81%, respectively). Consumption of PP by goats constituted 27% of total legume offered and 16% of total forage intake. In summary, chemical composition and CPD was improved as percentage of PP increased in PP:GG mixtures, however, inclusion of PP in proportions higher than 25% decreased IVDMD and NDFD. Diets containing 40% PP also decrease forage intake and digestibility in goats.

Key Words: pigeon-pea, nutritive value

W330 Effects of feeding peanut skins on growth performance and carcass traits of Kiko × Spanish growing male goat kids. A. Stone*[1], N. Gurung[1], S. Solaiman[1], D. Rankins, Jr.[3], G. Abdrahim[2], and W. McElhenney[1], [1]*Tuskegee University*, *Tuskegee, AL*, [2]*Alabama A & M University*, *Normal*, [3]*Auburn University*, *Auburn, AL*.

Peanut skins (PS), a year-round by-product of the peanut blanching industry, are readily available in southeast Alabama and southwest Georgia. It is typically used as animal feeds; however its feeding value has not been fully evaluated for goats. Objectives of this study were to evaluate effects of various dietary levels of PS on DM intake, growth performance and carcass quality of meat goats. Twenty four Kiko cross-bred intact male goats (18.2 ± 1.41 kg initial BW and 3 to 4 months of age) were randomly assigned to one of the four experimental diets (6 goats/diet) containing 47.3% bermudagrass hay plus 52.7% concentrate mix

with 0, 10, 20, and 30.0% of peanut skins, on as-is basis. Feed offered and refusals were collected daily. Body weights were recorded every 4-wk. After 92-d, goats were slaughtered and carcass characteristics were measured. The feed intake, growth, feed efficiency, and carcass quality data were analyzed as a completely randomized design. Initial BW (P = 0.87), final BW (P = 0.20), and average daily gain (P = 0.29) were not different between treatments. The DM intake (P = 0.65) and gain: feed ratio (P = 0.28) were similar among diets. Dressing percent, longissimus muscle area and chilled carcass weight (P < 0.05) decreased linearly with increasing level of PS. No differences were observed (P > 0.05) in hot carcass weight, body wall fat, and kidney and pelvic fat between treatments. The results indicate that PS is a viable feedstuff for meat goats and up to 30% of PS, on as-is basis, can be included in the diet for growing goats without any compromise in DM intake, growth performance and carcass quality.

Key Words: goats, peanut skins, performance

W331 Effects of soybean small peptide on absorption of free amino acids and small peptide in lactating goats. L. Wang, Z.-J. Cao*, H. Liu, and S.-L. Li, *College of Animal Science and Technology, China Agricultural University*, *Beijing, China*.

The objective of the experiment was to study the effects of intraduodenally infused soybean small peptide (SSP) on absorption of free amino acids and small peptide in lactating goat. Four late lactating dairy goats (38.24 ± 2.73 kg BW, milk production 0.5 - 1.0 kg/d) were used in a 4×4 Latin square design. Goats were fitted with duodenal cannulas and implanted with indwelling catheters in carotid artery, proximal and distal mesenteric vein and portal vein. Each goat received four treatments, respectively: infused normal saline, 60 g/d, 120 g/d and 180 g/d SSP into duodenum. Each period of the experiment lasted 17 d, including a 10-d adaptation period and a 7-d infusing period. Throughout the experimental periods, the diets were delivered in 12 equal meals at 2 h intervals by automatic feeders and water was available ad libitum. Normal saline and SSP were dissolved in 700 mL of normal saline continually infused into the duodenum within 24 h during the 7-d infusing period. The mesenteric and portal plasma flows were measured by dye dilution with para-aminohippurric acid. Plasma was deproteinized and the difference in amino acid concentration of supernatant before and after hydrolysis was attributed to peptides. The results showed that the mesenteric-drained visceral net fluxes of total peptide amino acids (TPAA) and total free amino acids (TFAA) increased (P < 0.05 or P < 0.01) when the infused levels of SSP increased. The portal-drained visceral (PDV) net fluxes of TPAA of infused treatments with 60 g/d, 120 g/d and 180 g/d SSP were higher than that of infused normal saline (P < 0.05), but there were no differences among the infused SSP treatments (P > 0.05). The PDV net fluxes of TFAA increased (P < 0.05 or P < 0.01). These results suggest that increasing the PAA amount in duodenum may promote the absorption of PAA and FAA in small intestine.

Key Words: small peptide, free amino acids, absorption

W332 Protein requirements of Boer crossbred kids. I. A. M. A. Teixeira*[1], K. T. Resende[1], J. M. Pereira Filho[2], R. C. Canesin[1], and T. T. Berchielli[1], [1]*Universidade Estadual Paulista/Unesp*, *Jaboticabal, SP, Brazil*, [2]*2Universidade Federal de Campina Grande/UFCG*, *Patos, PB, Brazil*.

Two experiments were conducted to determine protein requirement for maintenance and growth of 64 ½ Boer ½ Saanen crossbred, intact male kids (5 and 15 kg of initial BW for experiment 1 and 2, respectively). In the first experiment, the baseline group was 6 randomly selected kids, averaging 5.6 ± 0.8 kg of BW. An intermediate group consisted of 6 randomly selected kids, fed for ad libitum intake, that were slaughtered when they reached an average BW of 10.0 ± 0.4 kg. The remaining kids (n = 18) were randomly allocated to one of 3 levels of DMI (ad libitum and restricted to 70% or 40% of the ad libitum intake) within 6 slaughter groups. Kids were slaughtered when the ad libitum treatment kid reached 15 kg of BW. In the second experiment, the baseline group was composed of 7 kids, averaging 15.3 ± 0.3 kg of BW. An intermediate group consisted of 6 kids, fed for ad libitum intake, that were slaughtered when they reached an average BW of 20.4 ± 0.7 kg. The remaining kids (n = 21) were randomly allocated to one of 3 levels of DMI, similar to the first experiment, within 7 slaughter groups. Kids were slaughtered when the ad libitum treatment kid reached 25 kg of BW. Individual empty bodies were weighed, ground, mixed, and samples were collected for chemical analyses. The equations to estimate protein body composition and requirements for maintenance and growth were different for each experiment. The metabolic and endogenous nitrogen losses were 395 and 410 mg/ $kg^{0.75}$ of empty BW (EBW)/d for kids in the first and second experiment, respectively. For young animals (experiment 1), the calculated NP for growth ranged from 165 to 168 mg/$kg^{0.75}$ of EBW. On the other hand, older kids presented lower net protein requirements, which ranged from 144 to 135 mg /$kg^{0.75}$ of EBW. These results suggest that meat goat protein requirement is different from the established recommendations. *Sponsored by FAPESP, 04/06626–0.*

Key Words: body composition, goat, maintenance requirements

W333 Nitrogen balance of Saanen goats in early lactation fed diets with different protein: energy ratio. L. Rapetti*, S. Colombini, G. M. Crovetto, and G. Galassi, *Department of Animal Science, University of Milan*, *Milan, Italy*.

Aim of the experiment was to evaluate the protein:energy ratio (MP/NEl) of the diet in early lactating goats on N balance. 8 Saanen goats were used in two consecutive N balance trials at 8-14 (P1) and 28-34 (P2) DIM. The dietary treatments were as follows: 56 (LOW) or 65 (HIGH) g MP/Mcal NEl, estimated with INRA model (2007). The CP contents of the diets were 15.1 (LOW) and 17.3% (HIGH) on DM. Both diets had 1.69 Mcal of NEl on DM. The forages fed (DM basis) were corn silage (28%) and dehydrated alfalfa hay (22%); in diet HIGH, soybean meal and corn gluten meal partially substituted corn grain. 4 d after kidding, goats were confined to metabolic cages. During each 6 d of trial, individual DMI, milk production and total collection of excreta were recorded. All data were statistically analyzed by GLM procedure (SAS, 2008) considering the diet and period effect and their interaction. DMI was influenced only by period, not by dietary treatment (2.06 and 2.97 kg/d, in P1 and P2 respectively; *P*<0.001); milk yield had the same trend increasing from 3.91 to 5.49 kg/d (*P*<0.001). Milk fat, crude protein and casein contents (%) were affected (*P*<0.01) only by period (4.77 *vs* 3.55, 3.67 *vs* 3.47, 2.63 *vs* 2.46, for fat, CP and casein, in P1 and P2, respectively). Milk urea nitrogen (MUN) was directly related to MP/Mcal NEl ratio: on average 6.9 and 15.3 mg/dL with LOW and HIGH diets (*P*<0.001). The higher SBM inclusion in diet HIGH determined a higher CP digestibility (73.3 *vs* 67.8%, *P*<0.001); however, urinary nitrogen excretion resulted higher for this diet (19.7 *vs* 12.9% of N intake, *P*<0.01). N utilization for milk production (milk N, % of N intake) was higher in diet LOW (42.8 *vs* 36.7, *P*<0.01) and lower in the second period (41.4 *vs* 38.2, *P*<0.05) because of the higher DMI. These results suggest that a MP/NEl ratio of about 60 (with approximately 16% CP

on DM), should be adequate to meet the requirements of high yielding dairy goats during early lactation.

Key Words: goats, N balance, protein:energy ratio

W334 Nitrogen balance and ruminal and blood metabolites of Sannen dairy goats infused abomasally with different levels and combination of starch and pectin. M. Sari, A. A. Naserian*, R. Valizadeh, and S. Salari, *Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran*.

The objective of this study was to examine the effect of abomasal infusion of starch, pectin or combination of both on production and urinary nitrogen excretion of lactating Sannen dairy goats. Four abomasally cannulated goats (average BW 44 ± 2.3 kg, DIM 114 ± 2.1 and milk production 1.65 ± 0.41 kg) were used in a 4×4 Latin square design. Goats were housed in metabolic cages with free access to water and were fed a basal diet consisting of 40% alfalfa hay and 60% concentrates. Each goat was offered the basal diet at 95% of its estimated ad libitum intake throughout the experiment. Treatments were abomasal infusion of different, isoenergetic ratio of starch to pectin: T1 (0.84 g/d), T2 (26.56 g/d), T3 (52.28 g/d), and T4 (77.0 g/d). Purified maize starch and high-methoxyl slow-set citrus pectin were continuously infused from d 9 to 21 of each period. Total collections of urine and feces were conducted for last 4 d of each period and blood and rumen fluid samples were taken 3 h after feeding on d 1 and 3 during each collection period. Milk yield was recorded daily and samples were collected at each milking over the last 2 d of each period. Data were analyzed using the GLM procedure of SAS (2001). Infusions had no significant effect on basal ration intake (P > 0.05). Replacement of abomasal pectin infusion with starch linearly increased urinary N (16.3, 17.9, 18.7, and 19.4 g/d, for T1, T2, T3, and T4 respectively), plasma urea N (14.9, 15.5, 16.3 and 16.5 mg/dL, respectively) and tended to increase milk urea N (P = 0.09). Decreasing amount of infused pectin resulted in linearly decreased fecal N (14.2, 12.7, 12.4, 11.4 g/d, respectively) but did not affect milk and retained N, ruminal NH3-N and pH, plasma concentrations of glucose, triglyceride and cholesterol. Results indicated that increasing carbohydrate fermentation in large intestine by pectin infusion may shift some N from urine to feces and reduce manure ammonia volatilization.

Key Words: fecal and urine N, pectin, starch

W335 Efficiency of energy utilization by lactating Alpine goats. I. Tovar-Luna*[1,2], A. L. Goetsch[1], R. Puchala[1], T. Sahlu[1], and H. C. Freetly[3], [1]*American Institute for Goat Research, Langston University, Langston, OK*, [2]*Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Aridas, Bermejillo, Dgo., México*, [3]*USDA, ARS, US Meat Animal Research Center, Clay Center, NE*.

Thirty-six lactating Alpine does (50.5 ± 1.2 kg BW) were used to determine the effect of stage of lactation on energy utilization. Twelve does were assigned for measurement periods in early, mid-, and late lactation (28-35, 91-98, and 189-196 d of lactation). For six does of each group, after measures with ad libitum consumption of a 60% concentrate diet, feed intake was restricted to the ME requirement for maintenance (ME_m) for 8 d followed by a 4-d fasting period. For the other six does, fasting immediately followed ad libitum consumption. Heat production or energy expenditure (EE) was measured using a head-box calorimetry system the last 2 d with ad libitum intake, near maintenance intake, and fasting. Ad libitum intake of ME was affected (P < 0.05) by stage of lactation (22.2, 24.0, and 18.4 MJ/d), and was similar when fed near ME_m (9.8, 10.4, and 10.8 MJ/d) in early, mid-, and late lactation, respectively. Recovered energy in milk did not differ in early and mid-lactation and was lower (P < 0.05) in late lactation (8.77, 7.84, and 5.40 MJ/d respectively; SE = 0.418). Efficiency of ME utilization for maintenance (k_m) based on ME intake and EE by does fed near maintenance and when fasting was similar (P > 0.05) among stages of lactation (0.780, 0.813, and 0.803 in early, mid-, and late, respectively; SE = 0.0459). However, ME_m (based on fasting after ad libitum intake divided by k_m) was similar (P > 0.05) in early and mid-lactation and lowest (P > 0.05) in late lactation (494, 472, and 412 kJ/kg $BW^{0.75}$; SE = 23.7, respectively). Efficiency of use of dietary ME for lactation (k_{l-d}) was not influenced (P > 0.05) by stage of lactation (0.615, 0.574, and 0.569 in early, mid-, and late lactation, respectively; SE = 0.0191). Although k_m and k_{l-d} by lactating goats were similar among stages of lactation, the ME_m requirement appears lower in late lactation than at early times.

Key Words: goat, energy expenditure, lactation

W336 Blood mineral concentration of goats in semiarid rangelands of central zone in Mexico during the rainy and dry season. R. Rojo-Rubio*[1], A. Z. M. Salem[1,2], A. Olmedo-Juárez[1], A. Hernández-Rodríguez[1], B. Albarrán-Portillo[1], D. López-Aguirre[1], S. Rebollar-Rebollar[1], J.F. Vázquez-Armijo[1], D. Cardoso-Jiménez[1], and J. Hernádez-Martínez[1], [1]*Centro Universitario UAEM, Temascaltepec. Universidad Autónoma del Estado de México, Temascaltpec, Estado de México, México*, [2]*Department of Animal Production, Faculty of Agriculture, Alexandria University, Alexandria, Egypt*.

In semiarid rangelands of central zone in Mexico the annual rainfall is 750 mm. During dry season, rainfall (from October to May) is scarce, thus, most forage species are withered and grazing animals forage intake is too low to meet energy, protein and mineral requirements. This study was carried out to evaluate the effects of season (rainy and dry) and sample location of three different places selected randomly (L1:Luvianos one; L2:Luvianos two; and L3:Luvianos three) at the province of Luvianos in Mexico State on mineral status of blood plasma in crossbred adult goats (LW 35 ± 2 kg), during transition period under the semi-arid rangelands of central zone in Mexico. Blood samples were collected from 66 adult goats (22 per each location) before morning feeding. Blood mineral concentration of P, Na, K, Cu and Zn were assayed and data were analyzed using one way ANOVA test; significant differences between means were tested by Tukey. Results are summarized in Table 1. The information shows little difference between season for mineral concentration in goats, and this maybe due to their native grazing behavior on browse shrubs and tree foliages in the province of Luvianos in México State.

Table 1. Blood mineral concentration (mg/dl) of goats in semi-arid rangelands of central zone in Mexico, during rainy and dry season, 2008.

Season	Location	P	Na	K	Cu	Zn
Rainy	L1	3.82^{ab}	362.8^{b}	21.8^{ab}	0.080	0.052^{b}
	L2	3.19^{ab}	356.4^{b}	17.1^{bc}	0.105	0.065^{b}
	L3	4.74^{a}	362.4^{b}	16.4^{c}	0.088	0.050^{b}
Dry	L1	2.93^{b}	423.4^{a}	26.5^{a}	0.128	0.137^{a}
	L2	2.73^{b}	413.2^{a}	22.1^{ab}	0.101	0.107^{a}
	L3	4.20^{ab}	398.57^{ab}	23.2^{a}	0.105	0.108^{a}

Means with different superscripts within a column differ (P<0.05).

Key Words: status mineral, goats, semi-arid region

W337 Anti-obesity effect of ethanol extract of seed sprouts in porcine preadipocytes. M.-Y. Lee[1], J.-J. Lee[1], H.-J. Lee[2], and S.-H. Oh*[3], [1]*Department of Food and Nutrition, College of Natural Sciences, Chosun University, Gwangju, Chonnam, South Korea*, [2]*Department of Nutrition and Culinary Science, Hankyong National University, Ansung, Gyeonggi, South Korea*, [3]*Department of Animal Sciences, North Carolina A&T State University, Greensboro*.

This study was performed to investigate the anti-adipogenic effect of ethanol extract of various seed sprouts, such as broccoli, alfalfa, barely, rapeseed, red radish, red brussels, Chinese cabbage and buckwheat on porcine preadipocytes in vitro. Anti-obesity effects of various seed sprouts were investigated by measuring proliferation and differentiation in porcine preadipocytes. In addition, triglyceride (TG) level, lipoprotein lipase (LPL) activity and the gene expression of LPL, as indicators of lipid accumulation in cultured porcine preadipocytes, were also examined. The preadipocytes were isolated from the backfat of newborn female pigs by collagenase digestion. Data were analyzed with ANOVA in SAS 8. Fifty μg/ml of the ethanol extracts of broccoli, rapeseed, barley and buckwheat sprouts were able to both reduce TG concentration and retard differentiation of cultured porcine preadipocytes compared with control group ($P < 0.05$). The inhibitory effects of seed sprouts ethanol extracts on proliferation of peadipocytes were small, compared to the effects on differentiation. Anti-obesity effects of barley sprout ethanol extracts were the highest among the seed sprout ethanol extracts. The inhibitory effects on differentiation of porcine preadipodytes were higher in the barley, broccoli, buckwheat and rapeseed sprouts ethanol extracts treated groups than in the alfalfa, red radish, red brussels and chinese cabbage sprouts ethanol extracts treated groups ($P < 0.05$). These results suggest that the ethanol extract of seed sprouts may have potential to reduce the fat accumulation and obesity.

Key Words: porcine preadipocytes, seed sprouts, anti-obesity

W338 The relationship between ammonia concentration in the farrowing room and liver enzymes of sows exposed during lactation: A preliminary study. G. Rocha-Chavez*[1], J. M. Tapia-Gonzalez[1], M. A. Pinto[2], A. Sepulveda- Montes[1], S. Hernandez-Gutierrez[1], O. D. Montañez-Valdez[1], and M. Sanchez-Fabian[1], [1]*CUSUR Univ de Guadalajara, Cd Guzman, Jalisco, Mexico*, [2]*Private practice, Guadalajara, Jalisco, Mexico*.

Ammonia and other noxious gases are always present, in greater or lesser degree depending on type of ventilation, inside pig barns. In animals, these gases can cause stress and respiratory or liver damage that can later impair the health of individuals. Previous studies have demonstrated a close relationship between liver enzyme levels and reproductive problems. The objective of this work was to determine the existing relation between levels of ammonia in the farrowing room and plasmatic levels of two hepatic enzymes of sows exposed during lactation. A total of 20 air samples were obtained in summer and winter from farrowing rooms of a farm in southern Jalisco Mexico using a suction pump connected to an indicator tube. Ammonia measures were done two times a day for 5 consecutive days on both seasons. At the same time, blood samples were collected from 10 lactating sows that were kept in the farrowing room for at least 18 d. Plasmatic levels of glutamic-oxaloacetic transaminase (GOT) and glutamic-pyruvic transaminase (GPT) were determined. Ammonia concentration was higher than expected in both seasons (see Table) and much higher than recommended levels (25 ppm). Hepatic enzymes were also slightly increased ($P > 0.05$) but no correlation was found between both parameters ($r = 0.04$).

Table 1. Ammonia levels in the farrowing room and its relationship with plasma concentration of liver enzymes in lactating sows.

Season	Ammonia	(ppm)	GPT	GOT
	Avg	SD	(iu/ml)	(iu/ml)
Summer	49.2	6.4	29.5 ± 4.7	35.7 ± 3.8
Winter	51.7	8.9	23.6 ± 5.2	28.4 ± 8.6

Ref value for GPT: 9-17, for GOT 8- 21. No significative difference was found ($P>0.05$)

Key Words: ammonia, liver enzymes, sows

W339 Variation in backfat depth and its relations to testicular hypertrophy and reproductive development in boars. D. O. Umesiobi*, *Field of Animal Reproductive Physiology, School of Agriculture and Environmental Sciences, Central University of Technology, Bloemfontein, South Africa*.

The aim of this study was to determine the effectiveness of the use of backfat depth (P2) as a selection model for the determination of lifetime reproductive capacity in boars. Forty eight Large White boars were selected at the onset of puberty (20 wk of age) and evaluated until 60 wk of age. Sixteen boars were randomly assigned to each of the three treatment combinations based on their P2 at selection and designated as: (1) lean group = 8 to 10 mm (L); (2) moderate group = 11 to 13 mm (M); and (3) fat group = 14 to 18 mm (F). At 60 wk of age, the M boars had a greater paired testes weight (463.1 ± 9.6 g) than L (338.3 ± 4.6 g) and F (295.5 ± 6.2 g) groups. Boars in M group had 15% greater daily sperm production per gram testicular parenchyma (DSP/g) than L (40.7 ± 0.3 vs 34.6 ± 0.02 x106) and 10% greater than F (40.7 ± 0.3 vs 36.63 ± 0.3 x106) groups, respectively. Total daily sperm production (DSP) was 25% and 10% greater ($P < 0.05$) for M boars than L (25.3 ± 0.4 vs 19.0 ± 0.6 x109) and F (25.3 ± 0.4 vs 22.8 ± 1.7 x109) boars. Boars in the M group from 20 wk to 60 wk of age had 30% greater ($P < 0.05$) caput-corpus epididymal sperm reserves than L and 38% than F boars. The caudal epididymal sperm reserves were significantly ($P < 0.05$) higher compared to those of L and F boars. The M boars produced semen with highest sperm motility (92.2 ± 1.9%), sperm concentration per ml (285.6 ± 12.3 x106), sperm concentration per ejaculate (56.4 ± 1.1 x109) and normal acrosome (95.4 ± 2.1%). We conclude that the rate of fat deposition seems to be one of the determinants of reproductive development in boars. Thus, selection of males with medium fat deposits appears to enhance the reproductive traits and genetic progress in a breeding herd.

Key Words: boar, backfat thickness, reproductive capacity

W340 Performance of weanling pigs consuming varying levels of a genetically modified corn expressing an alpha-amylase. K. L. Price*[1], A. F. Harper[1], M. E. Persia[2], and J. Escobar[1], [1]*Animal & Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg*, [2]*Syngenta Biotechnology, Inc., Research Triangle Park, NC*.

The increased demand for renewable fuels has lead to the development of a genetically modified corn that expresses high levels of alpha-amylase, an enzyme required for dry grind ethanol production. Although this corn was developed specifically for ethanol production, it is not known if this enzyme-containing corn would also be effective

when fed to growing pigs. Thus, the objective of this experiment was to quantify growth performance in weanling pigs consuming varying levels of corn containing alpha-amylase. Pigs were weaned at 21 days of age (6.6 ± 0.2 kg), blocked by weight and randomly assigned to one of four dietary treatments in a 28-day experiment. There were 3 pigs per pen and 7 pens per treatment. Pigs were fed a 3-phase nursery diet protocol (Phase 1, 0 to 7 days; Phase 2, 8 to 21 days; and Phase 3, 22 to 28 days) and had ad libitum access to water and feed. All diets were formulated to meet or exceed NRC (1998) nutrient requirements. For each phase, a basal diet was prepared that contained all ingredients with the exception of 15% experimental corn. This basal diet was then mixed with both alpha-amylase corn and an isogenic corn to obtain 0 (control), 5, 10, or 15% inclusion of alpha-amylase corn. At the end of the 28-day growth trial overall ADFI (P = 0.64), ADG (P = 0.29), final BW (P = 0.40), and G/F ratio (P = 0.75) were not different among treatment groups. Furthermore, the growth performance of pigs consuming alpha-amylase corn diets was not different from that of pigs fed the control diet: ADFI, P = 0.85; ADG, P = 0.58; final BW, P = 0.67; and G/F ratio, P = 0.38. Although the alpha-amylase corn is efficacious under high temperature conditions in ethanol production, the present results demonstrate that there are neither adverse nor positive effects on growth performance of weanling pigs when fed alpha-amylase corn.

Key Words: weanling pig, corn amylase, growth performance

W341 A survey of North American sow farm reproductive management. R. Knox*[1], T. Safranski[2], D. Levis[3], and W. Singleton[4], [1]*University of Illinois*, *Urbana*, [2]*University of Missouri*, *Columbia*, [3]*University of Nebraska*, *Concord*, [4]*Purdue University*, *West Lafayette, IN*.

Responses from 115 Midwest (74%) and Canadian farms (14%) showed farms were segregated as breed-wean (68%). Inventory in >85% was 500-4000 sows. Weaning age was 18-21 d in >70%. Feeding in lactation was by gradual increases and ad libitum. Labor varied from 1 person:10-400 sows in breeding/gestation with most hours spent on estrus and AI, then on feeding, moving sows, animal health, and cleaning, and then on records and equipment repair. People influenced fertility in >70% and training was valued on 67% of farms. Boar exposure began at weaning and as late as day 4. Most checked for estrus in AM (>75%), but varied from 1-2X/d. Duration of boar contact varied (1-4 min), as did method of boar control, boars used/sow, and alternate boar use. Semen was supplied by studs (>80%) in multiple deliveries/week of 10-60 doses/shipment. Semen was stored at 17 C and rotated daily. AI was consistent among farms occurring with a boar present (87%), double AI, and catheter left in post-AI (76%). AI timing was based on estrus (85%), but varied from within minutes (49%) to the next AM/PM (31%) and whether adjusted on wean to estrus interval (53%). Farms required boar exposure (88%), back pressure (93%), flank rubbing (79%) and gravity semen flow (79%) during AI and did not squeeze semen into the uterus (64%). Farms did not warm semen before AI, use IUI, or add hormones to semen. Gestation management was mixed; some relocated sows 1-3 times, while others prohibited this. Sows were moved only within the first week (19%) or only after four weeks (58%) post-breeding. Pregnancy was diagnosed with real time ultrasound (75%), and culling varied by rebreeding attempts (1-2) and weeks from open diagnosis to culling (1-5 weeks). Infertility in Jul-Aug was reported on most farms, with reduced estrus and increased returns. Yearly production was consistent for sows bred within 7 days of weaning (>80%), not in pig (<5%), farrowing rates (>80%), and liveborn pigs (10-12, >70%). These outcomes suggest consistencies and variation in management, but uncertainty as to which may be advantageous for achieving reproductive efficiency.

Key Words: reproduction, swine, management

W342 Combined *Acanthopanax senticosus* extract and inulin improves growth performance, diarrhea and intestinal morphology in weaned piglets. X. Wu[1], Y. Yin*[1], F. Yan[1], X. Kong[1], R. Huang[1], T. Li[1], and L. Chen[2], [1]*Laboratory of Animal Nutritional Physiology and Metabolic Process, Institute of Subtropical Agriculture, the Chinese Academy of Sciences*, *Changsha, Hunan, China*, [2]*Guang An Biological Technique Company*, *China*.

Acanthopanax senticosus (AS) is used widely in eastern Asia as a tonic and sedative Chinese herb to enhance overall well-being. Inulin is used increasingly in feed because it has unusual nutritional characteristics. Combination of AS extracts (ASE) and inulin were tested as possible alternatives to antimicrobial growth promoters for early weaned pigs on growth performance, diarrhea and intestinal morphology. A total of 96 Duroc×Landrace×Yorkshire piglets weaned at 21 days of age with an average initial body weight of 5.64±0.18 kg were randomly assigned to one of 3 groups with 4 replicate pens per treatment. The piglets were fed a basal diet (BD), BD+ASEI (ASE 1 g/kg and inulin 25 g/kg), and BD+antibiotics (10% bacitracin zinc 400 mg+15% carbadox 300 mg), respectively for 14 days. On d 21, eight piglets per group (two piglets per pen) were slaughtered for evaluation of small intestinal morphology. Results showed that ASEI and antibiotics improved ADG by 18.05 and 19.78% (P<0.05), decreased F/G by 19.79 and 21.39% (P<0.05), respectively, compared with the control group. However, there was no difference between the ASEI and antibiotic groups (P>0.05). Compared to the control group, both ASE and antibiotics decreased (P<0.05) the incidence of diarrhea by 52.7 and 55.0%, respectively. The villus height of jejunum and ileum increased by 13.41, and 14.00% (P<0.05), respectively, in response to the dietary supplementation with ASEI. These findings suggested that dietary supplementation with the combination ASE and inulin could decrease diarrhea occurrence resulting from weaning stress, and improve health of intestinal morphology in weanling piglets instead of antibiotics.

Key Words: *Acanthopanax senticosus* extracts, inulin, weaned piglets

W343 Microarray analysis of genes in small intestine of IUGR piglets. R. Chen, Y. Yin*, J. Pan, Y. Gao, and X. Song, *Key Laboratory of Animal Nutritional Physiology and Metabolic Process, Institute of Subtropical Agriculture, the Chinese Academy of Sciences*, *Changsha, Hunan, China*.

In this study, Affymetrix porcine GeneChips were used to explore differentially expressed genes in the small intestinal mucosa of IUGR (Intrauterine growth restriction) and NBW (normal birth weight) piglets. Five NBW (birth weight: 1503±310 g) and five IUGR (birth weight: 806±35 g) piglets were killed 21 days after birth by jugular puncture after anesthesia, Samples were immediately placed in liquid nitrogen and stored at -80 °C. cDNA synthesis, microarray hybridization, microarray slide washing, and array scanning were performed following Affymetrix protocols. Standard post-hybridization washes and double-stain protocols were used on an Affymetrix GeneChip Fluidics Station 450. Arrays were scanned on an Affymetrix GeneChip Scanner 3000. Statistical analysis of array data was analyzed using GeneChip Operating Software. The dividing point of the genes relative expression level was 2-fold. There were 561 differentially expressed genes in the small intestine from IUGR compared to NBW piglets. Compared with age-matched NBW piglets, mRNA levels for 255 genes were reduced in the small intestine of IUGR piglets, whereas 306 genes were increased. For example, the expression levels of the argininosuccinate synthetase 1 and cytochrome P450 3A29 genes were 6-fold and 4-fold higher in tissues of the IUGR

piglets than those of NBW piglets, respectively; whereas the expression level of the metallothionein and urate transporterchannel protein genes were reduced 10-fold and 5-fold in the IUGR piglets, respectively. Our results not only provide new insights into the molecular mechanisms of small intestinal mucosa in IUGR piglets, but also serves as a valuable resource to researchers investigating IUGR piglets.

Key Words: IUGR, piglet, microarray

W344 Conjugated linoleic acid (CLA) isomers and its effect on proliferation of CD4 and CD8 T lymphocytes of pigs. J. R. Peralta-Quintana, S. Y. Moya-Camarena, J. Hernández, M. Reséndiz, V. Mata-Haro, and A. Pinelli-Saavedra*, *Centro de Investigación en Alimentación y Desarrollo A.C.*, *Hermosillo, Sonora, México*.

In several studies CLA has been shown to enhance some aspects of immune response. Most pig studies have focused in pro-inflammatory cytokines, immunoglobulin production, using a mixture of isomers. The aim of this study was to evaluate the effect of individual isomers of CLA and a mixture of them (1:1) on proliferation of CD4 and CD8 T lymphocytes. Peripheral blood mononuclear cells (PBMC) (5×10^6) from 9 conventional pigs (25 d of age) dyed with carboxyfluorescein succinimidyl ester (CFSE) were stimulated with phytohaemagglutinin (PHA) (5µg/mL), supplemented *in vitro* with CLA. Cells were incubated at 37°C under atmosphere controlled with 5% CO_2 for 72 h, and with monoclonal antibodies (mAb) anti-CD4 o anti-CD8 labelled with phycoerythrin (PE). Analysis was by flow cytometry fluorescence activated cell sorting (FACS) Calibur. Treatments were as follows: A. non-stimulated; B. PHA; C. 10µ M 9*cis*-11*trans*; D. 10 µM 10*trans*-12*cis*; E. 10 µM mixture; F. 100 µM 9*cis*-11*trans*; G. 100 µM 10*trans*-12*cis*; H. 100µM mixture. Data were analysed by one way ANOVA using NCSS2005 package. Our results showed that 100 µM 9*cis*11*trans*-CLA decreased significantly ($P < 0.05$) the proliferation of PBMC. In contrast, no effect was found with 10*trans*-12*cis*-CLA and the mixture irrespective of the amount used. Regarding the proliferation of CD4 and CD8 T lymphocytes, it was not affected ($P > 0.05$) for any isomer nor the mixture of them, irrespective of concentration used. However, 100 µM 9*cis*-11*trans*-CLA tended to reduce the proliferation ($P = 0.06$) of CD8 T lymphocytes. Our results suggest that CLA is isomer specific, but CLA does not appear to affect CD4 lymphocytes.

Key Words: conjugated linoleic acid, CD4 and CD8, pigs

W345 Dietary requirement of true digestible lysine for growing pigs. Y. Zhang*[1,2], Y. Yin[1], J. Li[1], R. Huang[1], and Y. Chen[1,2], [1]*Key Laboratory of Subtropical Agro-ecology, Institute of Subtropical Agriculture, The Chinese Academy of Sciences*, *Changsha, Hunan, The People's Republic of China*, [2]*The Graduate University of Chinese Academy of Sciences*, *Beijing,The People's Republic of China*.

Sixty healthy growing pigs (Duroc×Landrace×Yorkshire) with an average BW of 21.6±1.1 kg were used to determine the true digestible lysine (TDL) requirement of growing pigs on the basis of growth performance and lysine digestibility. Pigs were assigned randomly to one of five dietary treatments (12 pigs/diet), representing five levels of TDL (0.72, 0.82, 0.92, 1.02 and 1.12%). There were three replications per treatment, with four pigs (2 barrows and 2 gilts) in each replication (2 pigs/pen). A randomized-block design was used, with pen as the experimental unit. Experimental diets were formulated to provide the 5 TDL levels offered to pigs at 5% BW during the experimental period. The results show that: the ADG of pigs was affected by dietary TDL levels as described by Equation 1: y1=-3217.9X2+6117.1x-236.2 (R2=0.9435, y1 = ADG, g/d; x=dietary TDL, %). The ADG/BW0.75 of pigs was affected by dietary TDL levels as described by Equation 2: y2=-429.79x2+808.86x-326.97 (R2=0.9589, y = ADG/BW0.75, g; x=dietary TDL, %). The F/G of pigs was affected by dietary TDL levels as described by Equation 3: y3=33.071x2-62.781x+32.534 (R2=0.9957, y = F/G; x=dietary TDL, %). When dietary TDL level was 0.950%, ADG was highest (511 g/d). When dietary TDL level was 0.941%, ADG/BW0.75 was highest (53.60 g). When dietary TDL level was 0.949%, F/G was lowest (2.74). The results abrove indicated that growth performance of growing pigs was most improved when dietary TDL was 0.947%. The digestible nitrogen, nitrogen digestibility and nitrogen retained values were highest when dietary TDL was 0.92%. The ileal true digestibility of amino acids was highest when dietary TDL was 0.92%. Collectively, these results indicate that the optimal TDL requirement of growing pigs is 0.92%-0.95% of the diet.

Key Words: requirement, growing pigs, true digestible lysine

W346 Effect of diet enriched with rapeseed or sunflower oil on fatty acid profile of backfat and intramuscular fat in gilts. G. Battacone*, A. Nudda, M. G. Manca, C. Dimauro, and G. Pulina, *Dipartimento di Scienze Zootecniche, Università di Sassari*, *Sassari, Italy*.

An experiment was carried out in order to study the fatty acid profile in the backfat and intramuscular fat from carcasses of gilts fed diets enriched with either rapeseed or sunflower oils for the last 4 weeks before slaughter. Twenty Landrace x Large White crossbred gilts were allotted to one of two experimental diets obtained by adding either rapeseed oil (RSO) or sunflower oil (SFO) to the commercial feed (at 2%). Fatty acid composition of Longissimus muscle (Lm) and backfat (Bf) of each carcass was quantified. Both tissues of RSO pigs had a higher percentage of C18:3n3 (1.15 vs 0.95%; P<0.01) and a lower n6/n3 ratio (13.9 vs 15.9; P<0.01) than those fed SFO. On the contrary, the fat of pigs fed SFO had a higher content of C14:0, C16:0 and C16:1 (P<0.05). The dietary oil did not affect (P=0.38) the CLAc9,t11 content in both tissues (0.11 vs 0.10% in RSO and SFO, respectively). The content of MUFA was higher in Lm than in Bf (48.0 vs 42.1%; P<0.01), due to its higher concentration of C18:1c9 and C16:1. The CLAc9,t11 concentration was higher in Bf than in Lm(0.12 vs 0.09%; P<0.05). The PUFA content was higher in Bf than in Lm (21.0 vs 15.0%; P<0.01). Our data confirmed that: i) it is possible to modify the fatty acid composition of pork meat by altering the source of fat in the diet; ii) the adipose tissues from Lm and Bf of pig differ for their fatty acid composition.

Key Words: swine carcass, fatty acid, backfat and intramuscular fat

W347 Mechanisms for transcellular transport of glucose in swine small intestine. M. Al-Rammahi*[1], A. Moran[1], D. Batchelor[1], E. Coulter[1], N. Jones[1], C. Ionescu[2], D. Bravo[2], and S. Shirazi-Beechey[1], [1]*Department of Veterinary Preclinical Sciences, University of Liverpool*, *Liverpool, UK*, [2]*Pancosma SA*, *Geneva, Switzerland*.

Dietary glucose is transported across the luminal membrane of intestinal absorptive cells (enterocytes) by the Na^+/glucose cotransporter, SGLT1. Glucose exits the cells across the basolateral membrane into the systemic system by the Na^+-independent monosaccharide transporter, GLUT2.

It has been proposed that in rats fed high carbohydrate diets, GLUT2 may be recruited to the luminal membrane where it can transport either glucose or fructose. In order to determine the expression of monosaccharide transporters in swine small intestine, 28 day old piglets of both sexes were housed in separate pens and were weaned to isocaloric diets containing either 7%, 35.9% or 60.3% digestible carbohydrates. The animals were maintained on these diets for 3 days and had access to water at all times. At the end of the experimental period piglets were sacrificed by giving intravenous pentobarbitone (Approved by the UK Home Office under schedule 1). Intestinal tissue samples were fixed and used for immunohistochemical localisation of SGLT1 and GLUT2 using specific antibodies. The data show that in the intestinal samples of animals on all three diets, SGLT1 protein was expressed on the brush border membrane and GLUT2 on the basolateral membrane of all villus enterocytes. There was no labelling of GLUT2 on the luminal membrane. We conclude that SGLT1 is the major protein responsible for the absorption of monosaccharides across the brush border membrane under all dietary carbohydrate levels.

Key Words: Intestine, SGLT1/GLUT2, Glucose Transport

W348 Expression of sweet taste receptor, gustducin and carbohydrate responsive gut hormones in swine small intestine. M. Al-Rammahi*[1], A. Moran[1], D. Batchelor[1], E. Coulter[1], N. Jones[1], C. Ionescu[2], D. Bravo[2], and S. Shirazi-Beechey[1], [1]*Department of Veterinary Preclinical Sciences, University of Liverpool*, *Liverpool, UK*, [2]*Pancosma SA*, *Geneva, Switzerland*.

We have shown previously that dietary sugars and artificial sweeteners increase SGLT1 expression and glucose absorptive capacity in wild type mice, but not in T1R3-, a subunit of the sweet taste receptor, and α-gustducin-, the partner G-protein, knockout mice. We proposed that T1R2+T1R3, the sweet taste receptor, expressed on the luminal membrane of villus enteroendocrine cells senses the lumenal glucose concentration. Lumenal glucose above a threshold level activates, in enteroendocrine cells, a signaling pathway involving T1R2+T1R3, gustducin and other signalling elements. This results in secretion of candidate gut hormones. These hormones bind to receptors on target cells and, through a paracrine mechanism, enhance SGLT1 expression. In this study we determined the expression of T1R2, T1R3, gustducin and the gut hormones in the intestine of 28 day old weaned piglets. Using specific antibodies we show, by immunohistochemistry, that the sweet taste receptor subunits, gustducin and gut hormones are expressed in subpopulations of cells along the crypt villus axis. In contrast, SGLT1 is expressed on the brush border membrane of all villus enterocytes. Furthermore, there was co-expression of T1R2/R3 and gustducin with chromogranin A, a classical marker of enteroendocrine cells. Our data indicate that the sweet taste receptor and other signaling elements are expressed in swine intestinal enteroendocrine ells and that the intestine has the capacity to detect, via T1R2/R3, changes in the concentration of lumenal sugars/artificial sweeteners. The findings that gut hormones are expressed in the same cells as those possessing taste receptors indicates that the swine intestine is capable of secreting gut hormones known to be responsive to dietary carbohydrates.

Key Words: intestine, sweet taste receptor, gut hormones

W349 Microbiological and molecular analysis of bacterial community by probiotic mixture in wearing pig *in vivo* intestinal models. Y. S. Kim[1], Y. Kim[1], K. Y. Whang[2], S. H. Kim[2], and S. Oh*[1], [1]*Division of Animal Science, Chonnam National University*, *Gwangju, Korea*, [2]*Department of Food Bioscience and Division of Biotechnology, Korea University*, *Seoul, Korea*.

Recently, it has been reported that the balance or ratio of the intestinal microbiota resulting from health promoting probiotic bacteria plays an important role in human and animal health. Here, we monitored the dynamic microbial diversity by probiotic mixture including *Lactobacillus acidophilus* 30SC and *Saccharomyces cerevisiae* using *in vivo* feeding trials supplemented with probiotic mixture by traditional plating method and polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) techniques. Experimental period was divided into Phase I (14 days) and Phase II (14 days). The Phase I diet contained 3600 kcal/kg ME, 22.6% CP, 1.56% Lys, 0.54% Met, 0.82% Ca, and 0.75% P. The Phase II diet contained 3430 kcal/kg ME, 19.5% CP, 1.30% Lys, 0.47% Met, 0.80% Ca, and 0.55%P. Dietary treatments were; 1) Basal diet (no antibiotics), 2) Basal diet with 0.2% antibiotics 3) Basal diet with probiotics mixture (*ca* 1.0 x10^9 of *L. acidophilus* and 2.0 x 10^{10} of *S. cerevisiae*). Pigs consumed feed and water ad libitum. Cr_2O_3 (0.2%) included diets were supplied from day 12 and day 26 to day 14 and day 28, and feces was collected at the end of each Phase (day 14 and 28). During 28 days administrations using wearing pigs, a specific reduction in coliforms was observed compared to the control, whereas the population of lactobacilli increased. Unexpectedly, supplemental probiotic mixture did not dramatically affect the counts of total aerobes and yeast/mold under standard plating method. In addition, DGGE analysis showed a significant difference in the 16S rRNA gene products by specific-genus target primer sets (eubacterial, lactobacilli, and bifidobacteria groups) on administering probiotic mixture. Selected twenty bands were sequenced and most of them were identified with uncultured bacterium clones or a *Lactobacillus*-like community. Therefore, our study suggests that probiotic mixture including *L. acidophilus* and *S. cerevisiae* could significantly regulate the specific bacteria population such as lactobacilli and coliforms via a dynamic interaction with other microbial communities in the intestinal tract.

Key Words: probiotics, DGGE, lactobacillus

W350 Administration of probiotics influences enterotoxigenic *escherichia coli* F4 attachment and expression of intestinal cytokines in weaned pigs. J.-F. Daudelin*[1,2], M. Lessard[2], F. Beaudoin[2], N. Bissonnette[2], E. Nadeau[1], and J. M. Fairbrother[1], [1]*Reference laboratory for E. coli (EcL), Université de Montréal*, *St-Hyacinthe, Quebec, Canada*, [2]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*.

Post-weaning diarrhoea associated with F4-positive enterotoxigenic *E. coli* (ETEC F4) causes important economic losses for pig producers. The use of probiotics as feed additives to prevent such enteric infections and reduce the use of antimicrobial treatments, possibly due to an improved host intestinal health, has recently gained in interest. The aim of this study was to evaluate the effects of two probiotics, *Pediococcus acidilactici* (PA) and *Saccharomyces cerevisiae boulardii* (SCB), on ETEC F4 attachment, colonization and cytokine expression in the ileum of weaned pigs. At birth, different litters of pigs were allocated to the following treatments: 1) control group without antibiotic or probiotic treatment (CTRL), 2) control with antibiotics (aureomycin (110 ppm/kg) and tiamulin (31.2 ppm/kg) added to weanling feed (ATB), 3) PA, 4) SCB, and 5) PA + SCB. During lactation and the post-weaning period, a daily

dose of probiotics (1×10^9 CFU) was orally administered to pigs using disposable pipets. At seven days post-weaning, F4-receptor-positive pigs, thus susceptible for ETEC F4 infection, were orally inoculated with an ETEC F4 strain. The necropsy was performed 24 h after infection and intestinal samples were collected. The immunofluorescence assay, ETEC F4 bacterial counts and real-time PCR analysis for cytokine expression were performed. In the probiotic groups, the attachment of ETEC F4 to the intestinal mucosa was significantly lower than in the ATB group ($P < 0.05$). Moreover, colonization of the ileal mucosa tended to be lower in PA + SCB pigs than for pigs of the ATB group ($P = 0.07$). Finally, proinflammatory cytokines and beta-2 defensin, which are involved in the innate immune defence against ETEC F4, were upregulated in PA and PA + SCB groups in comparison with the CTRL group ($P < 0.10$). Futhermore, IL-6 tend to be upregulated in PA and PA + SCB groups in comparison with the ATB group ($P < 0.10$). These results suggest that administration of probiotics could be an alternative to attenuate ETEC F4 infection in pigs.

Key Words: probiotics, *E. coli*, immune response

W351 Inclusion of live yeast *S. cerevisiae boulardii* (CNCM I-1079) in sow lactation diets: Effects on sows and nest performances. F. Mariella[1], A. Agazzi[1], G. Invernizzi[1], G. Savoini*[1], E. Chevaux[2], and Y. Le Treut[2], [1]*University of Milan Faculty of Veterinary Medicine, Milan, Italy*, [2]*Lallemand S.A.S., Blagnac, France.*

The aim of the trial was to evaluate the inclusion live yeast (S. cerevisiae boulardii, CNCM I-1079) in sow lactation diets on sows and nest performances. A total of 50 sows were subdivided into the following two groups based on parity and date of birth: Control (C = n 20) and Live yeast (LY = n 30). Sows were fed a basal diet with (LY) or without (C) the inclusion of live yeast during lactation. Yeast supplementation started 3 weeks before farrowing at 109 cfu/kg, with an additional 2 x 1010 cfu/d provided upon entrance into the farrowing room, until 2 d after parturition. The following parameters were observed for each sow: rectal temperature and fecal score at entrance into the farrowing room one week before parturition, and at 3, 10, and 28 d after parturition, percentage of live piglets and number of piglets born alive. Rectal temperature, fecal score at birth and 1, 3, 10 d after birth, ADG and weight gain were determined for each piglet. All the parameters were analyzed by a Mixed procedure for repeated measures of SAS (2006) using treatment, parity and sex as fixed effects and sows as random factor. Live yeast led to an increase in number of piglets born alive (12.15 for LY vs 11.80 for C, P<0.05) and percent of live piglets (85.54% for LY vs 76.07% for C, P<0.05); an increase in overall ADG of piglets (183.12 g for LY vs 174.07 g for C, P<0.01), in particular for 2nd-6th parity sows (208.36 g for the LY group vs 175.05 g for the C group, P<0.01); and increased weaning weights (6969.54 g for LY vs 6495.54 g for C, P<0.01). Average piglet rectal temperature was slightly higher for LY than for C (38.65°C for LY vs 38.46°C for C, P<0.05). No difference was noted in sow rectal temperatures or on piglet fecal scores. The inclusion of live yeast in sow lactation diets positively affected their productive performance as shown by increased live litter size and growth of piglets.

Key Words: live yeast, sow, nest

W352 Consumer preferences for U.S. pork in urban China. D. Ortega*[1], H. Wang[1], and L. Wu[2], [1]*Purdue University, West Lafayette, IN*, [2]*China Agricultural University, Beijing, P. R. China*.

The emergence of China onto the world economic stage has many implications for U.S. hog producers. China is making a transition from a developing economy to a developed one. Its population is becoming wealthier, demanding more goods, and eating more high-quality food. Pork, being the primary meat in Chinese diets, will face a demand surge that will need to be met by increasing domestic production and supply-chain efficiency or increased imports. With a market of 1.32 billion consumers and growing, China offers many opportunities for U.S. pork. The identification of specific factors that influence consumer purchasing decisions regarding imported pork will aid policy makers and companies wishing to enter the growing Chinese urban market. The objective of this research is to assess and evaluate factors which influence consumer demand for U.S. pork in China. The data for this study comes from a survey of urban Chinese consumers that was administered in May 2008. A double-bounded dichotomous question format was used to measure an individuals' willingness-to-pay for U.S. pork. An ordered logit model was then developed to determine the factors that influenced a consumer's willingness-to-pay for U.S. pork. Specifically, this study looks at food safety issues affecting urban consumers, especially their acceptance of the lean-meat additive ractopamine (commonly sold in the U.S. as Paylean). Results from this study show that age, shopping location, and food safety concerns, among other factors, have a significant effect on willingness-to-pay for U.S. pork. Food safety was determined to be an important factor in pork purchasing decisions, making urban consumers reluctant to purchase pork fed with ractopamine. This is an issue tied specifically to a lack of consumer confidence on the Chinese food inspection system due to previous lean-meat additive scares. U.S. hog producers looking to enter the Chinese market should consider either removing ractopamine supplementation to cater to Chinese consumers who prefer fattier pork, or invest in educating the Chinese public that ractopamine-fed pork is safe for human consumption.

Key Words: willingness-to-pay for U.S. pork, ractopamine, China

W353 Gastrointestinal morphology of pigs farrowed in indoor versus outdoor management systems and weaned into an indoor, off-site nursery. E. Davis*[1], C. V. Maxwell[2], J. D. Spencer[3], R. L. Moser[3], J. Rehberger[1], and T. Rehberger[1], [1]*Agtech Products, Inc., Waukesha, WI*, [2]*University of Arkansas, Fayetteville*, [3]*JBS United, Inc., Sheridan, IN*.

Two swine herds of similar genetics (PIC C-22 × PIC 280) were used to evaluate the effects of indoor and outdoor management on gastrointestinal (GI) morphology during the pre- and post-weaning periods. Pigs were farrowed in a conventional (CONV), confinement facility located in Sheridan, IN or in an outdoor pasture facility in Springfield, CO. Pigs were weaned from both locations simultaneously at 19 ± 2 d of age and averaging 5.5 kg BW, were transported to an off-site nursery facility at the University of Arkansas, and housed in separate rooms. Pigs were blocked by BW and fed common Phase 1 (d 0 to 14), Phase 2 (d 14 to 28), and Phase 3 (d 28 to 42) diets. Six pigs from each group were euthanized and GI tracts sampled to measure GI morphology and goblet cell enumeration at 6, 13, and 18 d of age prior to weaning (d 19) and on d 1, 3, 10, and 24 post-weaning. Duodenal villus height was greater ($P \leq 0.05$) pre-weaning in CONV pigs compared to those farrowed in the outdoor system. However, outdoor reared pigs had greater ($P \leq 0.05$) duodenal villus height the day after weaning compared to CONV pigs, as well as greater ($P \leq 0.05$) duodenal and jejunal crypt depth, villus height, and villus area on d 24 post-weaning. The number

of acidic mucin-producing goblet cells on ileal villi was greater ($P \leq 0.05$) in CONV pigs at 13 d of age and lower ($P \leq 0.05$) at 18 d of age compared to outdoor reared pigs (treatment x day interaction, $P \leq 0.05$). Outdoor reared pigs had a greater ($P \leq 0.05$) number of acidic mucin-producing goblet cells along the duodenal villi on d 3 post-weaning and fewer ($P \leq 0.05$) along the jejunal villi on d 24 post-weaning compared to CONV pigs; however, numbers of goblet cells were similar between treatments on the other post-weaning sampling days (treatment x day interaction, $P \leq 0.05$). These data indicate that pigs farrowed in an outdoor management system and weaned to an indoor facility experience less gut integrity disruption at weaning compared to pigs farrowed in CONV facilities.

Key Words: swine, management, weaning

W354 The relationship between radiated heat loss and feed conversion in grower pigs. W. Caine*, L. Holt-Klemic, J. Aalhus, I. Larsen, T. Liu, J. Colyn, M. E. Dugan, W. Robertson, S. Landrey, and A. L. Schaefer, *Agriculture and Agri-Food Canada*, *Lacombe, Alberta, Canada*.

With all-in-all-out swine marketing systems the uniform grouping of individual pigs within a pen can significantly influence the body weight and carcass index variation at marketing. Excessive weight or index variation can incur economic discounts. The purpose of the present study was to examine whether the non invasive quantification of radiated heat loss from grower pigs could be used to stratify pen mates into more uniform growth efficiency groups such that a given pen would display greater uniformity in target market weights. In a pilot trial, 20 grower pigs balanced by sex (gilts and barrows, Hypor Comp. genetics) were monitored during the grower period (60 to 90 kg live weight) for individual growth efficiency or feed/gain and also for radiated heat loss using infrared thermography. All pigs were individually housed in a thermoneutral environment in pens measuring approximately 2.5 meters × 1.5 meters and fed a conventional cereal based grower diet which met or exceeded NRC requirements. Feed intake and growth were monitored weekly for individual pigs. Towards the end of the grower period of 90 kg the pigs were scanned on the orbital region (eye) using a FLIR broad range infrared camera (IRT). The feed conversion value for all pigs during the growth phase was 2.3 ± 0.2 (SD) and the thermal radiation value averaged 33.6 ± 0.7 C. Of interest was the observation that the feed conversion ratio and the IRT values displayed a significant Spearman Ranking value ($P<0.05$). In other words, animals that were more efficient displayed a lower radiated heat loss. For example, the six most efficient pigs displayed a feed conversion value of 2.1 ± 0.05 and an IRT value of 33.5 ± 0.7 compared to the six animals that were least efficient displaying a feed conversion of 2.6 ± 0.2 and an IRT value of 34.1 ± 0.7. These data suggest that it may be possible to use IRT to stratify pen mates during the growing period so that an all-in-all-out marketing system could create a more uniform growth efficiency and more uniform carcass index values.

Key Words: swine, feed conversion, infrared

W355 The effect of a *Bacillus* based direct fed microbial on the microbiota of grow-finish pigs. J. Rehberger*[1], E. Davis[1], C. V. Maxwell[2], and T. Rehberger[1], [1]*Agtech Products, Inc.*, *Waukesha, WI*, [2]*Department of Animal Science, University of Arkansas*, *Fayetteville*.

MicroSource® "S" is a *Bacillus* based direct fed microbial (DFM) included in the grow-finish diet to improve the decomposition of manure. In order to determine the effect of MicroSource S on the microbiota of the grow-finish pig, terminal restriction fragment length polymorphism (TRFLP) analysis was performed on gastrointestinal tracts of pigs whose diets were supplemented with MicroSource S at 0.5 g per kilogram of feed or fed a control diet. Gastrointestinal tract samples were taken from five treated and five untreated pigs when their average weight was 36 kg, 68 kg, 91 kg, and 113 kg. After TRFLP was performed, a GLM procedure was used to determine which gastrointestinal TRFs were impacted by the inclusion of MicroSource S in the grow-finish diet. The addition of MicroSource S increased the microbial diversity in the duodenum as indicated by greater incidence ($P < 0.05$) of 15 TRFs identified with BfaI and 41 TRFs identified with MspI when compared to control pigs. Combining the data generated by both enzymes made it possible to putatively assign a genus to some TRFs. There were several putatively assigned species of *Lactobacillus* that were more prevalent ($P < 0.05$) in pigs whose diets had been supplemented with MicroSource S. The incidence of *Ruminococcus* and *Brevibacillus* were greater ($P < 0.05$) in animals that were administered MicroSource S compared to animals that received the control diet. Additionally, TRFs putatively assigned to the phylum Bacteroidetes, possibly from the genus *Bacteroides*, were also more prevalent ($P < 0.05$) among animals that were administered MicroSource S. Evaluation of the TRFLP results indicates that the inclusion of MicroSource S alters the microbiota of the grow-finish pig, as illustrated by the number of TRFs in the duodenum that were more commonly present in animals administered the DFM.

Key Words: swine, *Bacillus*, microbiota

W356 A preliminary comparison of the bacterial communities of foaming and non-foaming swine manure pits. J. Rehberger*, E. Davis, A. Baker, T. Parrott, A. Veldkamp, and T. Rehberger, *Agtech Products, Inc.*, *Waukesha, WI*.

The accumulation of foam in manure pits is an emerging problem in the swine industry and effective solutions have not yet been identified. Although the definitive cause of foaming is unknown, microbial activity in the swine manure pit is a likely factor and investigation of the differences in the microbial communities of foaming and non-foaming swine manure pits may provide initial insight on the cause of the problem. In order to examine the difference between the microbial communities in foaming and non-foaming manure pits, terminal restriction length polymorphism (TRFLP) analysis was performed using four restriction enzymes; BfaI, HaeIII, MspI, and BstUI. To analyze the TRFLP data the GLM procedure was used to determine which TRFs were present or more abundant in foaming or non-foaming swine manure pits. When the binary TRFLP data were analyzed, six TRFs were more prevalent ($P < 0.05$) in foaming pits than non-foaming pits. There were also four unique binary TRFs more commonly found ($P < 0.05$) in non-foaming pits than foaming pits. The binary microbial profiles from all four enzymes suggested that there were six operational taxonomic units (OTUs) that differed between foaming and non-foaming swine manure pits. When the quantitative TRFLP data were analyzed, four peaks were found in greater ($P < 0.05$) quantity in foaming pits and twelve TRFs were found in greater ($P < 0.05$) quantity in non-foaming pits. The comparison of the TRF profiles generated by all four enzymes from the quantitative analysis suggested that eight unique OTUs differed between foaming and non-foaming swine manure pits. The analysis of both the binary and quantitative TRFLP data illustrates that there are different microbial communities present in foaming pits and non-foaming pits, suggesting further evaluation of these microbial differences may explain the foaming phenomenon.

Key Words: swine, manure, microbiota

W357 Effects of supplementing piglets post-weaning with an oral rehydration solution or lactic acid on growth and performance. L. Seefeldt*, S. I. Kehoe, and G. Onan, *University of Wisconsin, River Falls*.

According to a survey performed in 2000, 2.4% of piglets die before exiting the nursery stage. Of those, 12.6% are due to diarrhea and 13.3% are due to starvation (USDA, 2000). The objective of the first trial was to evaluate the effects of adding an oral rehydration solution (ORS; Tech-Mix Bluelite Swine Formula) to the drinking water (all water sources were well water) of newly weaned piglets (17-21 d of age) on gain and performance. The objective of the second trial was to evaluate whether lowering pH of the drinking water would have any effects on gain and performance. For experiment 1, a randomized complete block design consisted of a treatment of water (W; n=98 piglets) and added oral rehydration solution (ORS; n=111 piglets). For experiment 2, the same design was used with a third treatment using lactic acid (LA; n=55 piglets). The ORS groups were administered the ORS product at labeled rates through their water supply for the first 5 days post-weaning. For each trial, litters were initially sorted at weaning and placed into one of six tubs or one of two floor pens. Piglets were weighed every 2 days for week one and weekly thereafter for the next 3 weeks. Hematocrits, glucose, bodyweights, drinking water and behavior were recorded every 2 days for the first week. Feed intake and body weights were recorded weekly throughout the trial. The Mixed procedure of SAS 9.1 was used with pen as the experimental unit and housing as a covariate. For experiment 1, there were no significant differences in gain per piglet (W:284.86g/d and ORS:299.5g/d), feed intake (W:100.9kg and ORS: 114.3kg), water intake (W:195.8L and ORS:110.9L), or blood parameters. For experiment 2, means of water pH at the nipple were 4.5 which were similar to ORS treatment. There were no significant differences in gain per piglet (W:284.86g/d, ORS:299.5g/d and LA:307.54g/d), feed intake (W:101.1kg, ORS:114.7kg and LA:121.6kg), water intake (W:105.7L, ORS:179.5L and LA:133.2L), or blood parameters. This research concludes that supplementation with ORS or lactic acid for the first 5 days post weaning results in little benefit.

Key Words: piglets, oral rehydration, weaning

W358 Comparison of growth performance for pigs raised indoor and outdoor. T. White*, I. Martinez, T. Barrios, and S.-H. Oh, *Department of Animal Sciences, North Carolina Agricultural & Technical State University, Greensboro*.

Monitoring the growth patterns of pigs raised in alternative and conventional systems is important in understanding their physiological characteristics and performance. Studies comparing alternative and conventional pig systems have been variable and further studies comparing specific breeds have been limited. Two trials were conducted to compare the feed efficiency and growth output between Landrace and Yorkshire pigs raised under conventional confinement and pasture grazing systems post-weaning. Eight weight measurements were collected in Trial 1 comparable to six weight measurements collected in Trial 2 with each trial lasting 36-days. Custom grow-out feed was weighed and distributed ab libitum to calculate feed intake. In Trial 1, a significant difference for feed efficiency between the indoor (0.429) and outdoor (0.553) environments was determined via analysis with Duncan's test. Only mean weights of 21.40 kg and 16.94 kg were significant between indoor and outdoor systems during the second measurement out of 36-days. In Trial 2, Duncan's tests revealed no significant differences for mean weight between breeds, gender, and production system for any of the measurement intervals. There was however, a significant difference in mean weight gain ranging between four litters measuring 19.19, 17.72, 15.45, and 12.44 kg. MANOVA observed an interaction ($P<.0001$) for breed and the number of days allotted for growth effect throughout the 36-day period. The results of this study suggest that breed selection and the amount of days designated for rearing in certain systems are key in determining positive outcomes for optimal growth performance. Further research in this area may help small farm producers decide the optimal time to move pigs out to pasture systems following post-weaning.

Key Words: outdoor, growth, pig

Animal Behavior and Well-Being: Behavior-Nutrition Interaction

504 Behavior-nutrition interaction in goats. A. L. Goetsch*[1], T. A. Gipson[1], and A. R. Askar[2], [1]*American Institute for Goat Research, Langston University, Langston, OK*, [2]*Animal and Poultry Nutrition Department, Desert Research Center, Cairo, Egypt*.

Factors influencing feeding behaviors of goats include grazing management practices, type of vegetation and season, breed and stage of production, group size, and properties of diets fed in confinement. Considerable information has been gathered from methods such as visual observation during daylight. However, there are now tools available to characterize feeding behavior of goats while grazing and in confinement throughout 24-h periods. Global positioning system collars with motion/position sensors can be used to assess horizontal and vertical distances traveled, up/down position of the head, and movement within pasture/rangeland areas. A commercially available leg activity monitor allows estimation of the number of steps and time spent standing, lying, and moving rapidly without grazing. However, these measurements do not directly determine grazing. Therefore, prediction equations based on visual observation must be developed. Classification tree analysis is a robust method in developing these equations because the decision tree can be pruned or expanded to provide the best fit. Another equipment system is based on patterns of jaw movement to determine time spent eating, ruminating, and idle, although in some instances differentiation between eating and ruminating is subjective. In addition to use of n-alkanes as internal markers to estimate digestibility, their profile can provide an indication of botanical composition of the selected diet. Automated feeding systems for confined goats permit determinations such as number of feeder visits and meals, eating time, and rate and pattern of feed intake. Heart rate measured while goats are in normal production settings can be used to predict total energy expenditure through multiplication by energy expenditure per heart beat of individual animals. To partition the activity energy cost, an estimate of ME intake or measures of change in body energy status and milk energy yield are needed to determine other sources of heat to be subtracted from total energy expenditure. These methods create opportunity to gain a fuller understanding of factors influencing feeding behaviors of goats and their relationships with levels and efficiencies of production.

Key Words: goat, feeding behavior, activity

505 Selection of tannins by sheep in response to gastro-intestinal nematode infections. J. J. Villalba*[1], F.D. Provenza[1], J.O. Hall[2], and L.D. Lisonbee[1], [1]*Utah State University, Department of Wildland Resources, Logan*, [2]*Utah State University, Department of Animal, Dairy and Veterinary Sciences, Logan*.

Herbivores select compounds that attenuate the aversive effects of plant secondary metabolites (PSM), but can they learn to increase intake of PSM with medicinal effects when experiencing illness? We hypothesized that herbivores learn to increase intake of PSM-containing foods to combat gastrointestinal parasites. In Exp. 1, four groups of lambs (n=8 lambs/group) were assigned to a 2 x 2 factorial design with parasitic burden (parasitized or not parasitized) and supplemental tannins (yes, no) as the main factors. Parasitized (P) lambs ate more of the tannin-containing food than non-parasitized (NP) lambs (1.4 vs. 0.5 g/Kg $BW^{0.75}$; SEM= 0.2; P = 0.01) for the first 12 d of the study, when fecal egg counts (FEC) were high (234 eggs/g), but differences became smaller and disappeared toward the end of the study when parasite burdens decreased (P = 0.58). In Exp. 2, 10 lambs with natural gastrointestinal parasitic burdens (P) and 10 non-parasitized lambs (NP) were offered a choice of alfalfa and alfalfa mixed with 10% of quebracho tannin (alfalfa:tannin) before and after they were conditioned with the postingestive effects of tannins in a split-plot design. When tested with a parasite burden, lambs in P consumed more (14 vs. 10 g/Kg $BW^{0.75}$; SEM= 1.8; P = 0.07), showed greater preference (22 vs. 13%; SEM= 2.9; P = 0.05) for alfalfa:tannin, and consumed less alfalfa (53 vs. 65 g/Kg $BW^{0.75}$; SEM= 4.8; P = 0.06) than lambs in NP. Preference for alfalfa:tannin did not differ between groups before conditioning, or when parasite loads were terminated due to the administration of ivermectin (P > 0.1). Ingestion of tannins by lambs in P reduced FEC and a direct proportional relationship was observed between preference for alfalfa:tannin and FEC (P = 0.07). Thus, parasitized lambs modified their selection and intake of tannins when they experienced a parasite burden. These results suggest herbivores can self-medicate with potentially toxic compounds. Self-selection of PSM has implications in the quest for alternatives to chemoprophylaxis in the treatment and well-being of wild and domestic animals grazing in pasturelands and in confinement.

Key Words: helminthes, diet selection, plant secondary metabolites

506 Feed volatile compounds affect lambs and ewes palatability. T. Rapisarda[1], A. Mereu[2], A. Cannas[2], V. Giovanetti[3], S. Carpino*[1], and G. Licitra[1,4], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*Dipartimento di Scienze Zootecniche, University of Sassari, Italy*, [3]*Agris Sardegna, DRPA, Olmedo, Italy*, [4]*D.A.C.P.A. University of Catania, Italy*.

Aroma characteristics of feeds can affect their palatability in ruminants. The aim of this research was to correlate the palatability of several feeds used for ruminants with their aromatic profile. Fourteen feeds (soybean meal 44, soybean meal 49, soybean hulls, corn grains, canola meal, wheat grains, beet pulps, sunflower meal, oat grains, pea grains, wheat brans, corn middlings, corn gluten meal and dehydrated alfalfa) were subjected to 6-min palatability tests by using 14 Sarda lambs and 14 Sarda dry ewes in two trials, following 14 (days) x 14 (feeds) Latin square designs. Before the experiments started, the animals went through a training period of two weeks. In the palatability test, the animals were fed a basal diet and were exposed to only one feed per day. The 14 feeds were analyzed by gas chromatography olfactometry and MS for aroma profile and to identify chemical families associated with animal's intake responses. Both sheep and ewes had high intakes of wheat grains, pea grains, corn grains, and beet pulps, probably because of the many pleasant odour compounds present in these feeds. On the other side, both lambs and ewes refused canola meal, dehydrated alfalfa, sunflower meal and oat grains. Sulphur compounds may have influenced negatively the acceptability of dehydrated alfalfa and sunflower meal by lambs and ewes, and a terpene, α-pinene, likely affected negatively the palatability of oat grains. The presence of methanamine, which gives an off-flavour

of rotted fish odour, in sunflower meal and soybean meal 44 probably determined the almost total refusal of the former by both lambs and ewes and the low palatability of the latter in lambs. These results showed that the aroma of several feeds affected animal short-term intake responses. However, more research is needed to better understand the specific compounds and the mechanism underlying feed palatability.

Key Words: palatability, volatile compounds, sheep

507 Behavior-nutrition interactions in horses. D. Sigler*, *Department of Animal Science, Texas A&M University*, *College Station*.

Domesticated horses sometimes develop abnormal behavioral patterns not observed in feral horses. This has led to undesirable vices, digestive problems and other management issues for horse owners. Imposed stressful environmental conditions also lead to numerous health and nutritional maladies in the domesticated horse. Research has been reported on factors which influence feed intake, feeding behavior and digestion. Recently, much attention has been given to management of digestive abnormalities attributable to behavior and high stress environments. Equine Gastric Ulcer Syndrome (EGUS) is a prevalent condition affecting horses across multiple equestrian disciplines, from racehorses to recreational show horses. Estimates of occurrence range from 40% to 90% of horses, with various stress and management factors being implicated as contributors to ulceration. As EGUS can be detrimental to normal behavior and athletic performance, pharmaceuticals have been employed for the treatment and prevention of ulcers. However, these products are expensive, thus prompting investigation into alternative solutions. Research evaluating the effect of diet on ulceration has found significant relationships between diet and the incidence and severity of EGUS. Specifically, hay type appears to play a role in the severity of EGUS with alfalfa hay causing a reduction in the severity of ulcers when compared to grass hay. In a recent study, EGUS severity scores were reduced in yearlings fed alfalfa hay vs. grass hay. The causative mechanism by which this happens is still unknown. Research which attempts to isolate favorable factors contained in alfalfa hay is ongoing. Other nutritional considerations which also may affect EGUS are protein, mineral levels, concentrate amount and feed forms. Any environmental and behavioral changes which may increase stress also negatively affect EGUS. Researchers should continue to look for management techniques which effectively reduce stress and improve the health and well-being of domesticated horses.

Key Words: equine, nutrition, behavior

508 Effects of Protimax® and Betaine feed supplements on activity in dairy calves. S. C. Tutt*, G. Holub, T. H. Friend, S. M. Garey, and J. E. Sawyer, *Texas A&M University*, *College Station*.

Dairy calves are often housed in hutches with limited interaction or exercise for up to 8-wk. The objective of this research was to determine the ontogeny of motivation of dairy calves to exercise as they aged from 5-d to 8-wk when housed in hutches and fed different supplements. Forty-four Holstein calves where randomly assigned to four treatment groups: Protimax® supplement (n = 11), Betaine supplement (n = 10), no supplementation (n = 11), and Protimax® and Betaine supplements (n = 12). Recommended feeding of Protimax® is up to 3-wk, at which time Protimax® was discontinued. Calves where housed in hutches with a 2-m x 1.2-m yard and turned loose together for one 2.5-hr period every 7-d. Calves were fitted with pedometers and the percentage of calves that were active, standing, and lying was recorded at 15-min intervals when loose. Recorded steps, analyzed by repeated measures with calf as the subject in an autoregressive covariance structure, increased during the 8-wk study, from a mean of 1,589 steps in wk 1 to 2,763 in wk 8 ($P < 0.001$). There were no week by treatment interactions, but treatment significantly influenced steps ($P = 0.028$). Calves that were not fed supplement took the most steps, averaging 2,367 steps, while calves given Protimax® averaged 2,243, Betaine 1,961, and both supplements 2,082. To help determine ontogeny, the sum of the percentage of animals lying, standing, and active was multiplied by -1, .5, and 1 respectively, and used as a weekly activity score. Activity scores increased linearly ($\hat{y} = -0.087 + 0.037x$) over the 8-wk period ($P < 0.01$), from -15.5% to 18.4% for wk 1 and 8 respectively. These results suggest that calves' activity consistently increases with age through 8-wk. Assuming steps taken is an indirect measure of health, the supplements did not significantly improve health. Additional research is needed to determine if turning calves loose at regular intervals is useful in improving well-being in production.

Key Words: calves, supplement, activity

509 Effect of feeding method on the learning of feeding behavior in dairy heifers. A. M. Greter*[1], K. E. Leslie[2], G. J. Mason[3], B. W. McBride[3], and T. J. DeVries[1], [1]*Department of Animal and Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, ON, Canada*, [2]*Department of Population Medicine, Ontario Veterinary College*, *Guelph, ON, Canada*, [3]*Department of Animal and Poultry Science, University of Guelph*, *Guelph, ON, Canada*.

Dietary habits of ruminants are affected by learning early in life. The objective of this study was to determine if long-term exposure to different feeding methods influences the feeding behavior of growing dairy heifers when they are switched to a novel TMR. Thirty-two Holstein heifers (237.2 ± 21.9 d of age; mean ± SD), divided into 8 groups of 4, were exposed for 13 weeks to 1 of 2 treatments: 1) TMR or 2) top-dressed ration (TDR), each containing 65% grass/alfalfa haylage and 35% textured concentrate (DM basis). All heifers were switched to a novel TMR containing 56.1% grass/alfalfa haylage, 21.0% corn silage, 21.0% high moisture corn, and 1.9% mineral supplement (DM basis) for 7 weeks. Group DMI was recorded daily. Feeding behavior was recorded using time-lapse video for 7 d during weeks 1, 4, and 7. Fresh feed and orts were sampled each day of the recording weeks and subjected to particle size analysis. The particle separator contained 3 screens (19, 8, and 1.18 mm) and a bottom pan, resulting in 4 fractions (long, medium, short, and fine). Sorting activity for each fraction was calculated as the actual intake expressed as a % of the predicted intake. To determine if sorting occurred, each fraction was tested for a difference from 100% using t-tests. Effect of treatment was tested using a general linear mixed model with repeated measures. Animals were fecal scored for stool consistency twice weekly using a scale from 1 (liquid) to 4 (normal). Neither DMI (9.2 kg/d) nor ADG (1.0 kg/d) differed between treatments. Sorting also did not differ between treatments. Daily feeding time tended to be higher for the TDR (198.8 vs. 186.8 min/d; SE=4.2; P=0.09). As done prior to the dietary change, TDR heifers spent more time at the bunk in the 2 h after feed delivery (40.6 vs. 25.9 min/d; SE=3.8, P=0.03). Fecal scores were lower for heifers originally fed the TDR (3.2 vs. 3.7; SE=0.1; P=0.02). The continued difference in feeding time suggests that TDR heifers retained this behavior when switched to a novel diet. Furthermore, lower fecal scores for TDR heifers indicate altered rumen fermentation, possibly due to altered diurnal consumption patterns.

Key Words: heifers, feeding behavior, learning

ASAS Graduate Student Symposium: Decisions, Decisions, Decisions. How to make informed decisions on your future career opportunities to developing a successful research program.

510 Extension employment opportunities following the completion of a M.S. degree in animal science. G. P. Lardy*, *North Dakota State University, Fargo*.

The Extension Service continues to undergo change as many land grant universities face budgetary shortfalls and smaller numbers of people are employed in production agriculture. But rather than viewing this as a reason not to pursue an M.S. degree, it should be viewed as an opportunity for students interested in extension work. Livestock producers continue to require expertise which will help them improve efficiency of production, reduce or eliminate costs, and remain financially competitive in a business environment which is increasingly demanding additional technical competence in a wide variety of disciplines. This is driven, in part, by regulatory agencies at the federal and state level, customers, suppliers (e.g. processors), and service providers (e.g. lending institutions). Producers need additional expertise to ensure production systems are not only technically and financially sound, but also meet consumer standards for a wide variety of traits and/or expectations related to production practices (e.g. animal welfare, humane handling). Students seeking employment as regional extension educators or county extension personnel must have an appreciation for how to apply technical expertise at the farm or ranch level. They must also possess the following skills (either through life experiences or training): knowledge of animal husbandry techniques, written and oral communication skills, and an ability to interpret technical data and create useful information. The greatest challenge for students in the future may be identifying meaningful ways of gaining "on-farm" experiences if they did not grow up on a farm or ranch. Students expressing an interest in extension-related careers should be encouraged and mentored. Animal science departments should also consider additional ways to work within the Extension Service in their state to provide meaningful internship opportunities for M.S. students interested in extension careers. In the future, as more explore regionalizing extension programs, there will likely be increasing opportunities for M.S. level personnel not afraid to get manure on their boots!

Key Words: extension service, M.S. degree, job opportunities

511 Career opportunities in the animal science industry for graduate students. W. J. Platter*, *Elanco Animal Health*.

Dramatic changes in animal agriculture during the first decade of the new millennium, including the trends of consolidation, globalization and increased market volatility, have raised the competition for positions within the industry. However in recent years, companies have recognized a need for employees with a higher level of critical-thinking capacity, an enhanced understanding of data interpretation and a greater degree of scientific and technical training. The increased technical nature of the business has created more job opportunities for graduate students in the areas of sales and marketing, quality assurance, technical service and research. For those students with an interest in applied industry jobs, a multi-disciplinary understanding of key scientific areas related to animal production, an increased level of business acumen and a general understanding of practical applications of science in production settings are vital. The influx of biotechnology and molecular biology in animal agriculture has increased the need for employees in research and development positions with these areas of expertise. Leveraging the knowledge and skills gained during graduate school will increase the rate in which new employees learn and advance in their careers. Regardless of the area or position within the animal agricultural industry, those students with an entrepreneurial spirit and the motivation to continuously learn throughout their career will be of most interest to employers.

Key Words: animal science, careers, graduate education

512 Unique and non-traditional opportunities with an advance degree in animal science. J. L. Garrett*, *JG Consulting Services, Dowling, MI*.

Traditional animal science degree programs include farm and companion animal applications in biosciences, veterinary sciences, nutrition, health, reproduction, metabolomics and genomics. Non-traditional career opportunities for animal scientists commonly include the same areas of scientific application, but for the benefit of humans rather than animals. Both traditional and non-traditional employers wish to hire people to solve their work problems, so that the employer's short-term financial needs and long-term vision are pursued. Since problem solving is a primary interest and skill for most animal scientists, employers from industry, academia, government and non-profits have positions, traditional and non-traditional, for animal scientists. In today's global environment, animal scientists with advanced degrees who are interested in pursuing non-traditional opportunities must invest in an honest assessment of their abilities, interests, knowledge, skills and work styles (AIKSW), and understand their strengths and weaknesses in these areas. Beyond a resume or curriculum vita, development of an effective Personal Marketing Plan (PMP) will help animal scientists proactively sell their strengths to non-traditional employers, and may help employers determine potential fit more quickly and accurately. In this session, a brief discussion of determining AIKSW and developing an effective PMP will be reviewed, along with examples of where animal scientists are currently employed in unique and non-traditional roles.

Key Words: career development, non-traditional careers, animal science careers

513 Should I go get a Ph.D. and if so, is a post-doc warranted? M. Hogberg*, *Iowa State University, Ames*.

Students face several decisions as they progress through their college days. As undergraduates, the question is often "Should I get a job or should I go on to graduate studies?". As graduate students approach finishing their M.S. degree, they again are faced with the question of whether to terminate their formal education or continue on in pursuit of a Ph.D. This paper will explore the reasons for pursuing a Ph.D. and also reasons not to pursue this terminal degree. Career goals and aspirations play a major role in this decision. At the conclusion of a Ph.D. students again have a choice to make as to whether to seek a post-doc position or look for employment. This paper will discuss the objectives of post-doctoral training and what students should consider in making this decision. The role of career goals and objectives will be reviewed and used as a guideline on pursuing this issue. Major objectives for post-doctoral training of expanding training as an independent researcher, expanding grant writing experiences and the opportunity for depth of training will be covered.

Key Words: graduate school, post-doctoral training

514 Developing a competitive research program and securing tenure as a new faculty hire. B. W. Hess*, *University of Wyoming*, *Laramie*.

Developing a competitive research program and securing tenure can be a daunting task for a new faculty hire. There is no special formula that suits all; however, the task may be less daunting if one considers several principles that are common among those who have trudged down the path leading to success. The following nouns are offered as examples of key elements to developing a competitive research program and securing tenure: Courage; Confidence; Compatibility; Consistency; Collaboration; Colleagues; and Commitment. Embarking on a career in academia certainly requires courage. A new faculty hire must face many new challenges and guard against being deflected from a major career hurdle. Building a research program that garners support hinges upon one's ability to convince those whom are in a position to make decisions that the program possesses the prowess required for success. The trick is to strike a balance between exuding sufficient confidence without exaggerating capabilities. Furthermore, it is critical to research topics that are compatible with one's training and interests. Focusing on strengths will naturally generate consistency and lead to the ability to maintain a research program. Although independent research is of utmost importance, collaboration with others may be necessary to realize a program's full potential. Colleagues can provide invaluable insight and lend expertise that enhances the program's competitive advantage. It is prudent to welcome the advice of those who have completed the journey successfully. Additionally, because procurement of funds to support a research program is inherently essential, commitment to pursuing all possible mechanisms of funding is critical. Presenting and publishing results also demonstrates commitment to establishing a reputation necessary to maintain a competitive research program and securing tenure. The level of commitment required to accomplish these goals supersedes the tangibles; a commitment to those who are engaged in the research is also required. Practicing some or all of the seven "Cs" may help a new faculty hire develop and maintain a competitive research program and attain tenure.

Key Words: research, tenure, success

Breeding and Genetics: Beef Cattle & Sheep Breeding

515 Genotype by region and season interactions for postweaning gain in beef cattle. J. L. Williams*[1], M. Lukaszewicz[1,2], I. Misztal[1], and J. K. Bertrand[1], [1]*University of Georgia*, *Athens*, [2]*Institute of Genetics and Animal Breeding, Polish Academy of Sciences*, *Jastrzebiec, Poland*.

The objective of this study was to determine if sires perform consistently across different environments and calving seasons in the US. Data and pedigree information were provided by the American Angus Association. A preliminary bivariate analysis containing yearling contemporary group as the sole fixed effect was conducted for postweaning gain in the Southeast (SE) and in the Northwest (NW) as these regions are perceived as opposite extremes in climate. In a second analysis, gains in these two regions were further divided based on season of birth (spring and fall) and fit in a four trait model with fixed effects as previously mentioned. Spring records included 6304 and 37129 observations in SE and NW, respectively. Fall records consisted of 38987 and 5800 observations in the SE and NW, respectively. Heritability estimates from the first analysis were 0.20 ± 0.01 and 0.27 ± 0.01 for gain in SE and NW, respectively. The genetic correlation between the two regions was 0.79 ± 0.02. Heritability estimates from the second analysis were 0.25 ± 0.04 and 0.18 ± 0.02 for spring and fall gain in SE and 0.26 ± 0.02 and 0.16 ± 0.03 for spring and fall gain in NW, respectively. Genetic correlations between NW and SE were 0.56 ± 0.15 and 0.76 ± 0.07 for spring and fall, respectively. Correlations between spring and fall were 0.85 ± 0.06 and 0.57 ± 0.11 for SE and NW, respectively. The genetic correlation between spring in NW and fall in SE was 0.58 ± 0.08 and that between fall in NW and spring in the SE was 0.44 ± 0.17. Sires may perform differently across both seasons and regions suggesting it may be better for producers to select bulls based on performance in the calving season utilized in their production region. Subsequent analyses will be performed on weaning weight to determine if strong selection at weaning is leading to low correlations in postweaning gain.

Key Words: Angus, genotype by environment, postweaning gain

516 Estimation of genetic parameters for mature weight in Angus cattle. R. B. Costa*[1], I. Misztal[1], J. K. Bertrand[1], and S. Northcut[2], [1]*University of Georgia*, *Athens*, [2]*American Angus Association*, *St. Joseph, MO*.

The objective of this study was to estimate genetic parameters for weight of up to 5 years in Angus and to investigate options for including mature weight (MW) as a trait in a genetic evaluation. Data were obtained from American Angus Association. Only female records in herds with at least 500 animals and with > 10% of animals with weights at ≥ 2 years were included. Traits in the analysis included weaning weight (WW, n=81,525), yearling weight (YW, n=62,721), and weights measured from 2 to 5 years of age (MW2, n=15,927, MW3, n=12,404, MW4, n=9,805, MW5, n=7,546). Genetic parameters were estimated using a multiple-trait animal model with fixed effects of contemporary group and linear effect of (actual age - standard age), both in days (205, 365, 730, 1,095, 1,460, and 1,825 for WW, YW, MW2, MW3, MW4, and MW5, respectively). The random effects were animal direct, maternal, and maternal permanent environment. Estimates of direct variances were 298, 563, 925, 1221, 1406, and 1402; maternal variances were 167, 153, 123, 136, 167, and 110; the variances of maternal permanent environment were 124, 120, 61, 69, 103, and 134; and residual variances were 258, 608, 829, 1016, 1017, and 1202 for WW, YW, MW2, MW3, MW4, and MW5, respectively. For the direct effect, the genetic correlation of WW and YW was 0.84 and of WW and MW ranged from 0.66 (WWxMW4) to 0.72 (WWxMW2). The genetic correlations of YW and MW ranged from 0.77 (YWxMW5) and 0.85 (YWxMW2). Among MW2, MW3, MW4, and MW5, the genetic correlations were ≥ 0.98. Correlations between maternal effects ranged from 0.52 (WWxMW4) and 0.95 (WWxYW). Regarding only MW, the correlation between maternal effects ranged from 0.54 (MW4xMW5) to 0.94 (MW2xMW3). Variability of maternal effects at MW may be an artifact due to low heritabilities and low number of records. A genetic evaluation for mature weight may include MW2, with weights at higher ages accommodated by variance adjustments to the scale of MW2.

Key Words: mature weight, growth, multiple-trait

517 Rate of maturing and proportion of mature body weight at puberty of crossbred cows. H. C. Freetly* and L. A. Kuehn, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Cows born (1999 – 2000) resulting from AI breeding Hereford (n = 58), Angus (n = 61), Red Angus (n = 70), Simmental (n = 74), Limousin (n = 80), Charolais (n = 74), or Gelbvieh (n = 78) bulls to Angus (A; n = 69), Hereford (H; n = 173), or MARC III composite (M; n = 253) cows were weighed 6 times as calves and then twice a year as cows through 7 years of age. Body condition scores (BCS; 1 through 9 scale) and BW were collected at the beginning of breeding and then again in 4 mo. Cow BW was standardized to a BCS of 6 by allowing ± 45 kg BW/BCS different than 6. Individual growth curves of BW on age (wk) were fit with the nonlinear function $f(\text{age}) = A - Be^{kxage}$ using the Gauss-Newton iterations to minimize error sum-of-squares. Proportion of mature weight reached at puberty (n = 459) was solved for age at puberty with $f(\text{age}) = 1 - (B/A)e^{kxage}$. Sire and dam breed effects were tested with a model including sire breed (S), dam breed (D), birth year (Y), S x D, S x Y, and D x Y. Sire nested within S, was treated as a random effect. There was no S x D interaction for k ($P = 0.49$), B/A ($P = 0.21$), and maturity at puberty ($P = 0.61$). Main effects for S differed for k ($P = 0.01$), B/A ($P = 0.04$), and tended to differ for maturity at puberty ($P = 0.09$). Main effects for D differed for k ($P < 0.001$; H -0.01308 ± 0.00024, A -0.01426 ± 0.00015, M -0.01365 ± 0.00013), and for maturity at puberty ($P < 0.001$; H 0.523 ± 0.007, A 0.542 ± 0.004, M 0.523 ± 0.003), but not for B/A ($P = 0.88$). There were S x Y ($P = 0.005$), and D x Y ($P = 0.02$) interactions for k, and S x Y ($P = 0.006$), and D x Y ($P = 0.02$) interactions for B/A.

Table 1. Sire breed means and standard errors

Breed	k	B/A	Maturity at puberty
Hereford	-0.01244 ± 0.00034	0.9135 ± 0.0035	0.508 ± 0.011
Angus	-0.01382 ± 0.00029	0.9123 ± 0.0030	0.529 ± 0.007
Red Angus	-0.01397 ± 0.00030	0.9075 ± 0.0031	0.532 ± 0.008
Simmental	-0.01396 ± 0.00030	0.9099 ± 0.0031	0.532 ± 0.008
Limousin	-0.01362 ± 0.00027	0.9178 ± 0.0027	0.545 ± 0.007
Charolais	-0.01393 ± 0.00027	0.9200 ± 0.0027	0.538 ± 0.007
Gelbvieh	-0.01390 ± 0.00027	0.9132 ± 0.0028	0.521 ± 0.007

Key Words: cow, maturity, puberty

518 Breed comparison of post partum ovarian activity in cows. C. Disenhaus*[1], E. Cutullic[1], F. Blanc[2], and J. Agabriel[3], [1]*INRA UMR1080 Dairy Production, Rennes, France*, [2]*ENITAC, Lempdes, France*, [3]*INRA UR1213 Unité de recherches sur les herbivores, Saint-Genès-Champagnelle France.*

Recent references about postpartum ovarian activity are available only in Holstein cows. The aim of the study is to compare post partum (pp) ovarian activity in Charolaise (beef, CH), Normande (dual purpose, NO) and Holstein (dairy, H) cows. A data set including 367 progesterone profiles established between 2006 and 2008 was used (CH: N=125; NO: N=106; H: N=136). Twice a day, cows were or milked (NO and H) or suckled (CH). The onset of luteal activity (C-LA), length of normal estrous cycles and characterization of the pp activity were determined. Breed and parity effects were analyzed. The resumption of ovarian activity was slower in CH breed than in others (Table 1; P<0.01). At 50 days pp, more H than NO cows (P<0.05) were still inactive. In all breeds, C-LA 50d were lower for primiparous cows than for multiparous (CH: 50% vs.74%: P< 0.01; NO: 84% vs.100%; P<0.05; H: 70% vs. 84%; P<0.01). Once estrous cycles have been established, CH cows showed good further cyclic activity without any abnormal cycles. In agreement with the literature, the main cycle abnormality was prolonged luteal phase (PLP). 23% of H-cows showed PLP vs. 8% of NO cows (P<0.01). Duration of cycles seemed to be related to breed milk potential. Normal cycles were longer for H than for NO cows (22.6 ± 2.3 vs. 21.4 ± 2.1 days, N= 136 and 155; P<0.001) with a median value of 23 vs. 21 days. Cycles were shorter for CH than for NO cows (20.2 ± 2.2 vs. 21.4 ± 2.1days, N=77 and 155; P<0.05) with the same 21 days median value. In conclusion, pp ovarian activity impairment seems to explain partially poor reproductive performances in H breed.

Table 1. Breed effect on resumption of ovarian activity: cumulative percentage of cows which have achieved C-LA at 30 day pp (C-LA 30d) or 50 day pp (C-LA 50d).

Breed*	N	C-LA 30d (%)	C-LA 50d(%)
CH	125	32[a]	68[a]
NO	106	63[b]	92[b]
H	136	57[b]	79[c]

*Values within column with different superscripts differ significantly (a≠b, b≠c, P< 0.01; a≠c, P<0.05)

Key Words: ovarian activity, cows, breed

519 Prediction of wool fibre diameter from protein and metabolisable energy digestibility coefficients in crossbred sheep. A. E. O. Malau-Aduli*, R. E. Walker, and W. C. Bignell, *University of Tasmania, Hobart, Tasmania 7001, Australia.*

Our objective in this study was to investigate the interactions between sire breed and supplement on digestibility and to ascertain its accuracy in predicting wool fibre diameter. Forty first-cross Merino weaner sheep sired by Texel, Coopworth, White Suffolk, East-Friesian and Dorset sires with initial BW range of 22.9 and 31.3 kg (average of 26.8 ± 3.2 kg) were randomly assigned to four treatment groups in a 5 × 2 × 2 × 2 factorial experimental design representing 5 sire breeds, 2 supplementary feeds (canola and lupins), 2 feeding levels (1 and 2% of bodyweight) and 2 sexes (ewes and wethers). The feeding trial lasted for six weeks with an initial 3-week adjustment period and the last 7 days for faecal collection. Factorial ANOVA with orthogonal contrasts in SAS was used for statistical analysis to test for the interactions between sire breed and supplement on digestibility and wool fibre diameter. Our results demonstrated that sire breed × level of feeding interactions significantly influenced digestibility (P<0.01) whereby Coopworth-sired sheep supplemented at 1% of their body weight recorded the highest ME and N digestibility of 54% and 67% compared to 42% and 62% respectively, in their counterparts fed at 2% of body weight. There was a highly significant (P<0.01) effect of type of supplement x level of feeding interaction on wool fibre diameter at the end of the trial because sheep fed canola supplements at 1% of body weight had finer wool (22.1 microns) than their 2%-fed counterparts (25.4 microns). Regression of wool fibre diameter on digestibility revealed very poor prediction accuracy (R^2 = 0.0087-0.169). We concluded that sire breed variation in digestibility is unlikely to be a useful predictor of genetic merit for wool fibre diameter in first cross sheep under the same management.

Key Words: digestibility, wool, fibre diameter

520 Wool quality and growth traits of Tasmanian pasture-fed crossbred lambs and relationships with plasma metabolites. A. E. O. Malau-Aduli*, C. F. Ranson, and C. W. Bignell, *University of Tasmania, Hobart, Tasmania 7001, Australia.*

Wool quality, growth and plasma metabolite traits of 500 F_1 progeny from Merino dams sired by 5 ram breeds were investigated to study the influences of sire breed, sex and their interactions with plasma metabolites aimed at dual-purpose crossbreeding options. Coopworth, Texel and White Suffolk sired progeny had significantly ($P<0.05$) heavier weaning weights (WWT) and average daily gains (ADG) than those sired by Dorset or East-Friesian rams. Coopworth-sired sheep had the highest WWT (31.3±1.7Kg) and East-Friesian sired sheep the lowest (22.9±3.1Kg) with ADG ranging from 0.15kg/day in East-Friesian to 0.23 Kg/day in Texel and White Suffolk sire breeds. Highly significant ($P<0.01$) sex by sire breed interaction were evident; Coopworth-sired ewe lambs had the highest WWT and ADG (34Kg, 0.27 Kg/day) and Dorset-sired ewe lambs the least (22kg, 0.15 Kg/day). Greasy fleece weight ranged from a minimum of 964g to a maximum of 1303g in Dorset and Coopworth-sired lambs respectively, with Coopworth and Texel sire breeds having significantly heavier ($P<0.05$) fleece weights than either Dorset, White Suffolk or East-Friesian. Texel-sired sheep had significantly larger ($P<0.05$) micron fibre diameter (23.4μm) than the 21μm recorded in White Suffolks and East-Friesians. There were also highly significant differences ($P<0.01$) between sire breeds in staple length (range 50-68mm) and staple strength (range 39-52Nktex), with males having finer fibre diameter (21 vs 23μm) and shorter staple length (55 vs 60mm). Regardless of sire breed or gender, blood plasma metabolites were well within the normal range. A strong, positive and significant phenotypic correlation of 0.72 existed between marking and weaning weights. There were no significant correlations between the wool quality and growth traits, essentially implying that producers can select for finer wool without compromising growth. Coopworth x Merino first cross was the overall best performing sheep breed studied because of its heavier liveweight, faster daily gain, heavy fleece weight and a comparatively lower micron fibre diameter than the other crossbreds.

Key Words: Tasmanian crossbreds, wool quality, plasma metabolites

521 Bayesian estimation of genetic parameters for body weight traits and litter size of Moghani sheep using Gibbs sampling. N. Ghavi Hossein-Zadeh*[1,2], [1]*University of Tehran, Karaj, Iran*, [2]*University of Guilan, Rasht, Iran*.

The objective of the present study was to estimate genetic parameters for body weights at different ages and litter size in Moghani sheep. Traits were included birth weight (BW), 3 months weight (3MW), 6 months weight (6MW), 9 months weight (9MW), yearling weight (YW) and litter size (LS). Data and pedigree information used in this research were collected at Breeding Station of Moghani sheep (Ardebil, Iran) during 1987–2005. Linear and threshold animal models with additive genetic, maternal genetic, maternal permanent environmental and residual effects were implemented by Gibbs sampling methodology. A single Gibbs sampling with 100,000 rounds was generated by the MTGSAM program. The posterior means of genetic parameters were estimated based on the 900 samples that were left after elimination of 10,000 rounds in the burn-in period and 100 rounds of each thinning interval. Posterior means of direct heritability estimates for BW, 3MW, 6MW, 9MW, YW and LS were 0.29, 0.13, 0.14, 0.10, 0.31 and 0.10, respectively. Posterior mean estimates of maternal heritabilities were 0.29 for BW, 0.08 for 3MW, 0.11 for 6MW, 0.06 for 9MW, 0.10 for YW and 0.17 for LS. All the posterior mean of phenotypic correlation estimates among body weight traits at different ages were positive and changed from 0.08 to 0.68. But, the estimates of phenotypic correlations between litter size and body weights were negative and ranged from -0.69 to -0.08. A moderate negative direct genetic correlation has been estimated for 9MW-YW, but the estimates of direct genetic correlation between other body weight traits were positive and ranged from 0.08 to 0.88. But, there were negative medium to high direct genetic correlations between body weights at different ages and litter size, ranging from -0.92 to -0.28. Thus, selection for increased growth or LS may have a negative genetic effect on the other trait. The medium to high negative estimates of direct-maternal correlations for body weight traits or litter size suggest that it would be difficult to jointly improve direct and maternal growth ability for Moghani sheep.

Key Words: Bayesian inference, Moghani sheep, body weight

Dairy Foods: Dairy Foods/Microbiology

522 Molecular and technological characterization of lactic acid bacteria isolated from the Egyptian white pickled cheese. M. El Soda*, M. Mohammed, S. Anwar, and S. Awad, *Department of Dairy Science, Faculty of Agriculture, Alexandriau University, Alexandria, Egypt*.

Egyptian white pickled cheese samples were collected from different areas in Egypt. One hundred isolates obtained from the cheese samples were identified using repetitive genomic element-PCR (Rep-PCR) fingerprinting. The identified isolates were tested for efficiency of biomass production and separation, acidifying activity, autolytic, aminopeptidase and antagonistic activities and exopolysaccharide production. The obtained results revealed that *Enterococcus faecium*, *Enterococcus faecalis*, *Lactobacillus paracasei* subsp. *paracasei*, *Lactobacillus plantarum* and *Lactobacillus delbrueckii* subsp. *lactis* were the predominant species in Egyptian white pickled cheese. Fifteen percent of *Lactobacillus* and 2% of *Enterococcus* isolates showed fast acidifying activity. Aminopeptidase and autolytic properties were generally higher for *Lactobacillus* strains when compared to the enterococci. Among the lactobacilli, *Lactobacillus paracasei* subsp. *paracasei* was the highest in aminopeptidase activity and autolytic properties. Antagonistic activity was detected in 70% of *Lactobacillus* and 30% of *Enterococcus* isolates. Two strains of *Lactobacillus paracasei* subsp. *paracasei* and one of *Lactobacillus plantarum* were capable of producing exopolysaccharides in milk.

Key Words: Rep-PCR, Egyptian white pickled cheese, lactic acid bacteria

523 Physiological and transcriptional response of *Lactobacillus casei* ATCC 334 to acid stress. R. Thompson*[1], V. Deibel[2,3], J. Steele[2], and J. Broadbent[1], [1]*Utah State University, Logan*, [2]*University of Wisconsin, Madison*, [3]*TracMicro, Madison, WI.*

Lactobacillus casei is used as a starter culture in fermented foods, as a probiotic, and in the industrial production of lactic acid. *Lb. casei* produces lactic acid as a major end product of carbohydrate fermentation, which acidifies the environment. Cell survival in acidic environments is critical to industrial application of *Lb. casei*, so a fundamental knowledge of cellular physiology during acid stress may reveal strategies to enhance its industrial performance. Here, we investigated the effect of acid adaptation of *Lb. casei* ATCC 334 on viability during acid chal-

lenge at pH 2.0, cytoplasmic membrane fatty acid (CMFA) composition, and cellular transcriptome using microarray technology. Experiments investigating the effect of acid adaptation at several pH values (range=pH 3.0-5.0) on viability of *Lb. casei* at pH 2.0 indicated that some degree of acid tolerance was induced over a broad range in pH, but the highest survival was noted in cells that were acid adapted for 10 min at pH 4.5. Fatty acid (FA) methyl esters of CMFAs were prepared, separated and quantified by gas chromatography. The ratio of saturated:unsaturated FAs increased from 0.4 in non-adapted control cells to 4.3 and 5.3 after 10 and 20 min of acid adaptation (AA), respectively. The level of cyclopropane FAs increased from 5% in the control to 17 and 18% after 10 and 20 min of AA, respectively. Several differences were noted between the transcriptome of cells grown at pH 6.0 (control) to that from cells that were acid adapted for 5 min (AA1) or 20 min (AA2) at pH 4.5, or acid adapted for 20 min and acid shocked at pH 2.0 (AA-AS). For example, AA1 significantly ($P<0.05$) affected the expression of 15 genes, of which one (7%) was up-regulated. AA2 significantly affected 322 genes (of which 105 [33%] were up-regulated), while AA-AS significantly affected the expression of 66 genes (12 [19%] up-regulated). Real-time quantitative PCR (RT-PCR), an independent assay to confirm microarray data, was performed on ten selected genes. In general, the microarray results were validated by the RT -PCR data, and there was a positive correlation ($r = 0.89$) between the two methods.

Key Words: lactobacillus, acid shock, stress response

524 Genotyping for strain-level differentiation of *Bifidobacterium animalis* ssp. *lactis*. J. R. Loquasto*[1], E. P. Briczinski[2], A. M. Roberts[1], E. G. Dudley[1], R. Barrangou[3], and R. F. Roberts[1], [1]*Pennsylvania State University, State College*, [2]*University of Wisconsin, Madison*, [3]*Danisco USA Inc., Madison, WI.*

While numerous health benefits are attributed to probiotic organisms, these benefits are generally considered to be strain-specific. *Bifidobacterium animalis* ssp. *lactis* strains are widely used in dietary supplements and fermented and non-fermented dairy foods for their probiotic function. However, the high level of genetic homogeneity reported among *B. animalis* ssp. *lactis* used in commercial dairy products presents a challenge to differentiation using common phenotypic or DNA-based techniques. In an effort to differentiate *B. animalis* ssp. *lactis* isolates, 22 strains obtained from national culture collections (2) and commercial culture suppliers (20) were characterized using a variety of phenotypic and DNA-based methods (PFGE and RAPD-PCR). The only phenotypic difference observed was the inability of 10 strains to ferment glucose and only one strain (ATCC 27536) could be differentiated by PFGE after restriction with *Xba*I and *Spe*I. In an effort to locate genetic targets for strain-level differentiation, the genomes of *B. animalis* ssp. *lactis* DSMZ 10140 (the Type strain) and Bl-04 (a commercial strain) were sequenced and compared. Comparative analyses of the genomes revealed four insertion/deletion sites (for a total of 443 bp) and 47 single nucleotide polymorphisms (SNPs), confirming a high level of genetic relatedness. PCR primers designed to amplify the INDELs and regions containing each identified SNP were used to determine the allele in each of the 22 strains under study. To date, evaluation of two INDELs, one containing a portion of the CRISPR locus, and 15 SNP sites has identified 9 unique allelic types. To our knowledge, this represents the first SNP-based typing scheme for differentiating strains of *B. animalis* ssp. *lactis* and perhaps the first practical strain-level typing scheme for *B. animalis* ssp. *lactis*. This typing scheme will be useful to starter manufacturers, dairy products processors and clinical researchers who are interested in verifying strain identity for this subspecies.

Key Words: *Bifidobacterium animalis* ssp. *lactis*, SNP, probiotic

525 CpG oligodeoxynucleotide from *Streptococcus thermophilus* regulates anti-inflammatory responses. T. Shimosato*[1], M. Tohno[2], T. Sato[3], and H. Kitazawa[2], [1]*Shinshu University, Kamiina, Nagano, Japan*, [2]*Tohoku University, Sendai, Miyagi, Japan*, [3]*Yokohama City University, Yokohama, Kanagawa, Japan*.

Immunostimulatory sequence of oligodeoxynucleotides (ISS-ODNs) from lactic acid bacteria, such as CpG and AT ODNs, are recently found as potent stimulators of innate immunity (1-3). In this study, we identified a strong immunostimulatory CpG ODN, which we named MsST, from the *lac*Z gene of *Streptococcus thermophilus* ATCC19258, and we precisely evaluated its immune functions. In vitro studies revealed that MsST had a similar ability as the murine prototype CpG ODN 1555 to induce inflammatory cytokine production and lymphocyte mitogenicity. In mouse splenocytes, MsST increased the number of $CD80^+$ $CD11c^+$ and $CD86^+CD11c^+$ dendritic cells and $CD4^+CD25^+$ regulatory T cells. We also analyzed the effects of MsST on the expression of various cytokines by real-time quantitative PCR. MsST was more potent at inducing anti-inflammatory cytokines such as interleukin (IL)-10 and IL-33 expression after 48 h of stimulation, whereas IL-6 was down regulated. Together with recent findings, these results indicate that MsST may be a potential therapeutic ODN for inflammatory disease by secreting IL-10 and IL-33. In addition, *Streptococcus thermophilus*, which contains a strong ISS-ODN, may also be a good as a candidate starter culture for the development of new physiologically functional foods. 1. Shimosato T., et al., Anim Sci J. in press. 2. Shimosato T., *et al., Cellular Microbiol*.8(3):485-95.2006. 3. Shimosato T., *et al., Biochem Biophys Res Commun*. 326(4):782-7.2005.

Key Words: CpG ODN, *S. thermophilus*, IL-33

526 Survival of probiotic adjunct cultures added to low-fat, reduced-fat, and full fat cheddar cheese. C. J. Oberg*[1], L. Moyes[1], C. Brothersen[2], and D. J. McMahon[2], [1]*Microbiology Department, Weber State University, Ogden, UT*, [2]*Western Dairy Center, Utah State University, Logan*.

A variety of delivery systems are used to deliver probiotic bacteria such as yogurt and milk. Cheese may have benefits over other dairy delivery systems including greater in vivo survival, longer shelf life, and being a more common component in the average diet. Cheese was made at three different fat levels (33, 16, 6%) using *Lactococcus lactis* ssp. *lactis*. Commercial strains of *Lactobacillus acidophilus*, *Lactobacillus casei*, *Lactobacillus paracasei*, and *Bifidobacterium* were added as adjuncts. Selective media, designed to promote growth of certain lactic acid bacteria (LAB) over others, were used to detect individual LAB types during cheese storage. Microbial flora of the cheese was analyzed at 1, 30, 60, 90, 120, 180, and 270 d. Between 90 and 120 d of storage, bacterial counts changed on selective media for *Bifidobacterium* indicating NSLABs may be appearing. Differences in cheese chemistry, particularly the salt-in-moisture levels related to cheese fat levels appears to play a role in probiotic adjunct counts since NSLABs appear on *Lb. casei* selective media (MRS + vancomycin) after only 30 d in low fat control cheeses. In low fat cheese, one *Lb. acidophilus* adjunct was observable to 60 d while *Lb. casei* and *Lb. paracasei* maintained high counts through the entire storage period. In some cheeses, one *Lb. casei* adjunct had the ability to grow on both *Lb. casei* and *Bifidobacterium* selective agar. Since no *Bifidobacterium* had been added to these cheeses *Bifidobacterium* counts could be discarded. In all cheeses with added *Bifidobacterium*, counts decreased after 90 d of storage. In full fat cheese, *Lb. acidophilus* counts remained high to 120 d. For many cheeses, nonstarter LABs seemed to appear on a number

of the selective media during aging. Probiotic adjunct cultures can be detected in cheddar cheese out to 90-120 d when growth of nonstarter LABs obfuscates results on selective media. Some adjunct cultures can be detected beyond this time, particularly *Lb. casei* and *Lb. paracasei*. Results indicate selected probiotic adjuncts can survive for at least 90 d in low-fat, reduced-fat, and full fat Cheddar cheese.

Key Words: probiotic, cheese, lactic acid bacteria

527 Intrinsic resistance and stress responses to hydrogen peroxide in bifidobacteria. T. S. Oberg*[1], S. C. Ingham[2], J. L. Steele[2], and J. R. Broadbent[2], [1]*Utah State University*, *Logan*, [2]*University of Wisconsin*, *Madison*.

The interest and use of bifidobacteria as a probiotic in function foods has increased dramatically in recent years. Due to the anaerobic nature of bifidobacteria, however, oxidative stress can pose a major challenge to the viability of bifidobacteria during storage in functional foods. To better understand oxidative stress resistance in two industrially important species of bifidobacteria, we examined the response of three strains of *Bifidobacterium longum* and three strains of *Bifidobacterium animalis* subsp. *lactis* to hydrogen peroxide. Each strain was exposed to a range of hydrogen peroxide concentrations (0.1mM to 10mM) to evaluate and compare intrinsic resistance to H_2O_2. Next, strains were tested for the presence of an inducible oxidative stress response by 20 or 60 min exposure to a sublethal level of H_2O_2 followed by challenge at a lethal H_2O_2 concentration. Results showed *B. longum* subsp. *infantis* ATCC 15697 and *B. lactis* D2908 had the highest level of intrinsic H_2O_2 resistance among tested strains of *B. longum* and *B. lactis*, respectively. Inducible H_2O_2 resistance was only detected with two strains; *B. longum* NCC2705 showed a 17-fold increased survival in 5.25mM H_2O_2 after a 60 min induction in 1.25mM H_2O_2, and survival of *B. lactis* D2908 increased 2.5-fold in 5.25mM H_2O_2 after 20 min induction in 1.25mM H_2O_2. Other strains showed either no difference or increased sensitivity to H_2O_2 after induction treatments. These data indicate that intrinsic and inducible resistance to hydrogen peroxide is strain specific in *B. longum* and *B. lactis* and suggest that for some strains, sublethal H2O2 treatments could help increase cell resistance to oxidative damage in production and storage of probiotic foods.

Key Words: bifidobacteria, probiotic, oxidative stress

528 Cholesterol removing ability and bile tolerance of lactic acid bacteria isolated from fermented yak milk. Y. Jiao[1], L. Zhang*[2], and H. Yi[2], [1]*Heilongjiang University of Chinese Medicine*, *Harbin, China*, [2]*College of Food science and engineering, Harbin Institute of Technology*, *Harbin, China*.

Cholesterol assimilating ability and bile tolerance of 23 strains of lactic acid bacteria isolated from fermented yak milk of Gansu province were examined. All strains have varying capabilities to remove cholesterol in vitro. The ability of cholesterol assimilation of most of the strains in the media with oxgall was better than without. The heat killed strains assimilated less cholesterol than the normal ones. All types of bile salts could inhibit the growth of strains, the most powerful of which was sodium glycocholate, bile acid took the second place, oxgall was the weakest. There was no relationship between bile salts tolerance and cholesterol assimilation. Finally, it was found that the strains of H1, I10,and W2 acted better, indicating that these strains may be promising candidates for use as a dietary adjunct to lower serum cholesterol in vivo.

Key Words: fermented yak milk, lactobacillus, cholesterol removal

529 Factors affecting the total bacteria count of raw milk preserved with azidiol (liquid or tablet) and bronopol. M. O. Leite*[1,2], N. J. Andrade[3], M. M. O. P. Cerqueira[1,2], L. M. Fonseca[1,2], and R. Rodrigues[1,2], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis, UFMG*, *Belo Horizonte, MG, Brazil*, [3]*Federal University of Viçosa*, *Viçosa, MG, Brazil*.

The objective of the present work was to evaluate the influence of several parameters on the milk quality results of electronic analyses for total bacteria count (TBC), somatic cell count (SCC) and composition. The parameters were: storage time and temperature, azidiol (liquid and tablet), and bronopol. Six samples were collected, subdivided, added preservative and stored at room temperature for up to eight days, and incubated under three different temperatures (4, 7, and 10°C) for until ten days. An electronic equipment, Bentley CombiSystem 2300® was used for the composition and SCC analyses. The total bacterial counting (TBC) was analyzed using an electronic equipment Bactocount IBC (Bentley®) and standard plate counting for mesophilic aerobic microrganisms. The design was split-plot, and the results were evaluated by Analysis of Variance with analysis of minimal significant difference by Duncan Test. The results showed that samples kept at 30°C can be analyzed, for composition and SCC until the fourth and fifth day, respectively, after collection. Cooled samples can be analyzed for composition, SCC and TBC until 10 days after collection. However the samples can not be stored at room temperature for TBC. There was a significant statistical difference on the levels of lactose and SCC for samples preserved with azidiol instead of bronopol. Therefore azidiol is not suitable for sample preservation in the electronic analysis for composition and SCC. Sample preserved with bronopol is not indicated for TBC because it underestimates the bacterial population. The results indicated that the tablet of azidiol can be used to replace the liquid presentation of this preservative in raw milk samples. *Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq; CAPES.*

Key Words: azidiol tablet, milk quality, bronopol

Extension Education

530 A diagnostic tool to assess calf welfare and management on-farm. E. Vasseur*[1], J. Rushen[2], A. M. de Passillé[2], D. Lefebvre[3], G. Fecteau[4], and D. Pellerin[1], [1]*Université Lavalé*, *Quebec city, Quebec, Canada*, [2]*Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada*, *Agassiz, British Columbia, Canada*, [3]*Valacta, Dairy Production Centre of Expertise Quebec-Atlantic*, *Sainte-Anne-de-Bellevue, Quebec, Canada*, [4]*Veterinary Faculty, Université de Montréal*, *Sainte-Hyacinte, Quebec, Canada*.

Unweaned calf morbidity remains high, which is a costly animal welfare concern. A previous survey, of 115 Quebec dairy farmers found mean perinatal calf mortality of 8.8%, which was underestimated by 20 to 50% by producers with 94% believing calf morbidity was not a problem.

Diagnostic tools to assess calf health and welfare on-farm are needed to improve production and consumer assurance. From this survey, we identified 10 areas of concern: calving management, care of the newborn and painful procedures, colostrum management, calf-dam separation, weaning, calf feeding, calf housing, heifer feeding, heifer housing, and health. We then developed a diagnostic and intervention tool with recommended goals for each area of concern and material was assembled to explain on-farm those goals. An expert committee validated the scoring system and recommendations. The tool was tested in 28 Quebec dairy farms for feasibility, producer satisfaction and repeatability. Farmers were asked to take colostrum and blood samples, and record health data. The on-farm evaluation included an interview on management practices and in-barn measurements related to calf and heifer welfare. The efficiency and usefulness of the tool was evaluated by the producers during a final debriefing. The visit required 3:38±1:07 h (Mean±SD). We found that 100% of producers were convinced of the effectiveness of our diagnostic tool for identifying areas in need of improvement, and that our tool was useful as an advisory tool for technical advisors and veterinarians. Involving producers in the collection of data (e.g. checking colostrum quality by using a colostrodoser) and providing realistic targets, helped in putting emphasis on problem areas and in discussing ways of improvement. Thus, 75% of producers would continue using in routine the colostrodoser and keeping stock of colostrum. Although 65% found it useful to keep health records, only 32% continued to do so over a 6-month period. Voluntary improvements in animal welfare can be facilitated by using appropriate tools to educate producers and help them change their attitudes towards management and animal welfare.

Key Words: on-farm tool, welfare, calf

531 Expanding use of high accuracy AI sires in Missouri beef cattle enterprises. D. C. Busch*, N. R. Leitman, D. A. Mallory, J. F. Bader, D. J. Wilson, S. E. Poock, M. F. Smith, J. L. Parcell, and D. J. Patterson, *University of Missouri*, *Columbia*.

Implementation of existing and emerging reproductive technologies (fixed-time AI; FTAI) in beef cattle enterprises affords producers a competitive advantage over beef enterprises that do not implement these same technologies. Field demonstrations involving 34 cow-calf producers across Missouri were conducted to demonstrate the feasibility of using FTAI. In addition, 14 educational meetings with ~ 650 people in attendance were held to review results highlighting successes in using FTAI in cows. These programs reviewed criteria for implementing a FTAI program, and the expected improvement in calving distribution, genetics, and carcass quality of calves that result from AI sires with high accuracies for various production and carcass traits. Based on pregnancy diagnosis performed with transrectal ultrasonography, 2420/4083 (59%) cows conceived to a single FTAI (CO-Synch + CIDR with FTAI at 66 h) among the 34 farms. Calving data summarized from these demonstrations show an increase in calf age ranging from 6 to 22 days in comparison to the previous year′s calving profiles; resulting in older, heavier, and more uniform calves at weaning. A group of steers (n = 145) resulting from FTAI and subsequent natural service (NS) matings were weaned and preconditioned for 45 d before placement in the same feedlot. Sires of these steers were categorized on the basis of EPD accuracies: High Accuracy AI (HA; n = 42); Low Accuracy AI (LA; n = 62); Calving Ease AI (CE; n = 27); or NS (n = 14). The HA sire group had EPD accuracies ≥ 0.85 for BW, WW, and YW. Individual carcass data was collected for all steers at harvest. The number of steers grading Choice or better was increased in the HA sire (78%) and CE sire groups (84%) compared to the LA sire (59%) and NS groups (27%). In summary, beef operations in Missouri are realizing improvements in reproductive management and genetics resulting from FTAI to genetically proven superior sires. *This project was supported by National Research Initiative Competitive Grant No. 2007-55618-18238 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: artificial insemination, beef cows, estrus synchronization

532 On-line access to the Cattle Producer's Library for disseminating beef cattle educational information. J. C. Whittier[1], J. W. Oltjen*[2], J. A Paterson[3], D. R. Zobell[4], and Western Beef Resource Committee[5], [1]*Colorado State University*, *Fort Collins*, [2]*University of California*, *Davis*, [3]*Montana State University*, *Bozeman*, [4]*Utah State University*, *Logan*, [5]*WBRC*, *12 Western USA States*.

Our objective is to report on-line use of The Cow-Calf Management Guide & Cattle Producer's Library (CL) during 2008. The CL is an educational resource for cattle producers and educators prepared by the Western Beef Resource Committee (WBRC) comprised of extension specialists in 12 western states. The first printed edition of the CL was in 1980, with a second edition in 1992. In 1999 a CD-ROM version was added. The CL contains approximately 250 factsheets in sections on quality assurance, nutrition, reproduction, range and pasture, animal health, management, marketing, finance, genetics, drought and other natural disasters. The CL is revised annually by WBRC. In 2005, Colorado State University (CSU) was charged by WBRC to develop a site for on-line electronic access to the CL. Concurrently, CSU was enhancing their web delivery of beef cattle information as the URL CSUBeef.Com. The CL was added as a menu item and requires users to have a user name and password to access the CL. This on-line CL is in Adobe PDF format and registered users can download and print factsheets individually. The site contains a search function to find terms and phrases in the CL. During 2008, Google and similar search engines were allowed search capabilities of the CSU CL site. By February 2008 there were 399 registered on-line CL users and 11,117 total factsheet downloads. This increased to 496 users by February 2009 with cumulative downloads increasing to 55,710, over a 5-fold increase in 1 year. The on-line CL contains 15 factsheets translated into Spanish. Of the top 10 downloads, 4 were Spanish, including the Spanish table of contents as the most frequent download (1,243 downloads). This report demonstrates that the internet provides an effective tool for disseminating information about beef cattle production and management topics.

Key Words: Cattle Producer's Library, on-line, internet

533 Using audience response software in equine extension programs. K. Martinson*, *University of Minnesota*, *St. Paul*.

The use of audience response software is an effective tool in encouraging audience participation and interaction. Audience response software can also be used to collect survey data, evaluate teaching effectiveness, and ensure that important concepts are understood. The objectives of using audience response software at Extension programs were to encourage participation, evaluate teaching effectiveness, determine nutrition knowledge, collect data on hay preferences, and determine demographics of horse owners. The use of audience response software began in February 2008. A total of 50 horse owners at three different locations used audience response software during a basic horse hay presentation. Participants were asked the same pre and post presentation questions

to assess nutrition knowledge, determine teaching effectiveness, and to ensure that important concepts were learned. Throughout the presentation, additional questions were asked to determine horse owner hay preferences and collect demographics. Pre-presentation questions demonstrated the lack of horse owner's nutrition knowledge, but provided the ability for the presenter to immediately focus on certain concepts and correct any misconceptions. The survey data showed that a majority of horse owners (69%) bought all of their hay, fed small square bales (57%), and fed a mixture of grass and alfalfa (78%). When asked why participants fed the type of hay they did, 45% indicated they fed what they thought was best for their horse, 42% fed whatever was available, and only 5% had ever worked with an equine nutritionist. A majority of participants (78%) had never had their hay tested for nutritional quality. A majority of participants (72%) owned between one and five horses, 66% were female, 80% were 30 to 69 years old, and 43% had owned horses for less than 5 years. The use of audience response software has resulted in audience participation and interaction, provided immediate feedback regarding teaching effectiveness and participant learning, identified future educational and research needs, and has given insight to horse owner hay preferences and demographics.

Key Words: audience response software, extension, equine

534 Partnering with outside entities to broaden extension's reach: Theory, practice, challenges, implications, and impact. E. A. Greene*[1], R. E. Greene[2], and R. L. Parsons[1], [1]*University of Vermont, Burlington*, [2]*Kleine Lelli Consulting, Wayland*.

With decreasing funding, Extension professionals constantly seek innovative means to produce and provide effective programming that demonstrates impact and meets the needs of the clientele. One potential avenue is to partner with strategic community entities to provide mutually beneficial opportunities for all parties involved. Everything Equine, one of New England's largest equine educational events, is a collaboration between University of Vermont Extension, Champlain Valley Exposition, and other equine businesses that combines a consumer trade show with 75 educational seminars/demonstrations over two days. This collaboration provides a measure of program impact and an opportunity to link Extension, 4-H, the community and equine businesses. Due to sponsors and the enormity of this event, Extension clientele are able to learn from national experts, whose normal fees can exceed entire equine extension budgets. Publicity, educational material, volunteer instructor time contributed to Extension for this event is worth more than $50,000. Commercial exhibitors and equine professionals benefit from interaction with thousands of attendees, while participants benefit from exposure to multiple workshops at one location. For educators, this is a rare opportunity to offer a smorgasbord of educational workshops that would not normally be possible. Extension gains economical and educational benefits while also reaching a large crowd. In 2008, over 8,500 equine enthusiasts attended with at least 1,100 participating in workshops. Calculations indicate that workshops cost less than 40% of traditional Extension workshops, and equine extension received a donation for planning the program. These events have challenges. Partners' roles must be clearly identified and respected by the team and communication is critical. Extension administrators covet monetary benefits but fail to recognize financial risk involved. At such large events, change in behavior can be difficult to measure; we use prize drawings incentives, evaluation cards, and computer surveys.

Key Words: extension, collaboration, programming

535 Maximizing reach via the internet while providing tools for information dissemination in traditional extension environments. E. A. Greene*[1], A. S. Griffin[2], K. P. Anderson[3], and C. D. Skelly[4], [1]*University of Vermont, Burlington*, [2]*University of Kentucky, Lexington*, [3]*University of Nebraska, Lincoln*, [4]*Michigan State University, Lansing*.

eXtension is an online resource transforming how faculty can collaborate and deliver equine education. As the first Community of Practice launched from eXtension, HorseQuest (HQ) offers free, interactive, peer-reviewed, on-line resources on a variety of equine related topics at www.extension.org. This group has learned how to adapt traditional content to the online environment to maximize Search Engine Optimization (SEO), in order to be more discoverable and relevant in the online world. This means that HQ resources are consistently being found on the first page of search results. Also, by researching keywords searched by Internet users, HQ has guided new content direction and determined potential webcast topics based on relevance and frequency of those searches. In addition to establishing good SEO, HQ has been utilizing the "viral networking" aspect of the popular social network, YouTube™. By uploading clips of existing equine educational videos to YouTube™, HQ content appears in mainstream media, is passed on by the user, and helps HQ effectively reach their community of interest (horse enthusiasts). HorseQuest partners with My Horse University to produce webcasts that combine concise knowledge exchange via a scripted presentation with viewer chat and incoming questions. Locally, multiple specialists have used the 24/7/365 web resource in classrooms and programming throughout their states. Examples include using archived webcasts to bring national talks to local audiences (e.g. Dr. Lenz on The Unwanted Horse), video clips to show digesta moving through the horse's system, or showing examples of equine artificial gaits (e.g. rack), which can be difficult to find. Additionally, animations of the parts of the hoof and the interactive learning lesson for body condition scoring have been used in the field and classroom to supplement presentations. HorseQuest is a resource for several state 4-H advancement and competition programs, and will continue to be incorporated into traditional extension, while reaching and impacting global audiences.

Key Words: eXtension, HorseQuest, social networking

Growth and Development: Fetal Development

536 Inadequate protein levels during gestation in gilts affect gestation body mass and fatness as well as offspring birth weight and insulin sensitivity at 10 wk of age. C.C. Metges*, I.S. Lang, S. Goers, P. Junghans, U. Hennig, B. Stabenow, F. Schneider, W. Otten, and C. Rehfeldt, *Research Institute for the Biology of Farm Animals (FBN), Dummerstorf,MV,Germany*.

We have studied whether maternal gestational protein supply affects glucose metabolism in pig offspring. Isoenergetic diets with low (LP, 6% CP; n=15 sows), high (HP, 30%; n=15) or adequate protein (AP, 12%; n=15) levels were fed to German Landrace gilts (age ≈ 8 mo, 149 kg BW) from insemination to parturition. Gilt gestation BW, backfat thickness (BFT; ultrasound) and offspring birth weight were recorded. Piglets were cross-fostered to control sows (standardized litters, 11 piglets), weaned at 28 d and fed according to recommendations. Two pigs per litter (age ≈70 d, ≈23 kg, n=10 litters/diet) were fitted with venous and arterial catheters and received an i.v. bolus of 200 mg/

kg BW unlabeled and 1.5 mg/kg BW [U-13C]glucose after overnight food withdrawal. Plasma 13C glucose enrichment was measured by GC-MS. Plasma glucose and insulin concentrations were determined by a glucose kit and by radioimmunoassay, respectively. Areas under the curve (AUC, 30 min) were calculated. Results were evaluated by ANOVA. Gilts fed LP gained less BW until 109 d gestation than in AP and HP (45.6, 67.8, 63.1; P<0.05). During the same time period BFT increased by 3.57, 4.73, and 5.45 mm in HP, LP and AP, respectively (P<0.05). Mean piglet birth weight was lower in LP and HP than in AP (1.19, 1.21, 1.41 kg; P<0.01) with no difference in litter size. The AUC of 13C glucose enrichment and glucose concentration of the offspring did not differ in respect to gestation diet. The AUC of insulin response to i.v. glucose administration was higher in LP and HP offspring as compared to AP (461, 584, 363 μU/ml • min; P<0.1). This suggests that more insulin was required to metabolize glucose in these groups and LP as well as HP offspring was less insulin sensitive. We conclude that LP and HP diets during gestation are detrimental to growth of the fetuses and metabolism of glucose by the progeny.

Key Words: Fetal programming, swine offspring, glucose meatbolism

537 Dam parity influences offspring liveweight and abdominal adiposity. P. R. Kenyon*, H. T. Blair, S. T. Morris, E. C. Firth, and C. W. Rogers, *Massey University, Palmerston North, New Zealand*.

Evidence indicates that the in-utero environment an animal is exposed to, can have long term consequences, with a restricted environment reported to negatively affect an animals physiology, growth and health status. First parity offspring display reduced fetal growth and birthsize, with potentially negative long term consequences. Most studies to date have compared offspring born to differing sires and dams managed separately in pregnancy which result in confounding due to the timing of lambing, dam nutrition and lamb genetics. The present study compared singleton male offspring born to either mature (3-5 years of age) multiparous (n=20) or young (8 month) primiparous (n=17) ewes bred with the same rams and managed as one cohort during pregnancy and lactation. Offspring born to primiparous dams were lighter (P<0.05) at birth (4.22 ±0.23 vs. 5.98 ±0.22kg), 4 months of age (20.38 ±0.98 vs. 24.90 ±0.89kg) and tended to be lighter (P=0.06) at 10 months of age (40.37 ±1.41 vs. 44.19 ±1.25kg) than those born to multiparous dams. At slaughter at 10 months of age offspring born to primiparous dams tended (P=0.08) to have lighter carcass weights (18.84 ±0.80 vs ±20.10 0.85kg) although there was no difference (P>0.10) in GR or abdominal fat compared to those born to multiparous dams. When adjusted to the same liveweight those born to primiparous dams tended (P=0.07) to have more abdominal fat (0.57 ±0.05 vs. 0.41 ±0.05kg) compared to those born to multiparous dams. DXA scanning of the hind leg indicated there were no differences (P>0.10) between the groups for bone mineral content, lean or fat mass or the ratio of bone mineral content and lean mass. This study suggests that offspring born to young primiparous dams are programmed to deposit more abdominal fat which could have implications for efficiency of growth and long term health status. Further studies are underway.

Key Words: fetal programming, parity, adiposity

538 Metabolic maturity at birth and neonate lamb survival and growth. I. The effects of maternal low dose dexamethasone treatment at two time points in late gestation. D. R. Miller*[1], R. B. Jackson[1], D. Blache[2], and J. R. Roche[1], [1]*Tasmanian Institute of Agricultural Research, Mt Pleasant, TAS, Australia*, [2]*University of Western Australia, Perth, WA, Australia*.

Perinatal mortality is a major contributor to reproductive wastage in grazing sheep industries. Maternal glucocorticoid treatment may increase lamb metabolic and endocrine maturity at birth, promoting behavioral competency, thermoregulation, and survival over the first 72 h of life. Multiparous, fine-wool Merino ewes (n = 150) were divided into 3 groups to lamb on pasture. Within each group, 5 single-lamb and 5 twin-lamb bearing ewes were randomly allocated to one of 5 treatments. Treatments were either 1.5 or 3.0 mg of dexamethasone (DEX) injected i.m. at either Day 130 or Day 141 of gestation, or 1 ml saline solution injected into half of the relevant ewes at each of these times. DEX had no effect on lamb survival to 72 h after birth (P > 0.05); although there tended (P = 0.09) to be a lower proportion of treated lambs dying due to dystocia, with heart girth reduced (P < 0.01) at the greater dose rate. DEX reduced birth weight by 5% in twin lambs, and reduced pre-suckling rectal temperatures by about 1ºC in both twin and female lambs. Treatment at Day 130 produced lambs that took longer to bleat than lambs of untreated ewes (P < 0.05), otherwise behavior was unaffected. Treatment at Day 141 increased (P < 0.05) pre-suckling plasma ghrelin concentrations in singleton and male lambs but did not alter glucose, NEFA, urea or leptin concentrations or gestation length. DEX did not affect the concentration of plasma metabolites or hormones at weaning, which occurred 78 d after lambing started, or BW recorded 73 d later. In conclusion, maternal glucocorticoid treatment did not have a positive effect on neonate thermoregulation or behavior, or alter perinatal survival. The sensitivity of ghrelin to maternal DEX treatment at Day 141 of gestation warrants further investigation.

Key Words: neonate, dexamethasone, survival

539 Metabolic maturity at birth and neonate lamb survival and growth. II. Association among maternal factors, litter type, lamb birth weight, plasma metabolic and endocrine factors, lamb survival and behavior. D. R. Miller*[1], D. Blache[2], R. B. Jackson[1], E. Downie[1], and J. R. Roche[1], [1]*Tasmanian Institute of Agricultural Research, Mt Pleasant, TAS, Australia*, [2]*University of Western Australia, Perth, WA, Australia*.

Neonate metabolic and endocrine maturity was studied using stepwise multiple regression analysis to explore relationships among litter type, birth weight and ewe nutritional status and lamb endocrinology, physiology, behavior at birth, and survival to 72 h of life. Multiparous, fine-wool Merino ewes (n = 150, equal numbers of single and twin lamb bearing status) were lambed on pasture, with low dose dexamethasone treatments applied at d 130 or d 141 of gestation. Improved lamb viability at 72 h after birth (n = 99 of 215 born) was related (P < 0.05) to increased ewe pre-lambing plasma ghrelin and lower lamb pre-suckling plasma glucose (GLUC) concentration (CONC), lower chill index at birth, greater pre-suckling rectal temperature (RT), singleton litter status, heavier birth weight, and female sex. Greater RT were associated (P < 0.05) with increased birth weight and gestation periods shorter than 146 d. Neonate behavioral progress was not related to RT or GLUC CONC, but there was a decline in 72 h survival rates as time to suckle increased. GLUC CONC were greater in singletons, lambs from ewes of high BCS at d 95 of gestation, and lambs of heavier birth weight. GLUC CONC was associated with lower pre-suckling RT; maybe reflecting a delay in GLUC utilization during metabolic rate adjustment to the cold external environment. Singleton lambs had lower plasma NEFA CONC. Birth weight was less in lambs born to ewes with high pre-lambing GLUC

and leptin CONC. Greater pre-suckling ghrelin CONC were measured in lambs from shorter gestations, and when born to ewes with high pre-lambing leptin CONC. Lamb leptin CONC declined with increasing gestational age at birth. In conclusion, lambs exhibiting greater metabolic and endocrine maturity at birth had improved survival to 72 h after birth in a cold environment.

Key Words: neonate, survival, sheep

540 Maternal over-nutrition induces inflammatory response in large intestine of fetal sheep in late gestation. X. Yan*[1], M. Du[1], B. W. Hess[1], S. P. Ford[1], P. W. Nathanielsz[1,2], and M. J. Zhu[1], [1]*University of Wyoming*, *Laramie*, [2]*University of Texas Health Sciences Center*, *San Antonio*.

The intestinal mucosal immune system (MIS), which develops largely during the fetal period, plays a key role in defending against potentially pathogenic bacteria. It was hypothesized that maternal over-nutrition induces an inflammatory response in the fetal large intestine which may permanently alters fetal MIS development and, thus, the prevalence of bacteria in their gastrointestinal tract postnatally. Non-pregnant ewes were assigned to a control (Con, 100% of NRC recommendations, n=8) or obesogenic (OB, 150% of NRC, n=8) diet from 60 d before to 135 d after conception, when fetal large intestine was sampled for western blotting and real-time PCR analyses. mRNA expression of Toll-like receptor (TLR) 2 and TLR4 was increased ($P<0.05$) by 108 ± 23% and 53 ± 7% in OB versus Con fetuses. The mRNA level of macrophage markers, CD11b, CD14 and CD68 was also increased ($P<0.05$) by 75 ± 42%, 69 ± 17% and 204 ± 52%, respectively. The proinflammatory cytokines TNFα and IL6 were increased ($P<0.05$) by 91 ± 33% and 167 ± 29%, respectively. The expression of IL-1α and IL8 was increased ($P<0.05$) by 68 ± 16% and 97 ± 22%, respectively, while IL-Iβ tended to increase (48 ± 15%: $P = 0.06$). Monocyte/macrophage chemotactic protein-1(MCP-1) was upregulated in the OB group by 30 ± 13% ($p = 0.05$), and upregulation ($P<0.05$) of phos(p)-JNK (36 ± 13%), pIKKβ (52 ± 13%) and its downstream component p-p65 (29 ± 11%) was demonstrated in OB versus Con fetuses. In summary, maternal over-nutrition enhances expression of pro-inflammatory cytokines in the fetal large intestine, which may permanently alter MIS development. Since the MIS is responsible for the body defense against opportunistic pathogens, alteration of fetal MIS development in response to maternal over-nutrition may have long-term impacts on offspring health, and the safety of their meat products.

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Key Words: sheep, fetus, gut

541 An *in vivo* comparison of muscles formed from broiler and layer chick somites. P. E. Mozdziak*, D. Hodgson, and J. N. Petitte, *Department of Poultry Science, North Carolina State University*, *Raleigh*.

Unique avian genetic resources at NC State University were employed to test the hypothesis that the embryonic environment has a greater impact on muscle size than the genetic growth potential of muscle-precursor cells. The somites (#17-20; including a portion of the associated neural tube) that form the right *Pectoralis thoracicus* were removed from broiler chick embryos, which are genetically predisposed to form large muscles, and replaced with tissue containing the somites from transgenic, layer strain chick embryos (eGFP or *lacZ*), which are genetically pre-disposed to form small muscles. Broiler somites were also transplanted into a layer background, and broiler somites were also transplanted into a broiler background as a sham control. Subsequently, 18 day embryos were harvested and myofiber diameters were assessed for the left (background) and right (experimental) *Pectoralis thoracicus*. Myofiber cross-sectional area was significantly lower ($P< 0.05$) for layer-derived-muscle (right side; 11.2±1.0 μm^2) than the broiler-derived muscle (left side; 19.2±2.8 μm^2). However, myofiber cross-sectional area of broiler-derived muscle (right side; 8.8±1.7 μm^2) in a layer background was not significantly ($P > 0.05$) different than observed for the layer background muscle (left side; 8.3±1.1 μm^2). No significant difference was found between sides when broiler somites were cross-transplanted between broiler embryos (14.2±3.5 μm^2; 15.8±4.8 μm^2). Embryos with layer somites were transplanted into a broiler background were cultured through hatching, and chicks were grown to 8 weeks of age. Muscle weights were lower ($P < 0.05$) in the transgenic layer-derived muscle (233 g) than the broiler-derived background muscle (244 g). However, the layer-derived muscles were also larger than expected for un-manipulated layer chicken of the same age. It appears that the *in vivo* environment drives the donor cells to exceed their normal *in vivo* potential, but the donor muscles retain a lower growth potential than the higher growth potential of the host animal.

Key Words: avian, embryo, development

International Animal Agriculture: ASAS-EAAP Global Issues

542 Animal agriculture in developing countries: Population pressures, income growth, climate change, and the management of global genetic resources. D. Gollin*, *Williams College*, *Williamstown, MA*.

The UN predicts that world population will rise from 6.5 billion today to 9.1 billion in 2050, with all the increase taking place in today's less developed countries. Among the countries experiencing large absolute increases are some, such as China and India, where incomes are also rising. Taken together, rising populations and incomes will drive up demand for animal products. Projections suggest that meat demand in developing countries could grow by 2.4% annually to 2030, with milk demand rising at 2.7%. Growth in animal agriculture in the developing world will interact significantly with climate change. More animals, raised in more intensive production systems, will add to emissions of greenhouse gases. Even absent these emissions, the IPCC's projections suggest that mean temperatures will rise by about 1-1.5° C in much of developing Asia and Africa by 2050. Temperature increases will stress traditional crop and livestock systems. Production systems that involve controlling the environment are likely to flourish, taking market share from traditional systems. Thus, intensive production systems seem likely to gain at the expense of backyard production. These trends are likely to have a double effect on animal genetic resources. On the one hand, traditional phenotypes and genotypes may be displaced by the shift towards intensive management systems. On the other hand, the demand for traits associated with tolerance to biotic and abiotic stresses may increase, especially with continued advances in biotechnology. This implies an urgent need to pursue intensive collection and conservation of animal genetic resources. Market forces are unlikely to meet this challenge. On

the contrary, the "tragedy of the commons" applies to genetic resources. Many producers would like continued access to the genes of traditional breeds, but none has much incentive to bear the costs of collection and maintenance. The international community needs mechanisms to provide this global public good. Public-private partnerships hold promise; industry support for public initiatives will be essential.

Key Words: animal genetic resources, climate change, demand growth

543 Adaptation of the livestock sector to global climate change: Opportunities and options for animal genetic resources and management systems in developing countries. S. Fernandez-Rivera*, *Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias*, *Mexico City, D.F., Mexico*.

Model simulations are used to identify hot spots in developing countries where climate changes may result in new challenges to livestock production. Areas where climate changes may result in favorable situations for livestock production are also identified. The production systems practiced in those hot spots and their driving forces are described and their likely responses to temperature and rainfall variations are discussed. Variations in rainfall will have a major effect on quantity and quality of feed resources available, whereas higher temperatures will influence the prevalence of disease related factors and will have a direct effect on animals. Opportunities for livestock producers to adapt to those changes, with emphasis on animal genetic resources and specific traits are presented.

Key Words: climate change, livestock, developing countries

544 The role for animal genetic resources under global climate change conditions and rapid development of the livestock sector. I. Hoffmann*, *FAO*, *Rome, Italy*.

The livelihoods of one billion poor people are sustained by livestock. The livestock sector is the world's biggest land user and is associated with 18% of total greenhouse gas emissions. In large areas of developing countries, climate change threatens the livelihood of smallholders and pastoralists and may accelerate the erosion of animal genetic diversity. The paper will explore how animal genetic diversity is affected by climate change, and how it contributes to adapt to and mitigate climate change. Developed and developing countries differ in their adaptation capacity and the expected interactions between climate change adaptation and mitigation. Developing countries will have to apply a closer relationship between climate change adaptation and development policy. They also have weak capacity for high-tech breeding programes to increase their breeds' adaptation. Depending upon the ecosystem changes brought about by climate change and other pressures, the portfolio of breeds demanded by society will change. We assume that climate change itself, and the resulting disintegration of the components of (agricultural) ecosystems, together with human migration will increase the pressure to maintain wide access to animal genetic resources. Comprehensive policy frameworks that foster access to genetic resources as well as the development and use of appropriate technologies need to be developed. The recent adoption of the Global Plan of Action for Animal Genetic Resources provides for the first time an internationally agreed framework to promote creating these crucial conditions for the global livestock sector.

Key Words: animal genetic resources, climate change

545 The impact of global climate change, utilization of genetic resource management and livestock sector development on nutrition and health in developing countries. Y. Plante*[1] and H. Blackburn[2], [1]*Agriculture and Agri-Food Canada*, *Saskatoon, SK, Canada*, [2]*United States Department of Agriculture*, *Fort Collins, CO*.

Globally livestock employ 1.3 billion people and create livelihoods for one billion of the world's poor. In addition they provide one third of humanity's protein intake and therefore are a remedy for undernourishment. Livestock's growing role in developing country food security is evidenced by an increase (from 1960 to 2003) of milk (70%) and meat (190%) consumption when compared to an 18% increase in cereal consumption during the same time period. The full ramifications of global climate change, its interaction with animal genetic resources for food and agriculture and the ultimate ability of local production systems to provide animal products and to sustain food security or income to developing country smallholder farmers and landless people is unclear. Predicted climate changes will affect soil erosion and fertility, crop, forage and livestock management in terms of decision making regarding water resources, seeding and harvesting different varieties, pest and disease control, and locally adapted livestock species and breeds, especially in tropical and sub-tropical regions. Clearly mitigating actions are needed to buffer such events and to insure that livestock's contribution to health, nutrition and economic growth continues. It has been suggested that livestock producers will make the necessary adjustments, for example by abandoning traditional cattle breeding and adopting small ruminant husbandry practices. However, a number of policy and technological changes will have to occur for a systematic transition to new animal production systems so that livestock smallholders and pastoralists may be protected against greater levels of food insecurity. How these producers can buffer themselves from such changes is important and exploration into this subject is crucially needed so that governments and multilateral agencies can work toward potential solutions.

Key Words: climate change, animal genetic resources, food security

Lactation Biology: Lactation Biology 2

546 Prolactin, insulin and cortisone regulate expression of GLUT8 gene in bovine mammary explants. K. Zhao*, H. Y. Liu, and J. X. Liu, *Institute of Dairy Science, Ministry of Education Key Laboratory of Molecular Animal Nutrition, Zhejiang University*, *Hangzhou, P.R. China*.

Lactogenic hormones are known to regulate milk synthesis and secretion in lactating dairy cows, but knowledge about their possible effects on glucose transporters in mammary gland at tissue level remains controversial. GLUT8 is a newly identified member of the facilitative glucose transporter family, and may play an important role in glucose uptake in the lactating mammary gland. This study was aimed at investigating effects of the three primary lactogenic hormones, prolactin, insulin, and cortisone, on expression of GLUT8 mRNA in cultured bovine mammary tissue taken from the mid-lactating dairy cows. The mRNA expression was determined by SYBR green method of quantitative reverse tran-

scription PCR (ABI 7500). The explants were cultured in DMEM/F12 medium containing 10% fetal bovine serum (FBS) and treated by prolactin (0, 50, 1000, 5000 ng/ml), insulin (0, 5, 50, 500, 5000 ng/ml), and cortisone (0, 50, 1000, 10000 ng/ml), respectively for 48 hr after 24 hr starvation of FBS. Compared with control (no hormone), prolactin (50, 1000 ng/ml) decreased GLUT8 gene expression ($P<0.05$), but had no effects at 5000ng/ml. Insulin above 50ng/ml doubled the abundance of GLUT8 mRNA, while 5ng/ml had no effect. The expression of GLUT8 mRNA was enhanced firstly and then depressed with the increasing level of cortisone, with highest abundance at 1000ng/ml of cortisone ($P<0.05$). The regulation pattern and sensitivity of GLUT8 to lactogenic hormones were different from those of GLUT1 that is the predominant glucose transporter in bovine mammary gland (data not shown). The results demonstrate that GLUT8 expression may be regulated by lactogenic hormones in a dose-dependent manner, suggesting that lactogenic hormones may influence glucose transportation in bovine mammary gland through regulation of transporter gene expression.

Key Words: bovine mammary gland, GLUT8 gene expression, lactogenic hormone

547 Effect of the milking-induced prolactin release on galactopoiesis in dairy cows. V. Lollivier*[1], R. M. Bruckmaier[2], P. Lacasse[3], and M. Boutinaud[1], [1]*INRA, AGROCAMPUS OUEST, UMR1080, St. Gilles, France*, [2]*University of Bern, Bern, Switzerland*, [3]*AAFC, Dairy and Swine R&D Centre, Sherbrooke, Canada*.

In ruminants, milking induces the release of prolactin (PRL). Milking-induced PRL release decreases as lactation advances and PRL is a survival factor for mammary epithelial cells (MEC) of cows, suggesting a galactopoietic role of this hormone. Nevertheless, suppression of PRL by bromocriptine has produced ambiguous effects on milk yield in cows. To assess the effect of inhibition of PRL release in lactating dairy cows, nine Holstein cows were assigned randomly to treatments during 3 5-d periods: 1)daily i.m. injection of 2 mg of Quinagolide (a PRL release inhibitor), 2)daily i.m. injection of 2 mg of Quinagolide and twice a day (milking time) i.v injection of PRL (2µg/kg of body weight),3) daily injection of vehicle as control. Blood and milk samples were harvested at milking. MEC were purified from milk. Daily injections of Quinagolide reduced milking-induced PRL release ($P<0.05$). The amount (area under curve) of PRL during milking after the PRL injections was similar to that of endogenous PRL discharges in control treatment. Quinagolide decreased milk production ($P<0.05$), milk protein content ($P<0.05$) and milk lactose content ($P<0.05$), without modification of milk fat composition or fat globule size. PRL injections had no effect on milk yield and milk fat composition but tended to increased milk protein content ($P<0.10$). Injections of Quinagolide increased the number of MEC harvested from milk ($P<0.05$) but PRL injections tended to decrease it ($P=0.10$). PRL injections also increased viability of MEC harvested from milk ($P<0.05$). Injections of Quinagolide decreased kappa-casein ($P<0.05$) and alpha-lactalbumin ($P<0.05$) mRNAs in milk MEC. Exogenous PRL have no affected the level of these mRNA. In conclusion, chronic administration of Quinagolide reduces milk production in dairy cows by affecting MEC activity. PRL injections at milking time were not sufficient to restore milk yield but influenced the viability of MEC purified from milk.

Key Words: prolactin, milking, dairy cows

548 Effects of unilateral frequent milking of dairy heifers during early lactation. J. B. Wright*, E. H. Wall, and T. B. McFadden, *University of Vermont, Burlington*.

In multiparous cows increasing milking frequency from 2X to 4X/d during days 1 to 21 of lactation stimulates an immediate response in milk yield that partially persists throughout lactation. However, it is unknown if dairy heifers respond similarly. The objective of this study was to investigate the response of dairy heifers to frequent milking during early lactation using a half-udder design. Holstein heifers were assigned at parturition to unilateral frequent milking (UFM). On days 1 to 21 of lactation Heifers were milked twice daily at 0130 h and 1330 h, with additional milking of the right udder half at 0430 h and 1630 h. Thereafter, heifers were milked twice daily. Half udder milk yields and teat end scores were measured weekly on days 1 to 35 of lactation. Teat ends were scored on a scale of 0 to 4, with 0 representing no apparent teat end damage and 4 representing severe damage to the teat end. A 1-sided paired t-test was used to compare milk yields of 2× vs. 4× udder halves. Effects of time, milking frequency and their interaction on teat end scores were analyzed using the mixed procedure of SAS. During UFM milk production of 4× udder halves rapidly increased relative to that of 2× udder halves ($P < 0.001$). After cessation of UFM the difference in milk yield was no longer significant at day 28, but was partially restored by day 35. Teat end scores increased over time ($P < 0.001$), but were not effected by milking frequency. We conclude that frequent milking of heifers during early lactation stimulates an increase in milk yield that partially persists after treatment. These results are similar to those of mature cows.

Table 1. Effect of Unilateral Frequent Milking on Milk Yield and Teat End Score in Heifers

DIM	1	7	14	21	28	35
n =	5	7	7	7	6	6
4X-2X, kg/d	-0.2	2.0*	4.1*	3.3*	0.5	0.9^{+}
Teat Score	0.3	0.6	1.0	1.1	1.6	1.6

*$P < 0.01$, $^{+}P < 0.1$

Key Words: frequent milking, heifer, teat end

549 Effects of reduced frequency of milk removal on gene expression in the bovine mammary gland. M. Littlejohn*[1], C. Walker[1], H. Ward[2], K. Lehnert[2], R. Snell[2], G. Verkerk[1], R. Spelman[3], D. Clark[1], and S. Davis[2,3], [1]*DairyNZ Ltd, Hamilton, New Zealand*, [2]*ViaLactia Biosciences Ltd, Auckland, New Zealand*, [3]*Livestock Improvement Corporation, Hamilton, New Zealand*.

In mammals, reduced suckling frequency by the offspring initiates the down-regulation of milk synthesis and the induction of apoptotic pathways and structural remodeling of mammary tissue. This effect on milk synthesis and secretion has been shown to be mediated through local (intra-mammary) mechanisms, however the physiological triggers and discrete signaling pathways that comprise the response to milk removal frequency remain largely undefined. To gain insight into the pathways and individual molecules involved in this response, an analysis of mammary gene expression was conducted in 12 lactating cows milked at two different frequencies. Animals milked twice a day were sampled by mammary tissue biopsy and then milked once daily for five days. A second biopsy was then taken from the adjacent rear-udder quarter of these animals, allowing changes in gene expression to be assessed within each animal. Expression analysis was conducted

using Agilent bovine oligonucleotide arrays representing 21,495 transcripts, and revealed a range of genes differentially expressed as a result of less frequent milk removal. These changes included an increase in abundance of transcripts related to apoptotic signaling (NFKB, JUN, ATF3, GADD45A, IGFBP5, TNFSF12A) and mechanical stress and epithelial tight junction synthesis (CYR61, CTGF, CLDN4, CLDN8). Concomitant with a reduction in milk yield, a downregulation of molecules related to milk synthesis (LALBA, B4GALT1, UGP2, CSN2, GPAM, LPL) was also observed. Quantitative real time PCR was used to assess the expression of 13 genes in the study, and all were highly correlated ($p<0.05$) with values derived from array analysis. It can be concluded that the apoptotic signaling pathways characteristic of recognizable involution and mammary regression occur early in response to a reduction in milk removal frequency. Further, these results suggest that mechano-signal transduction cascades (initiated as a result of udder distension) play roles in initiating the apoptotic signaling networks that orchestrate this response.

Key Words: milking frequency, involution, gene expression

550 The ability of exogenous growth hormone to maintain milk production during prolonged lactation in the mouse is more evident with reduced nursing frequency. D. L. Hadsell*[1], W. Olea[1], A. F. Parlow[2], and R. J. Collier[3], [1]*Baylor College of Medicine*, *Houston, TX*, [2]*Harbor-UCLA Medical Center*, *Torrance, CA*, [3]*The University of Arizona*, *Tucson*.

Although growth hormone (GH) increases milk production in dairy animals, the milk production response of lactating rodents to this treatment has been variable. Milk removal frequency in the lactating mouse is about 10-fold higher than that of lactating dairy cows. The hypothesis tested in this study was that the ability of GH to stimulate milk production during prolonged lactation would be greater in mouse dams subjected to reduced nursing frequency than in dams allow to nurse ad-libitum. The growth of 8-day-old crossfoster litters maintained on groups of lactating mice was studied either from day 14 to 21 postpartum, or from day 21 to 27 postpartum using a litter cross-fostering protocol that prevents natural mammary involution. There were four treatments that consisted of ad-libitum (AL) or reduced nursing frequency (4×) in combination with subcutaneous injections of either saline (SAL) or recombinant murine GH (GH). The GH was tested at 2 doses of either 6 or 18 mg/kg/day. Reduced Nursing frequency caused a dramatic decrease in litter gain ($P<0.0001$) in both SAL- and GH-treated dams. At 6 mg/kg/day, GH failed to significantly increase day 14 to 21 litter gain in either AL or 4× dams (12.4±1.4, 15.4±1.2, 24.5±1.6 and 25.5±0.9 g for 4×-sal, 4×-GH, AL-SAL, and AL-GH, respectively). At a dose of 18 mg/kg/day, GH increased day 14 to 21 litter gain in 4× ($P<0.02$), but not in AL litters (10.56±0.8, 16.03±1.4, 30.1±1.9, and 30.1±0.8 g for 4×-SAL, 4×-GH, AL-SAL, and AL-GH, respectively). Litter gain from day 21 to 27 was increased by GH in both AL ($P<0.01$) and 4× ($P<0.001$) litters (2.4±1.9, 11.0±0.7, 13.5±0.5, and 18.8 g for 4×-SAL, 4×-GH, AL-SAL, and AL-GH, respectively). These results support the conclusion that the ability of GH to stimulate milk production in lactating mice is affected both by stage of lactation and the frequency of milk removal. *This project was supported by National Research Initiative Competitive Grant no. 2007-35206-17831 from the USDA Cooperative State Research, Education, and Extension Service.*

Key Words: milking frequency, growth hormone, mouse

551 Mammary transcript profiles due to prepartum dietary energy level and bacterial lipopolysacharide challenge in dairy cows early postpartum. D. E. Graugnard*, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, J. K. Drackley, and J. J. Loor, *University of Illinois*, *Urbana*.

Immunosuppression renders cows highly susceptible to mastitis pathogens as well as metabolic diseases after parturition. We hypothesized that plane of dietary energy prepartum can affect tissue response to inflammatory challenges through changes in gene expression. Twenty–eight Holstein cows with average composite SCC of ~128,000 in the previous lactation were assigned (n = 14/diet) to a control (high-straw; NE_L = 1.52 Mcal/kg) or moderate-energy (ME; NE_L = 1.64 Mcal/kg) diet during the entire dry period. All cows were fed a common lactation diet (NE_L = 1.69 Mcal/kg) postpartum. At 7 DIM, cows (n = 7/prepartum diet) were assigned to receive an intramammary bacterial lipopolysacharide (LPS) challenge (200 μg) in one rear mammary quarter or served as controls. Cows used were bacteriologically–negative in all mammary quarters. A percutaneous mammary biopsy was collected at 2 h post–LPS for transcript profiling using a 13,257 annotated bovine oligonucleotide microarray. LPS challenge of cows fed ME prepartum resulted in >100 differentially expressed genes (DEG, $P < 0.01$). Among DEG, the most enriched biological functions were response to stimulus (n = 21) and immune response (n = 11). We also observed genes with higher mRNA abundance due to LPS that were related with regulation of immune response (e.g. *MBP, SIT1*), inflammatory response (e.g. *TLR9*), and chemotaxis (e.g. *CXCL2*). In the comparison of ME vs. control–fed cows receiving LPS postpartum there were >20 DEG due to prepartum diet. The most affected biological function among DEG was transport regulation (n = 10). Genes with higher mRNA due to feeding the control diet prepartum were involved primarily in immune response regulation (e.g. *CD59*). Results showed that a mammary inflammatory challenge early postpartum caused rapid alterations in tissue gene expression profiles. However, the transcriptomic response to inflammation was not greatly affected by prepartum dietary energy level.

Key Words: transcriptomics, inflammation, mastitis

552 Fluoxetine and phenelzine disrupt tight junctions in primary bovine mammary epithelial cells. L. L. Hernandez*[1], R. J. Collier[2], and N. D. Horseman[1], [1]*University of Cincinnati*, *Cincinnati, OH*, [2]*University of Arizona*, *Tucson*.

Serotonin (5-HT) acts via autocrine-paracrine mechanisms on mammary epithelial cells in a variety of species. In human mammary cells, 5-HT treatment disrupts tight junctions (TJ) in a biphasic manner. Low doses and short exposures increase TJ integrity, and high, sustained treatment disrupts TJ. TJ remain "tight" throughout lactation, preventing leakage of milk components out of the luminal space, and become "leaky" during involution. The 5-HT reuptake transporter and the enzyme monoamine oxidase (MAO) regulate 5-HT concentrations in the extracellular space by allowing 5-HT to re-enter the epithelium to be degraded to 5-hydroxyindole acetic acid. In these experiments, we investigated the effects of treatments with fluoxetine, a selective 5HT reuptake inhibitor (SSRI), and phenelzine, a monoamine oxidase inhibitor (MAOI) on transepithelial resistance (TEER) in primary bovine mammary epithelial cell (BMEC) cultures. BMEC were grown on Transwells® for 6 d, and then treated with 40 and 400 μM, and 1.4 mM SSRI, 40 and 400 μM, and 1.4 mM MAOI, and 40 and 400 μM, and 1.4 mM SSRI in combination with MAOI for 48 h. Media was exchanged daily and TEER was measured prior to media changes. Percent change was calculated for all treatments relative to the control. The 40 μM SSRI treatment resulted in 15% and 27% decreases in TEER, 24 and 48 h

after treatment, respectively ($P < 0.001$). The 400 μM and 1.4 mM SSRI treatments resulted in 86% decreases in TEER 24 h after treatment, and decreased 75% after 48 hr after treatment ($P < 0.001$). The 40 μM, 400 μM, and 1.4 mM MAOI treatments decreased TEER 1.63, 17.8, and 12.2% respectively, 24 h after treatment and 16.2, 37.9, and 41.9% respectively, 48 hr after treatments. Treatment of pBMEC with SSRI + MAOI, resulted in similar decreases in TEER seen with SSRI treatment alone. In conclusion, while both SSRI and MAOI resulted in tight junction disruption in pBMEC. SSRI resulted in larger decreases in TEER relative to the control when compared to MAOI treatments. *Project supported by NRI Grant #2007-35206-17898 from USDA-CSREES.*

Key Words: serotonin, tight junctions, serotonin reuptake transporter

553 Detection of bioluminescent *Staphylococcus aureus* through bovine mammary gland tissue *ex vivo*. J. Curbelo*, K. Moulton, E. Schenck, and S. Willard, *Mississippi State University*, *Mississippi State*.

Mastitis infections caused by *Staphylococcus aureus* (*S. aureus*) causes serious problems for the dairy industry due to its high degree of pathogenicity, and new models are needed for monitoring mastitis infections. The objectives of this study were 1) to conduct photonic imaging (PE) of a transformed bioluminescent *S. aureus*-lux (Caliper Life Sci.) through bovine mammary gland tissue (BMGT); and 2) to evaluate the significance of an optical clearing agent (OCA; corn syrup, 75%) in increasing transference of PE through BMGT. To accomplish this, n=10 bovine mammary quarters with intact teats were excised in half (n=20 sections) and placed over 5 ml of concentrated *S. aureus*-lux inoculums (3.5×10^{14} CFU) inside a black plastic box (opened top) for imaging and PE quantified in relative light units per second (RLU/s). Then, one of the teat sections was treated with OCA for 3 h and the other section was used as control and imaged, as previously described. Due to the high degree of variation of PE between the 20 teat sections, they were categorized by color (black, mixed and white). The mean PE of all teats (non-OCA treated) was 2.30 ± 0.53 RLU/s. However, when analyzed by color, PE through black teats were significantly lower than mixed and white teats ($P=0.01$; 0.68 ± 0.08 vs. 3.77 ± 1.50 and 3.48 ± 0.78 RLU/s, respectively). In addition, when applying OCA to teats, resulted in a greater detection of PE numerically, but not statistically ($P=0.18$); however when the significance of the OCA was evaluated by color, a higher PE was found in mixed colored teats treated with OCA vs non-OCA treated ($P=0.01$; 1.44 ± 0.12 vs 0.53 ± 0.05 RLU/s, respectively). In summary, this study indicates that detection of *S. aureus*-lux through BMGT is questionable due to the low PE detected; however, higher PE were detected through white and mixed colored teats. The OCA used in this study did not increase PE overall. For future studies, the color of the teats may need to be considered due to differences in PE transference, and further studies are needed to enhance penetration of the dense tissue of the mammary gland for photonic pathogen detection.

Key Words: *S. aureus*, biophotonics, mammary gland tissue

Nonruminant Nutrition: Minerals and Vitamins

554 Effects of phytase supplementation on apparent and standardized total tract digestibility of P in corn, soybean meal, and distillers dried grains with solubles (DDGS) fed to growing pigs. F. N. Almeida* and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was conducted to measure the apparent total tract digestibility (ATTD) and the standardized total tract digestibility (STTD) by growing pigs of P in corn, soybean meal (SBM), and distillers dried grains with solubles (DDGS) without and with supplementation of microbial phytase. Seven diets were prepared. Two diets were based on corn, 2 diets were based on SBM, 2 diets were based on DDGS, and 1 diet was a P-free diet. Corn, SBM, or DDGS were the only sources of P in the diets. One of the diets with each ingredient contained no microbial phytase while the other diet contained 500 units/kg of phytase (Optiphos, Enzyvia LLC, Sheridan, IN). A total of 42 growing barrows (initial BW: 13.5 ± 3.9 kg) were randomly allotted to the 7 dietary treatments with 6 pigs per treatment. All pigs were fed experimental diets for 10 d with the initial 5 d being an adaptation period to the diet, whereas feces were collected quantitatively during the final 5 d of the experiment using the marker to marker procedure. The ATTD of P was calculated for corn, SBM, and DDGS and the effect of microbial phytase was calculated as well. The basal endogenous losses of P (ELP) were measured from pigs fed the P-free diet and values for ATTD of P in the 6 P-containing diets were corrected for the basal ELP to calculate STTD values for P in each of these diets. Results showed that the addition of phytase increased ($P < 0.001$) ATTD of P from 19.9 to 57.8% in corn and from 41.5 to 68.4% in SBM, but the ATTD of P in DDGS without phytase (68.6%) was not different from the ATTD of P in DDGS with phytase (71.0%). The ELP was 199 mg/kg DMI. The addition of phytase also increased ($P < 0.001$) STTD of P in corn and SBM (from 26.4 to 64.4% and from 48.3 to 74.9%, respectively), but the STTD values of P in DDGS without and with phytase (72.9 and 75.5%, respectively) were not different. In conclusion, the addition of phytase increased the ATTD and STTD of P in corn and SBM, but had no influence on the ATTD and STTD of P in DDGS.

Key Words: digestibility, pigs, phosphorus

555 Determination of the stability of Zn, Mn, Cu and Fe glycinates in aqueous solution by electrospray QqTOF mass spectrometry. S. Oguey*[1], V. Vacchina[2], R. Lobinski[3], and D. Bravo[1], [1]*Pancosma*, *Geneva, Switzerland*, [2]*UT2A*, *Pau, France*, [3]*CNRS*, *Pau, France*.

The crystalline structure of trace mineral complexes based on glycine (BT) was well known, however setting analysis methods of the products in diluted media (feed, stomach juice, plasma,...) required a previous identification and characterisation of the complexes existing in aqueous solution. The chemical structure of BT with elements of the first transition series (Fe, Cu, Mn and Zn) in aqueous solution was investigated by mass spectroscopy with an electrospray QqTOF mass spectrometer (ESI-QqTOF-MS) either in full scan TOF mode or in tandem mass spectrometry (MS/MS) mode. Each BT was dissolved in a 50% methanol and 10 mM ammonium acetate buffer at pH 7. BT Fe solutions were previously degassed to prevent iron oxidation and iron hydroxide precipitation. Once the chemical structures determined at pH 7, the pH of the BT solutions was varied from 2 to 7 by step of 1 in order to determine the stability of the complexes in solution, and the evolution of the amount of the complex and free glycine ions was observed. BT in aqueous solution at pH 2 were still detected as glycine complexes. The chemical structure was slightly different from the structure found in solid, except for manganese which was identical. Their general formula

was $[M(Gly)(SO_4)(H_2O)_x]_n$. For M=Zn and M=Fe, 2 complexes were detected (n=1, x=1 and n=2, x=0), for M=Cu, 3 complexes were found (n=1, x=1; n=2 x=1 and n=3 x=0) and for M=Mn, 4 anhydrous (x=0) complexes were observed (n=1,2,3,4). All the complexes were detected on the whole pH range. An acid pH induced a partial degradation of the complexes, as free glycine seemed to be more abundant while the acidity of the solution was increased. The small complexes were more degraded than the larger complexes. The identification of glycine complexes in aqueous solution rendered possible the development of analytical traceability methods.

Key Words: chelate, traceability, trace mineral complex

556 Analysis of Zn, Mn, Cu and Fe glycinates by size-exclusion liquid chromatography coupled to an inductively coupled plasma mass spectrometry detection. S. Oguey*[1], V. Vacchina[2], R. Lobinski[3], and D. Bravo[1], [1]*Pancosma, Geneva, Switzerland*, [2]*UT2A, Pau, France*, [3]*CNRS, Pau, France*.

Analyzing trace mineral complexes based on glycine (BT) in diluted media (feed, stomach juice, plasma, etc.) required us to find separation conditions where BT could be detected specifically. The intent of the study was to investigate size exclusion chromatography (SEC) with an inductively coupled plasma mass spectrometer detector (ICP-MS) to determine the stability of BT on a chromatographic column and to separate the glycine complexes from metal sources present in the matrix (like metal sulfates). Ammonium acetate (AAC) was chosen as a buffer and the mobile phase was optimized in terms of ionic strength (10 to 200 mM AAC) and pH (6, 7.4 and 8). A SEC column with an optimal separation range between 0.1 and 7 kDa was chosen. The BT solutions were injected with the selected mobile phase and the ICP-MS data were recorded. The metal remaining on the column was eluted by EDTA, which was removed before the next injection. The recovery was evaluated by comparison of the quantity of metal injected with the quantity collected at the retention time of the glycinate. BT Cu and Mn were eluted with an ionic strength equal or over 10mM AAC. Both were stable at pH 6 and 7.4. At pH 8.5 BT Cu was stable while BT Mn slightly interacted with the column. The stability of BT Zn was maximized with a high ionic strength (200 mM AAC) and a neutral pH. BT Fe required a deoxygenated mobile phase to avoid oxidation and precipitation in the column, an ionic strength of 40 mM AAC or higher, and a slightly acid or neutral pH. At 200 mM AAC and pH 7.4, the recovery was always over 85% for all 4 BT. Metal sulfates also had variable behaviors. Zinc sulfate did not elute from the column while copper, iron and manganese sulfate eluted with a slight time decay. Consequently size-exclusion could be used as a purification method for BT.

Key Words: chelate, traceability, size-exclusion chromatography

557 Femurs are more accurate than fibulas as predictors of whole body bone mineral content in growing pigs. T. D. Crenshaw*, L. E. Hoffman, J. R. Danielson, and D. K. Schneider, *University of Wisconsin*, *Madison*.

An assessment of skeletal tissue is considered standard procedure for quantifying animal responses to supplemental sources and amounts of Ca and P. If the primary concern involves entire animal responses, then a measure of whole body bone mineral content offers a logical standard. However, individual excised bones are often used to minimize costs and expedite project completion. Justification for selection of a specific bone is often vague and dependent on ease of collection rather than documented accuracy of the individual bone as a reliable predictor. Variable responses in nutrient bioavailability among experiments may be explained, in part, by the bone chosen for assessment. The pig fibula has been proposed as the preferred bone based on ease of collection and processing. The current objective was to compare accuracy of fibula and femur ash as predictors of whole body bone mineral content in growing pigs. Data were collected from 96 pigs (~ 25 kg final wt.) that were fed diets with various concentrations and sources of Ca and P over a 27 d trial. Pigs were scanned with a GE Lunar Prodigy DXA instrument (software version 10.10.038, adult standard scan mode) to determine whole body bone mineral content (BMC, g). Pigs were killed and the ash content of the fibula and femur from the right leg were determined. Regression analysis were used to predict whole body BMC from either fibula or femur ash. Femur ash predicted BMC ($R^2 = 0.94$) and showed minimal deviation in residual patterns or slope of responses across BMC values. However, fibula ash had a lower prediction of BMC ($R^2 = 0.78$) and deviated with BMC magnitude. Fibula ash over estimated BMC at low values, but under estimated BMC values at high values. The pattern in fibula ash allowed a reduction in the ability to detect differences between mineral sources and allowed a bias in detection of differences in relative bioavailability compared with estimates based on femur ash or whole animal BMC. Thus, femurs provide a more accurate assessment of mineral status in young growing pigs than fibulas.

Key Words: ash, bioavailability, DXA

558 Effect of supplemented mined humate on growth, loin quality, and pathological status of liver and kidneys in pigs. C. M. Ballou*, Y. Zhao, Y. B. Kim, A. C. Chaytor, and S. W. Kim, *North Carolina State University*, *Raleigh*.

This study used mined humate from Utah (LiveEarth Prodcuts, Emery, UT) to test its supplemental effect on growth, loin quality, and liver health of pigs. Forty-eight pigs at 24.0±0.8 kg BW were allotted to 2 treatments, 6 replicates per treatment, and 4 pigs per pen. Treatments were CON (control) and HA (0.5% humate). Pigs were fed the assigned experimental diets ad libitum for 6 wks. Body weight and feed intake were measured biweekly. At the end of wk 6, 2 pigs representing the average BW of each pen were selected and bled (8 mL) through jugular vein at 0900. After bleeding, pigs were euthanized to collect loin, liver, and kidney. Loin samples were used for quality measures including loin eye area, loin color, marbling score, and fat content. Serum samples were used to measure indicators of liver function including levels of creatinine, total protein, albumin, total bilirubin, alkaline phosphatase alanine aminotransferase, aspartate aminotransferease, and cholesterol in serum. Liver and kidneys were weighed and tissue samples were used for histological evaluation for tissue damage measurements including vacuolation, necrosis, inflammation, megakaryosis, fibrosis, and bile ductule hyperplasia. Pigs fed HA tended to grow faster (P=0.054, 917.2 vs. 868.5 g/d) than pigs fed CON during 6 wk feeding period. Feed intake (2.08 vs. 2.03 kg/d) and gain/feed ratio (0.44 vs. 0.43) did not differ between treatments. Loin eye area, loin color, marbling score, and loin fat content did not differ between treatments. Measurements for liver function test did not differ between treatments. Weight of liver and kidneys did not differ between treatments. Microscopic examinations of the livers and kidneys did not reveal any evidence of toxicity in both CON and HA groups. Collectively, dietary supplementation of mined humate at 0.5% can improve the growth of pigs but did not cause clinical or pathological changes in the liver and kidneys of pigs.

Key Words: growth, humate, pig

559 Effects of EcoCare® Feed on mineral excretion of pigs during the finishing phase. T. Walraven*[1], S. Carter[1], M. Lachmann[1], J. Bundy[1], J. Jarrett[1], and B. De Rodas[2], [1]*Oklahoma State University, Stillwater*, [2]*Land O'Lakes Purina Feed, Gray Summit, MO*.

We have previously reported that EcoCare® Feed reduced N and P excretion of finishing pigs without affecting growth performance or carcass traits. To determine mineral excretion, eighty crossbred (D x (L x Y)) pigs (30 kg BW) were blocked by BW and sex, and randomly allotted to 1 of 2 dietary treatments. Pigs were housed in an environmentally-controlled building with 4 identical rooms (20 pigs/room, 2 rooms/trt). Each room contained a shallow pit, pull plug system. A fortified corn-soybean meal-based diet served as the control. The test diet (EcoCare®, EC) was similar to the control diet except that CP and available P were reduced (~2.6% units for CP; ~0.11% unit for avail. P) with additions of Lys, Thr, Met, EC Pak (containing phytase) and EC premix. To maintain similar Ca:P ratio, Ca content of the EC diet was reduced. The EC premix provided approximately 20% less Fe, Zn, Cu, and Mn than the mineral premix used in the control diet. All trace minerals were included in an inorganic form with the exception of Se. Pigs and feeders were weighed at each phase change, and pit volume was measured. Feed and pit samples were collected for mineral analysis. On d 0 and 122, 6 and 24 pigs (6/room), respectively, were ground to estimate initial and final body composition. There was no difference ($P > 0.10$) in initial or final ash or mineral concentration; thus, accretion was similar ($P > 0.10$) for pigs fed the control or EC diet. The intake of minerals was reduced ($P < 0.05$) for pigs fed EC. The excretion (g/d) of Ca (7.44 vs. 4.51), P (8.2 vs. 5.7), K (18.4 vs. 14.6), Mg (2.91 vs. 2.55), S (2.12 vs. 1.79), Fe (0.433 vs. 0.343), Zn (0.247 vs. 0.205), Cu (0.026 vs. 0.020), and Mn (0.080 vs. 0.064) was reduced ($P < 0.05$) for pigs fed EC compared to those fed the control. In general, the excretion of minerals as a % of intake was reduced ($P < 0.05$) for pigs fed EC. These results suggest that EcoCare® Feed reduced mineral excretion without affecting mineral accretion or growth performance.

Key Words: pigs, mineral, excretion

560 Effects of combining multiple dietary manipulations on growth performance and nutrient excretion of finishing pigs. T. Walraven*, S. Carter, J. Jarrett, M. Bible, and H. J. Kim, *Oklahoma State University, Stillwater*.

Eighty-eight crossbred (D × (L × Y)) pigs (32 to 114 kg BW) were used to evaluate the effects of reducing dietary CP, Ca, and P with the additions of phytase and organic trace minerals on nutrient excretion during a 94-d finishing period. Pigs were stratified by sex, weight, ancestry and randomly allotted to 1 of 2 dietary treatments. Pigs were housed in an environmentally-controlled building with 4 identical rooms. Each room contained a shallow pit, pull plug system (22 pigs/room, 2 rooms/trt). Dietary treatments were fed in 4 dietary phases and consisted of a fortified corn-soybean meal diet and a Reduced Excretion (REx) diet. The REx diet had a 3% units decrease in CP with Lys, Thr, Met, and Trp added as needed and a reduction in available phosphorus of 0.10% with phytase inclusion. Also, in the REx diet, monocalcium P replaced dicalcium P and CaCl replaced 50% of the $CaCO_3$ in the control diet. Furthermore, organic sources of Fe, Zn, and Cu replaced inorganic sources of these minerals in the control diet. All diets within phase were formulated on a SID lysine basis (0.92, 0.79, 0.65, and 0.56% for Phases 1 to 4). Feed and slurry samples were collected weekly along with pig weights, feed intake, pit volume, and pH of slurry. Diet did not affect ($P < 0.10$) ADG (822 vs. 839 g), ADFI (2.27 vs. 2.28 kg), or G:F (0.365 vs. 0.367). Daily DM intakes were similar ($P > 0.10$), but N (57.8 vs. 47.4 g/d) and P (11.1 vs. 8.6 g/d) intakes were reduced ($P < 0.05$) for pigs fed REx. Also, slurry pH for pigs fed REx was reduced (7.4 vs. 6.8; $P < 0.05$). Slurry DM concentration was similar ($P > 0.05$), but slurry N (15.1 vs. 11.8%) and P (2.84 vs. 1.98%) tended to be reduced ($P < 0.10$) with REx. The daily excretion of DM, N (33.9 vs. 24.4 g) and P (6.8 vs. 4.5 g) for pigs fed REx was reduced ($P < 0.05$) compared to those fed the control. These results suggest that combining dietary manipulations is an effective method of reducing N and P excretion. *This project was supported by the National Pork Board.*

Key Words: pigs, diet, excretion

Physiology and Endocrinology: Impact of Gonadal Steroids on Brain Development and Function

561 Feedback and fitness: Consequences of non-classical estrogen receptor α signaling in the brain. J. E. Levine*, *Northwestern University, Evanston, IL*.

Ovarian estrogens exert critically important actions in hypothalamic neurons to regulate ovulatory cyclicity, reproductive behaviors, and energy homeostasis. Estrogen receptor alpha (ER) appears to mediate most of these effects, as disruption of ER signaling leads to infertility and metabolic syndrome. ER signaling mechanisms may include "classical genotropic" effects mediated by direct binding of receptor dimers to DNA, "non-classical genotropic" effects involving tethering of ERs to other transcription factors, and "non-classical non-genotropic" actions mediated by cytoplasmic ERs coupled to membrane-initiated signal transduction pathways. Our studies make use of novel ER mutant mouse models to ascertain the cellular mechanisms by which ER mediates E2 effects on these physiological and behavioral processes. We have utilized a novel mutant ER knock-in mouse model, which confers non-classical genotropic and non-genotropic signaling in the absence of classical signaling, to determine that non-classical ER signaling can convey E2 effects integral to homeostatic feedback control of reproductive hormone secretions, as well as E2 actions governing paracopulatory behavior and body weight regulation.

Key Words: estrogen, body weight, reproduction

562 Nongenomic actions of estrogens directly on the ovine pituitary facilitates LH secretion. T. Nett*[1], A. Arevalo-Arreguin[1], and T. Davis[2], [1]*Colorado State University, Fort Collins*, [2]*University of Idaho, Moscow*.

In addition to the well known genomic actions of steroid hormones, there are nongenomic effects of these hormones that are only now being recognized. Our laboratory has investigated the nongenomic effects of estradiol (E) on secretion of LH in sheep. For these studies, we have employed E conjugated to either BSA (E-BSA) or to a novel 15 amino acid peptide (E-PEP), neither of which appear to induce classic genomic effects attributed to estradiol. Both compounds (as well as E) inhibited ($P<0.01$) GnRH-induced secretion of LH from cultured ovine pituitary cells in a dose dependent manner. Each of the estrogens essentially abolished the LH secretion induced by 2 nM GnRH when present in the culture media at 20 nM or greater. Based on these data, ovariectomized (OVX) ewes were administered E or E-BSA and concentrations of LH were monitored for the next 24 hr. Both E and E-BSA resulted in a rapid decrease (<20 min, $P<0.01$) in serum concentrations of LH. Interestingly, only E decreased secretion of FSH. Likewise, E, but not E-BSA stimulated an ovulatory-like surge of LH beginning approximately 12 hr after treatment. Although there was no ovulatory-like surge of LH in ewes treated with E-BSA, there was a slight increase in LH at the

time an ovulatory-like LH surge would have been expected. These data indicate that acute inhibition of GnRH-induced LH secretion is mediated by a nongenomic action of estradiol directly on gonadotropes. *Supported by NRI grant No. 2005-35203-15376 from the USDA-CSREES.*

Key Words: estrogen receptors, nongenomic, luteinizing hormone

563 Actions of androgens in regulating sexual differentiation of the sheep brain and consequent effects on sexual behavior. C. E. Roselli*[1,2] and F. Stormshak[2], [1]*Oregon Health and Science University, Portland*, [2]*Oregon State University, Corvallis*.

During a critical period in early life, the male-typical mammalian brain develops via direct actions of testicular testosterone, while the female-typical brain develops in the absence of significant exposure to testosterone. Many sex-specific behaviors and neuroendocrine functions that will later be expressed in adults are programmed during this time. In our laboratory the domestic ram is used to study the early programming of the neural mechanisms underlying same sex partner preference. As many as 8% of domestic rams are sexually attracted to other rams (male-oriented) in contrast to the majority of rams that are attracted to estrous ewes (female-oriented). Male-oriented rams thus express a female-typical sexual attraction that may have arisen from atypically low exposure to testosterone during early fetal life. To test this hypothesis we compared the structure of the preoptic area/anterior hypothalamus among female-oriented rams, male-oriented rams and ewes. We found that sexual partner preferences correlate with the volume of the ovine sexual dimorphic nucleus (oSDN) and the number of aromatase-expressing neurons it contains. We also studied the ontogeny of the oSDN and found that it develops prenatally under the influence of testosterone arguing that the circuitry for sexual attraction is assembled prior to birth. The high level of aromatase mRNA in neurons of the oSDN raised the question of whether local aromatization of testosterone to estradiol is required to masculinize brain structure and sexual attraction. Prenatal treatment with an aromatase inhibitor did not alter the expression of male-typical behaviors, including sexual preference for females or neuroendocrine responses; nor did it reduce the size of oSDN in genetic males. These results argue that male-typical sexual differentiation of the sheep brain does not depend on locally synthesized estradiol, but rather is programmed through androgen receptor mechanisms. *Supported by NIH grant R01 RR014270.*

Key Words: sexual partner preference, sexual differentiation, sexually dimorphic nucleus

Production, Management and the Environment: General

564 Heat stress does not alter immune status of Holstein calves but slick genotype confers reduced immune function. J. W. Bubolz*, S. Tao, B. C. do Amaral, M. J. Hayen, T. A. Olson, and G. E. Dahl, *University of Florida, Gainesville*.

Environmental factors such as photoperiod and heat stress influence health and hormone secretion in dairy cattle. Genetic background may also modulate immune status in cattle. The objective of the present study was to test the hypothesis that heat stress depressed immune function in cattle. A second objective was to examine the affect of the *Slick hair* gene on immune status. Calves defined as slick-haired possess a dominant gene of Senepol orgin that when expressed produces a very short, sleek coat. Slick (n=4) and wild-type (n=4) calves were kept in controlled-temperature chambers for a period of 9 weeks. Calves were exposed to heat stress and neutral thermal conditions with a 1 week pre-treatment acclimation and 2 week recovery period between temperature treatments in a 2x2 cross-over design. Dry matter intake (DMI), water intake and infrared (IR) skin temperature were measured daily. Jugular blood samples were collected weekly and evaluated for lymphocyte proliferation, neutrophil phagocytosis and neutrophil oxidative burst activity. Relative to thermoneutral condtions, heat stress increased AM (35.0 vs. 30.6°C; $P < 0.001$) and PM skin temperatures (36.8 vs. 31.6°C; $P < 0.001$). Calves under heat stress increased daily water consumption (29.2 vs. 17.8 L; $P < 0.04$) and decreased DMI as percentage of body weight (2.29 vs. 3.83%; $P < 0.001$) compared with the thermoneutral period. Relative to thermoneutral treatment, no difference in any immune variable was observed during heat stress. However, neutrophils from wild type calves had greater phagocytic ($P < 0.01$) and oxidative burst ($P < 0.07$) activity compared with slick-haired calves. In addition, lymphocytes from wild type calves had greater proliferation relative to slick calves ($P < 0.05$). Results indicate that wild type calves had improved immune status compared to slick-haired calves regardless of environmental temperatures. Immune status of slick-haired calves was depressed relative to wild type, but heat stress did not influence immune status of Holstein calves in controlled-temperature chambers.

Key Words: slick-haired calves, heat stress, immune status

565 Clinical stopping rules in sequential field trials. D. B. Nielsen* and C. Enevoldsen, *Faculty of Life Sciences, Department of Large Animal Clinical Sciences, University of Copenhagen, Denmark*.

Trials performed by field veterinarians can integrated in health programs in large dairy herds to enhance treatment efficiency. The objectives of this study were to identify the requirements to trial designs if they were to be accepted and performed non-subsidized by veterinarians in commercial herds and, by means of simulation, to illustrate a potentially useful design. Semi-structured research interviews of 12 veterinarians working within a similar type of health program were conducted. The veterinarians elaborated on their experience, present methods and future needs for evaluation of efficiency of metritis treatments (as a general disease model). Qualitative analysis was performed to identify coherent meanings across interviews. We performed a simulation of a sequential design (double triangular test with 'Christmas tree correction') with the PEST 4 program ®. This design can potentially reduce the sample size by early stopping based on interim analysis of an important parameter and adjustable significance levels. The interviews showed that all the interviewed veterinarians preferred to evaluate efficiency by means of production parameters like milk production and fertility. However, the majority of the veterinarians emphasized that clinical cure (e.g., no need for follow-up treatment) imposed a constraint. They expressed unwillingness to perform trials without the possibility to apply early stopping in case of clinically significant adverse effects. The simulation (10,000 runs, alpha 0.05, power 0.8) showed that if an existing difference in probability of follow-up treatment was 0.3 in favor of the conventional treatment, a sample size of 54 cows (SD 19) would result in early stopping of the trial (fixed sample size of 72 cows). The simulation indicated 79% probability of showing inferiority of the experimental treatment and 21% probability of showing no difference between treatments. We conclude that implementation of scientifically acceptable production-oriented field trials could be accepted by field veterinarians as integrated parts of a health program if the designs include possibilities for early stopping based on valid statistical evaluations of clinical cure.

Key Words: field trial, stopping rules

566 Modeling cow body shape for objective estimation of body condition score from digital images. G. Azzaro[1], M. Caccamo*[1], J. D. Ferguson[2], S. Battiato[3], G. M. Farinella[3], G. C. Guarnera[3], G. Puglisi[3], and G. Licitra[1,4], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*University of Pennsylvania, Kennett Square*, [3]*IPLAB, University of Catania, Italy*, [4]*D.A.C.P.A., University of Catania, Italy*.

Body Condition Score (BCS) is considered an important tool for management of dairy cattle. The feasibility of estimating the BCS from digital images has been demonstrated in recent works. Regression machines have been successfully employed for automatic BCS estimation, taking into account information of the overall shape or information extracted on anatomical points of the shape. Despite the progress in this research area, such studies have not addressed the problem of modeling the shape of body cows to build a robust descriptor for automatic BCS estimation. Moreover, a benchmark dataset for quantitative evaluation and comparison of different methods for automatic estimation of BCS from images is still missing. The main objective of this study was to develop a technique able to describe the shape of body cows in a reconstructive way. Shapes of cows are reconstructed by using a linear combination of basis shapes obtained through robust principal component analysis used to model the variability of the shapes of cows within a large set of examples. In this manner, cows body shape was described considering the different variability from the average shape. The method produced a compact description of the shape to be used for automatic estimation of BCS through kernel regression approach. A benchmark dataset useful for dairy cattle research purpose, available through the Internet, was also built. The images used to build the benchmark dataset were taken by using 2 cameras placed above an exit alley from the milking robot. The cameras were positioned at 3m from the ground and in such a position to allow capturing images of the dorsal area and of the rear of cows. The BCS of each cow was estimated on site by 2 technicians and properly associated to the cows' images by means of a software tool developed ad-hoc, used for anatomical point annotation and labeling. The benchmark dataset contained images with associated BCS, anatomical points, and shapes. It was used for quantitative evaluation. Preliminary results showed that the proposed model was robust in terms of cow body shape description and accurate in terms of BSC estimation.

Key Words: body condition score, digital imaging, body shape

567 Effects of calf bedding acidification on microbial content and fly larvae density. M. S. Calvo*, T. L. Armitage, Y. E. Pan, A. Gerry, J. McGarvey, and F. M. Mitloehner, *University of California, Davis*.

Environmental stressors, such as high fly density, can impact calf well-being. Past studies have demonstrated that microbes provide nutrients to growing larvae, which are necessary for the development and survival of the adult fly. Sodium bisulfate (SBS) is an acidifier that reduces the pH of its surrounding environment, which potentially creates a medium that neither microbes nor larvae can thrive in. Two studies were conducted to investigate the application of SBS to rice hull bedding in calf hutches to reduce both fly larvae density and microbial content. A completely randomized design with four SBS treatment levels and four replications was used. Exp. 1 tested the effects of SBS on larvae density and Exp. 2 the effects of acidification on microbial levels. In Exp. 1, SBS was applied to 16 one-liter calf bedding samples, each containing 2500 house fly (*Musca domestica* L.) eggs and calf slurry. The control (CON) bedding with 0 g of SBS was compared to three treatment applications with 8.9, 17.7, and 26.5 g of SBS. Total larvae counts were reduced in all SBS treatments vs. CON ($P < 0.05$), but the three SBS treatments were similar to each other. CON showed greater live larvae counts ($P < 0.05$), but the three SBS treatments were similar to each other. In Exp. 2, the same SBS treatments as before were applied to calf bedding samples containing calf slurry and analyzed for survival of total aerobic bacteria counts. A correlation was observed between time and SBS treatment: an increase in both frequency and amount of SBS decreased microbial counts ($P < 0.001$). The results of these studies demonstrate the effectiveness of acidification on larvae density and microbial levels, which could have a profound impact on reducing adult fly populations and thereby pest related stress in calves.

Key Words: calf, larvae, welfare

568 Effect of a plant extract on cutaneous inflammation in growing chicks challenged with phytohemagglutinin. J. C. Garcia-Lopez*, G. Alvarez-Fuentes, Y. Jazzo-Pineda, J. M. Pinos-Rodriguez, B. E. Balderad-Gonzalez, and H. I. Contreras-Treviño, *Universidad Autonoma De San Luis Potosi, San Luis Potosi, SLP, Mexico*.

Recently a strong interest has arisen to study natural alternatives to counteract poultry backyard diseases, in rural areas where chick performance is severe affected by different diseases. Several issues have been investigated, such is the case of plants that have showed some bactericide activity, the aim of this study was to test the effect of *Chrysactinia mexicana* extract on Cutaneous Bashopil Hipersensitivity (CBH) response by measuring wing-web inflammation of chicks challenged with Phytohemagglutinin (PHA). 120 Cobb day old chicks were used in a complete randomized design with the following treatments: control (T1), control + PHA (T2); control + *C. Mexicana* + PHA (T3). The plant extract dose used was 20mg /ml per day per bird via esophagus. At 14 d post-hatch birds in treatment 2 and 3 were injected into the wing web with PHA 100 ug/bird, birds were examined by measuring wing web thickness (mm) in the injected wing and the uninjected wing with low pressure digital calipers at 3, 6, 12, 24 and 48 h postinjection. Chick performance was evaluated by feed intake, weight gain and feed conversion ratio. There were no differences ($P>0.05$) in chick performance variables. Inflammation of wing web was different ($P<0.05$) during all the different times of measure, between T2 and T3 with the highest values of thickness for birds challenged without plant extract, birds treated with plant extract and challenged with PHA had lower thickness values. It is concluded that the use of the plant extract *C. mexicana* may have some anti inflammatory activity due to its secondary metabolites and could be a good tool to treat some poultry backyard diseases in rural areas, more studies are warranted to elucidate the possible role of this and other plants to treat poultry diseases.

Key Words: chick, plant extract, inflammation

569 Nutritional value of fresh cocoa husk mucilage as a sole feed for African giant land snail (*Archachatina marginata*). R. A. Hamzat*[1] and J. Babayemi[2], [1]*Ochaja Research Station, Cocoa Research Institute of Nigeria, Egume, Kogi State, Nigeria*, [2]*Department of Animal Science, University of Ibadan, Ibadan, Oyo State, Nigeria*.

The advocate for large-scale afforestation in Nigeria has led to the production of vast quantities of tree crop by-products, which are becoming a nuisance in our plantations. One of such by-products is cocoa husk mucilage (CHM). CHM is the succulent part of the cocoa husk (CH). African giant land snails (AGLS) are known to feed on plant materials and many crop by-products thereby converting the inedible by-products to the edible snail meat. This premier investigation was aimed at evaluat-

ing the potential of cocoa husk mucilage (CHM) as an alternative feed resource to AGLS. 144 AGLS with weight ranging from 20g-45g were used for this study. The experimental snails were allotted into 4 treatments and 3 replicates. Treatments included; 100% PPF (fresh pawpaw leaf) (control), 100% ORP (fresh orange pulp), 100% KNT (fresh kolanut testa) and 100% CHM. This experiment was designed to be completely randomized. Results from the performance assessment of experimental snails showed significant differences ($P<0.05$) in average total weight gain, average total shell length increment, average total shell width increment, average total aperture radius increment. The values of average total weight gain, total average shell length increment, total average shell width increment and total average aperture radius increment were ranked as follows: PPF>CHM>KNT>ORP; PPF>CHM>ORP>KNT; CHM>PPF>ORP>KNT and PPF>ORP>CHM>KNT respectively. Results of carcass analysis showed the dressing percentage of snails fed PPF as 38.46%, ORP 36.9%, KNT, 27.16% and CHM, 33.68%. Statistical analysis showed significant differences ($P<0.05$) in scores for flavour, tenderness and overall acceptability. Average scores for overall acceptability were 7.4 for PPF, 6.9 for ORP, 5.5 for KNT and 6.1 for CHM. Values can therefore be ranked as PPF>ORP>CHM>KNT. Although the cocoa-husk mucilage had lower yield in terms of carcass than PPF and ORP, the study revealed no detrimental effect on nutrient composition of the meat samples. It could therefore be inferred that the use of cocoa husk mucilage in feeding AGL snails enhanced performance.

Key Words: fresh cocoa husk mucilage, sole feed, African giant land snails

570 Acclimation to salinity and survival of Lahontan cutthroat trout *Oncorhynchus clarki henshawi*. J. P. Bigelow*[1,2], W. M. Rauw[2], and L. Gomez-Raya[2], [1]*U.S. Fish and Wildlife Service, Lahontan National Fish Hatchery Complex*, *Reno, NV*, [2]*University of Nevada*, *Reno*.

The goal of this study was to assess the effect of acclimation to salinity on survival of Lahontan cutthroat trout reared at the Lahontan National Fish Hatchery on well water (pH=7.8; Total Dissolved Solids (TDS)=292 mg/L) and challenged with Walker Lake water (pH=9.6; TDS=17,800 mg/L). Six-month-old fish (N=2,400) were assigned to three treatments comprised of 4 replicates (tanks). Fish were acclimated for 0, 3, or 8 days by increasing the ratio of lake water to hatchery water on a daily basis. Blood was collected from fish (n=12) in each of the three tanks in the 3 and 8 day treatments prior to and after acclimation to determine plasma osmolarity(mmoles/Kg). After acclimation, a subsample (n=76) from each tank was challenged with 100% lake water for one week. Mortalities were monitored at two-hour intervals. Fish fork lengths and weights were determined at time of death or at the end of the challenge if they survived. A mixed model was used to estimate the effect of acclimation time on survival time (in hours). Other independent variables were: Fulton's Body condition factor (covariate), fork length (covariate), and tank (random effect nested within acclimation treatment). The effects of acclimation treatment, condition factor and fork length were significant with P-values of 0.048, 0.035, and <0.0001. The least square means for survival at 0, 3 and 8 acclimatizing days were 7.95±5.70, 8.06±5.69, and 28.55±5.70 hours, respectively. Only fish acclimated for 8 days survived the entire challenge experiment, but at a low rate (2.3%). A linear model using plasma osmolarity as dependent variable and acclimation time (fixed), tank (random and nested within acclimation treatment), time of blood collection (fixed), and acclimation time by blood collection time interaction (fixed) as independent variables revealed only significant results for the interaction term (P-value=0.044). Osmolarity (before and after acclimation) increased in fish acclimatizing 3 days (from 251.07 to 262.65 mmoles/Kg) but decreased in fish acclimatizing 8 days (from 258.08 to 244.01 mmoles/Kg). Implications of the results for fish repopulation are discussed.

Key Words: Lahontan cutthroat trout, salinity acclimation

Ruminant Nutrition: Dairy Calves

571 Effects of fat concentration of a high protein milk replacer on calf performance and digestion. T. M. Hill*, H. G. Bateman II, J. M. Aldrich, and R. L. Schlotterbeck, *Akey*, *Lewisburg, OH*.

Fat concentration was varied (14, 17, 20, and 23%; all units on DM basis) in a 27% CP milk replacer (MR) fed at 660 g DM/calf daily to achieve CP to ME ratios from 52 to 57 g CP/Mcal ME. The hypothesis was that high fat concentrations would reduce intake of starter, digestibility, and ADG. Forty-eight Holstein calves (initially 42.4 ± 1.5 kg BW, 2 to 3 d of age) were fed the MR (12 calves/treatment) and were weaned after 28 d. Measurements were continued from d 28 to 56. A 20% CP starter and water was fed ad libitum all 56 d of the trial. Measurements of digestion were made using chromic oxide as a marker in the MR and starter from fecal samples collected on d 19 to 23 from 4 calves/treatment. Selected serum constituents were measured on d 21. Calves were housed individually in pens bedded with straw within a naturally ventilated barn with no added heat between January and March. The barn temperature based on hourly measurements was 2°C. Data were analyzed as a completely randomized design using polynomial contrasts to separate differences in the means. Significance was declared at $P < 0.05$. Pre-weaning apparent digestibility of OM, fat, Ca, and P and serum amylase concentration were linearly reduced as fat increased from 14 to 23% in a 27% CP milk replacer powder fed at 0.660 kg DM/calf daily. Pre-weaning starter intake responded quadratically to fat, being lowest at 14 and 23% fat. A reduction in digestibility and starter intake contributed to less ADG at the higher fat concentrations in the MR. A 27% CP, 17% fat MR with 55 g CP/Mcal ME optimized ADG when fat concentration was varied from 14 to 23%.

Key Words: fat, digestion, calf

572 Effects of free-access feeding and milk replacer acidification on calf performance and development of digestive anatomy. C. G. Todd*[1], T. J. DeVries[2], K. E. Leslie[1], J. M. Sargeant[1], N. G. Anderson[3], and S. T. Millman[4], [1]*Department of Population Medicine, University of Guelph*, *Guelph, ON, Canada*, [2]*Department of Animal Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, ON, Canada*, [3]*Ontario Ministry of Agriculture, Food and Rural Affairs*, *Fergus, ON, Canada*, [4]*Veterinary Diagnostic and Production Animal Medicine, Iowa State University*, *Ames*.

The aim of this research was to examine the effects of free-access feeding and milk replacer acidification on calf performance and development of

digestive anatomy. Holstein male calves (n=16) were randomly assigned at birth to 1 of 4 feeding programs: 1) free-access (ad libitum) feeding of milk replacer (22% CP and 17% fat), 2) free-access feeding of acidified milk replacer, 3) restricted (6 L/d) feeding of milk replacer and 4) restricted feeding of acidified milk replacer. Formic acid was used to acidify the milk replacer to a target pH of 4.0 to 4.5. Milk replacer, starter ration and water intakes were measured daily, while body weight gain was determined weekly for each calf. One calf from each feeding program was euthanized at 28, 42, 56 and 70 d of age. Rumen tissue samples were collected and wall thickness, papillae length, width and density were measured. Multivariable regression models were constructed to examine the effects of free-access feeding and acidification on important outcome variables. Free-access feeding resulted in higher milk consumption (9.2 vs 5.0 L/d, $p<0.01$); acidification did not affect milk intake ($p>0.05$). Restricted-fed calves began consuming starter ration significantly earlier (HR=12.3, $p<0.01$) and had greater starter intake (3.8 vs 1.0 kg, $p<0.01$) over the free-access calves. Milk replacer acidification was associated with reduced time to initiation of starter consumption (HR=3.7, $p<0.05$). Free-access calves had higher body weight gain than restricted-fed calves (26.0 vs 14.3 kg, $p<0.05$); acidification did not affect body weight gain ($p>0.05$). Restricted-fed calves had increased rumen wall thickness ($p<0.05$), longer ($p<0.05$) and wider papillae ($p<0.05$), and reduced papillae density ($p<0.05$); acidification did not affect rumen development ($p>0.05$). These results indicate that free-access feeding of milk replacer supports improved body weight gain, but delays starter ration consumption and rumen development. Milk replacer acidification had little impact on calf performance and digestive anatomy development.

Key Words: milk replacer, free-access feeding, acidification

573 Effect of weaning age and feeding rate of a high protein calf milk replacer on diet digestibility. T. M. Hill*, H. G. Bateman II, J. M. Aldrich, and R. L. Schlotterbeck, *Akey*, *Lewisburg, OH*.

A 27% CP, 17% fat, 55 g CP/Mcal ME milk replacer (MR; all units on DM basis) was fed at 660 g DM/calf daily and calves were weaned at either 28 (Treatment A) or 42 d (Treatment B). Additionally, the same MR was fed at rates stepped up to 1090 g DM/calf daily and calves were weaned at 42 d (Treatment C). The hypothesis was that calves weaned early would gain less BW and that calves fed up to 1090 g MR would have reduced digestion of starter post-weaning. Holstein calves (initially 42.8 ± 1.5 kg BW, 2 to 3 d of age) were fed the MR (5 calves/treatment). Measurements were made through 56 d. A 20% CP starter and water were fed ad libitum all 56 d of the trial. Measurements of digestion were made using chromic oxide as a marker in the MR and starter from fecal samples collected during three time periods (P1: d 21 to 24; P2: d 36 to 39; P3: d 53 to 56). Additionally, selected serum constituents were measured on d 21, 36, and 56 to correspond with the time periods. Calves were housed individually in pens bedded with straw within a naturally ventilated barn with no added heat between July and September. The barn temperature based on hourly measurements was 24°C. Data were analyzed as a completely randomized design using pre-planned contrast statements to separate the means (A vs. B; B vs. C). Significance was declared at $P < 0.05$. During all periods, starter intake was B > C. During P2 and P3, starter intake was A > B. During P1, Ca digestibility was B > C and g of DM, OM, CP, fat and P digested was C > B. During P2, digestibility of DM, OM, fat, Ca, and P was B > A and B > C. During P3, digestibility of DM, OM, Ca, and P was B > C. During all periods, serum amylase concentration was B > C. Feeding up to 1090 (vs. 660) g MR/calf daily reduced starter intake, serum amylase concentrations, and post-weaning DM, OM, fat, Ca, and P digestibility in calves weaned at 42 d. Weaning at 28 vs. 42 d did not change post-weaning digestibility in calves fed 660 g MR/calf daily.

Key Words: fat, digestion, intake

574 Effects of weaning strategy on calf performance and health status during transition. A. Bach*[1,2], A. Ferrer[2], and J. Ahedo[3], [1]*ICREA*, *Barcelona, Spain*, [2]*Ruminant Production-IRTA*, *Caldes de Montbui, Spain*, [3]*Rancho Las Nieves*, *Mallen, Spain*.

This study aimed to assess whether continuing to offer 2 L/d of milk replacer (MR) at 15% dilution rate after moving animals from individual hutches to groups of 8 at weaning would improve animal performance and immunity, and diminish respiratory afflictions during the transition period (57 to 112 d of life). A total of 160 female Holstein dairy calves (initial BW=72±6.1 kg; age=56±3.2 d) were randomly allocated to one of 2 treatments: weaning in individual hutches (at the age of 57 d) and moved in groups of 8 (Control), or weaning 2 wk after moving (at the age of 71 d) calves from individual hutches to groups of 8 animals. When calves were moved from individual hutches to groups, they also changed diet from a starter to a dry TMR. Feed and MR consumption (by pen) was determined daily for the first 3 wk of study. Body weight was determined at the beginning and at the end of the study. Health condition was monitored daily. In addition, half of the animals in each pen were blood-sampled at 0, 14, and 21 d of the study. Pen was the experimental unit. The proportion of animals affected by respiratory problems was not influenced by treatment (44±5.6% for Control vs 35±5.4% for MR-supplemented calves). However, the number of days until the first respiratory case was greater in the MR-supplemented group (29±2.5 d) than in the Control group (19±2.2 d), and this incidence was lower in the MR-fed than in control calves during the first 4 wk of study. Average daily solid feed intake was greater in Control (3.2±0.14 kg/d) than in MR-supplemented calves (3.0±0.14 kg/d). Solid feed consumption was lower for MR-fed than for Control calves for the first 2 wk (2.6 vs 3.1 kg/d), but it was greater afterwards (3.7 vs 3.5 kg/d). The number of circulating blood lymphocytes decreased when MR was offered compared with Control (2.79±0.69 vs 3.06±0.69 x 10^3 cells/ μL, respectively). Mean platelet volume decreased in MR-fed calves compared with Control. Providing additional MR for 2 wk in groups improved ADG, but failed to sufficiently stimulate the immune system and thus diminish the incidence of respiratory problems during the entire transition period.

Key Words: pneumonia, milk replacer, immunity

575 Determination of oro-sensorial preferences for energy ingredients in weaned calves. C. Montoro*[1], F. Boe[1], I. Ipharraguerre[2], and A. Bach[1,3], [1]*IRTA-Ruminant Production*, *Caldes de Montbui, Spain*, [2]*LUCTA S.A.*, *Barcelona, Spain*, [3]*ICREA*, *Barcelona, Spain*.

The objective of this study was to determine oro-sensorial preferences among common energy feed ingredients used to manufacture calf starters. A total of 28 assays involving 280 calves were conducted to rank calf oro-sensorial preferences for: barley, corn, corn gluten feed, oats, rice, sorghum, wheat, and wheat middlings. To minimize the effect of feed texture, all ingredients were ground at 3 mm. In each assay, 20 naive calves were offered a choice ad libitum of 2 ingredients and feed consumption was monitored every 30 min for 6 h. Each assay involved a group of 20 calves, and each group was used in two different assays

which were conducted 3 and 5 d after weaning. No calf was presented twice with the same ingredient. Oro-sensorial preferences were calculated as the mean difference in feed consumption every 30 min over a 6-h period. The most preferred energy ingredients were wheat, sorghum, corn, and barley; whereas oats, rice, and corn gluten feed were the least preferred (Table 1). Wheat was the most preferred ingredient in all assays but one. On the other hand, corn gluten feed was the least preferred ingredient in all assays but one.

Table 1. Significant differences (*P*< 0.05) in consumption (g/30 min) due to oro-sensorial preferences of several ingredients

Feed1[a]	Feed2[a]	Diff.[1]	Feed1	Feed2	Diff.[1]
W	CGF	10.0	C	R	48.9
W	R	77.9	C	O	44.5
W	O	23.1	C	WM	8.6
W	WM	28.8	C	B	-12.8
W	B	16.8	B	CGF	9.9
W	S	44.2	B	R	59.3
S	CGF	3.5	B	O	66.1
S	R	33.4	B	WM	-16.5
S	O	42.3	WM	CGF	19.5
S	B	21.0	WM	R	19.7
S	C	12.8	WM	O	-55.3
C	CGF	47.4	R	CGF	12.1

[1] Feed1 - Feed2; [a]C = Corn; B = Barley; CGF = Corn gluten feed O = Oats; R = Rice; S = Sorghum; W = Wheat; WM = wheat middlings

Key Words: palatability, preferences, intake

576 High dietary iron negatively impacts gene products important in iron and manganese metabolism in young calves. S. L. Hansen*, M. S. Ashwell, R. S. Fry, and J. W. Spears, *North Carolina State University*, *Raleigh*.

Fourteen weaned Holstein calves were used in a 56-d experiment examining the impacts of high dietary iron (Fe) on proteins involved in Fe and manganese (Mn) metabolism. Calves were stratified by weight and randomly assigned to one of two diets: 1) no supplemental Fe (normal Fe) or 2) 750 mg supplemental Fe/kg DM (high Fe). Blood was collected on d 0, 35 and 56. At the end of the trial 6 calves per treatment were harvested and liver and duodenal scrapings were collected for analysis. Feeding a diet high in Fe decreased ($P < 0.05$) average daily gain, dry matter intake and feed efficiency. Hemoglobin and serum Fe concentrations did not differ due to dietary treatment. Feeding a diet high in Fe increased concentrations of Fe in the liver ($P = 0.03$), but did not affect heart or duodenal Fe. Duodenal Mn concentrations were lowered ($P = 0.05$) by feeding a high Fe diet, but liver and heart Mn concentrations were not affected. As determined by real-time RT-PCR, relative hepatic expression of the gene which encodes the Fe regulatory hormone hepcidin was 5-fold greater ($P < 0.01$) in calves fed high dietary Fe. Hepcidin is released in response to increased Fe status and binds to the Fe export protein ferroportin causing it to be degraded, thereby reducing dietary Fe absorption. Confirmation of this result was achieved through Western blotting of duodenal protein which revealed that expression of ferroportin was decreased ($P = 0.03$) due to high dietary Fe. Duodenal expression of divalent metal transporter 1 (DMT1), a Fe import protein which can also transport Mn, tended (P = 0.13) to be reduced by high dietary Fe. In summary, feeding calves a diet high in Fe induced a signal cascade (hepcidin) designed to reduced absorption of Fe (via reduced expression of ferroportin and DMT1) in a manner similar to that reported in rodents. Additionally, reduced levels of DMT1 protein appeared to decrease duodenal Mn, suggesting that Mn is also a substrate for DMT1 in the bovine.

Key Words: cattle, iron, manganese

Ruminant Nutrition: Rumen Microbiology

577 Metagenomics analysis reveals shifts in functional profiles and population dynamics of rumen microbial communities in response to developmental and dietary changes. R. W. Li*[1], M. E. Sparks[1], Y. Huang[2], W. Li[2], E. E. Connor[1], R. L. Baldwin VI[1], C. Li[1], and T. Sonstegard[1], [1]*Unisted States Department of Agriculture, Agricultural Research Service, Bovine Functional Genomics Laboratory*, *Beltsville, MD*, [2]*University of California*, *San Diego*.

Physiologists have long attempted to manipulate rumen fermentation to enhance fibrolytic capacity and reduce proteolytic and methanogenic outputs of the rumen ecosystem. However, successful ruminal fermentation manipulation requires a solid understanding of rumen microbes and their interactions. ~8 gigabases of DNA from 6 metagenomes were generated using next-generation technologies. ~70% of short reads could be assembled into contigs using Velvet. ORFs were predicted using MetaGene, and resultant proteins were annotated using Pfam, TIGRfam and COG. Higher level metagenome features, such as phylogenetic profiles, functional compositions and population dynamics, were compared between relevant rumen microbial communities. For example, 34,948 and 14,700 proteins identified from 2 of the 6 communities studied (#911 and #103) belong to roughly the same number of Pfam protein families (1,983 and 1,835, respectively), of which ~80% were identical. Interestingly, 414 protein families were unique to #911 (from calf fed hay) while 266 families unique to #103 (from calf fed milk only). Thus, differences in biological functions and ecosystem outputs may be deduced. Both glycoside hydrolase (GH) families 70 and 42 were unique to #911, suggesting ruminal degradation of cellulose and xylans as a primary function of this community. One of the most abundant families was GH family 43, which contains arabinase activities for degradation of plant cell wall arabinan, reflecting more active fibrolytic activities in #911. Moreover, unique expression of >12 other GH families in the #911 community demonstrates its character for glycosidic bond hydrolysis. In contrast, Proteobacteria were abundant in #103, as evidenced by its unique expression of cytochrome cbb3 oxidases exclusive to this phylum. Many protein families typical of aerobic prokaryotes were also abundant in this community. In addition, #103 expressed proteins involved in N metabolism, such as a urea transporter and urease, which can be advantageous due to roles NH3 plays in microbial growth and maintaining rumen pH.

Key Words: metagenomics, rumen, microbial

578 pH dynamics and bacterial community composition in the rumen of lactating dairy cows. A. Palmonari*[1], D. M. Stevenson[2],

D. R. Mertens[2], C. W. Cruywagen[3], and P. J. Weimer[2], [1]*DIMORFIPA, University of Bologna, Bologna, Italy*, [2]*USDA-ARS-U.S. Dairy Forage Research Center, Madison, WI*, [3]*Department of Animal Science, University of Stellenbosch, Stellenbosch, Republic of South Africa*.

The effect of pH dynamics on ruminal bacterial community composition (BCC) was studied in 8 ruminally-cannulated Holstein cows fitted with indwelling electrodes that recorded pH every 10 min over a 2.4-d period. Cows were fed a silage-based TMR supplemented with monensin. Ruminal samples were collected each day just before feeding, and at 3 and 6 h after feeding. Solid and liquid phases were separated at collection, and extracted DNA was subjected to PCR amplification followed by Automated Ribosomal Intergenic Spacer Analysis (ARISA). Although cows displayed widely different pH profiles (mean pH= 6.11 to 6.51, diurnal pH range = 0.45 to 1.39), correspondence analysis of the ARISA profiles revealed that 6 of the 8 cows had similar BCC. The 2 cows having substantially different BCC from the other 6 had intermediate mean pH values (6.30 and 6.33) and intermediate diurnal pH ranges (averaging 0.89 and 0.81 pH units). These two cows displayed the lowest milk fat percentages of the 8, along with markedly higher ruminal populations of one bacterial OTU (Operational Taxonomic Unit) and reduced populations of two other OTUs. Cloning and sequencing of a DNA segment from the elevated OTU revealed phylogenetic similarity to *M. elsdenii*, a species known to produce t10-c12 conjugated linoleic acid (CLA, a known regulator of mammary lipogenesis). The higher populations of both *M. elsdenii* and OTU246 in these 2 cows were confirmed using quantitative real-time PCR with species-specific primers, and the population sizes of these two taxa were highly correlated (r^2=0.99, p<0.001). By contrast, the relative population sizes of *Streptococcus bovis* and genus *Ruminococcus*, two taxa expected to respond to ruminal pH, did not differ among cows (mean = <0.01% and 10.6%, respectively, of rRNA gene copy number, determined by real time-PCR). The results indicate that cows with widely differing pH profiles can have rather similar ruminal BCC, and that low milk fat can occur at intermediate ruminal pH. The results support recent reports that milk fat depression is associated with shifts in BCC in rumine, and are specifically related to the relative population size of *Megasphaera elsdenii*.

Key Words: ARISA, BCC, ruminal pH

579 Effect of supplemental carbohydrate source and level on in vitro gas production estimates. A. Britos*[1], N. Pomiés[1], J. L. Repetto[2], and C. Cajarville[1], [1]*Department of Animal Nutrition, Faculty of Veterinary, UdelaR, Montevideo, Uruguay*, [2]*Department of Bovines, Faculty of Veterinary, UdelaR, Montevideo, Uruguay*.

The aim of this work was to study the effect of source and level of supplemental carbohydrate mixed with forage on in vitro gas production. Substrates were composed of mixtures of 30, 70 and 100% of supplement (citrus pulp (CP), corn grain (C) or barley grain (B)) and high quality temperate pasture, also incubated with no supplemental carbohydrate source (0%). 0.5g of each substrate was weighed in triplicate (n=21) into 125mL fermentation flasks and 38.5mL of N-free media was added the evening before inoculation of 10mL of inoculum. Rumen fluid was collected from a lactating cow after 15 d of adaptation to a forage diet. Gas measurements were made at 2, 4, 6, 8, 10, 12, 18, 24, 48, 72 and 96h post-inoculation. Data were fitted to V=Vf/{1+exp[2+4*Rf*(T-L)]}+Vs/{1+exp[2+4*Rs*(T-L)]} where V is total gas volume (mL/g DM incubated), Vf is fast pool volume (mL/g DM incubated), Vs slow pool volume (mL/g DM incubated), Rf and Rs are specific rates (h^{-1}) of fast and slow pools respectively, T is time, and L is lag (h). Parameter means were analyzed by PROC GLM considering carbohydrate source, level and its interaction, and separated by LSmeans procedure of SAS®. All parameters were affected by carbohydrate source, level and its interaction. In 0% level fast pool volume provided 77% of the total gas volume. The total gas volume increased between 15% (corn) to 37% (barley), when the supplement reached 70%. *Acknowledgements: funded by PEDECIBA Biología; PDT 78/12; FCE2007_119 ANII.*

Table 1.

S	I	V	Vf	Rf	Vs	Rs	L
	0	189^{a}	146^{a}	0.09^{a}	43.5^{a}	0.02^{a}	-0.24^{a}
CP	30	194^{a}	156^{a}	0.09^{a}	38.4^{a}	0.02^{a}	0.14^{ac}
	70	230^{b}	149^{a}	0.12^{b}	80.9^{b}	0.04^{b}	0.37^{bc}
	100	227^{b}	131^{b}	0.12^{b}	96.2^{c}	0.03^{b}	0.29^{bc}
	0	189^{a}	146^{a}	0.09^{a}	43.5^{a}	0.02^{a}	-0.24^{a}
C	30	204^{ab}	137^{abc}	0.11^{bc}	66.8^{b}	0.03^{b}	0.57^{b}
	70	218^{b}	123^{bc}	0.10^{ac}	94.7^{c}	0.03^{b}	1.22^{c}
	100	219^{b}	123^{c}	0.11^{bc}	96.2^{c}	0.03^{b}	2.62^{d}
	0	189^{a}	146^{a}	0.09^{a}	43.5^{a}	0.02^{a}	-0.24^{a}
B	30	191^{a}	147^{a}	0.10^{ac}	43.8^{a}	0.02^{b}	1.21^{b}
	70	259^{b}	206^{b}	0.09^{a}	52.8^{b}	0.02^{a}	1.38^{b}
	100	260^{b}	211^{b}	0.10^{bc}	48.5^{ab}	0.02^{a}	2.72^{c}
P(**S**)		**	*	*	*	*	*
P(**S**×**I**)		**	*	*	*	*	*

abcd within S differ P<0.05; *: P<.001; **: P<.01 S: source, I: level

Key Words: carbohydrate, temperate pasture, gas production

580 Differential chemotaxis by entodiniomorphids and isotrichids toward glucose after incubation with emulsified polyunsaturated fatty acids. H. L. Diaz*, A. M. Stalford, K. N. Barr, and J. L. Firkins, *The Ohio State University, Department of Animal Sciences, Columbus*.

We previously documented extensive chemotaxis by isotrichid (IS) protozoa toward glucose; however, entodiniomorphids (EN) had less pronounced, but dose-responsive, chemotaxis to the same concentrations. We hypothesized that prolonged exposure to fat would blunt chemotaxis toward glucose and be increasingly inhibited when mixed ruminal protozoa were previously incubated for 0, 3, or 6 h in the presence of 0, 0.5, 1.0 or 2.0% (v/v) emulsified polyunsaturated fatty acids (PUFA; Liposyn II™). After preincubation, 20 mL of ruminal fluid were inoculated to beakers that contained capillary tubes previously filled with either saline or 1000 m*M* glucose (G1000) or else unfilled and uncapped (positive control; POS). Counts in capillary tubes at 20 min were corrected for 0-min blanks and $\log_{10}$-transformed to normalize data. For only POS, there was an interaction (*P*=0.01) for PUFA × time. At 3h, PUFA decreased counts with both linear (L) and quadratic (Q) responses (*P*<0.01); however, at 6h, counts decreased linearly (*P*<0.01; Q was *P*>0.20) with increasing PUFA. Counts for saline or G1000 were covariate-adjusted for the respective POS counts to assess chemotaxis irrespective of changing protozoal abundance. For EN, there was a PUFA × glucose presence × time interaction (*P*<0.05). At 3 h, the main effect mean was greater (*P*<0.01) for G1000 than saline. At 6 h, the interaction (*P*<0.01) between PUFA and presence of glucose was explained by a cubic (*P*<0.01) response to PUFA for saline without effect (*P*>0.10 for all contrasts) for G1000. There were no interactions (*P*>0.20) for IS populations. For POS, increasing PUFA linearly decreased (*P*=0.01) counts. After covariate adjustment for POS, the

IS populations remained constantly chemotactic toward G1000 (main effect, $P<0.05$). Although IS populations were inhibited by fat, chemotaxis to G1000 was unchanged; in contrast, chemotaxis by EN is more complex. Fat might be inhibitory by disrupting membrane structure or more selectively by disrupting the ability to sense a glucose gradient, blinding EN to newly ingested feed.

Key Words: rumen protozoa, chemotaxis, fat inhibition

581 From Redox potential field measurement to its bioenergetic meaning in the rumen. J. P. Marden*[1,2], E. Ungerfeld[3], R. A. Kohn[4], C. Julien[1], E. Auclair[2], R. Moncoulon[1], and C. Bayourthe[1], [1]*Université de Toulouse, INRA, Castanet-Tolosan, France*, [2]*Lesaffre Feed Additives, Marquette-Lez-Lille, France*, [3]*Agriculture and Agri-Food Canada, Lethbridge, Canada*, [4]*University of Maryland, College Park.*

Anaerobic microbial metabolism is driven by free energy change (ΔG) of fermentation reactions, but ΔG can be difficult to estimate in biological systems. Ruminal metabolism is highly controlled by dynamics of dihydrogen (H_2) production and utilization, e.g. methanogenesis ($CO_2 + 4\ H_2 \rightarrow CH_4 + 2\ H_2O$; $\Delta G = \Delta G° + RT \ln [CH_4][H_2O]^2/[CO_2][H_2]^4$) is highly dependent on H_2 availability. Redox potential (E_h), in conjunction with pH, can be used to calculate equilibrium H_2 availability to study ΔG in fermentation systems. E_h is defined as the tendency of a biochemical/chemical system to oxidize (lose electrons to) or reduce (gain electrons from) another system. E_h measurements have been applied in fields as diverse as understanding fermentation in soils to ripening of cheese and maturation of wines. In the rumen, this variable was initially measured during the late 1950's in sheep and later in goats and cattle. Some studies reported a clear relationship between E_h and metabolic rate of rumen microbes when animals were fed grain and hay diets. E_h can be used in combination with pH and temperature to calculate equilibrium H_2 partial pressure (P_{H2}), based on the Nernst Equation: $rH = -\log P_{H2} = E_h/30 + 2pH$ at 312 K. Since H_2 is readily transferred among organisms in the rumen, it is generally near equilibrium in reality, or moving rapidly in that direction, and is central to the feasibility of major fermentation pathways in the rumen. Three trials: a dry cow model with 8 kg DMI/d (T8) and 2 lactating cow models with 21 (T21) and 28 kg DMI/d (T28) were used to continuously measure pH and E_h over 9 h around the morning meal to finally calculate mean ruminal P_{H2}. Lower DMI was associated with higher estimated P_{H2}, with a 10-fold significant decrease ($P<0.001$) at each feeding level (T8 vs. T21 & T21 vs. T28). Calculated P_{H2} values from simultaneous and continuous E_h and pH measurements can be valuable to study ΔG of processes highly dependent on H_2 availability, like methanogenesis, propionate formation, or even microbial growth. Processes dependent on releasing H_2 (e.g acetate and butyrate formation), are also dependent on H_2 concentration.

Key Words: ruminal redox potential, free energy, partial pressure of H_2

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582 Pharmacological amounts of nicotinic acid can reduce isoproterenol-stimulated lipolysis in cattle, but also reduce feed intake. K. S. Spivey, E. C. Titgemeyer*, and B. J. Bradford, *Kansas State University*, *Manhattan*.

Six Holstein steers (225 kg) were used in a series of experiments to determine if pharmacological supplies of nicotinic acid could reduce lipolysis stimulated by beta-agonists. The ruminally cannulated steers were fed a grain-based diet (72% corn, 12% soybean meal, 10% alfalfa) near ad libitum intake. In the first trial, nicotinic acid was continuously infused into the abomasum at 0, 2, 4, 8, 16, or 32 g/d in a 6x6 Latin square with 1-d periods. Steers were challenged with a pulse dose of isoproterenol (ISOP; 0.225 mg) with blood samples collected 8 min after ISOP to measure plasma NEFA. Results were inconclusive, and 4 of 6 steers demonstrated reductions in feed intake during the trial. In a second trial, the same steers were used in a replicated 3x3 Latin square with continual infusion of nicotinic acid in amounts of 0, 8, or 16 g/d. ISOP was dosed at 0.1125 mg, and blood samples were collected just prior to and 8 min after ISOP. Nicotinic acid at 16 g/d inhibited ($P<0.05$) the ISOP-stimulated increases in plasma NEFA concentrations, whereas 8 g/d did not. All 6 steers were then fed 60 mg/d zilpaterol-HCl, and 3 were provided a continual abomasal infusion of 16 g/d nicotinic acid, whereas 3 were infused with water. Steers given 16 g/d nicotinic acid had large reductions in feed intake, and nicotinic acid infusions were terminated after 3 d. Plasma glucose and insulin were somewhat elevated in response to nicotinic acid, even in the face of reductions in feed intake. Following discontinuation of the nicotinic acid infusions, cattle were maintained on their diets for 4 d before they were euthanized. Total liver fatty acids tended ($P=0.16$) to be elevated for steers that had received the nicotinic acid, with C16:0 and C18:1cis-9 demonstrating the largest increases. It appears that nicotinic acid (16 g/d) can inhibit ISOP-stimulated lipolysis, but the large negative effect on feed intake suggests that caution should be exerted when providing pharmacological doses of nicotinic acid to cattle.

Key Words: nicotinic acid, cattle

583 Effects of niacin infusion on transcript and protein abundance of the niacin receptor GPR109A in bovine tissues. B. J. Bradford*, L. K. Mamedova, K. S. Spivey, and E. C. Titgemeyer, *Kansas State University*, *Manhattan*.

Pharmacological effects of niacin (nicotinic acid) are likely mediated by GPR109A, a G protein coupled receptor with affinity for niacin. In most species, GPR109A is expressed primarily in adipocytes and macrophages, accounting for antilipolytic and cutaneous flushing responses to niacin. Tissue distribution of GPR109A has not been thoroughly investigated in cattle. We determined where GPR109A is expressed in cattle and assessed effects of niacin infusion on abundance. Six ruminally-cannulated steers (225 kg) were fed a grain-based diet (with 60 mg/d zilpaterol-HCl) near expected intake. Three steers received continuous abomasal infusion of 16 g/d nicotinic acid in 2 L water, and 3 received water alone. Steers provided 16 g/d niacin had dramatic reductions in feed intake, requiring discontinuation of niacin infusion after 3 d. Thereafter, steers were maintained with no niacin treatment until the end of the planned 7-d period. Steers were then euthanized and tissue samples were collected from tailhead fat, backfat, kidney fat, longissimus muscle, and liver for analysis of GPR109A mRNA by quantitative real-time PCR and protein by Western blotting. The mRNA for GPR109A was found in all tissues analyzed, and was most abundant in liver tissue, despite the fact that it has not been observed in liver of other species. Tailhead and kidney fat contained more mRNA for GPR109A than did longissimus muscle, as expected. Protein analysis by Western blot demonstrated presence of GPR109A protein in all tissues, except 3 of 6 backfat samples. The greatest abundance of GPR109A protein was in tailhead fat, kidney fat, and liver. Niacin treatment had no impact on mRNA or protein abundance of GPR109A in any analyzed tissue ($P>0.17$), but this is confounded by reduced feed intake by niacin and removal of treatments 4 d before euthanasia. The novel identification of the niacin receptor in bovine liver may provide

insight into mechanisms underlying unique physiological responses to pharmacological doses of niacin in cattle.

Key Words: nicotinic acid, GPR109A, niacin receptor

584 Effects of encapsulated niacin on metabolism and production of periparturient dairy cows. S. D. Morey, B. J. Bradford*, L. K. Mamedova, and D. E. Anderson, *Kansas State University*, *Manhattan*.

Nicotinic acid (niacin) can suppress lipolysis, but responses to dietary niacin have been inconsistent in cattle. Our aim was to determine if a relatively high dose of encapsulated niacin (EN) alters lipid metabolism and productivity of transition cows. Primiparous (n=9) and multiparous (n=13) cows (BCS 3.63 ± 0.08) entered the study 21 days prior to expected calving and were sequentially assigned within parity to EN (24 g/d, provided with ration twice daily) or control treatments through 21 d postpartum. Throughout the study, liver biopsies were collected for triglyceride (TG) analysis and blood samples were collected for nonesterified fatty acid (NEFA) and β-hydroxybutyrate (BHBA) analyses. On d 22-23 postpartum, blood samples were collected every 8 h to monitor post-treatment NEFA responses. Data were analyzed using mixed models with repeated measures over time. There were no prepartum treatment effects on plasma parameters; however, there was a treatment x time x parity effect on prepartum dry matter intake (DMI, $P < 0.07$) caused by a 4 kg/d decrease in DMI of EN-treated cows compared to control cows during the final 5 d prepartum. There were no treatment effects on postpartum DMI. Treatment x time x parity effects were detected for NEFA ($P = 0.09$) and BHBA concentrations ($P = 0.03$) during the postpartum period. Plasma NEFA peaked at 1.7 and 1.3 mEq/L for control heifers and cows, respectively, compared to 0.7 and 0.8 mEq/L for EN-treated heifers and cows. EN treatment also suppressed peak BHBA concentrations in both parity groups. After treatments ended on d 21, there was a treatment x time x parity effect ($P < 0.09$) on plasma NEFA; however, treatment means showed a continued suppression of plasma NEFA by EN in cows, with no evidence of a rebound in either parity group. No treatment effects were observed for liver TG concentration, BCS, BW, or milk or milk component production. These results indicate that a high dose of EN can decrease postpartum plasma NEFA and BHBA, but may also decrease prepartum DMI.

Key Words: niacin, transition, ketosis

585 Effects of low vitamin A and D finishing diets on beef cattle carcass quality. C. L. Pickworth*, S. C. Loerch, and F. L. Fluharty, *The Ohio State University*, *Wooster*.

Vitamins A and D are known to decrease adipocyte differentiation in vitro. It was hypothesized that supplemental vitamin A and D in cattle diets suppress carcass quality. One hundred sixty-eight Angus-based steers (BW = 284 kg) were blocked by BW and allotted to 24 pens. The experiment had a 2x2 factorial arrangement of treatments. Main effects were: 1) no supplemental vitamin A (NA) vs. 3,750 IU/kg of DM supplemental vitamin A (SA) and 2) no supplemental vitamin D (ND) vs. 1,860 IU/kg of DM supplemental vitamin D (SD). The basal diet was 65% high moisture corn, calculated to provide 1,260 IU/kg of DM vitamin A equivalents via beta-carotene, or 60% of the NRC recommendation for feedlot cattle. When the vitamin A and D interaction was not significant (P>0.10) the main effects are presented. Serum and liver vitamin A and D concentrations were greater (P<0.0001) in SA and SD steers on d 184 than NA and ND, respectively. The ND steers were able to synthesize ample vitamin D from sunlight as indicated by no change (P>0.05) in liver concentration of ND steers over time. Subcutaneous and intramuscular fat vitamin A concentrations were lower (P<0.05) in NA than SA steers. Supplemental vitamin D tended (P<0.09) to decrease vitamin A concentration in liver and intramuscular fat. Dry matter intake, average daily gain, and feed efficiency were not affected (P>0.05) by supplemental vitamin A or D. Yield Grades (YG) were higher (P<0.05) for NAND than for other treatments. Backfat thickness (BF) was greater (P<0.05) for steers fed the NAND diet than NASD and SAND fed steers. These results contradict previous results in which YG and BF were not affected by low dietary vitamin A. Hot carcass weight and dressing percent were higher (P<0.05) in NA as compared to SA steers. Marbling scores, Quality Grades and percent grading Average Choice or above were higher (P<0.05) in the NA than the SA treatment, and tended to have higher (P=0.06) ether extracts as well. Carcass quality was not significantly impacted by vitamin D supplementation. In conclusion, NA diets increased total fat deposition and ND had minimal impact on carcass composition of feedlot steers.

Key Words: vitamin A, vitamin D, carcass quality

586 Effects of extended zilpaterol hydrochloride withdrawal on performance, carcass traits, and shear-force value of steaks from finishing heifers. G. L. Parsons*[1], B. E. Depenbusch[1], C. D. Reinhardt[1], D. A. Yates[2], J. P. Hutcheson[2], and J. S. Drouillard[1], [1]*Kansas State University*, *Manhattan*, [2]*Intervet Schering-Plough*, *Desoto, KS*.

Our objective in this study was to determine if extended withdrawal of zilpaterol hydrochloride (Z) would ameliorate negative effects on marbling score and shear force without sacrificing improvement in carcass weight. Crossbred heifers (n = 450; 465 kg ± 27.2) were blocked into heavy and light groups. Within block cattle were stratified by BW and allocated randomly to feedlot pens containing 7 to 10 heifers each, with 9 pens/treatment. Treatments were arranged as a 2 X 3 factorial, with factors consisting of Z fed at 0 or 8.33 g/tonne DM and withdrawal times (W) of 3, 10, or 17 d. Heifers were implanted with Revalor-H and fed flaked corn finishing diets *ad libitum* once daily, providing 300 mg monensin, 90 mg tylosin, and 0.5 mg melengestrol acetate per animal daily. Z was fed for 20 d. With the exception of yield grade, there were no significant ZxW interactions (P > 0.10). For yield grade, ZxW interaction occurred because Z improved USDA yield grade after 3 and 10 d of withdrawal, but no differences were detected by 17 d. Z did not affect DMI, ADG, or gain efficiency (P > 0.10), but increased HCW, dressing percentage, and longissimus muscle area (P < 0.01) and decreased marbling scores (P < 0.01). Z increased HCW by 12.8, 7.7, and 5.2 kg at 3, 10, and 17 d of withdrawal, respectively. Marbling scores were 457, 466, and 459 in control cattle, and 401, 445, and 442 in zilpaterol cattle after 3, 10, and 17 d of withdrawal, respectively. W increased final BW, HCW, and marbling scores (P < 0.04), and decreased back fat and KPH (P < 0.03). Whole loins were collected from 15 randomly selected cattle per treatment in each block and wet aged in vacuum bags for 7, 14, and 21d. Z increased shear force in steaks by 0.54 kg (P < 0.001), but shear force declined linearly with additional aging (P < 0.01), yielding loin steaks with acceptable shear-force after 14 or 21 d of aging.

Key Words: zilpaterol, shear force, performance

587 In vitro evaluation of four bacterial species as potential probiotics in the rumen. T. W. Priambodo, J. Hummel, S. Kehraus, and K.-H. Südekum*, *University of Bonn*, *Bonn, Germany*.

The current study evaluated effects of four potential probiotic bacterial cultures on ruminal in vitro gas production, and on fermentation acid and ammonia concentrations to compare the capability of probiotics and their survival during in vitro ruminal fermentation. Bacterial strains, namely *Lactobacillus buchneri*, *L. brevis*, *Enterococcus faecium* and *Propionibacterium jensenii* were investigated at two different concentrations, namely 10^7 and 10^9 colony forming units (cfu)/ml. The Hohenheim gas test was employed to determine in vitro gas production at 8- and 24-h incubation time, using four different ratios of grass silage to mixed concentrate (dry matter basis; 100:0; 75:25; 50:50; 25:75). The concentrations of ammonium (NH_4^+) and volatile fatty acid (VFA) were determined as well as probiotic cell counts to estimate probiotic activity and persistency. Protozoa were enumerated to estimate the effects of bacterial strains on the rumen fauna. Gas production and individual and total VFA concentrations were affected by probiotic colony concentrations as well as diet type, but only *P. jensenii* at 10^9 cfu/ml increased ($P < 0.05$) gas and VFA production over control values. Probiotic colony counts decreased over the 24-h incubation period, and were least pronounced for *P. jensenii*, indicating that it was the most adaptable strain. Treatments had no ($P > 0.05$) effects on NH_4^+ concentration and protozoal numbers. In general, autoclaved probiotics produced similar concentrations of gas and NH_4^+ as the live probiotics, which likely was a result of fermentation of the carrier material. Only the live *L. brevis* and *P. jensenii* produced more ($P < 0.05$) gas than their autoclaved forms.

Key Words: probiotics, rumen, in vitro

588 Feeding behaviour of wethers fed a temperate pasture with different time of access to food and supplemented or not with additives. A. Pérez-Ruchel[1], J. L. Repetto*[2], M. Michelini[1], L. Pérez[1], G. Soldini[1], and C. Cajarville[1], [1]*Departamento de Nutrición Animal, Facultad de Veterinaria*, *Montevideo, Uruguay*, [2]*Departamento de Bovinos, Facultad de Veterinaria*, *Montevideo, Uruguay*.

The effect of time of access to food (TAF) and supplementation with selected additives on feeding behaviour was studied. Twenty-four wethers were blocked by weight and fed fresh forage (*Lotus corniculatus*, CP 14%), housed in metabolic cages and allocated to 4 treatments. AD animals had access to forage all day (AD); R, RB, RS had forage available 6 h/day. RB and RS were supplemented (2% DMI of 75% NaHCO3-25% MgO and 6.2×10^9 UFC/d of *Saccharomyces cerevisiae*, respectively). Feeding behaviour was recorded for each animal every 3 minutes for 12 h via visual observation by trained operators. Four categories were used to classify animal behaviour: eating, ruminating, drinking and resting. Parameters were compared between treatments by GLM considering 'treatment' and 'block'. Orthogonal contrasts were performed on data to study the effect of TAF, use of additive and the type of additive. Animals with restricted TAF exhibited reduced eating and ruminating time (40% and 36%, respectively) and increased the resting time (47%) in comparison with those fed all day. Animals fed all day masticated 1.6 more times than animals fed 6h/d. The use of additives had no effect on the feeding behaviour. Restricted TAF changed the feeding behaviour of wethers fed forage. *Acknowledgements: PDT-DICyT (78/12 and S/PSP/02/48), CSIC, and CODENOR S.A.*

Table 1.

	Treatments					P contrast		
Cumulative time, min	AD	R	RB	RS	SE	AD vs R + RB + RS	R vs RB + RS	RB vs RS
Eating	328.5	187.5	215.5	194.5	18.1	<.001	ns	ns
Ruminating	169.5	106.0	106.0	114.5	12.6	<.001	ns	ns
Mastication*	498.0	293.5	321.5	309.0	15.4	<.001	ns	ns
Drinking	4.5	4.0	3.0	0.5	1.52	ns	ns	ns
Resting	217.5	422.5	395.5	410.5	15.7	<.001	ns	ns
Ruminating/ resting	0.53	0.66	0.50	0.67	0.12	ns	ns	ns
Mastication/ resting	2.41	0.71	0.83	0.78	0.13	<.001	ns	ns

*: eating + ruminating; SE: standard error; ns: non significant (P>0.05)

Key Words: feeding behaviour, magnesium, *Saccharomyces cerevisiae*

Small Ruminant: Nutrition

589 The effects of replacing alfalfa hay with fresh citrus pulp on ruminal fermentation and ewe performance. J. L. Sparkes, Y. T. E. Fung, I. van Ekris, R. D. Bush, and A. V. Chaves*, *The University of Sydney, Faculty of Veterinary Science*, *Sydney, NSW, Australia*.

Two studies were conducted to determine the effects of replacing alfalfa hay with fresh citrus pulp in Merino ewe diets: (i) an *in vitro* study which measured ruminal fermentation; and (ii) an *in vivo* study in which twelve Merino ewes pre- and post-lambing were fed treatments in a cross-over design over 120 d to evaluate effects on ewe performance (i.e. dry matter (DM) intake (DMI), average daily gain (ADG) and wool growth). In both the *in vitro* and *in vivo* studies, the control treatment consisted (in diet DM) of alfalfa hay (91.3%), lupins (8.3%) and phosphate (0.42%), while the citrus pulp treatment consisted of alfalfa hay (57.7%), lupins (9.5%), phosphate (0.48%) and fresh citrus pulp (32.3%). Data were analyzed with the mixed model procedure of SAS. In the *in vitro* study, gas production, total volatile fatty acid (VFA) yield, proportion of propionic acid to total VFA and *in vitro* dry matter digestibility (IVDMD) were higher (P<0.02) in the citrus pulp treatment compared to the control treatment. In contrast, *in vitro* ammonia production, pH and the acetate to propionate ratio were lower (P<0.03) for the citrus pulp treatment compared to the control treatment. In the *in vivo* study, DMI of ewes fed the citrus pulp diet was lower than their control ewe counterparts throughout both the pre- and post-lambing periods (928.9 vs. 1115.0 g/d pre-; 1285.0 vs. 1620.3 g/d post-lambing, P<0.01), however ADG was similar (P=0.12). Wool growth parameters and lamb performance did not differ (P>0.32) between treatments. In summary, the *in vitro* study demonstrated that the replacement of 30% of an alfalfa diet with fresh citrus pulp improved total VFA yield, increased total gas production and improved IVDMD, while decreasing the production of ammonia, acetic acid and rumen pH. In addition, the *in vivo* study demonstrated that the replacement of 30% of an alfalfa diet with fresh citrus pulp pre- and post-lambing decreased DMI but did not affect a ewe's performance in terms of ADG and wool growth. These findings would be of significant interest to producers endeavoring to control feed cost while maintaining productivity.

Key Words: in vitro, Merino sheep, wool growth

590 Effect of yeast (*Saccharomyces cerevisiae*) culture supplementation to medium-quality hay on nutrient digestibilities by goats of two different body sizes. D. V. G. Krishna Mohan[1], J. Hummel[2], and K.-H. Südekum*[2], [1]*Sri Venkateswara Veterinary University, Tirupati, Andhra Pradesh, India*, [2]*University of Bonn, Bonn, Germany*.

Yeast (*Saccharomyces cerevisiae*) products may exert beneficial effects on ruminant productivity by either increasing fermentability of fiber and/or allowing rumen microbes to more effectively metabolize end-products of ruminal starch fermentation. The objective was to evaluate the possible effect of increased fiber fermentability, independent of metabolism of starch fermentation end-products. Twenty male goats (German Improved Dairy Goat) were housed in individual pens and assigned to four treatments of five animals each in a 2 × 2 factorial design to study the effects of body weight (BW; heavy [HE], mean BW 45 kg, and light [LI], mean BW 25 kg) and live yeast (Levucell® SC 20) supplementation (YEA, yeast product supplemented at 2.5 x 10^5 colony forming units/g hay; CON, without supplementation) on nutrient digestibility of a hay-only diet. A high-fiber, medium-quality grass hay was fed to treatments: 1 (HEYEA) and 2 (HECON), hay at 1000 g/d, and 3 (LIYEA) and 4 (LICON), hay at 600 g/d. A digestion trial (3 wk adaptation period and 1 wk total fecal collection period) was conducted to measure nutrient digestibilities of the hay. The digestibilities of dry matter, organic matter, ether extract and of fiber fractions (acid and neutral detergent fiber) were not different ($P > 0.05$) among treatments. Only crude protein (CP) digestibility was greater ($P < 0.001$) for heavy compared to light goats. Within the light goats, CP digestibility was lower for the YEA supplemented animals. In the present experiment, neither yeast product nor BW of young male goats affected nutrient digestibilities in the gastro-intestinal tract.

Key Words: yeast, grass hay, digestibility

591 Performance of lambs fed ensiled orange pulp treated with exogenous enzymes. H. Gado*[1], A. Z. M. Salem[2,4], H. Alsersy[3], B. E. Borhami[2], and M. El-Adawy[2], [1]*Faculty of Agriculture, Ain Shams University, Egypt*, [2]*Faculty of Agriculture, Alexandria University, Egypt*, [3]*Animal Production ARC, Ministry of Agriculture, Egypt*, [4]*Universidad Autónoma del Estado de México, Centro Universitario UAEM, Temascaltepec, México*.

Eighty four Ossimi male sheep (21.0 ± 0.5 kg LW) were used in this study. The animals were randomly assigned among three experimental treatments using a complete block design. The period of this trial extended for 90 d. The objectives of this study were to evaluate the effects of ensiled orange pulp (EOP) in lamb diets in presence of exogenous enzyme on growth performance, digestibility and some blood metabolites (i.e. glutamic oxaloacetic transaminase (GOT) and glutamic pyruvic transaminase (GPT). The EOP was mixed (1:1) with rice straw (3-5cm) sprayed with ZAD (2 L/ton straw) as a liquid product which contains live anaerobic rumen bacteria and their enzymes, and ensiled for 30 d. The ensiled mix replaced 15% of the concentrate mix (corn, 30%, sugar cane molasses, 5.5%, cottonseed cake, 11% and soybean meal, 5%) in Diet 2 and similarly in Diet 3 plus 0.5% of ZADO/ton (product with natural enzymes derived from rumen bacteria). The addition of ZAD to the ensiled mix resulted in a decrease ($P < 0.05$) in the total phenolics, saponins and aqueous fraction. Digestibility coefficients for DM, OM, CP, CF, NDF and ADF were highest ($P < 0.05$; SEM = 0.36) for diet 3 followed by diet 2. Accordingly, the TDN of diet 3 was improved ($P < 0.05$; SEM = 0.24) in comparison with control (72.4 vs 68.8%, respectively). Average daily gain (ADG) was highest (250 g/d) for Group 3 followed by Group 2 (202 g/d) and control one (128 g/d). Feed efficiency was improved in Group 3 (3.2 kg feed /kg LW) and lowest ($P < 0.05$; SEM = 0.17) was for Group 1 (6.2 kg feed/kg LW). There were no differences between groups for the results of GPT and GOT. Meanwhile, there was an increase ($P < 0.05$; SEM = 0.06) in blood serum globulin and a decrease in the cholesterol with Diet 3 .The results reflect the possibility of replacing grains with citrus pulp silage and better results were obtained with the addition of ZAD and ZADO.

Key Words: orange pulp, ZAD, digestibility

592 Effect of tea saponin and soybean oil on performance of growing lambs and protozoa community in the rumen. H. L. Mao*, J. K. Wang, and J. X. Liu, *Institute of Dairy Science, Ministry of Education Key Laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou, P.R. China*.

Thirty-two Huzhou male lambs were used to investigate the effect of tea saponin (TS) and soybean oil (SO) on performance of growing lambs and the protozoa community in the rumen. Diets were formulated as a 2 × 2 factorial with TS (0 or 3g/d) and SO (0 or 3% of DM) and were fed for 60 d. Feed intake and refused, and body weight gain were recorded every two wk. After the feeding trial, four lambs in each treatment were slaughtered to obtain the rumen samples for analysis of protozoa community by using real-time PCR and denaturing gradient gel electrophoresis (DGGE) technique. Populations of protozoa were expressed as a proportion of total rumen bacterial 16S rDNA. The protozoa diversity and similarity were determined on the base of the position and number of bands in the DGGE gel. No significant effects were observed on feed intake and daily gain in growing lambs by inclusion of TS or SO in the diets ($P > 0.05$). Rumen protozoa population was decreased markedly when TS or SO was included into the diets, compared with the control ($P < 0.05$). A tendency was observed for a TS × SO interaction in the relative abundance of protozoa ($P = 0.08$). Six major bands occurred, but their abundance was different among the dietary treatments. Based on the results of sequence analysis, these bands were classified to genus *Epidium*, *Entodinium*, *Eudiplodinium*, and *Polyplastron*. The band representing genus *Eudiplodinium* only occurred for lambs fed the control or the SO-supplemented diet, while lambs supplemented with SO had the band representing genus *Polyplastron*. However, no significant difference was observed in protozoa diversity among the different diets ($P > 0.05$). From the present study, it is inferred that addition of TS and supplementary SO had an inhibitory effect on the protozoa population, but did not affect the productive performance of lambs and protozoa diversity in the rumen.

Key Words: rumen protozoa, soybean oil, tea saponin

593 The effects of replacing dried citrus pulp with barley grain on the performance of Iranian Saanen kids. Abasali Naserian*, Mohammad Mahdi Sargolzehi, and Hojat Gholizadeh, *Ferdowsi University of Mashhad, Mashhad/ Khorasan Razavi Province/Iran*.

This study was conducted to evaluate the effect of replacing barley with dried citrus pulp on the performance of growing kids. Twelve female Iranian Saanen weaned kids aged 88 ± 3 d with live weight 7 ± 0.7 kg were used in a completely randomized design. Kids were housed in well-ventilated individual metabolic cages. There were 3 treatments (n = 4 kids/treatment). The dietary treatments were T1, 30% lucerne with 70% concentrate supplement; T2 and T3, 7 and 14% of barley grain in supplements were replaced with dried citrus pulp, respectively. Each

animal was kept and fed in a separate cage during the entire experiment (60 d). Daily intake was determined. The growth of animals was monitored every 15 d. Rumen fluid was collected by stomach tube and pH measured. Blood samples were collected from each animal at the end of experiment via jugular vein 2 h after morning feeding. The results are shown in Table 1. Significant difference ($P < 0.05$) occurred for DMI, average daily gain, feed efficiency, rumen fluid pH and blood urea nitrogen (BUN). The pH of rumen tended to increase as the level of citrus pulp increased. Dry citrus pulp in ration of growing kids is not able to support requirements like starch sources, but citrus pulp could be incorporated into ruminant ration.

Table 1. Means of feed intake, gain, FE, rumen fluid pH, BUN and serum glucose

	T1	T2	T3	SEM
DMI (g/d)	849a	835b	793c	10.22
Gain (g/d)	198a	186b	167c	0.26
Feed efficiency	4.20	4.56	4.78	0.24
Rumen fluid pH	6.28a	6.41b	6.62b	0.004
BUN (mg/dL)	30a	31b	35c	0.06
Glucose (mg/dL)	51	51	52	0.07

Key Words: Saanen kids, citrus pulp, growth

594 Empirical modeling of the utilization of energy and of the methane production in dairy goats. D. Sauvant* and S. Giger-Reverdin, *AgroParistech-INRA, Paris, France*.

The objective was to develop a model of energy utilization and methane production in dairy goats by meta-analysis. A data base was built from 7 publications, number of experiments (nexp) was 14 including 37 (n) treatment groups. The following parameters, expressed on a metabolic live weight basis (MLW), were collected: Metabolizable energy intake (MEI/MLW = 224.1 ± 97.9 kcal/kgMLW; n = 37), energy losses as methane (ECH4 = 21.9 ± 8.5 kcal/kgMLW, n = 37), net energy used for milk production for lactating goats (NEL/MLW = 76.1 ± 40.9 kcal/kgMLW, n= 27), energy balance (EB/MLW = 37.3 ± 22.5 kcal/kgPM, n = 37), Energy digestibility 70.3 ± 5.6% and percentage of MEI loss as methane 10.3 ± 2.1%. The various items were correlated, thus the sum of (NEL+EB)/MLW was closely related to MEI/MLW, the intra experiment equation was: (NEL+EB)/MLW = –68.1 + 0.70(± 0.03) MEI/MLW (n = 37, nexp = 14, R2 = 0.99, RMSE = 4.3 kcal/MLW). These coefficients suggest that the efficiency of ME intake to milk and body reserves is 70%, slightly better than some proposed values. This could be the outcome of the increase of the dietary concentrate percentage with higher levels of milk production. Maintenance requirements were close to present values proposed by INRA since 1978 (68.1 vs 65.3 kcal NEL/MLW). This value corresponds to 97.3 kcal MEI/MLW. The results allowed to predict daily methane production of a goat in function of its LW and 3.5% FC milk yield: CH4 (g/d) = 0.41 LW + 6.70 FCMY (n = 37, R = 0.87, RMSE = 6.9 g/d). Thus a dairy goat of 70 kg LW with a 3 kg FCMY produces 49 g CH4/d. The 22 residuals of this regression concerning mixed diets were curvilinearly linked with proportion of concentrate (resCH4 = –2.7 + 20.9 PCO – 29.2 PCO2, n = 22, nexp = 9, RMSE = 1.7 g/d). In conclusion, these models allow to update basic parameters of energy utilization and methane production by dairy goats.

Key Words: dairy goat, energy requirements, methane production

595 Evaluation of performance predictions of the Small Ruminant Nutrition System model using growth and body composition data of South African Mutton Merino and Dorper. A. Cannas*[1], A. Linsky[2], L. J. Erasmus[2], L. O. Tedeschi[3], W. A. van Niekerk[2], and R. Coertze[2], [1]*Dipartimento di Scienze Zootecniche, University of Sassari, Sassari, Sardinia, Italy*, [2]*Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria, South Africa*, [3]*Department of Animal Science, Texas A&M University, College Station, TX*.

Since 2004, the biological model of the Cornell Net Carbohydrate and Protein System for sheep has been modified to include recent information, including a submodel to account for goat nutrition. This effort has led to the development of the Small Ruminant Nutrition System (SRNS) model. Considering the worldwide interest in nutritional models and the growth of the sheep industry in South Africa, the objective of this study was to evaluate the performance predictions of the SRNS model of South African Mutton Merino (late maturing) and Dorper breeds (early maturing) under South African conditions. The evaluation was carried out on the predictions of feed intake, average daily gain (ADG), empty body gain (EBG), and the composition of the EBG. Two different equations were compared to estimate energy value of gain and five different equations were compared to estimate the efficiency of conversion of ME to NE for gain. The original SRNS model gave the best predictions when compared to any of the modifications tested. Predictions of feed intake and ADG were accurate and precise with a low systematic bias (for feed intake: mean bias (MB) = 40 g/d, root of mean square prediction error (RMSPE) = 50 g/d, and $r^2 = 0.95$; and for ADG: MB = 2.4 g/d, RMSPE = 21.4 g/d, and $r^2 = 0.76$). However, the predictions for the EBG were on average over predicted (MB = 31 g/d, RMSPE = 38 g/d, and $r^2 = 0.69$). The model slightly over predicted both fat and protein contents of the EBG by 7.2% and 3.9%; respectively, showing high accuracy but very low precision, probably due to the fact that the measured range of variation of fat and protein content of gain was narrow. This evaluation indicated the SRNS model can be used under South African conditions, but modifications might be needed to more accurately predict body composition.

Key Words: growth, lamb, modeling

596 Factors affecting dietary intake and colostrum production in ewes. A. G. Fahey*, T. F. Crosby, and T. M. Boland, *School of Agriculture, Food Science, and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*.

The curvilinear increase in fetal mass in the final 8 wk of pregnancy and mammary development for lactogenesis highlights the necessity of nutrition in the pregnant ewe. Mortality associated with immunosupression in newborn lambs can be minimized through adequate availability of high quality colostrum. To analyze the effects of ewe profile and gestation characteristics on dietary intake and colostrum production, data were collected from a crossbred flock (n = 204 ewes). Daily average DMI, average crude protein intake (CPI), total colostrum yield and total immunoglobulin G (IgG) yield to 18 h post partum were measured. Ewes were divided into 3 groups based on their BW (high, n = 65; medium, n = 70; low, n = 69), gestation length (long, n = 69; medium, n = 66; short, n = 69), body condition score (BCS; high, n = 57; medium, n = 75; low, n = 72;) and lamb BW (large, n = 63; medium, n = 79; small, n = 62). High BW ewes had a higher DMI than low BW ewes ($P < 0.05$), while ewes with long gestation had a tendency to have lower DMI than ewes with short gestation ($P < 0.10$). High BW ewes tended to have a higher CPI than medium BW ewes ($P < 0.10$) and medium BW ewes had higher CPI than low BW ewes ($P < 0.05$). High BCS ewes had

lower CPI than low BCS ewes ($P < 0.01$), while ewes that gave birth to high BW lambs had higher CPI than low BW lambs ($P < 0.05$). High BW ewes had higher IgG yield than medium and low BW ewes ($P < 0.05$). Ewes with long gestation lengths tended to have lower IgG yield than those with short gestation ($P < 0.10$), and high BCS ewes tended to have higher IgG yield than low BCS ewes ($P < 0.10$). However, large BW ewes had higher colostrum yield than ewes with a low BW ($P < 0.05$). Ewes with low BW lambs tended to produce more colostrum than ewes with high BW lambs ($P < 0.10$). The data show that ewe profile influences feed intake and colostrum production. A better understanding of these may lead to an improvement in late pregnancy nutrition and reductions in lamb mortality.

Key Words: dry matter intake, immunoglobulin, colostrum

ADSA Production Division Symposium: Driving Forces in the Dairy Industry That Will Change Dairy Farm Management

597 The dairy scientist's role in re-connecting the dairy food-chain. K. Murphy*, *Food-Chain Communications, Lee's Summit, MO*.

The ideal food-chain is defined as the group of people and organizations working together to effectively respond to the demands of food consumers. Recent actions by grocery retailers, quick-service restaurants and branded product manufacturers have caused the food-chain to instead function more antagonistically, more closely resembling nature's food chain, in which each species within the chain cannibalizes the other in order to survive. Dairy scientists play—and will continue to play—an increasingly important role in returning the food chain to the cooperative effectiveness indispensable to feeding a growing population. To be effective in their role, scientists and their institutions must appreciate the necessity to communicate science beyond their own bounds, learn to effectively communicate and translate the complexities of science into a common consumer vernacular, understand the nature of "my science vs. your science" characteristic of post-modernism, understand how physical science must mesh with humanities and social science in communicating with consumers.

Key Words: food chain, consumer communication

598 The welfare of dairy cattle: Problems and solutions for the coming decade. M. A. G. von Keyserlingk*[1], R. Rushen[2], A. M. de Passillé[2], and D. M. Weary[1], [1]*University of British Columbia, Vancouver, BC, Canada*, [2]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada*.

Recent interest in animal welfare stems often from concerns related to intensive farming techniques. In many modern farms, especially in the industrialized world, dairy cattle are housed indoors, a system perceived by some as "unnatural" as it provides limited space and often a limited ability to engage in some natural behaviors. In contrast, many within the dairy industry see advantages to intensive, indoor systems, including protection of cows from the elements and the provision of high quality diet. Thus different people can reach different conclusions about management systems by favoring different welfare indicators. Clearly the best solutions will be those that satisfy the range of concerns (in this case allowing for natural behaviors that are important to the animal, along with good health and production). Taking this approach we provide a critical summary of the available welfare literature on intensively managed dairy cattle and show how scientific research can provide ways of resolving current concerns. Specifically we address dairy cattle welfare from three perspectives: improving health, reducing pain and distress, and facilitating natural behavior. Four major areas of concern are reviewed: 1) calf health and rearing practices, 2) lameness and transition cow disease, 3) housing, including access to pasture and, 4) painful procedures like dehorning that cause considerable pain that can be avoided using the right techniques and analgesics, or like tail docking that prevents the animal from performing natural fly avoidance behaviors, and fails to provide clear advantages to either the animal or the producer. In each example we show how research can identify solutions that improve dairy cattle welfare while remaining practical for dairy producers. We also identify some of the major welfare concerns for intensively managed dairy cattle where research is still required.

Key Words: welfare, dairy cattle, behavior

599 Accelerating genetic improvement with SNP chips and DNA sequencing. C. P. Van Tassell*[1], P. R. VanRaden[1], G. R. Wiggans[1], L. K. Matukumalli[1,2], S. Schroeder[1], J. O'Connell[1,3], R. D. Schnabel[4], J. F. Taylor[4], E. J. Pollak[5], M. Munson[6], D. Bailey[6], and T. S. Sonstegard[1], [1]*USDA-ARS, Beltsville, MD*, [2]*George Mason University, Manassas, VA*, [3]*University of Maryland School of Medicine, Baltimore*, [4]*University of Missouri, Columbia*, [5]*Cornell University, Ithaca, NY*, [6]*Illumina, Inc., San Diego, CA*.

The development of high-density single nucleotide polymorphism (SNP) assays is expected to have a profound impact on genetic progress in the U.S. dairy industry. In the 16 months since its initial availability, the Illumina BovineSNP50 BeadChip has been used to genotype nearly 20,000 Holsteins. These genomic data were included for the first time in the national dairy cattle genetic evaluation published by the USDA in January 2009. Substantial increases in genetic improvement have been predicted through the implementation of genome enabled selection. Currently, however, validation results are available only from the analysis of historic data, where populations have somewhat arbitrarily been divided into past and "future" populations. Availability of low-density but targeted SNP data could also dramatically impact genetic improvement. Low-density SNP data could be used to validate reported parentage and correct pedigree errors if comprehensive genotyping were conducted. These data could also be used to discover parentage and to more accurately characterize the degree of relatedness among animals in the population using genomics-based relationship coefficients. By accurately charactering the fractions of the genome inherited from each grandparent, genetic similarity that is currently described by statistical averaging using the pedigree could be refined to more accurately predict genetic merit early in life. Finally, individual animal genome sequencing is on the scientific horizon. Availability of such data could have implications beyond genetic improvement, and result in deeper understandings of basic biology, consequences of selection, and even animal and human health. Our ability to fully utilize these data will present enormous statistical and computational challenges.

Key Words: SNP, selection, genome

600 Affects of climate change and environmental regulation on management of dairy farms. W. Powers*[1] and D. Meyer[2], [1]*Michigan State University*, *East Lansing*, [2]*University of California*, *Davis*.

The dairy industry faces increasing environmental challenges. This is coupled with retailer pressure to discontinue use of bST, which will likely increase nutrient excretion per unit of milk produced and/or result in an increase in cow numbers to meet increasing product demand. As states adopt their own greenhouse gas reduction strategies, there is greater emphasis on adoption of a national policy. However, at the present time it is uncertain whether such a policy would include animal agriculture in a cap (e.g. a cow tax) or provide opportunities to the dairy industry to generate credits to be sold in a carbon market. Furthermore, the question remains as to whether or not greenhouse gas reduction strategies will result in increased emissions of criteria pollutants. Air quality issues remain at the forefront of challenges for the dairy industry. Recent reporting requirements under the Emergency Planning and Community Right-to-know Act (EPCRA) for large concentrated animal feeding operations (CAFOs) signifies that regulation of air pollutants may intensify for animal agriculture. Yet, it is uncertain what pollutants will be targeted and how standards will be established. As the Environmental Protection Agency winds down its National Air Emissions Monitoring Study many are eager to see how the data will translate to policy and what pollutants will be addressed. In the meantime, states continue to set their own policies, targeting a wide array of pollutants such as odor (PA), volatile organic compounds (CA) and hydrogen sulfide (IA and MN). In the face of all these changes is the increasing activity associated with adoption of practices to promote animal well-being and the uncertainty of how those practices affect the welfare of the environment. While many are discussing and calculating the carbon footprint of the U.S. dairy industry many holes in the data exist, making it all the more difficult to manage conflicting objectives.

Key Words: air, environment, water

Animal Health: Calf Health, Respiratory Disease, etc.

601 Calf enteric mortality etiologies 2004–2008. T. J. Baldwin, D. J. Wilson*, R. T. Skirpstunas, J. D. Trujillo, and E. J. Kelly, *Utah State University*, *Logan*.

Calves (1-90 d old, < 137 kg body wt) submitted dead to the Utah Veterinary Diagnostic Laboratory from 2004-2008 and diagnosed with enteric disease were retrospectively studied. 180 dairy and 123 beef (mainly Holstein or Jersey, Angus, respectively) calves from Utah and Idaho had post-mortem enteric cause(s) of death diagnosed. Agents of mortality included: Bovine Viral Diarrhea (BVD) 38% of cases, cryptosporidia 22%, coronavirus, rotavirus, E. coli each 20%. 10 different single agents killed 52% of calves; most common were BVD 21%, E. coli 9%. There were 21 combinations of 2 agents (28% of cases) and 12 combinations of 3 agents (9%). For calves 1-7 d old, common mortality causes were: dairy-coronavirus, rotavirus, cryptosporidia; beef - BVD, E. coli. 8-14 d, dairy - rotavirus, cryptosporidia, coronavirus; beef - BVD, E. coli. 15-45 d, dairy - BVD, Salmonella; beef - BVD, coccidia. From 45-90 d old, there was little beef calf mortality, but dairy calves died mainly from E. coli and BVD. Recent literature reports the vast majority of calf diarrhea cases are antibiotic-treated. The main causes of enteric mortality are viral, protozoal or a combination thereof. There are implications for therapy and importance of BVD control.

Key Words: calf, mortality, BVD

602 Assessment of the health status of newborn dairy replacement and veal calves. K. Waalderbos*[1], K. Leslie[1], T. Duffield[1], T. DeVries[2], and B. McBride[2], [1]*Department of Population Medicine, University of Guelph*, *Guelph, Ontario, Canada*, [2]*Department of Animal and Poultry Science, University of Guelph*, *Guelph, Ontario, Canada*.

Successful raising of healthy calves can be a challenge for dairy and veal producers. To date, in Ontario calves, little research has been reported on how the transfer of passive immunity and other health indicators may relate to calf health. A cross-sectional study is being conducted with 2306 newborn calves from 16 herds in southwestern Ontario. The objectives are to determine the health status of newborn dairy replacement and veal calves, with emphasis on quantifying transfer of passive immunity; to assess the influence of other metabolic and physiological indicators on calf health; and to evaluate differences between heifer and bull calves for these health indicators. During the study period of January to December 2008, weekly enrollment of heifer and bull calves, 1 to 7 days of age, occurred on commercial dairy farms in southwestern Ontario. At enrollment, calves were given a health score, measured for height, weight and body temperature, and two blood samples were collected. The whole blood sample was analyzed for complete blood count and selenium. Serum was harvested and analyzed for total protein, haptoglobin, magnesium and globulins. Birth records were completed for each study calf. Calves were followed until four months of age for disease events, treatment information and growth. Data analysis is in progress. In current results, the serum total protein values for 2306 calves ranged from 3.6 to 9.7g/dL, with a mean of 5.7g/dL (SD 0.68). Using a cut-off of >5.2g/dL to indicate success of passive transfer, 482 calves (20.9%) had a failure rate. Farm of origin and gender have an effect ($P<0.01$) on the distribution of serum total protein in calves. The distribution of whole blood selenium status for 876 newborn calves shows values ranged from 0.09 to 0.40 mg/mL, with a mean of 0.21 mg/mL (SD 0.05). Of note, the lab-provided reference interval for whole blood selenium is 0.20 to 1.2 mg/mL. Calves in this study tend toward the lower reference limit, with 369 calves (42.1%) falling below a 0.2 cut-off. These results suggest there is considerable variability in serum total protein and selenium levels of newborn calves both within and between farms.

Key Words: calf, total protein, selenium

603 Targeting therapy to minimize antimicrobial use in pre-weaned dairy calves: effects on health and occurrence of antimicrobial resistance in fecal *Escherichia coli*. A. C. B. Berge, D. A. Moore*, T. E. Besser, and W. M. Sischo, *Washington State University*, *Pullman*.

Antibiotics should be used prudently in production agriculture to reduce risks for antimicrobial resistance. The objectives of this study were to assess effects of raising pre-weaned calves without antimicrobials in the milk and reducing therapeutic antimicrobial treatment for diarrhea on morbidity, mortality, weight gain and antimicrobial resistance fecal *Escherichia coli*. Newborn calves (N=358) were randomly allocated to 4 groups, housed in individual hutches and observed for 28 days. Day

2 serum IgG levels, weights on day 1, 28 and weaning were obtained. Calves in the conventional treatment (CT) group were treated by dairy staff with their protocol of bismuth-pectin, sulfisoxazole/trimethoprim, spectinomycin and penicillin for diarrhea. The targeted treatment (TT) group received bismuth-pectin and antimicrobial treatment only in cases of fever or depressed attitude. Within CT and TT groups, calves were equally stratified to receive neomycin and tetracycline in the milk for the first 2 weeks (ABMILK) or no antimicrobials (NoABMILK). Daily evaluations included fecal consistency, respiratory signs, attitude, appetite and milk and grain consumption. Fecal samples were obtained on the day 1, 14 and 28. Three fecal E. coli per sample were isolated and susceptibility-tested to 12 antimicrobials using disk diffusion. A multivariate negative binomial model evlauted the likelihood of diarrhea on any observation day. An ANOVA model assessed differences in weight gain and grain consumption. Potential covariates included serum IgG, birth weight and gender, and interaction effects. The CT calves were twice as likely to have diarrhea compared to TT calves. The ABMILK calves were 1.3 times more likely to have diarrhea compared to NoABMILK calves. The TT calves tended to have a higher average daily gain at 28 days and consumed more grain than CT calves. Antimicrobial resistance patterns in fecal E. coli showed low levels of multi-drug resistance in day-old calves but higher levels in isolates from 2 and 4 week old calves.

Key Words: calves, antimicrobial resistance, treatment

604 Factors affecting performance of pre-weaned dairy calves under Kuwait's environment: Effects of immunoglobulins and age on diseases and mortality. M. Razzaque*, T. Al-Mutawa, S. Abbas, and M. Bedair, *Aridland Agriculture and Greenery Department, Kuwait Institute for Scientific Research, Kuwait, Safat, Kuwait*.

Abstract: Objectives of the study were to investigate the effects of dam vaccination, age, serum immunoglobulin (Ig) on disease syndromes and mortality in pre-weaned calves. Late pregnant Holstein Friesian dairy cows and heifers were divided into two herds from five farms: Treatment (T) vaccinated using Lactovac against Rotavirus, Coronavirus and Escherichia coli and control (C) unvaccinated. Total of 1088 newborn calves of above herds were also divided as T and C for the study from their birth to weaning at 90 d. Calves were weighed at birth, fed colostrum 12.5% of their live weight within 8 hrs from birth until 24 hrs. Serum proteins and Ig (IgG, IgM and IgA) were measured, disease syndromes, morbidity and mortality rates were evaluated until weaning of calves at 90 d. The mean birth weight (34.25±SE 0.21kg) of calves did not differ between the herds (P=0.05). Crude mortality rates (2.83 to 22.83%) in calves varied significantly ($P < 0.01$) among five farms. Highly significant differences between dairy herds were observed in Ig classes: IgG (F 3.47 P< 0.010), IgM (F 3.52 P<0.009) and IgA (F 3.66 $P < 0.008$). The effects of Ig levels on calf morbidity rates were significant ($P < 0.05$) on three disease syndromes: pneumonia, diarrhea, and pneumo-enteritis. Vaccination of pregnant dams and oral administration of antibodies to newborn calves reduced calf morbidity and mortality rates ($P < 0.01$). Predominant disease syndromes were pneumo-enteritis (34.6%), pneumonia (33.8%) and combined accounted for 68.4% of all mortality. The younger calves were greatly affected by the disease syndromes. Results showed that inadequate levels of passive immunity of young calves were commonly found in the dairy farms of Kuwait adversely affecting their performance. This first study demonstrates importance of ensuring adequate levels of serum Ig and proteins levels in calves of Kuwait's dairy herds. *Acknowledgement: Partial support of Kuwait Foundation for Advancement of Sciences (KFAS) and Public Dairy Establishment (PDE), Kuwait to this study is highly appreciated and acknowledged.*

Key Words: dairy calves, mortality, morbidity

605 Associations between herd risk of high precalving NEFA and management, feed additive, and facility factors. T. F. Duffield*[1], M. Carson[1], M. Capel[5], S. Godden[2], M. Overton[3], J. Santos[4], and S. J. LeBlanc[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*University of Minnesota, Minneapolis*, [3]*University of Georgia, Athens*, [4]*University of Florida, Gainesville*, [5]*Perry Veterinary Clinic, Perry, NY*.

A field study was conducted in 4 regions of Canada and the USA (ON and NY; MN and WI; CA; and GA and FL) to explore herd risk factors for high precalving serum non-esterified fatty acids (NEFA). Once weekly, blood was collected from cows in the week before calving. For this analysis data from 2048 cows in 47 Holstein dairy herds with a completed herd management survey were utilized. Median cows sampled per farm was 36 (min of 20, max of 97). The median NEFA value for all precalving cows was 0.37 mmol/L. A cutpoint of ≥ 0.5 mmol/L was used to define high NEFA at the cow level. Using this cutpoint, the range in the prevalence of high NEFA across herds was 6.5 to 75% and the median herd prevalence of high NEFA cows was 25%. High herd risk for elevated precalving NEFA (HNEFA, n=24 herds) was defined at a prevalence of $\geq 25\%$ of cows with NEFA ≥ 0.5 mmol/L and low risk NEFA (LNEFA, n=23) herds had a prevalence < 25%. Two by two contingency tables were constructed to screen survey variables for association with HNEFA within 3 categories: facilities, additives/therapeutics, management. Variables associated with HNEFA were then subjected to logistic regression. Bunk space, cow density, feeding frequency, and frequency of group changes through the transition period were not significantly associated with the probability of HNEFA in the close-up period. The use of anionic salts in the close-up diet was associated with a reduced risk of an HNEFA classification (odds ratio (OR) =0.31, P=0.06). The use of individual maternity pens versus a group calving pen was associated with HNEFA (OR=2.6, P = 0.1). The mixing of close-up heifers and cows was associated with an increased risk of HNEFA (OR=5.6, P=0.05). These results do not refute the importance of feeding and lying space but underline that the use of single calving pens and mixing of close-up heifers with cows may be associated with social stressors that might reduce DMI and raise serum NEFA. The lowered risk of HNEFA with the use of anionic salts may represent a surrogate measure of other aspects of transition nutrition and merits more investigation.

Key Words: NEFA, risk factors, precalving

606 Associations between herd risk of high precalving NEFA and dietary factors. T. F. Duffield*[1], M. Carson[1], M. Capel[5], S. Godden[2], M. Overton[3], J. Santos[4], and S. J. LeBlanc[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*University of Minnesota, Minneapolis*, [3]*University of Georgia, Athens*, [4]*University of Florida, Gainesville*, [5]*Perry Veterinary Clinic, Perry, NY*.

The objective of this study was to explore possible nutritional risk factors for high serum non-esterified fatty acids (NEFA) in the close-up period. A field study was conducted in 4 regions of Canada and the USA. Once weekly, after the morning feeding, blood was collected from cows in the week before calving. For this analysis data from 1572 cows in 35 Holstein dairy herds from ON, NY, MN, and CA with a completed herd

management survey and completed feed analysis of the pre-calving TMR were utilized. The close-up TMR was sampled from each participating farm in four places in the bunk, mixed together and submitted to the same laboratory. Wet chemistry analysis was used for minerals and all other analyses were performed using near infrared spectroscopy. In addition, each TMR was evaluated for particle size using the Penn State particle separator (PS). Dietary cation anion difference was calculated using the following formula: DCAD = ((Na*435*100)+(K*256*100)) - ((chloride*282*100)+(S*624*100)). Mean herd NEFA for each farm was calculated for all cows sampled and was used as the outcome of interest. Univariable associations between each ration parameter and herd NEFA were calculated using a mixed model linear regression, controlling for the random effect of region. Variables significant at $P < 0.2$ were submitted to a multivariable model. In preliminary screening, indicators of fiber (NDF, proportion on the top screen of the PS) and DCAD were positively associated with herd NEFA, while energy indicators (starch, ADF, fat) were negatively associated with herd NEFA. The final model revealed significant associations of NDF ($P = 0.01$) and DCAD ($P = 0.01$) with herd average NEFA. In this dataset, lower to moderate dietary NDF (mean = 43%, range was 32 to 52%) and limiting DCAD (mean= 64, range was -139 to 286) in the close-up diet was associated with lower herd NEFA pre-calving.

Key Words: NEFA, precalving diet, risk factors

607 Rumen metabolomic profile and hierarchical clustering analysis in dairy cows fed grading amounts of grain. Q. Zebeli, M. Lewis, S. M. Dunn, D. S. Wishart, and B. N. Ametaj*, *University of Alberta*, *Edmonton, Alberta, Canada*.

Feeding dairy cows high grain diets is related to high incidence of metabolic disorders; however, the underlying mechanism(s) are not yet clear. Metabolomic profiling is a new technology that identifies and quantifies multiple small molecular weight compounds in biological fluid samples. The aim of this study was to explore changes in rumen fluid metabolomic profile in dairy cows fed graded amounts of barley grain using NMR and GC-MS technologies as well as hierarchical clustering analysis. Eight primiparous Holstein lactating cows (~100 DIM) were assigned to one of the 4 mixed diets containing 0, 15, 30, and 45% barley grain (on DM basis) in a double 4 × 4 Latin square design with 21-d periods. After an 11-d adaptation period, samples of rumen fluid were collected shortly before morning feeding on d 1, 3, 5, 7, and 10 of measurements period. Across all diets, the average linkage hierarchical clustering analysis revealed a minimum similarity of 55% in the expression patterns of the 24 organic compounds identified in the rumen fluid. The highest similarity provided the cluster built by leucine, valine, and acetate (90%) followed by a cluster of butyrate, alanine, lactate, and valine (83%) as well as clusters of 3-phenylpropionate (3PP) and 3-hydroxy-phenylacetate (3HP; 71%). Increasing the level of barley grain in the diet linearly increased the concentration of methylamine (MET; P=0.01), phenylacetate (PHE: P=0.02), and 3HP (P=0.08) but decreased that of 3PP (P<0.01). The analysis also showed negative quadratic relationship between MET and dimethylamine to rumen pH (P<0.01). The results showed positive correlations between MET and PHE and rumen lipopolysaccharide (LPS; P<0.001), a highly pro-inflammatory compound, as well as negative correlation between LPS and 3HP (P<0.001). In conclusion, rumen metabolomic cluster analysis reliably describes changes in the rumen fluid during feeding of high-grain diets and suggest further research to better understand rumen physiology.

Key Words: dairy cow, rumen metabolomics, clustering analysis

608 Intrapulmonary *Mannheimia haemolytica* (MH) challenge increases nitrooxidative stress (NOxS) in heifers phenotypically selected for tumor necrosis factor-α (TNF-α) hyper-responsiveness. T. Elsasser*[1], J. Goff[2,3], R. Briggs[2], S. Kahl[1], H. Lehmkuhl[2], M. Ackerman[3], C. Li[1], and R. Horst[2], [1]*USDA-ARS*, *Beltsville, MD*, [2]*USDA-ARS*, *Ames, IA*, [3]*Iowa State University*, *Ames*.

We assessed the degree to which NOxS contributes to the pulmonary and extrapulmonary pathological consequences of MH infection. Two populations of 8-mo old Angus × Hereford heifers were selected based on the patterns of plasma TNF-α evoked following 2 endotoxin (LPS, *E. coli* 055: B5, 0.2 μg/kg BW) challenges 4 d apart; normal animals (N) presented low TNF-α responses and displayed tolerance to the second LPS challenge and hyper-responsive heifers (H) presented higher plasma concentrations of TNF-α and failed to display LPS tolerance. Animals were transported from Beltsville, MD to Ames IA, unloaded, and challenged with MH (NADC D153 serotype 1; intrapulmonary, 9×10^8 CFU/animal). Blood samples, rectal temperature and clinical observations were made at time 0, 24 h and 48 h postinfection (PI). Animals were euthanized at 48 h PI. Lungs and livers were excised, weighed, and scored for appearance; samples were fixed in buffered formalin for subsequent immunohistochemical (quantitative image analysis) examination. Animals included in the statistical analysis (N, n=6; H, n=5) had no clinical signs at time 0 and met 4 of 5 criteria (fever, respiratory signs, lung score ≥ 1, appropriate positive tissue gram stain, increased white blood cell count) of infection after MH. Lung weight (as a % BW) increased to a greater extent in H than in N. Mean lung TNF-α immunoreactivity was 47.7% greater in H than in N (P<0.04). Mean protein tyrosine nitration immunoreactivity, a biochemical marker for peroxynitrite (ONOO)-mediated NOxS damage in cells overproducing nitric oxide and superoxide anion, was higher in H than N in liver (87%, P<0.03) and lung (34%, P<0.04) after MH. The data suggest that MH infection generates ONOO in the lung and liver where tissue damage is more extensive in animals with a propensity to overrespond to Gram-negative proinflammatory challenge.

Key Words: *Mannheimia haemolytica*, respiratory disease, cattle

609 Transcriptome analysis of muscle tissue from calves infected with bovine viral diarrhea virus and *Mannheimia haemolytica*. R. L. Mills*, L. Carlos-Valdez, L. O. Burciaga-Robles, D. Stein, D. L. Step, R. W. Fulton, U. DeSilva, and C. R. Krehbiel, *Oklahoma State University*, *Stillwater*.

Bovine respiratory disease (BRD) is the most economically important ailment of cattle in the U.S. Cattle with this disease produce lighter carcasses with decreased dressing percentages and *longissimus dorsi* area. To understand the effects of common BRD pathogens on muscle gene expression, 8 crossbred beef steers (283.6 ± 37.4 kg) were exposed to a calf persistently infected with bovine viral diarrhea virus type 1b for 72h followed by intratracheal inoculation with *Mannheimia haemolytica* serotype A. Muscle biopsies were taken prior to exposure to either pathogen and 24h following inoculation. Total RNA was extracted and bovine oligonucleotide microarray hybridization performed (n = 6). Genes were categorized according to biological process and/or function. Significance was set at fold change greater than 1.5 and $P < 0.01$. We found 30 genes were induced and 32 genes were suppressed by 24h of infection. Protein metabolism, transcription regulation, and the cell cycle were the predominant biological processes affected. Among upregulated genes, protein metabolism, transcription regulation, cell cycle, and signal transduction processes were most affected. Among downregulated genes, transcription regulation, binding, and

cell cycle genes were most affected. We observed mRNA for several genes involved in tissue remodeling and regeneration to be induced by 24h of infection (tropomyosin 4, 2.84 fold; ankyrin repeat domain 2, 2.29 fold; cathepsin H, 2.09 fold). Genes involved in the cell cycle were coordinately regulated to promote cell proliferation and differentiation (eukaryotic translation initiation factor, 1.59 fold, calreticulin, -1.63 fold, and prolyl endopeptidase, -1.77 fold). Results from this experiment indicate that cattle challenged with BRD pathogens alter gene expression to promote cellular proliferation and differentiation with concomitant tissue regeneration. A corollary to this would suggest that during the first 24h of infection by BRD pathogens, skeletal muscle deterioration is occurring which may partially explain the lighter carcass weights associated with cattle treated for BRD.

Key Words: beef cattle, bovine respiratory disease, gene expression

610 Effect of times treated for bovine respiratory disease during preconditioning on gene expression in muscle and adipose tissue of beef heifers. J. Johnson*, D. R. Stein, L. O. Burciaga-Robles, B. P. Holland, D. L. Step, J. W. Ritchey, U. DeSilva, and C. R. Krehbiel, *Oklahoma State University*, *Stillwater*.

Bovine respiratory disease (BRD) is the most costly disease to the cattle feeding industry. Our objective was to determine the effects of BRD on gene expression in economically important tissues. Tissue biopsy samples from the LM and s.c. fat (SCF) were collected between the 12th and 13th rib from heifers never treated against BRD (HEALTHY; n = 5), treated once (n=5), treated twice (n=5), treated three times (n=5), and heifers classified as chronically morbid (CHRONIC; n = 5) after a 63 d preconditioning period. CHRONIC was defined as animals with at least three antimicrobial treatments and loss of BW during the previous 21 d on feed. Microarray comparisons were performed against HEALTHY and CHRONIC animals to determine differentially expressed genes important in pathways that decrease growth and performance or are involved in immunological functions. Subsequently, 14 genes were evaluated using RT-PCR including tumor necrosis factor alpha (TNFα), interleukin 6, toll-like receptor 4, and nuclear factor kappa B (NFκB). The Proc Mixed procedure of SAS was used to evaluate the significance of number of antimicrobial treatments. Components of the ubiquitin pathway were different among treatments, including greater (P<0.09) expression of Fbox WD repeating domain 12 in SCF, and greater (P=0.10) expression of 26S proteasome subunit ATPase 1 in LM. TNFα was more highly expressed (P<0.007) in muscle of CHRONIC than HEALTHY heifers. Other genes that were differently expressed in adipose tissue of CHRONIC vs. HEALTHY animals were haptoglobin (down regulated; P<0.02) and NFκB (up regulated; P<0.10). These results suggest that muscle wasting via the ubiquitin pathway, as well as increased expression of TNFα may decrease growth potential in heifers treated several times for BRD.

Key Words: animal growth, bovine respiratory disease, gene expression

611 Evaluation of enzymatically hydrolyzed yeast in vitro and in vivo for control of *Cryptosporidium parvum* infections in dairy calves. S. Jalukar*[1] and J. Nocek[2], [1]*Varied Industries Corporation*, *Mason City, IA*, [2]*Spruce Haven Farm and Research Center*, *Auburn, NY*.

Effect of enzymatically hydrolyzed yeast and yeast culture (EHY) (Celmanax®, Varied Industries Corporation, IA, USA) was evaluated to determine efficacy on *Cryptosporidium parvum* challenge. EHY contains complex sugars like galactosamine, mannose and mannan oligosaccharide (MOS) which have been shown to interfere with *Cryptosporidium spp* attachment to intestinal epithelium. Experiment 1 evaluated EHY (40, 20 or 2 mg/mL) treated *C. parvum* sporozoites to interfere with the binding and infection of Madin - Derby bovine kidney (MDBK) cells and live porcine intestinal cells (IPEC-J2) by an in vitro immuno-florescence assay. Experiment 2: Sixteen calves (10-12 days old) naturally infected with *C. parvum* were randomly assigned to two treatments: without and with 4ml/calf/twice a day EHY for 5 days. Fecal samples were taken at initiation and completion of the trial for oocysts count, consistency and calves were scored for dehydration. Experiment 1: There was a decrease ($P < 0.001$) in the number of attached sporozoites to bovine MDBK cells when EHY was present at 40 and 20 mg/mL, compared to un-treated control (11.97 and 19.60 vs. 40.80 sporozoites/field, respectively). Ability of *C. parvum* sporozoites to infect porcine IPEC-J2 cells decreased with increase in EHY concentration in a cell-monolayer assay. A 90% decrease in infection was noted with 40 mg/mL EHY treatment compared to control. Experiment 2: Calves supplemented with EHY demonstrated 3 fold less oocyst shedding within 5 days after supplementation. Fecal and dehydration scores were significantly less for calves supplemented with EHY. Enzymatically hydrolyzed yeast plus yeast culture (Celmanax®) demonstrated the ability to bind and prevent *C. parvum* from infecting tissue in vitro, reduced oocyst shedding, improved fecal consistency and hydration status in infected calves.

Key Words: cryptosporidiosis, calf

612 Neem-tree extract as a feed-additive against ticks in sheep. S. Y. Landau*[1], D. R. Gardner[2], J. A. Pfister[2], E. L. Knoppel[2], D. Kababya[1], F. D. Provenza[3], C. Peterson[3], and J. J. Villalba[3], [1]*Agricultural Research Organization*, *Bet Dagan, Israel*, [2]*SDA-ARS Poisonous Plant Research Laboratory*, *Logan, UT*, [3]*Utah State University*, *Logan*.

Ticks are affected by the composition of the blood of their hosts. Immersion in solutions of fruit and kernel extracts from trees of the Meliaceae family inhibits egg production and embryogenesis in *Hyalomma spp* and *Boophilus spp.* ticks in vitro. The tetranor-triterpenoid Azadirachtin A (AzA) is the main acaricidal compound in these extracts. We investigated the effects of an extract of the neem tree (*Azadirachta indica* Juss.) containing 43% AzA, given as a feed additive to lambs artificially infested with adult engorging *Dermacentor variabilis* ticks. We assessed feed acceptance and toxicity to lambs, AzA concentration in peripheral blood using a novel LC/MS assay, and tick engorgement and egg production. After tick attached, the lambs were allotted to 3 dietary treatments:AzA0 (Control, n=10), AzA0.3 (n=5), and AzA0.6 (n=5), with feed containing 0, 0.3, and 0.6% AzA on a DM basis. Four days after attachment, ticks were sprayed in half of the AzA0 lambs with an ethanol:water:soap emulsion containing 0.6% AzA (Aza0S). In spite of its very pungent odor, the neem extract was well accepted by all but one lamb. No differences were found between groups in muscle and liver enzymes in blood, and there was no indication of toxicity. Plasma AzA concentrations after 7 and 14 days of feeding AzA were (3.32; 4.81) and (1.88, 4.35 μg/ml) for the AzA0.3 and AzA0.6 treatments, respectively, suggesting increased liver detoxication during the second week. Treatments were not lethal to ticks, but tick weight at detachment was 0.64, 0.56, 0.48, and 0.37 g for ticks from the AzA0, AzA0.3, AzA0S, and AzA0.6 treatments ($P<0.004$), suggesting that blood AzA was detrimental to ticks. As Azadirachtin affects embryo development and ticks at the moulting stages, we expect that one-host ticks will be more

affected than the three-host tick *D. variabilis*. Our results thus suggest that ingestion by herbivores of plants containing compounds such as AzA may reduce external parasites.

Key Words: lamb, tick, azadirachtin

Beef Species: Health, Efficiency and Beef Quality

613 mRNA expression of genes regulating oxidative phosphorylation in the muscle of beef cattle divergently ranked on residual feed intake. A. K. Kelly*[1], S. M. Waters[2], M. McGee[2], C Carberry[1,2], D. H. Crews Jr[3], T. M. Boland[1], and D. A. Kenny[1], [1]*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin*, *Belfield, Dublin 4, Ireland*, [2]*Animal Bioscience Centre, Teagasc, Grange Beef Research Centre*, *Dunsany, Co. Meath, Ireland*, [3]*Colorado State University*, *Fort Collins*.

The objective was to evaluate the effects of ranking on phenotypic residual feed intake (RFI) and diet type on the transcription of genes coding for mitochondrial biogenesis in the muscle of beef cattle. Individual dry matter intake and growth was recorded for 90 yearling Limousin × Friesian heifers offered a high energy TMR diet over 120 days. All animals were ranked retrospectively on phenotypic RFI. The 10 highest (inefficient) and 10 lowest (efficient) animals were selected for this study. Animals were then re-allocated to a grass silage diet and feed intake was recorded for a six week period. The experiment was therefore arranged in a 2 (high v low RFI) × 2 (high v low energy diet) factorial design. Biopsies of the *M. longissimus dorsi* were harvested at the end of each dietary period. Total RNA was extracted and real-time PCR was used to quantify mRNA transcripts of genes coding for five enzymes from the respiratory chain complex, two electron carriers, mitochondrial protein and five transcription factors. mRNA expression of the transcription factors PGC1-α and PPAR-γ were 2.0 and 2.8-fold higher ($P < 0.01$) respectively, in inefficient compared with efficient animals. There was a phenotype × diet interaction ($P < 0.05$) for *ant-1* mRNA involved in exchange of ADP and ATP between the mitochondrial matrix and the cytosol. A tendency ($P = 0.09$) for a phenotype × diet interaction was also observed for *atpase*, a critical regulator of the ATP-synthesizing enzyme complex. These data suggest an association between mitochondrial biogenesis and RFI in cattle and could be useful in the development of molecular markers for this trait.

Key Words: residual feed intake, muscle, gene expression

614 Relationship between metabolic hormones, metabolites and energetic efficiency in growing beef heifers. A. K. Kelly*[1], M. McGee[2], D. H. Crews Jr.[3], T. M. Boland[1], and D. A. Kenny[1], [1]*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin*, *Belfield, Dublin, Ireland*, [2]*Teagasc, Grange Beef Research Centre*, *Dunsany, Co. Meath, Ireland*, [3]*Colorado State University*, *Fort Collins*.

Measurement of residual feed intake (RFI) is expensive and thus identification of cost-effective physiological indicators is necessary to facilitate wide-scale adoption. Our objective was to examine the potential of selected metabolic hormones and metabolites as indicators of energetic efficiency in growing beef heifers. Individual dry matter intake and growth was recorded for 90 yearling Limousin × Friesian heifers offered a high energy TMR diet for 120 days. Blood samples (n=4) were collected by jugular venipuncture on a monthly basis for each animal. Concentration of plasma IGF-1 was measured using RIA, insulin was quantified using fluoro-immunoassay, while selected metabolites were measured using an automated biochemical analyzer. Residual feed intake was computed, for each animal, as the residuals from the regression of DMI on ADG and mid test $BW^{0.75}$ (MWT). Residual feed intake averaged 0.00 kg/d and ranged from -1.25 to 1.87 kg/d. As expected, RFI was not correlated with MWT or ADG, but was correlated ($P < 0.001$) with DMI ($r = 0.48$) and FCR ($r = 0.46$). Plasma IGF-I was positively correlated ($P < 0.05$) with ADG ($r = 0.25$) but not ($P > 0.10$) with DMI, FCR or RFI. Correlations coefficients between insulin and DMI, ADG, FCR or RFI were not different from zero ($P > 0.10$). Plasma glucose was negatively correlated ($P < 0.05$) with FCR ($r = -0.20$) but not associated with DMI, ADG or RFI. Urea concentrations were related to DMI ($r = 0.33$) and FCR ($r = 0.31$) but not ADG or RFI. Plasma NEFA was negatively associated ($P < 0.05$) with DMI (-0.36), FCR (- 0.36) and RFI (-0.23). Positive associations ($P < 0.05$) were observed between BHB and DMI (0.34), FCR (0.25) and RFI (0.39) but an association with ADG was not detected. It is unlikely that the plasma analytes measured here, *per se*, will be useful in the early identification of energetically efficient cattle.

Key Words: residual feed intake, plasma analytes

615 Predicting body weight in beef heifers using various body measurements. A. G. Fahey*, A. K. Kelly, R. P. McDonnell, and D. A. Kenny, *School of Agriculture, Food Science, and Veterinary Medicine, University College Dublin*, *Belfield, Dublin 4, Ireland.*

Accurate assessment of body weight (BW) is an important management tool in commercial beef enterprises. However, many farmers may not have easy access to weighing facilities. Body measurements (BM) such as wither height or depth of chest require inexpensive equipment. In order to determine the potential of various BM as predictors of BW, back length, wither height, pelvic width, chest depth, and chest girth were measured along with BW. Heifers were divided into two age groups; 6-13 months (mean = 286.8 ± 44.7 d; n = 87 heifers, 176 records), and 17-24 months (mean = 642.3 ± 45.6 d; n=60 heifers, 106 records). Body weight was regressed on BM, and linear, quadratic and cubic effects of the BM variables were considered: $Y = b_0 + age + b_1X + b_2X^2 + b_3X^3 + \varepsilon$. Where Y = body weight, b_0 = the intercept, X = independent variable (i.e. wither height, back length, chest depth, chest girth, or pelvic width). Cubic regression models with and without age were best predictor equations for BW for both age groups. The R^2 value was used to determine the variation accounted for by the various regression models (Table 1). Overall, the cubic regression models had a better fit for the 6-13 month group for all measurements with the exception of chest girth which was stronger for the 17-24 month heifers. The cubic regression equation for chest depth + age had the best fit for the 6-13 month group , while chest girth + age was the best BW prediction model for the 17-24 month group. These results indicate the potential for the use of BM as indicators of BW, although different BM may have to be used depending on the age of the animal.

Table 1. Cubic regression models with and without age for heifers in both age groups.

Parameter	R^2 (6 – 13 months)	R^2 (17 - 24 months)
Back Length	0.71	0.31
Back Length + age	0.84	0.31
Pelvic width	0.83	0.26
Pelvic width + age	0.83	0.24
Chest Girth	0.57	0.70
Chest Girth + age	0.79	0.71
Chest Depth	0.91	0.15
Chest Depth + age	0.92	0.25
Wither Height	0.83	0.18
Wither Height + age	0.88	0.29

Key Words: beef cattle, body weight, body measurement

616 Effect of residual feed intake on body composition traits in growing beef heifers. A. K. Kelly*[1], M. McGee[2], T. M. Boland[1], D. H. Crews Jr.[3], and D. A. Kenny[1], [1]*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*, [2]*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*, [3]*Colorado State University, Fort Collins*.

Live animal measurements can be useful predictors of carcass composition and thus may act as early indicators of carcass value. The objective of this study was to assess various ultrasonic and body composition measurements in beef heifers divergently ranked on phenotypic residual feed intake (RFI). Ninety Limousin × Friesian heifers were used in the current study. Individual daily feed intake and bodyweight gain were calculated over a 120 day experimental period. The test diet consisted of *ad libitum* access to a maize silage and pelleted concentrate total mixed ration offered at a ratio of 30:70 respectively. Physical measurements including height at withers, chest girth, pelvic width and length of back as well as ultrasonic fat and muscle depths were recorded on four equally spaced occasions during the experimental period. Residual feed intake was computed, for each animal, as the residuals from a multiple regression model regressing DMI on ADG and mid test $BW^{0.75}$ (MWT). Standard deviations above and below the mean were used to group animals into high (>0.5 SD), medium (± 0.5 SD), and low RFI (<0.5 SD). Gain in body composition traits was computed as the coefficient of the linear regression of body composition measurements on time. Residual feed intake ranged from -1.27 to 1.87 kg/d. representing a mean daily difference of 3.14 kg/DM in feed consumed between the most and least efficient animals. Low RFI animals consumed 15.7 and 7.6% less feed than animals with medium and high RFI, respectively. The high RFI group deposited more ($P < 0.05$) lumbar fat compared to the medium or low RFI groups. There was no difference ($P > 0.10$) in gain of muscle or rump fat or in any other body measurement recorded between RFI groups. The results suggest lower lipid accretion in energetically efficient animals. Attempts should be made to account for this in the estimation of RFI.

Key Words: residual feed intake, body composition

617 The immune response of heifers divergently ranked for residual feed intake. A. G. Fahey*[1], B. Earley[2], A. K. Kelly[1], M. McGee[3], and D. A. Kenny[1], [1]*School of Agriculture, Food Science, and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland*, [2]*Teagasc, Animal Bioscience Centre, Dunsany, Co. Meath, Ireland*, [3]*Teagasc, Grange Beef Research Centre, Co. Meath, Ireland*.

Feed intake accounts for 70% of the variable costs of beef production. Therefore, the efficiency with which an animal converts feed energy into meat is an economically important trait. An animal's response to stress is characterized by increases in metabolic rate, energy consumption and utilization mediated through alterations in the functioning of the hypothalamic–pituitary–adrenal axis. The objective of this study was to examine the immune response to physiological stress in cattle divergently ranked for residual feed intake (RFI). Limousin × Friesian heifers (n=86) were ranked on phenotypic RFI. The 15 highest and 15 lowest ranking animals were assigned to high and low RFI groupings respectively. All heifers were fitted aseptically with an indwelling jugular catheter for repeated blood sampling. On d 0, two blood samples were taken at -120 and 0 min prior to an intramuscular administration of dexamethasone (20μg/kg). On d 1, blood samples were taken at -40 and 0 min and then animals were intravenously administered bovine corticotrophin releasing hormone (bCRH; 0.3μg/kg). Further blood samples were taken at 60, 120, 240, 350, and 410 min after bCRH. Blood samples were analyzed for lymphocyte, neutrophil and leukocyte (LUC) counts, haemoglobin (HGB) concentration and haematocrit percentage (HCT). A repeated measures ANOVA was conducted with the main effects of bleed time (T), group (G; high or low RFI), T × G, and the average of the two blood samples pre-dexmathasone was used as a covariate. A significant time effect was found for LUC and HGB ($P<0.01$), and for HCT ($P<0.05$). There were no significant effects for G or T × G. These data suggest that selection for animals with low RFI will not compromise immune function.

Key Words: residual feed intake, stress, immune response

618 Rubber mats improve finishing beef cattle welfare. M. R. Elmore*, M. F. Elischer, M. C. Claeys, and E. A. Pajor, *Purdue University, West Lafayette, IN*.

Housing beef cattle on concrete can negatively impact welfare, as evidenced by increased lesions and joint swelling. The aim of this study was to compare the effect of rubber mats on the growth, health, hygiene and behavior of finishing beef cattle. Crossbred Angus steers (48, n=4/trt) were housed in pens of 4 and assigned to either slatted concrete (C), slatted rubber mat (S) or solid rubber mat (M) from 36-48 weeks of age. Performance data were collected at 2 week intervals, while frequency of postural changes (indicator of floor traction/comfort) at weeks 0 and 12. Data were analyzed using GLM and post-hoc Tukey tests. There was no effect of flooring on weight ($P=0.429$) or ADG ($P=0.950$). The S steers showed a decrease in lameness (1.69 ± 0.04) compared to M (1.95 ± 0.04) and C (1.98 ± 0.04; both $P<0.001$), M and C did not differ ($P>0.05$). The S steers showed less joint swelling (knees [K]: 0.17 ± 0.05, hocks [H]: 0.15 ± 0.07) compared to M (K: 0.41 ± 0.05, H: 0.51 ± 0.07) and C (K: 0.74 ± 0.05, H: 0.62 ± 0.07; all comparisons $P<0.001$); while M showed less K swelling compared to C ($P=0.007$), but no effect on H ($P>0.05$). The M steers showed an increase in lesion score (0.80 ± 0.08) compared to S (0.38 ± 0.08) and C (0.37 ± 0.08; $P<0.001$ and $P=0.003$, respectively), though S and C did not differ ($P>0.05$). The M (2.88 ± 0.04) and S (1.02 ± 0.04) pens were less clean than C (0.86 ± 0.04; $P<0.001$ and $P=0.023$, respectively) and M was less clean than S ($P<0.001$). Additionally, M steers were dirtier (3.64 ± 0.05) than S (2.27 ± 0.05) and C (2.19 ± 0.05; both $P<0.001$), S and C did not differ ($P>0.05$). The S steers changed their posture more frequently (22.50 ± 1.21) than C (17.38 ± 1.21) and M (17.03 ± 1.21; $P=0.036$ and $P=0.026$, respectively), M and C did not differ ($P>0.05$). Compared to C, M

showed a reduction in knee swelling, but an increase in leg lesions and a reduction in cleanliness; while S showed a decrease in joint swelling and lameness and an increase in postural changes. This data suggests that the addition of slatted rubber mats to concrete pens should be considered as a method to improve beef cattle welfare.

Key Words: beef cattle, rubber mats, welfare

619 Feedlot growth performance and carcass characteristics of heifers treated for clinical signs of bovine respiratory disease during preconditioning. B. P. Holland*, L. O. Burciaga-Robles, C. J. Richards, D. L. Step, and C. R. Krehbiel, *Oklahoma State University*, *Stillwater*.

Heifers (n = 337; initial BW = 241.3 ± 16.6 kg) were assembled by a western Kentucky order buyer and shipped to Stillwater, OK. During a 63-d preconditioning period, morbidity and mortality attributed to Bovine Respiratory Disease (BRD) was 57.6% and 8.6%, respectively. At the end of preconditioning, 193 heifers were selected and allotted to finishing pens (5 to 7 heifers/pen) based on the number BRD treatments received. Heifers were never treated for BRD (0X; n = 9 pens), treated one time (1X; n = 9 pens), two times (2X; n = 6 pens), 3 times (3X; n=6 pens), or designated as chronically ill (C; 2 pens). Arrival BW were not different (P = 0.21) among treatment categories. However, disease incidence during preconditioning decreased (P < 0.01) performance, resulting in BW of 318, 305, 294, 273, and 242 kg for 0X, 1X, 2X, 3X, and C, respectively, at the start of the finishing period. On d 65 and 122, LM measurements were made by ultrasound to estimate average end point within category and block. On average, heifers were slaughtered on d 163 for 0X, 1X, and 2X, d 182 for 3X, and 189 for C (P < 0.01). Final BW was similar for heifers treated 0, 1, 2, or 3 times, but was lower (P = 0.05) for heifers deemed chronically ill. Overall ADG was not different among BRD treatment categories, but DMI was lower (P < 0.01) for chronically ill animals. Therefore, G:F was greatest (P < 0.01) for C, intermediate for heifers that received either 2 or 3 BRD treatments, and least for heifers never treated or treated 1 time. Similar to BW, HCW was lower (P = 0.03) for C than other categories. Marbling score tended (P < 0.10) to be lower for 3X and C than 0X, 1X, and 2X, but other differences in carcass characteristics were not detected ($P \geq 0.12$). Less than 20 additional days on feed were required for heifers treated 3 times to have similar weights and carcass characteristics to heifers never treated for BRD. Segregating and re-starting animals during finishing may be a viable alternative to realizing chronically ill animals.

Key Words: bovine respiratory disease, cattle, feedlot

620 Effects of growing phase diet on fatty acid profile of beef steers. K. E. Hudelson*, C. R. Krehbiel, G. W. Horn, J. W. Dillwith, M. P. McCurdy, R. D. Madden, and R. G. Mateescu, *Oklahoma State University*, *Stillwater*.

Fatty acid composition of intramuscular (IM) beef fat depots is influenced by diet. Previous research indicates that the benefits of grass-feeding beef cattle include decreased omega-6/omega-3 fatty acid ratio and atherogenic index and increased concentration of conjugated linoleic acid (CLA), all healthfulness traits that are becoming increasingly important to consumers. However, the effects of growing phase diet on the fatty acid profile of IM fat after the finishing phase are unclear. The purpose of this study was to investigate the effects of feeding regimen during the growing phase on fatty acid profile pre- and post-finishing. Thus, 36 British crossbred steers were randomly assigned to one of four treatment diets: high-concentrate ad libitum (CF); wheat pasture (WP); sorghum silage-based (SF); or high-concentrate program (PF). Steers in the WP, SF, and PF treatments were managed such that rate of gain was approximately equal across groups. Four steers from the WP, SF, and PF groups were harvested at the end of the 112 day treatment; the remaining 24 steers were finished on a concentrate diet until they reached a 12th rib fat thickness of 1.26 cm. Rib eyes were collected from the left side of each steer for analysis of fatty acid content. Rib eyes were trimmed of subcutaneous fat and powdered in liquid nitrogen prior to total lipid extraction in triplicate from approximately 40 mg tissue using a 2:1 chloroform: methanol method. Acid and base catalyzed derivitizations were performed. Extracts were analyzed using an Agilent 6890 GC with FID and a DB-23 column. Percent composition of each fatty acid was calculated and fatty acids were grouped by class prior to assessment of variation between treatments using the GLM of SAS followed by orthogonal contrasts with 1 degree of freedom. Significant differences in saturated (P=0.029) and monounsaturated (P=0.035) fatty acids, atherogenic index (P=0.039), and omega-6/3 ratio (P=0.001) were detected between treatments prior to finishing. Except for the omega-6/3 ratio (P=0.010), no significant differences were detected post-finishing suggesting that finishing diet is the determining factor of fatty acid profile at harvest.

Key Words: lipids, grass-fed, marbling

621 Comparison of fatty acid profiles of longissimus muscle from Angus and Charolais finishing steers. A. K. Lunsford*, J. W. Dillwith, C. R. Krehbiel, and R. G. Mateescu, *Oklahoma State University*, *Stillwater*.

Beef is a rich source of protein and micronutrients, however beef is perceived as having high fat content with undesirable composition: high percentage of saturated fatty acids. Genetic variability in beef fatty acid composition consists of differences between breeds and between animals within breed. The effect of breed on fatty acid profile in beef was evaluated in longissimus muscle from Angus (n=19) and Charolais (n=14) feedlot finished steers. Steers were fed a total of 140 d before slaughter. Longissimus muscles were biopsied on d 127 of the finishing period between the 10th and 13th ribs and fatty acid composition was determined. Lipids were extracted in triplicate with a 2:1 (v,v) methanol:chloroform solution then acid and base deritivitized before separation by gas chromatography on an Agilent 5890 gas chromatograph with 7673 autosampler. Percent composition of each fatty acid was calculated and the effect of breed was analyzed using the general linear model of SAS. Hot carcass weights did not differ, however, Angus steers had higher marbling scores (P=0.01) and more backfat (P=0.01) than Charolais steers. Although percent of saturated fatty acids did not differ between Angus (44.9%) and Charolais (44.0%) steers, Angus steers LM had a higher percent of monounsaturated fatty acids (43.7 vs. 39.4%; P=0.01) and a lower percent of polyunsaturated fatty acids (11.1 vs. 16.3%; P=0.03), omega-3 fatty acids (0.58 vs 0.82%; P=0.04) and omega-6 fatty acids (10.5 vs. 15.5%; P=0.03). Specifically, Angus had a higher (P<0.04) percentage of palmitic (16:0), palmitoleic (16:1), hetadecenoic (17:1), and oleic (18:1) acids in LM than Charolais steers. Angus steers had a lower (P<0.03) percentage of behenic (22:0), lignoceric (24:0), linoleic (18:2), linolenic (18:3), eicosadienoic (20:2), arachidonic (24:0), and docosahexaenoic (22:6) acids in LM than Charolais steers. The challenge for the beef industry is to develop and implement a program aimed at improving healthfulness of beef utilizing existing natural genetic variation in fat composition. These

results indicate the possibility of manipulating beef fat composition through breed selection.

Key Words: beef, fatty acid, longissimus

622 Fatty acid profile in beef meat and baby food based on beef meat. A. Nudda*[1], G. Battacone[1], R. Boe[1], M. G. Manca[1], M. Mele[2], A. Serra[2], and G. Pulina[1,3], [1]*Dipartimento di Scienze Zootecniche*, *University of Sassari, Italy*, [2]*Dipartimento di Agronomia e Gestione dell'Agroecosistema*, *University of Pisa, Italy*, [3]*Agricultural Research Agency of Sardinia - AGRIS Sardegna*, *Sassari, Italy*.

The aim of this study was to compare fatty acid (FA) profile of fresh beef meat with that of baby foods based on beef meat. For this purpose, 20 samples of homogenized beef–meat baby food (80–g jars; HO) and 18 samples of lyophilized (freeze–dried) beef–meat baby food (30–g jars; LIO), produced by various infant–food companies, and 10 samples of fresh beef meat (FM) were collected and analyzed by gas chromatography. The content of each fatty acid methyl ester (FAME) was expressed as a percentage of total FAME. Data were analyzed with one–way ANOVA using type of product as the main effect. All fatty acids, except for α–linolenic acid (C18:3 ω3) and c9,t11 conjugated linoleic acid (CLA), differed among the three products tested. The sum of ω6 FA was higher in HO (21.2%) compared to FM (12.5%) and LIO (4.0%) samples, due to its higher content of linolenic acid. Therefore, ratio ω6/ω3 FA was markedly higher in HO (32.1) compared to FM (9.0) and LIO (8.4) samples. On the other hand, the content of arachidonic acid (C20:4 ω6) was more than 9–fold higher in FM compared to LIO and HO. The content of total PUFA ω3 was highest in FM (1.5%), because of greater content of EPA, DPA and DHA compared to HO (0.8%) and LIO (0.6%) baby foods. Fatty acid composition was more similar between LIO and FM samples than between HO and FM samples, probably as a consequence of the high level of vegetable oil added to HO products. This study suggests the possibility of enhancing the FA profile of commercial baby food based on beef meat by using meat with a healthier FA profile. *Acknowledgements*: *Research supported by the Fondo di Ateneo per la Ricerca Scientifica (FAR, ex 60%).*

Key Words: beef meat, fatty acid, baby food

Breeding and Genetics: Breeding & Genetics Workshop

623 Solving a dilemma in graduate education: Animal Breeding and Genetics Online. R. M. Lewis*[1], B. B. Lockee[1], M. S. Ames[1], G. C. Márquez[1], R. M. Enns[2], J. M. Rumph[3], T. W. Wilkinson[1], and E. J. Pollak[4], [1]*Virginia Tech*, *Blacksburg*, [2]*Colorado State University*, *Fort Collins*, [3]*Michigan State University*, *Lake City*, [4]*Cornell University*, *Ithaca, NY*.

Diminishing faculty numbers has reduced opportunities for coursework tailored to the needs of future scholars in quantitative aspects of genetics. Existing faculty must focus on basic content, limiting their ability to offer advanced instruction. A potential solution to this dilemma is utilizing distance learning technologies within a collaborative framework. Distance delivery programs have advantages: more students can access expertise within a technology-enriched learning environment. However, challenges exist. There is risk of a â€œpsychological distanceâ€ separating students and faculty. Furthermore, distance education increases demands on faculty time, particularly with course design and implementation across institutions. A consortium of four universities has combined efforts to develop eight graduate-level online courses in animal breeding and genetics. The instructional design adopted embraces both the advantages and challenges of distance delivery. Discussion boards and virtual office hours have been used to encourage communications. A game-based genetic simulation was developed, with across-institutional teams competing through a common web-based interface. An annual face-to-face event has been held to allow social and academic interactions. Thus far, students from 19 universities have participated, with each course enjoying an enrollment of 10 to 30 students. Originally, seven courses were planned. However, based on student feedback and performance, it became clear that pre-requisite knowledge varied widely among participants. Therefore, an eighth course was added to provide foundational knowledge. Consistency in course design and implementation remains a challenge. Joint working sessions will be held to define common instructional and assessment strategies. With such a concerted effort, the Animal Breeding and Genetics Online curriculum offers promise for solving a dilemma in graduate education.

Key Words: graduate education, distance learning, quantitative genetics

624 Recent developments in genetic evaluation tools. D. Garrick*, *Iowa State University*, *Ames*.

The principal tool for genetic evaluation is a sound and practical statistical basis to determine linear functions for combining recorded performance on an individual, its relatives and contemporaries in order to minimize the prediction error variance of the estimated genetic merit of each animal. Hazel and Lush's methodology, known as best linear prediction or selection index, was limited to circumstances where observed performance had been corrected, prior to analysis, with the true or parametric adjustment factors for non-genetic effects such as herd-year. In practice, their method was applied using estimated adjustments for non-genetic effects and ignoring the contributions of all animals except a few close relatives. Henderson extended the method. First, to account for the estimation of fixed effects from the data, by restricting analysis to certain linear combinations of observations that resulted in translation invariant prediction, known as best linear unbiased prediction. Those evaluations had larger prediction error variance, but lacked the bias from errors in estimation of non-genetic effects. Second, a computing algorithm was developed to include information from all relatives. It used expected or average relationships between animals. A recent extension exploits the availability of genetic markers to characterize the realized rather than expected inheritance of chromosome fragments among close and distantly related animals. The combined use of genomic and phenotypic data is known as genomic prediction. It can provide genetic evaluations of animals without individual or progeny records that are more accurate than was the case using expected relationships.

Key Words: genomic prediction

625 Development and validation of SNP markers comprising the IGENITY® profile for carcass traits and ADG in beef cattle. B. W. Woodward* and J. D. Nkrumah, *Merial Ltd., Duluth, GA*.

Genomic markers have been used for several years to provide producers with an early prediction of differences in genetic potential in their animals. Discovery research at many institutions has allowed for rapid expansion of these panels to include larger numbers of markers in more genes to explain more variation in traits of economic importance. This abstract presents the results of panels of markers developed by IGENITY® for beef carcass traits and feedlot ADG. The initial step involved single marker analyses using an allele substitution mixed model in a population of 1,367 cattle. Compound covariate prediction methods were used along with single marker associations to develop panels of markers associated with each trait. Molecular breeding values (MBV) were computed and tested in independent populations, one internal and the other external, as part of a National Beef Cattle Evaluation Consortium validation process. Data used for internal and external validation of the MBV for each trait included 1,104 hd and 1,354 hd, respectively. All 3 data sets are comprised of purebred and crossbred steers and heifers with known sire and sire breed, representing at least 15 Bos taurus and Bos indicus breeds but with considerable Angus influence. All cattle were fed in commercial feedlots in the Midwest; however, they were born on cattle operations in eight states. All regressions of MBV on phenotype in the internal and external validations were highly significant for backfat, marbling score, quality grade (percent Choice or better), ribeye area, yield grade, and ADG. P-values for these traits from the internal validation regressions were 1.7×10^{-5}, 1.0×10^{-8}, 2.0×10^{-8}, 1.7×10^{-3}, 3.0×10^{-4}, and 2.4×10^{-2}, respectively; and external validation p-values were 2.2×10^{-4}, 5.0×10^{-8}, 9.2×10^{-5}, 4.7×10^{-4}, 1.5×10^{-6}, and 6.7×10^{-5}, respectively. Therefore, these results from internal and external analyses of independent populations support concluding these IGENITY trait panels are validated and can be used to predict differences in genetic potential for these traits in cattle.

Key Words: beef carcass traits, ADG, SNP

626 High-density SNP scan of production and product quality traits in beef cattle. R. M. Thallman*, W. M. Snelling, M. F. Allan, C. L. Ferrell, H. C. Freetly, T. G. Jenkins, T. L. Wheeler, S. D. Shackelford, D. A. King, L. A. Kuehn, J. W. Keele, and G. L. Bennett, *USDA, ARS, USMARC, Clay Center, NE*.

Genotypes from the BovineSNP50 BeadChip (50K)were obtained on animals derived from 150 AI sires from seven breeds (22 sires per breed; Angus, Charolais, Gelbvieh, Hereford, Limousin, Red Angus, and Simmental) as either progeny (F_1; 590 steers) or grandprogeny (F_1 x F_1 = F_1^2; 1,306 steers and 707 females). Single SNP associations were conducted for each of the 44,163 SNP with minor allele frequency > 0.05 in the F_1^2 generation. Records analyzed included birth weight (BWT), weaning weight (WWT) and postweaning gain (PWG) of 2,540 to 2,578 F_1 and F_1^2 steers and heifers; hot carcass weight (HCW), fat thickness (FT), ribeye area (REA), marbling score(MARB) and 14 d Warner-Bratzler shear force(WBS) of 1,667 to 1,693 F_1 and F_1^2 steers; and residual feed intake (RFI) and flight speed (FLS) of 1,187 to 1,192 F_1^2 steers. Models included fixed effects for additive substitution effect of the SNP as well as sex, age of dam, contemporary group (year-season-location), covariates for calf breed composition and heterosis, and random direct additive polygenic effects. Models for BWT, WWT, and PWG also included fixed dam SNP substitution effects, covariates for dam breed composition and heterosis, and random maternal additive polygenic and permanent environment effects. The number of SNP nominally significant at $P < 0.001$ and the false discovery rate (FDR), respectively, for each trait were BWT: 638, 0.07, WWT: 273, 0.16, WWT - maternal: 376, 0.12, PWG: 670, 0.07, PWG - maternal: 717, 0.06, FT: 115, 0.38, REA: 120, 0.37, MARB: 113, 0.39, HCW: 166, 0.27, WBS: 48, 0.92, RFI: 116, 0.38, and FLS: 51, 0.87. The number of SNP nominally significant at $P < 0.0001$ and their FDR, respectively, were BWT: 308, 0.01, WWT: 103, 0.04, WWT - maternal: 79, 0.06, PWG: 226, 0.02 and PWG - maternal: 192, 0.02. For FT, REA, MARB, HCW, and RFI, 29-37% of SNP significant at $P < 0.001$ are expected to be spurious. Many SNP could be identified with high confidence ($0.01 < FDR < 0.06$) for BWT, WWT, and PWG, the traits for which the greatest number of 50K genotypes and phenotypes were available. Only 7-16% of the many additional SNP significant for these traits at $P < 0.001$ are expected to be spurious associations.

Key Words: beef cattle

627 Whole genome candidate gene approaches to identifying gene SNP markers influencing fat deposition and carcass merit in beef cattle. C. Li*[1,2], M. Vinsky[1], R. Crews[3], E. Okine[2], S. S. Moore[2], and D. H. Crews Jr.[2,4], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*, [4]*Colorado State University, Fort Collins*.

Identification of DNA markers that affect quantitative traits is the first step towards successful implementation of marker assisted selection in order to improve the traits of economic importance. Single nucleotide polymorphisms (SNP) within a gene are of particular importance for association analyses of quantitative traits as they may be the causal allelic determinants that contribute to phenotypic variation. The aim of this study was a genome-wide identification of gene-specific SNP markers that are associated with fat deposition and carcass merit in beef cattle. The candidate genes were chosen based on their chromosomal locations within or in close proximity to reported quantitative trait loci (QTL) for fat deposition in cattle and(or) their possible function and involvement in fat metabolism, and a panel of 1536 SNPs in 418 candidate genes spanning 25 bovine autosomes was developed. The gene-specific SNPs were genotyped on 1027 steers from three unrelated beef cattle populations including 456 Hybrid, 313 Angus and 258 Charolais steers. Marker association analyses were carried out separately for each population on seven fat deposition and carcass merit traits including ultrasound backfat thickness, average daily gain of ultrasound backfat thickness during feedlot test, carcass average backfat, lean meat yield, carcass marbling score, carcass rib-eye area, and hot carcass weight. Single SNP marker association analyses identified a panel of between 18 to 53 SNP markers that were significantly associated with each trait of each population at a $P<0.05$. Comparison of the SNP markers across the three populations for a similar phenotypic trait identified common SNP markers as well as SNP markers specific to each population. These results will facilitate the development of breed-specific SNP panels for genetic improvement of carcass merit in the three populations.

Key Words: candidate gene association, single nucleotide polymorphisms (SNP), fat deposition and carcass merit in beef cattle

628 Association of single nucleotide polymorphisms in the CAST gene associated with longissimus tenderness in beef cattle. E. Casas*, T. L. Wheeler, S. D. Shackelford, G. L. Bennett, and T. P. L. Smith, *USDA, ARS U.S. Meat Animal Research Center, Clay Center, NE*.

The objective was to assess the association of single nucleotide polymorphisms (SNP) developed on the CAST gene, with longissimus tenderness. Forty one SNP were identified in the CAST gene and assays were developed. Markers were scattered throughout the gene. These markers, in conjunction with a commercially available SNP, were evaluated in a *Bos taurus* population (n = 556) that included crossbred animals derived from Hereford, Angus, Red Angus, Limousin, Charolais, Gelbvieh, and Simmental sires. The trait evaluated was longissimus tenderness measured as Warner-Bratzler shear force (kg). Of the 41 SNP developed, 21 were significantly ($P < 0.05$) associated with longissimus tenderness. The minor allele frequency (MAF) of the commercially available marker in this population was 0.20. Eleven of the 21 SNP, significantly associated with longissimus tenderness, had an average MAF = 0.366. The other 10 SNP significantly associated with longissimus tenderness, had an average MAF = 0.183. The 11 SNP with an average MAF = 0.366 had an additive effect. Animals homozygous for the allele with the lowest frequency had tougher longissimus than animals homozygous for the alternate allele. The average significance for these 11 SNP was $P = 0.032$. The commercially available marker had a dominant effect, where heterozygous animals had similar longissimus tenderness as homozygous animals with the MAF allele. These two groups of animals had tougher longissimus than those homozygous for the alternate allele ($P = 0.001$). The 10 SNP with an average MAF = 0.183 showed similar performance in longissimus tenderness as the commercially available marker. The average significance for these 10 SNP was $P = 0.004$. When evaluated in additional populations and their effects validated, these markers could be used as alternate candidates to characterize variation of longissimus tenderness in beef cattle.

Key Words: beef cattle, calpastatin, tenderness

629 Reproductive responses of dairy cows to supplemental fat. J. D. Ferguson[1], D. W. Remsburg*[1], E. Block[2], and Z. Wu[1], [1]*University of Pennsylvania, New Bolton Center, Kennett Square*, [2]*Arm and Hammer Animal Nutrition Group, Church & Dwight Co. Inc., Princeton, NJ.*

Measurements of reproduction function in cows fed supplemental fat were taken. Twenty-one multiparous Holsteins were fed a control diet (CO), a diet added with saturated fat (SF), or a diet added with a fat source high in linoleic acid and enriched with n-3 fatty acids (UF) (Megalac-R®, Church & Dwight Co., Inc.) beginning 3 wk prior to parturition and continuing for 16 wk after parturition. The supplemented diets were formed by adding fat sources to the control diet to provide 1% supplemental fat before parturition and 2.5% supplemental fat after parturition, resulting in higher NEL content. All cows were inseminated 80 to 86 DIM following estrous synchronization using the PreSynch-OvSynch protocol beginning 43 to 49 d postpartum. Blood samples were taken every 2 to 3 d beginning 2 d prior to breeding and continuing for 3 wk after breeding. The concentration of PGFM in blood plasma after breeding was lowest for UF ($P < 0.05$). There was no difference ($P > 0.05$) among treatments in the means for the concentration of progesterone, insulin, or IGF-1, but significant and non-significant interactions between dietary treatment and sampling day were observed in these analyses, showing some increased concentrations with supplemental fat. Dietary supplementation with linoleic and n-3 fatty acids may improve reproduction by increasing progesterone postpartum and decreasing $PGF_{2\alpha}$ in plasma during early pregnancy. *Research supported by Church & Dwight Co. Inc.*

Table 1.

Item	CO	SF	UF	SEM	Fat[1]	Fat source[1]
Progesterone (ng/mL)	5.0	5.7	5.2	1.0	0.73	0.75
PGFM (pg/mL)	582	704	391	83	0.73	0.03
Insulin (µg/mL)	0.7	1.0	0.8	0.2	0.49	0.38[a]
IGF-1 (ng/mL)	124	126	154	19	0.52	0.34

[1]*P* for difference between CO and SF plus UF, and between SF and UF. [a]Treatment and measuring day interaction ($P < 0.05$).

Key Words: reproduction, progesterone, fat

630 Differential gene expression in Suffolk ewes exposed to subacute dietary nitrate. R. C. Cockrum*[1], K. J. Austin[1], P. A. Ludden[1], J. F. Taylor[2], J. W. Kim[2], S. C. Fahrenkrug[3], J. R. Garbe[3], and K. M. Cammack[1], [1]*University of Wyoming, Laramie*, [2]*University of Missouri, Columbia*, [3]*University of Minnesota, St. Paul*.

Accumulation of nitrite (NO_2^-), by high dietary nitrate (NO_3^-) consumption in ruminants, leads to formation of methemoglobin, resulting in toxicity symptoms. Our objective was to identify genes differentially expressed in ewes identified as highly tolerant and lowly tolerant to subacute dietary NO_3^-. Purebred Suffolk ewes were administered a control supplement (n = 8) or a potassium nitrate supplement (300 mg KNO_3/kg BW daily; n = 47) for 8 d. Liver biopsies were conducted prior to (d 0) and on the last day (d 8) of treatment to collect tissue for gene expression analyses. Coefficients of variation (CV) indicated that supplement intake was more variable among NO_3^- treated ewes (CV = 59.3%) than among control ewes (CV = 13.6%). Among NO_3^- treated ewes, ewes highly tolerant (n = 6) and lowly tolerant (n = 6) to elevated dietary NO_3^- were identified based on individual performance and toxicity symptoms. Genes identified by microarray analysis and confirmed by real-time RT-PCR as differentially expressed between lowly tolerant and highly tolerant NO_3^- treated ewes included cytochrome P450 family 25, subfamily A, polypeptide 1, transcript variant 1 (CYP26A1); glutathione peroxidase 3 (GPX3); homeobox (HOP); fatty acid desaturase 2 (FADS2); thyroid hormone responsive gene (SPOT14); and cysteine sulfinate decarboxylase (CSD). Relative expression of CYP26A1, FADS2, and SPOT14 genes was downregulated ($P < 0.02$) in lowly tolerant ewes compared to highly tolerant ewes; furthermore, relative gene expression of CSD tended to be downregulated ($P = 0.07$) in lowly tolerant ewes compared to highly tolerant ewes. In contrast, relative expression of GPX3 and HOP genes was upregulated ($P < 0.05$) in lowly tolerant ewes compared to highly tolerant ewes. These results indicate that ewes identified as lowly tolerant and highly tolerant to subacute levels of NO_3^- varied in performance and hepatic gene expression. Identification of genes correlated to response to subacute dietary NO_3^- may allow producers to identify lowly tolerant animals and employ alternative management strategies for those individuals.

Key Words: gene expression, nitrate, toxicity

631 Effects of high-sulfur water on growth performance and gene expression of steers fed forage-based diets. K. L. Kessler*[1], K. C. Olson[2], C. L. Wright[2], K. J. Austin[1], K. McInnerney[3], P. S. Johnson[2], and K. M. Cammack[1], [1]*University of Wyoming, Laramie*, [2]*South Dakota State University, Brookings*, [3]*University of Montana, Bozeman*.

Sulfur-induced polioencephalomalacia (PEM), a neurological disorder affecting ruminants, is frequently associated with consumption of

high-S water. The objective of this study was to determine the effects of high-S water on performance and hepatic gene expression of steers. A secondary objective was to determine if clinoptilolite, a clay mineral high in cation-exchange capacity, ameliorates the effects of high-S water consumption. Yearling steers (n = 96; 318.2 ± 2.1 kg BW) were randomly assigned to one of four treatments for a 77 d period: low-S water control (566 mg kg^{-1} sulfate), high-S water (3,651 mg kg^{-1} sulfate), or high-S water plus clinoptilolite supplemented at either 2.5% or 5.0% of diet DM. Feed and water consumption were measured daily, and all steers were weighed on d -2, -1, 29, 53, 76, and 77. Liver biopsies were performed on all steers after the treatment period. Morbidity and mortality were higher ($P = 0.0014$) in steers receiving high-S water. No differences in animal health were observed among clinoptilolite levels, suggesting clinoptilolite is ineffective in negating the effects of high-S water consumption. Dry matter intake was lower ($P = 0.074$) in steers consuming high-S water regardless of clinoptilolite level; no differences in ADG were observed. Microarray analyses of hepatic tissues from selected control steers (n = 6) and healthy high-S water treated steers (0% clinoptilolite; n = 6) revealed that 264 genes were upregulated ($P < 0.05$) and 102 were downregulated ($P < 0.05$) due to high-S water treatment. Real-time RT-PCR confirmed numerical downregulation of aldo-ketoreductase family 1, major histocompatabiltity complex (MHC) class II DQA, transforming growth factor β, MHC class I heavy chain and amyloid-beta genes, and numerical upregulation of inhibin beta A, integrin β 2, MHC class I heavy chain, MHC class II DQB in high-S water treated steers compared to control steers. Results from this study suggest that administration of high-S water alters hepatic gene expression, which may explain the reduced performance associated with high-S water.

Key Words: sulfur, polioencephalomalacia, gene expression

632 Development and independent validation of SNP markers comprising the IGENITY® profile for feed intake and efficiency in indicus-influenced beef cattle. B. W. Woodward*[1], J. D. Nkrumah[1], P. A. Lancaster[2], G. E. Carstens[2], and D. J. Johnston[3], [1]*Merial Limited, Duluth, GA*, [2]*Texas A&M University, College Station*, [3]*University of New England, Armidale, NSW, Australia*.

Recent improvements in individual intake measurement technology have enabled producers and researchers to more accurately record intake (DMI) for calculation of feed efficiency, e.g., residual feed intake (RFI). These data are used to study the genome with the goal of finding molecular markers that are associated with these key economic traits. The objectives of this study were to 1) confirm SNP marker associations with feed efficiency traits discovered in a research program, 2) develop panels of the most informative markers, and 3) validate these panels in multiple resource populations. Single marker analyses using an allele substitution mixed model in a population of 464 purebred Brangus heifers with individual intake data (70 d) confirmed a number of the associations reported by discovery scientists. Panels of markers associated with each trait were developed and used to compute molecular breeding values (MBV) using compound covariate prediction methods along with single marker associations. These panels were evaluated in a combined analysis of two Beef CRC populations as part of a National Beef Cattle Evaluation Consortium validation process. Data used for testing the MBV included 1,270 hd of Santa Gertrudis, Belmont Red, and composite cattle based on Brahman, Senepol, and Belmont Red from the Beef CRC in Australia. Steers and heifers in these datasets had individual daily feed intake (DFI) recorded for an average of 60 and 71 d, respectively. Positive regression coefficients between MBV and phenotypes were found in the combined population analysis - RFI, P = 0.005 and DFI, P = 0.02. It is concluded that these DNA marker panels are validated (P < .05) and can be used to predict differences in genetic potential for feed intake and efficiency in indicus-influenced animals and for developing marker-based EPD.

Key Words: feed efficiency, SNP, indicus-influenced beef cattle

634 Effects of single nucleotide polymorphisms in stearoyl CoA desaturase and fatty acid synthase on milk yield, composition, and fatty acid profile in lactating Holstein cows. L. Clark*, S. Moore, and M. Oba, *University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to determine the effect of single nucleotide polymorphisms (SNP) in the stearoyl CoA desaturase (SCD) gene and the fatty acid synthase (FASN) gene on milk yield, composition, and fatty acid profile. A SNP in SCD found on the fifth exon of chromosome 26, which encodes an amino acid change from alanine to valine, and a SNP in FASN located in the thioesterase domain (TE) of chromosome 26, which encodes an amino acid change from threonine to alanine were evaluated in this study. Milk samples were collected from 215 lactating dairy cows at a commercial dairy farm. The distribution of genotypes was $111AA_S$, $85AV_S$, and $19VV_S$ cows for SCD, and $35AA_F$, $89AG_F$, and $91GG_F$ cows for FASN. Cows in one group were fed a diet containing 30.8% NDF, 18.0% CP, and 4.7% fat, and those in the other group were fed a diet containing 29.5% NDF, 18.2% CP, and 4.5% fat. The effects of SCD and FASN on milk composition and fatty acid profile were analyzed separately using the mixed procedure of SAS 9.1 with the fixed effects of genotype, stage of lactation, parity and their interactions, and the random effect of group. Milk yield and composition were not affected by SCD genotype. Fatty acid profile was affected by SCD where the ratio of C14:1 to C14:0 was greater for AA_S cows than both AV_S and VV_S cows (0.085 vs. 0.070; $P < 0.0001$), indicating greater activity of the desaturase enzyme for AA_S cows. However, the SCD genotype did not affect CLA concentration in milk fat, averaging 0.54%. For FASN genotype, GG_F cows had greater yields of milk (28.1 vs. 25.4 kg/d), milk fat (0.84 vs. 0.69 kg/d), and lactose (1.23 vs. 1.08 kg/d) than AG_F cows ($P < 0.04$), but fatty acid profile was not affected by FASN genotype. These results indicate that the genotype of SCD and FASN can affect milk and milk component production.

Key Words: SNP, stearoyl CoA desaturase (SCD), fatty acid synthase (FASN)

635 Genetic regulation of milk β-carotene content. S. D. Berry*[1], S. R. Davis[1], E. M. Beattie[1], N. L. Thomas[1], A. K. Burrett[1], H. E. Ward[1], A. M. Stanfield[1], M . Biswas[1], A. E. Ankersmit-Udy[1], J. L. Barnett[1], Y. van der Does[2], A. H. K. MacGibbon[2], R. J. Spelman[3], K. Lehnert[1], R. G. Snell[1], [1]*Vialactia Biosciences, Auckland, New Zealand*, [2]*Fonterra Research Center, Palmerston North, New Zealand*, [3]*LIC, Hamilton, New Zealand*.

Selection of cattle for milk β-carotene content, if genetically determined, could alter milk fat color, and produce β-carotene enriched milks. We identified QTL regions for milk β-carotene content on BTA15, BTA17, and BTA18 in a Friesian-Jersey crossbred herd (n~850) derived from six F1 bulls. This lead to the identification of three candidate genes: β-carotene oxygenase 2 (BCO2, on BTA15); scavenger receptor class B, member 1 (SCARB1, on BTA17); and β-carotene oxygenase 1 (BCMO1, on BTA18). For each gene, the coding regions were sequenced, along

with approximately 2kb of 5′ sequence. For BCO2, an A>G mutation was discovered in exon three, 240bp from the translation initiation site. The A allele creates a premature stop codon resulting in a putative truncated protein of 79 amino acids (compared to the wild-type protein of 530 amino acids), in the three F1 sires heterozygous for this mutation. BCO2 cows homozygous for the stop mutation produced milk with 78% and 55% more β-carotene than homozygous (GG) and heterozygous (AG) wild type animals, respectively. In BCMO1, three polymorphisms were discovered (one in the 5′ region of the gene, one in exon 6 causing a G>R amino acid change, and one in exon 7 causing a N>D amino acid change. The most striking of these, N341D, resulted in a 32% increase in milk β-carotene. In SCARB1, one polymorphism was discovered, in the 5′ regulatory region (-321 bp relative to the +1 translation start site), which resulted in a 10% increase in milk β-carotene content. The results establish important physiological roles for BCO2, BCMO1 and SCARB1 in bovine β-carotene metabolism, and consequently the regulation of milk β-carotene content. Thus, milk fat color may be decreased or increased, using genetic selection, for specific industrial applications, including the production of bovine milk enriched for β-carotene to alleviate vitamin A deficiency in humans.

Key Words: β-carotene, β-carotene oxygenase, milk fat color

636 Analysis of quantitative trait loci affecting female fertility and twinning rate in Israeli Holsteins on chromosome 7. J. I. Weller*[1], G. Glick[1], M. Golik[1], E. Ezra[2], Y. Zeron[3], E. Seroussi[1], and M. Ron[1], [1]*ARO, The Volcani Center, Bet Dagan, Israel*, [2]*Israle Cattle Breeders Association, Caesaria, Israel*, [3]*Sion, Shikmim, Israel*.

Female fertility and twinning rate were analyzed by the multitrait animal model with parities 1 through 5 considered correlated traits. Fertility was scored as the inverse of the number of inseminations to conception at each parity. Negative genetic correlations between all combinations of parities 1 through 3 between twinning rate and fertility were found by multitrait REML analysis. We have previously reported the existence of QTL affecting these traits segregating on BTA7. The objective of this study was to test if the overall genetic relationship between these two traits was maintained at the level of individual genes on BTA7 affecting the traits. In the preliminary analysis, 288 Israeli Holstein bulls were genotyped by the BovineSNP50 BeadChip (Illumina, Inc.). After edits there were 1752 valid SNPs on chromosome 7. Three hundred to 600 bulls were genotyped for an additional 225 SNPs on the first half of the chromosome. Significance of SNP effects on both traits was tested by a linear model that included the effects of allele and the bulls' birth year on the bulls' genetic evaluations. There were a total of 27 SNPs that were significant for both traits ($p<0.05$). The effects were located in three major clusters, between physical positions 14 and 52 Mbp (Build 4.0). Assuming independent association among the 27 effects, 4.9 significant effects were expected by chance, giving a false discovery rate of 0.18. Of these 27 SNPs the effects associated with the two traits were in opposite directions in all but 4 SNPs ($p<0.001$). Thus it can be concluded that the observed negative genetic correlation is due to specific quantitative trait loci with effects in opposite directions on twinning rate and female fertility.

Key Words: female fertility, genomic selection, twinning rate

Contemporary and Emerging Issues: Joint with Extension Education: Science-Based Approaches to Address Consumer Concerns with the Processing and Marketing of Animal Products

637 Effects of cattle production practices on environmental quality. F. M. Mitloehner*, *University of California, Davis*.

A recent United Nations report suggested that global livestock production is a significant threat to environmental quality, contributing to levels of greenhouse gas emissions that exceed those from all transportation sources. Furthermore, the report states that livestock is a major factor in degradation of air quality and surface and ground water resources. Indeed, livestock production in industrialized countries has consolidated, while at the same time production efficiencies per animal are at their near optimum. Over the last few decades, both beef and dairy production systems have dramatically improved efficiencies. For example, over the last 50 years, dairies have quadrupled milk output per lactation. This improvement in efficiencies per animal has considerably reduced the environmental impact per unit of production (milk or meat). However, in several regions of the industrialized world, cattle production has also spatially concentrated. A sustainable future in animal agriculture will require that the output of the cattle system will match the capacity of crops and soils to utilize these nutrients and that alternative uses of manure for fuel and energy production will be implemented. The ultimate goal must be to minimize unwanted nutrient losses to air and water while providing a growing human population with safe and nutritious food. Several recent papers have used a Life Cycle Assessment (LCA) to investigate the impacts of the entire milk- or meat chain on carbon footprint or energy use. To assess and compare production practices for their potential of releasing pollutants to air and water, a second, more comprehensive bio-geochemical modeling effort is required, often referred to as Process-based Modeling (PBM). Comparisons of cattle production systems like conventional versus organic or the use of production techniques with respect to effects on carbon footprint or pollutant contributions, will be feasible in the near future as numerous research teams are working on such assessment tools. These life cycle and emission prediction modeling tools will bring us closer to design and optimize sustainable production systems in animal agriculture.

Key Words: cattle, environmental impact, modelling

638 Effect of farm production practices on ruminant-derived foods: Fatty acid profile, product quality and human health outcomes. A. L. Lock*[1], J. Kraft[1], A. M. O'Donnell[2], and D. E. Bauman[2], [1]*University of Vermont, Burlington*, [2]*Cornell University, Ithaca, NY*.

There is increased consumer interest in the link between diet and health. A major focus of this has been the recognition that certain dietary fatty acids (FA) can impact human health. Related to this is the recent inter-

est in potential effects of different agricultural production practices on product quality, consumer perceptions and health outcomes. This presentation will utilize science-based approaches to address consumer concerns regarding these issues. First, we will address the impact of ruminant fats, particularly milk fat, on human health with a focus on saturated and *trans* FA which pose significant challenges because of their perceived negative effects on human health. The scientific evidence that some FA uniquely present in ruminant fat may have beneficial effects on human health and disease prevention (e.g., conjugated linoleic acids), and the recognition that not all saturated and *trans* FA have the same biological effects, may ultimately challenge the current public perception of ruminant fats. Second, we will discuss research which has investigated possible differences in nutritional value of ruminant products in conventional and emerging practices at the farm level. This discussion will also focus on FA. This has led to increased interest in the marketing of products from different production practices through the claim(s) of enhanced nutrient profile and/or benefits on human health. We will highlight physiological factors that have been examined for effects on the content of specific FA in ruminant fats. While some small differences in product composition have been reported between production practices, these must be taken within the context of the large impact of diet and the wide range among individual animals. Recent data from both meat and milk retail samples will be used to emphasize the similarity in nutrient composition of specific products regardless of production system, and importantly emphasize that all ruminant products are an excellent source of nutrients for the human population.

Key Words: production practices, ruminant fat, human health

639 Truth in labeling of dairy products: Legality, perception, and reality. J. S. Jonker*, *National Milk Producers Federation, Arlington, VA*.

As differentiation of dairy products accelerates in the marketplace, many dairy producers have become concerned about how this differentiation may lead to a perception of 'good' versus 'bad' milk. Label claims on dairy products can provide consumers useful information on nutrition of and production practices used in the manufacturing of those products. These label claims are governed by numerous Federal statutes and regulations overseen by the Food and Drug Administration, the Federal Trade Commission, and the U.S. Department of Agriculture. This presentation will explore the legal and regulatory basis for regulating labels on dairy products and examine how these shape marketing claims use in the marketplace.

640 Lactose intolerance and milk avoidance: An unnecessary risk for low calcium intake and poor bone health. D. A. Savaiano*, *Purdue University, West Lafayette*.

The potential for lactose intolerance causes an estimated 30 to 50 million Americans to avoid milk (NIH website 2008). The NIH estimate is supported by a survey by Elbon et al. (1999) demonstrating that 17% of whites and 35% of blacks indicated a perceived milk intolerance. The National Dairy Council African American Lactose Intolerance Study (Wooten and Price 2004) reported that 24% of respondents considered themselves lactose intolerant, and 49% reported some physical discomfort at some time following dairy food consumption, of which 27% said they experience discomfort all the time. African American and other maldigesters most likely have a similar potential for intolerance (Byers and Savaiano 2005). If the conservative estimate of 24% of the African American population is used for extrapolation (i.e., 35% African American maldigesters are estimated to be intolerant) to the general U.S. population, at least 25 million (1/3 of 75 million) Americans are avoiding dairy foods due to lactose intolerance. If the 17% percent number from Elbon et al is used, 50 million Americans are avoiding dairy foods. Milk avoidance is a significant causative factor for low bone density (Corazza et al. 1995; Di Stefano et al. 2002) and thus a risk factor for osteoporosis. Individuals who avoid milk, due to intolerance or learned aversion, consume significantly less calcium and have poorer bone health and higher risk of osteoporosis. Lactose intolerance is easily managed by: 1) regular consumption of milk that adapts the colon bacteria and facilitate digestion of lactose 2) consumption of yogurts and cheeses and other dairy foods low in lactose 3) consumption of dairy foods with meals to slow transit and maximize digestion 4) use of lactose digestive aids. This presentation will review the available scientific data on milk avoidance and calcium consumption, and dietary management of lactose intolerance.

Key Words: lactose intolerance, milk avoidance

641 Dairy foods: Inherent and added nutrition for health benefits. N. Auestad*, *Dairy Management Inc./National Dairy Council, Rosemont, IL*.

Increased consumer interest in improving overall health has fueled the demand for foods and beverages that offer health benefits. Nutrient rich dairy foods and dairy products with added nutrition offer many health benefits for consumers. Milk and other dairy foods are the major source of calcium in the U.S. diet, providing more than 70% of the calcium available in the food supply. Dairy products also contribute substantial amounts of other essential nutrients including phosphorus, riboflavin, vitamin B12, protein, potassium, zinc, magnesium, and vitamins A and D. Many dairy foods are excellent to good sources of many of these nutrients, making certain nutrition and health-related claims available. Label claims provide an opportunity to showcase the nutritive benefits of dairy foods. The good news for certain dairy products is the link between calcium and vitamin D and reduced risk of osteoporosis, a bone disease that is a major cause of disability in the U.S. This health claim can be featured on several dairy products. Other health claims that certain dairy products may qualify for include those related to sodium and hypertension, potassium and blood pressure, and saturated fat and the risk of coronary heart disease. The Dietary Guidelines for Americans (2005) recommends three servings of low-fat or fat-free milk or milk products each day. On average, Americans consume 1.7 servings per day. A 2007 IFIC survey found that many participants said that they are currently consuming or would be interested in consuming foods or beverages with added health benefits. In their commitment to help consumers get the recommended servings of milk and milk products each day, dairy processors and manufacturers have developed new dairy products with added health benefits (e.g. probiotics for digestive and immune health; omega-3 DHA to support brain development). Both the inherent nutrition in dairy foods and the added nutrition that some dairy products deliver can help consumers improve the overall nutritional quality of their diets.

Key Words: dairy, nutrients, health

642 Meat product safety. E. W. Mills*, *Pennsylvania State University, University Park.*

With an abundant and inexpensive food supply in the US consumer concerns for quality and safety have become preeminent. Rather than concern themselves with obtaining enough food, US consumers focus on perceived quality, safety and food production practices such as animal husbandry practices. Animal management practices such as confinement, castration, dehorning, use of antibiotics and growth promotants all come under criticism in the market place. The popularity of production claims such as organic, natural, and grass fed among others derives from a growing consumer desire to know more about how foods are produced. Such knowledge may lead to an increased perception that foods are safe and environmentally friendly. When consumers hear that millions of pounds of beef are being recalled they reasonably presume that this effort involves unsafe products. But, the idea that unsafe products are being withdrawn from commerce does not give consumers confidence that other products are safe. In fact, the occurrence of a recall leads, at least temporarily, to decreased consumer confidence in similar products which remain on the store shelves. Recently, in the peanut industry, a salmonella outbreak and recall by a small Georgia peanut processor has lead to a dramatic decrease in demand for a variety of peanut-containing products across the industry. Similar outcomes occur when meat or dairy products are recalled. There could be benefit throughout the food chain when consumers are better informed and understand what is going on during a recall. However, by the time you issue the recall news release you are already in the "minimize damage" mode. There is not much opportunity for positive spin or consumer education. Even if you have valid points to be made, your credibility is at its lowest when you are on the defensive. During a recall it is best to stick to the business at hand – retrieving product as efficiently as possible. Informing consumers about safety and wholesomeness of meat products and putting meat recalls into perspective is an ongoing task that we must pursue constantly.

Key Words: meat safety, product recall, consumer perceptions

CSAS Symposium: Functional Foods, Probiotics and Animal Health

643 Postnatal development of the mucosal immune system in domestic animals and consequences on health in adulthood. M. Bailey*, *University of Bristol, Bristol, U.K.*

In many mammalian species the immune system is poorly developed at birth. In the pig, the mucosal immune system is almost absent and develops over the first few weeks in conventional husbandry conditions. Sequentially, the intestine is populated by dendritic cells, CD4+ T-cells and CD8+ T-cells, while B-cell compartments firstly expand (Peyers patches) and then class-switch (to IgA). Much of this development is dependent on, or driven by, the presence of microbial flora in the intestine. Our observational studies have demonstrated that the complexity and type of microbial flora seems to depend on the genetics of the sows and piglets and on the environment (indoor, outdoor farms), and can be further manipulated by environmental modification (high-hygiene isolators). Similarly, there are marked differences in the rate of acquisition of memory T-cells between pigs on different farms, indicating environmental effects on immunological development. Consistent with these observational studies, direct manipulation of microbial flora in neonates using highly controlled conditions (caesarean-derived germ-free piglets reared in full gnotobiotic conditions and colonised with a defined, three-component flora) or conventional conditions (piglets fed a probiotic micro-organism from weaning) have also clearly demonstrated an impact of microbial flora on measures of immunological development and function. However, an important issue is the value, or otherwise, of such manipulations for subsequent 'enteric health' of the individual. The mucosal immune system is a complex, self-regulating system, capable of expression of active immune responses or tolerance directed at pathogens, commensals or food antigens. Manipulations directed at enhancing certain components may be advantageous under some circumstances but deleterious under others. Rational manipulation of early life flora will require considerably greater mechanistic understanding of the complexity of interactions between micro-organisms and the intestinal immune system.

Key Words: mucosal immunology, probiotics, neonate

644 Use of probiotics and prebiotics to modulate intestinal health in monogastric farm animals. M. Lessard*[1], X. Zhao[2], and F. Guay[3], [1]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [2]*McGill University, Department of Animal Science, Montreal, QC, Canada*, [3]*Université Laval, Département des sciences animales, Quebec, QC, Canada.*

There is increasing evidence that probiotics and prebiotics have beneficial effects on animal health through their potential to modulate intestinal microbiota and interaction between bacterial populations and host intestinal defenses. Probiotics are well-defined bacteria or yeasts and their functional properties are strain specific. Among proposed mechanisms, probiotics have the potential to increase resistance to enteric infections by inhibiting growth of pathogenic bacteria. However, the most common purported benefits of the consumption of probiotics are associated with their potential to modulate barrier properties of the intestinal wall and host immunity. Prebiotics are non-digestible food ingredients such as inulin, fructo-oligosaccharides and mannan-oligosaccharides. They are fermentable and can stimulate the growth and/or the activity of commensal intestinal bacteria such as bifidobacteria or bind to pathogenic bacteria that contribute to health. To modulate intestinal barrier functions and immunity, probiotics and commensal bacteria must interact with epithelial cells and immune cells. Recent data suggest that production of intestinal antimicrobial peptides and inflammatory cytokines are modulated by probiotics and commensal bacteria. This review will summarize mechanisms by which probiotics and prebiotics can affect health by modulating bacterial populations in the gut and mucosal immunity. The current understanding of the cross-talk between beneficial and commensal bacteria and the host remains limited and further research is still necessary to characterize complex interactions among probiotics/prebiotics, microbiota and gut health.

Key Words: probiotics, prebiotics, intestine

645 A review of the use of direct-fed microbials to mitigate pathogens and enhance production in cattle. T. A. McAllister*[1], K. A. Beauchemin[1], J. Baah[1], R. M. Teather[1], and K. Stanford[2], [1]*Agriculture & Agri-Food Canada Research Centre, Lethbridge, Alberta, Canada*, [2]*Alberta Agriculture and Rural Development, Lethbridge, Alberta, Canada*.

Direct-fed microbials (DFMs) or probiotics have been employed in ruminant production for over 30 years. Originally, DFMs were used primarily in young ruminants to accelerate establishment of the intestinal microflora involved in feed digestion and to promote gut health. Further advancements led to more sophisticated mixtures of DFMs that were targeted at improving fibre digestion and preventing ruminal acidosis in mature cattle. Thus, these second-generation DFMs undoubtedly contributed simultaneously to the improvements in milk yield, growth and feed efficiency that have been observed in some production studies involving DFMs, but results have been inconsistent. More recently, there has been an emphasis on the development of DFMs that exhibit activity in cattle against potentially zoonotic pathogens such as *Escherichia coli* O157:H7, *Salmonella* spp. and *Staphylococcus aureus*. Regulatory requirements have limited the microbial species within DFM products to organisms that are generally recognized as safe, such as lactic acid-producing bacteria (e.g., *Lactobacillus* and *Enterococcus* spp.), fungi (e.g., *Aspergillus oryzae*), or yeast (e.g., *Saccharomyces cerevisiae*). Development of DFMs of rumen origin has also been explored with lactate-utilizing species (e.g., *Megasphaera elsdenii*, *Selenomonas ruminantium*, *Propionibacterium* spp.) or cell wall-degrading isolates of *Butyrivibrio fibrisolvens*, but these products have not seen widespread commercial use. Our limited knowledge of gastrointestinal microbial ecology continues to present a challenge to the development of DFMs that are efficacious over a wide range of ruminant production systems. Few studies have employed molecular techniques to study in detail the interaction of DFMs with native microbial communities or the ruminant host. Advancements in the metagenomics of microbial communities and the genomics of microbial-host interactions could allow development of DFMs with the capacity to improve production and promote health in a manner analogous to that presently achieved through the use of antimicrobials.

Key Words: probiotic, lactobacilli, rumen

646 Influence of functional food on intestinal microbiota and their subsequent relationship with health. J. Escobar* and M. A. Ponder, *Virginia Polytechnic Institute and State University, Blacksburg*.

Food substances, containing carbohydrates, fats, protein and water provide nutrients for maintenance, production, and animal well-being. The term functional food describes foods with proven or purported health benefits beyond their nutritive functions. Because the lack of nutrient intake is deleterious to the health status of any living organism, it is then cumbersome to think about a food that is not "functional". However, the term "functional" typically refers to those foods that can be described as health promoting and disease preventative and commonly include carotenoids, fibers, fatty acids, flavonoids, minerals, phenolic acids, plant stanols/sterols, prebiotics, probiotics, phytoestrogens, soy proteins, etc. Addition of ZnO in broiler diets to provide Zn to achieve maximal growth will be considered a food, whereas pharmacological inclusion of ZnO in the diet of weaned pigs to reduce scouring can be considered a functional food. Minerals, prebiotics, probiotics, and phytoesterogens are common "functional" ingredients of animal feed. These functional dietary components may alter gut microbial populations, which undoubtedly leads to the preferential growth of certain microbes. Functional foods with intestinal effects include compounds directly interacting with the gut, like plasma proteins, and prebiotic (e.g., mannanoligosaccharides, fructooligosaccharides) and mineral (e.g., ZnO, $CuSO_4$) compounds capable of direct or indirect growth enhancement of certain microbial species. Recent findings in humans and rodents indicate that the intestinal microbial community may play a role in chronic diseases such as obesity and diabetes. Preliminary results in animal agriculture indicate significant differences in the microbial composition of pigs with different body conditions and genetic backgrounds. In general terms, reductions in pathogenic or undesirable bacterial with concomitant increases in desirable or beneficial microbial species in the intestine can result in reduced localized and systemic immune activation, and hence increasing the performance of healthier animals.

Key Words: functional food, iIntestinal microbiota, animal health

647 Influence of fermented products on health. E. Farnworth*, *Food Research and Development Centre, Agriculture and Agri-Food Canada, Saint Hyacinthe, QC, Canada*.

The fermentation process not only can preserve foods, but it can also cause changes to the food matrix that are beneficial to health. The challenge is to find bacteria that exert beneficial effects, and at the same time can survive in the food / beverage matrix. The list of potential health promoting probiotic bacteria grows; the number of foods into which they can be added is not as large. Cows' milk is the starting point for the most common fermented products (yogurt, Kefir, fermented milks) in Canada and the USA. World-wide, a variety of fermented foods are being consumed. With proper production, packaging, and storage, fermented products contain live bacteria when consumed. It is apparent, that for many probiotic products to exert their beneficial effects, the bacteria consumed must be alive when they reach their site of action, normally the lower gastrointestinal tract. Studies have now been published that show that consumption of yogurt is effective in protecting against, and reducing the duration of, several types of diarrhoea. There may be some cases, where the requirement for alive bacteria to be consumed may not be necessary. During the fermentation process, the responsible bacteria produce bioactives from the constituents of the food being fermented. For example, the action of bacterial proteinases and peptidases produce bioactives from cows' milk proteins. In other foods during the fermentation process, the bacteria can be carrying out metabolic processes themselves that generate bioactive compounds (such as exopolysaccharides). In both cases, it is these bioactives that are the source of beneficial effects; there is no requirement that the responsible bacteria be alive when consumed. Bioactives derived from cows' milk protein have been shown to have ACE inhibitor, antimicrobial, and antithrombotic properties. Bioactive exopolysaccharides have been shown to prevent the initiation and growth of certain cancers.

Key Words: fermented, health, probiotic

Dairy Foods: Challenges and Opportunities of Microencapsulation Technology in Application to Dairy Foods Symposium

648 Introduction to scientific principles and engineering technologies in microencapsulation as applicable to dairy foods. K. Kailasapathy*, *University of Western Sydney, Richmond, NSW, Australia*.

Development of technology driven functional and natural health products has a number of challenges since bioactive ingredients incorporated are unstable to processing with reduced absorption, low bioavailability and reduced shelf life. Encapsulation offers a great potential for protecting and delivering bioactive components and micro-organisms through technology driven products to enhance human health. Encapsulation is the technology of packaging bioactive core materials in miniature capsules that release their contents triggered by various factors such as shear, temperature, enzymes, an pH. The available technologies for microencapsulation can be grouped into two broad categories, one which uses a liquid as a suspending medium (complex coacervation, interfacial and in situ polymerisation or solvent evaporation from emulsions) and one which uses a gas as a suspending medium into which a liquid phase is sprayed (spray-drying or spray-cooling, fluidised-bed coating or coextrusion). Currently available commercial products are based on gel particles, spray-coating, spray-drying, extrusion and emulsions. Other encapsulation techniques such as liposomes, coacervation or molecular inclusion (cyclodextrins) as well as using nano emulsions are not widely available to protect bioactives in the development of technology driven functional dairy foods. This could be either because of cost or the requirement of non-food approved polymers used in the encapsulation. A number of both laboratory and commercial scale equipment had been developed and being used to produce micro and nano scale capsules. A UWS prototype encapsulator which uses a falling film technology capable of producing high capsule production capacity suitable for application on an industrial scale has been developed. This presentation will review the recent developments in relation to the science and technology of encapsulation, challenges and opportunities in the development of innovative functional dairy foods.

Key Words: microencapsulation, bioactive substances, functional dairy foods

649 Benefits of encapsulation of probiotics during processing and storage of dairy products. C. P. Champagne*, *Agriculture and Agri-Food Canada, St. Hyacinthe, QC, Canada*.

Viability is an important component of the functionality of probiotic bacteria in foods. Unfortunately, many processing (heating, freezing) and storage conditions (redox level, pH) used in dairy technology are detrimental to the viability of the probiotic bacteria. In this review-type presentation, the benefits of encapsulation to address these viability problems will be addressed. The three most widely used encapsulation technologies of probiotic bacteria (gel microentrapment, spray coating and spray drying) will be described. The benefits of encapsulation on the viability of probiotic bacteria during processing and storage will be examined in the following products: frozen desserts, yoghurt, cheese, unfermented milk, powders. Some of the factors which influence the effectiveness of encapsulation will be discussed; these factors include: strain variability, particle size, pH, multiple coating, packaging, cell density.

Key Words: probiotics

650 Strategies to improve survival of probiotic bacteria using microencapsulation and to reduce the size of microcapsules for food applications. W.-K. Ding and N. P. Shah*, *Victoria University, Melbourne, Victoria, Australia*.

Survival and stability of probiotic organisms in functional foods have been a major concern, because a high number of organisms is needed to confer health benefits to consumers. Microencapsulation of probiotic organisms in alginate beads is one of the methods of improving their viability. However adverse sensory qualities such as grittiness result when microcapsules are added to functional foods mainly due to their large size. The aim of this study was to improve the microencapsulation technique by making smaller more palatable capsules and provide the capsules with an extra coating for enhanced stability. A microfluidizer was used to manufacture microcapsules of reduced size. The surface structure and overall size of the microcapsules was measured and analyzed using electron microscopy. Palm oil and poly-L-lysine was used as added coating materials to enhance the capsule's stability. The porosity of the coated microcapsules was measured by monitoring the release of a water soluble dye. Our results show that microencapsulation helped protect probiotic bacteria from acidic conditions during storage, high concentrations of bile salts and mild heat treatment. The added coating materials, palm oil and poly-L-lysine helped maintain the capsule's integrity during exposure to acids, and provided the capsule with a much more smooth surface structure. The added coating material made the capsules less permeable to water soluble molecules. The production of microcapsules with a microfluidizer led to a significant decrease in the average capsule size from 132 µm to 35 µm, which would be much more palatable for consumers.

Key Words: microencapsulation, probiotics, size reduction

651 Food protein micro/nano particles for controlled nutraceutical delivery in functional foods. L. Chen*[1] and M. Subirade[2], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*Université Laval, Quebec, QC, Canada*.

The incorporation of nutraceutical compounds into food systems provides a simple way to improve public health and/or reduce the risk of disease. However, many of these compounds remain unavailable by oral administration, due to instability under the conditions encountered during food processing (e.g. high temperature, exposure to oxygen and light) or in the gastro-intestinal tract (e.g. low pH, digestive enzymes, presence of other nutrients), and low permeability and/or solubility within the gut. Micro/nano encapsulation systems can be used to overcome these limitations. Although numerous synthetic polymer based delivery systems to maximize drug action and minimize side effects in the biomedical and pharmaceutical sectors have been successfully developed, these formulations cannot be used in food applications that require materials generally recognized as safe (GRAS). As a vital macronutrient in food, food proteins possess unique functional properties and excellent biodegradability, which enable them to be GRAS for encapsulation of nutraceutical compounds. This presentation focuses on the current knowledge and techniques for development of food protein-based micro/nano particles of desirable structures at precisely controlled sizes for target release of nutracetuical compounds at the site of absorption. Their potential applications in functional foods are illustrated.

Key Words: food protein, nano/microparticles, nutraceutical delivery

652 Microencapsualtion of recombinant enzymes for application in accelerated cheese ripening. B. H. Lee*[1,2], [1]*Agriculture and Agri-Food Canada, Food R & D Centre, St-Hyacinthe, QC, Canada*, [2]*McGill University, Montreal, QC, Canada*.

Direct addition of enzymes to milk during cheesemaking appears to be the simplest method to accelerate cheese ripening. However, due to loss of most enzymes in whey, poor enzyme distribution, and texture defects by extensive proteolysis, alternative encapsulation technology can eliminate these defects. Previous approaches on the addition of free enzymes during salting stage and encapsulation of natural flavour-enhancing enzymes using different food gums and liposomes will be presented. In this study, aminopeptidase (PepN) of the cheese isolate, Lactobacillus rhamnosus S93 was genetically overproduced up to a 1,000 fold, purified and encapsulated in chitosan-coated alginate beads to investigate the effects of Cheddar cheese ripening for 6 months. The encapsulation efficiency was above 90%, and the experimental cheeses received higher scores for sensory properties than the control cheese. The amounts of PTA-N and total FAA in the cheese with the encapsulated enzyme after 2 months of ripening were close to those of the control cheese after 6 months, suggesting the acceleration of about 4 months in proteolysis. Although this study was aimed to develop an encapsulation method which can affect Cheddar cheese ripening, it would be useful for other type of cheeses.

Key Words: microencapsulation, enzymes, cheese ripening

Dairy Foods: Milk Protein and Enzymes Symposium

653 Indigenous enzymes in mammalian milk: Scientific, technological and physiological significance. A. Kelly*, *University College Cork, Cork, Ireland*.

The milk of all mammals contains a range of enzymes with a range of roles and functions; even in more well-studied species such as the bovine, the exact number of enzymes, factors affecting their activity, and their exact significance remains poorly understood. Some enzymes are recognised to have roles, either positive or negative, in the quality of milk and dairy products, such as milk lipoprotein lipase and the alkaline protease, plasmin. Other enzymes are of major industrial significance not for their function but due to their exploitation as surrogate indicators of the efficiency of processing, such as the use of alkaline phosphatase as an index of the efficiency of pasteurisation. In physiological terms, the activity of many enzymes is susceptible to secretory disturbances in the udder, reflecting their cellular or blood origins, and so levels can vary with factors such as stress, lactation and, in particular, mastitis. This presentation will give a brief overview of the profile and significance of the principal enzymes in mammalian milk. In addition, the results of some new research on the enzyme system of the human milk will be discussed, for comparison with the proteolytic system of the bovine, and highlights some potential insights into the physiological significance of modulation of hydrolysis of proteins in milk in terms of enhancing protein digestibility for the neonate.

Key Words: milk, enzymes, proteins

654 Enzymes associated with the bovine milk-fat-globule membrane with special reference to xanthine oxidoreductase. J.-K. Jeong, J. Xu, and I. H. Mather*, *University of Maryland, College Park*.

The enzymes of bovine milk-fat-globule membrane (MFGM) will be reviewed, with particular emphasis on their cellular origin and functional attributes. Over forty enzymes have been identified in the MFGM, including hydrolases, transferases and oxidoreductases. Hydrolases constitute the most abundant class, within which there are a large number of GTPases in the rab family. These enzymes originate from multiple cellular sources, including the mammary epithelium and immune cells, and have diverse physiological functions in milk synthesis and secretion, membrane trafficking, and immunity. The most abundant enzyme in the MFGM of dairy cows and many other species is xanthine oxidoreductase (EC 1.17.1.4) (XOR), a redox enzyme in the molybdyl hydroxylase family. XOR constitutes approximately 20% of globule-associated protein and over 10% of isolated MFGM. Besides its function as a purine oxidase, XOR, under certain physiological contexts can generate reactive oxygen and nitrogen species, which may function in the innate immune system and in signaling pathways. In addition, XOR binds with high affinity to the cytoplasmic domain of butyrophilin, the most abundant transmembrane protein in the bovine MFGM. Interactions between XOR and butyrophilin are postulated to be essential for formation of the MFGM, and the secretion of lipid droplets. Thus XOR is a multi-functional protein, required for diverse physiological processes in lactation and the immune system.

Key Words: xanthine oxidoreductase, butyrophilin 1A1, milk-lipid-globule membrane

655 Proteolytic enzymes associated with somatic cell count and their relevance in raw milk and dairy products. L. B. Larsen*, *Institute of Food Science, Faculty of Agricultural Sciences, Aarhus University, Denmark*.

Somatic cell count and mastitis are associated with increased activities of bovine proteases, such as plasmin, but also enzymes from somatic cells play a role. These cause proteolytic degradation of the caseins, which can lead to poorer quality of stored milk, and may also contribute to a lower cheese yield. Different proteolytic enzyme systems have been demonstrated in bovine milk, and include, apart from the plasmin system, lysosomal enzymes such as cathepsin B and D. It is, however, not clear to what extent the enzymes are actively secreted from the somatic cells, leaked from dead cells or to some extent secreted by the mammary tissue. This complex situation is reflected in the enzyme profile of e.g. the cathepsin D system, where both active enzymes and proenzymes have been demonstrated in purified preparations from milk, with procathepsin D being the major form present. The enzymes have been characterized in milk and their significance in some dairy products has been studied. The potential contribution of these different bovine enzymes to the proteolysis occurring in milk at acute mastitis as well as at low or moderately elevated somatic cell count has been further characterized by use of proteomic and peptidomic methods including 2D gel electrophoresis, LC MALDI spotting and MALDI ToF MS/MS of peptides and protein fragments. By these methods a range of casein-derived peptides, including some with apparent bioactive properties, were identified in the different milk types. Based in these identifications possibly responsible proteases have been suggested, and these included plasmin, cathepsin B, D and leucocyte elastase, in addition to apparent amino- and carboxypeptidase activities.

Key Words: cell count, proteolysis, MALDI ToF

656 Lipases and lipolysis in milk and dairy products. H. C. Deeth*, *School of Land, Crop and Food Sciences, University of Queensland, Brisbane, Queensland, Australia*.

The enzyme, lipase, which catalyses the hydrolysis of triglycerides to free fatty acids, partial glycerides and, in some cases, glycerol, is a constant concern in the dairy industry. It presents in different forms but chiefly as the indigenous milk lipoprotein lipase and a raft of lipases produced by contaminating microorganisms in milk and dairy products. Lipases can cause flavour problems as well as texture problems such as inhibition of foaming of milk used for making cappuccino coffee. However, not all lipases are detrimental to the quality of dairy products. For example, they play a very important role in the typical flavour of many cheeses. While much is now known about the nature of these enzymes and their action in milk and dairy products, lipase-related problems continually arise. This paper discusses some case studies where lipase has been involved and outlines the causes and solutions to the problems in the light of this knowledge.

Key Words: lipase, lipolysis, dairy industry

657 Native proteases in milk: Current knowledge and relevance to dairy industry. B. Ismail*[1] and S. Nielsen[2], [1]*University of Minnesota, St. Paul*, [2]*Purdue University, West Lafayette, IN*.

Plasmin is by far the predominant and most completely studied endogenous protease in bovine milk, so will be the primary focus of this talk on native proteases in milk. The hydrolysis of milk proteins by proteases, such as plasmin, affects the texture and flavor of dairy products, to have either beneficial or detrimental effects, depending on the extent of hydrolysis and type of dairy product. Plasmin is part of a complex protease-protease inhibitor system in milk that consists of active (plasmin) and inactive (plasminogen) forms of the enzyme, activators, and inhibitors. Considerable research has been done to isolate and characterize components of the plasmin system, determine how they interact, assess thermal stability, and develop and compare quantitation methods. Additionally, several studies have been carried out on the plasmin system activity and interactions as affected by cow characteristics, milk storage, processing conditions, bacterial proteases, and various milk proteins such as β-lactoglobuling and κ-casein. Depending on the end use, researchers have focused on either enhancing or minimizing the activity of plasmin system components. The intent has been to control protease activity in casein and whey fractions, depending on the food or ingredient application. Controlling the activity of endogenous milk proteases, such as plasmin, has great potential to improve dairy product quality and reduce their processing costs.

Key Words: milk proteases, plasmin, endogenous enzymes

Extension Education: Symposium: Models for Dairy Production Decision Making

658 To keep or cull a cow: An economic decision. A. De Vries*, *University of Florida, Gainesville*.

Dairy cow culling decisions are economic decisions. When a cow is culled, the producer expects to be better off without the cow. When no replacement is available, the open cow is often kept as long as her milk income exceeds her variable cost. When replacements are available, the typical recommendation is to keep the slot full, meaning that the culled cow should be immediately replaced by another cow, often a calving heifer. Alternatively, calving heifers may accelerate cow culling when space is limited. The decision to keep the current cow as long as her milk income exceeds her variable cost is then no longer optimal because earlier replacement might improve the profitability of the slot. When groups are overcrowded, culling might improve the performance of the remaining cows. In many of these situations, cash flow projections of the keep and cull decision may support the quality of decision making. Accurate cash flow projections are difficult to make without the help of computers and modeling. This difficulty arises because cash flow projections involve sequential cows in the same stall with differences in milk production, stage of lactation, and reproductive status, among others. Further, decisions in the future may or may not be optimized. Algorithms have been designed that provide cash flow projections of both the keep and cull decision for individual cows. Differences of the net present values of such projections allow for ranking of cows for future profitability, and hence identification of cows recommended for culling. Such algorithms have not been widely used on dairy farms because they were either not available, there was a lack of understanding of the calculations, or producers did not see the need for decision support. Newer algorithms allow for more accurate cash flow predictions based on daily updated cow performance data. They also allow for more insight in the calculations. Further, multiple decisions may be optimized simultaneously, such as insemination decisions, dry-off decisions, and replacement decisions. Collectively they provide added value to increasing amounts of data that is becoming available at a more rapid pace.

Key Words: culling, model, economics

659 Modeling the economic impact of reproductive change. M. W. Overton*, *University of Georgia, Athens*.

A spreadsheet-based model using partial budgeting was used to develop a stochastic simulation approach to estimate the economic benefit of improved reproductive performance in U.S. dairy herds. Through simulation, a herd is calved and followed through lactation. Time dependent culling risks and pregnancy rates for each cycle were used to project cumulative pregnancy rates following twelve potential breeding cycles. Distributions were fit to describe the potential cycle-specific conception and insemination risks and overall 305-day ME milk production for Holstein cows. Farm-level prices for milk, calves, market cows, and replacement animals from January 2007 through February 2009 were used to fit distributions for predicting future returns. Values associated with changes in pregnancy rate were obtained by comparison of a simulated reproductive management program with a simple estrus detection-based AI program. Final results were obtained by running 1000 iterations through the use of simulation software and are displayed as probability distributions, with a mean expected value and a 90% expected range. Sources of revenue include annualized milk per cow per day, annualized values of calves produced, and the annualized value of the market cows. Expenses include annualized replacement costs, the marginal feed consumed by cows producing marginal milk, feed consumed by additional non-lactating cows, additional costs for

housing, labor or medical expenses, and extra costs associated with the change in reproductive management. The estimated value derived from improving pregnancy rate from 10% to 32% is nonlinear, with the largest returns resulting from improvements to very low pregnancy rates. The relative value of improving pregnancy rate by one unit between 10% and 20% is more than six times higher than the value of a unit change, on average, between 22% and 32% pregnancy rate. Sensitivity analysis revealed that net returns per lactating cow slot per year were influenced by milk price, herd milk production level, feed cost, replacement cost, and heifer calf value, in decreasing order of magnitude.

Key Words: reproduction, economic model, stochastic simulation

660 Modeling nutrition decisions. M. D. Hanigan*, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Feed costs represent approximately half of the operating costs of a dairy. Because feed supplies the nutrients needed by animals to maintain themselves, grow, reproduce, and produce milk, it is critical to provide enough nutrients to achieve production goals. However, feeding excess nutrients has negative economic and environmental implications. Mathematical models of nutrient availability and animal requirements are used to make feeding decisions. The accuracy and precision of the feeding decisions are subject to the accuracy and precision of the models used to construct them as well as the input descriptors. The latest version of the NRC model appears to have greater precision than previous versions of that model, particularly for energy and metabolizable protein. The precision of the Cornell model also has improved over time although it does not appear to be as precise as the NRC model. Additional refinement of equations describing amino acid supply and requirements is required to maximize productivity and efficiency. Stochastic tools have been developed that allow consideration of variation in inputs and the variance in requirement models. These tools can be used to minimize the risk of underfeeding nutrients while minimizing the economic and environmental impacts associated with overfeeding. Future models need to allow economic optimization given a broader set of input and output constraints and costs. Nutritional decisions must be made while considering feed availability and cost, environmental constraints and penalties, management goals and capabilities, facilities, and the genetic potential of the herd.

Key Words: dairy management, nutrition, model

661 A large Markovian linear program model for dairy herd decision-making. V. E. Cabrera*, *University of Wisconsin*, *Madison*.

The purpose of the study was twofold: 1) propose an innovative modeling framework using Markovian linear programming to optimize dairy farm net returns under different decision schemes and 2) illustrate the model with a practical application. A dairy herd population was represented by cow state variables defined by parity (1 to 15), month of lactation (1 to 24), and pregnancy status (0 non-pregnant and 1 to 9 pregnant). A database of 326,000 lactations of Holsteins was used to parameterize reproduction, mortality and involuntary culling. Five diets were studied to assess economic, environmental, and herd structural outcomes. Diets varied in proportions of forage, corn grain, and soybean meal within and between lactations, which determined dry matter intake, milk production, and N excretion. The problem was set up as a Markovian linear program model containing 5580 decision variables and 2792 constraints. The model optimized the net return of the steady state dairy herd population having two options in each state: keeping or replacing an animal. Hence, the model identified the maximum net return that included a cost benefit function of the N excretion associated with the optimal policy. The problem was solved using the Risk Solver Platform with the Standard LP/Quadratic engine. The optimal policy with 2008 milk, feed, and livestock prices called to replace open cows between 11 and 14 months after calving depending on parity and diet, with higher culling rates for lower parities and high corn grain diet. High corn grain diet resulted in $22.8 and $61.8/mo per cow higher net returns compared with intermediate and no-corn grain diets. The model detected an opportunity to substitute corn grain for forage in mid and late lactation to increase net return and decrease N excretion. With lower milk prices and higher feed prices, the model suggested lower replacement rates and increased use of forage to increase net profit, which consequently decreased N excretion.

Key Words: Markov chain, linear programming, dynamic programming

662 Impact of disease on dairy production decisions. D. Galligan*, *University of Pennsylvania*, *Kennett Square*.

Dairy production involves the utilization of resources (animals, land, labour, capital etc.) in the production of products valued by society. Production efficiency of the process is based on the dilution of animal maintenance, replacement cost as well as dairy overhead cost. Yield per cow (milk lbs/cow/year) increased at 1.68% per year while herd consolidation (average number of cows/herd) increased at 4.96% per year from 1996 to 2006. Disease influences the production process in a variety of ways and thus can adversely affect the overall efficiency of resource conversion into useful products. In the US, catastrophic diseases have largely been controlled and now most production limiting diseases involve a complex dysfunction encompassing biology and management. At the herd level, the definition of health has been broadened to not only include attainment of normal physiological values, but also the attainment of specific production targets in an economic context. Diseases differ to the degree that management can mitigate production losses by timely treatments and or optimized culling of the diseased animals. At the public level, sensitivities regarding animal health and environmental impacts are largely based on perceptions regarding production and management practices. These sensitivities can affect product prices or indirectly increase production cost by restrictive legislative actions. Dairy management must understand the broad dimensions in which animal diseases can affect their operations and what tools are available to control their losses.

Key Words: health/disease, economic, management

663 Can bacterial inoculants improve the quality of rust-infested corn silage? O. C. M. Queiroz*, A. T Adesogan, and S. C. Kim, *University of Florida, Gainesville*.

Southern rust is an aggressive disease cause by *Puccinia polysora* which may provide ideal conditions for the growth of undesirable opportunistic fungi that adversely affect forage quality. Little is known about the effects of the disease on the nutritional value of corn silage. Less is known about whether microbial inoculants can improve the quality of rust-infested corn silage. This project aimed to determine how inoculant treatment affects the fermentation, nutritive value and aerobic stability of corn silage containing varying levels of southern rust infestation. Corn plants with no rust (NR), or medium (MR), or high rust (HR) infestation were harvested at random locations from a field, chopped and ensiled alone (Control) or after applying 1 × 106 cfu/g of *L. buchneri* and *P. pentosaceus*. Each treatment was prepared in quadruplicate in 20 l mini silos and ensiled for 97 days. As the level of rust infestation increased, concentrations of DM and NDF increased, whereas DM digestibility decreased by up to 13%. Control, HR silages also had lower NDF digestibility (NDFD; 36.2% of DM) than Control, MR (39.8%) or NR silages (38.1%). Inoculation increased the NDFD of NR (43.4%) and MR silages (45.7%) but not HR silages (33.0%). Concentrations of lactate and VFA decreased with increasing rust infestation in NR silages, but this trend was absent in inoculated silages. In HR silages, inoculation reduced mold counts (3.4 log cfu/g vs 0.95 log cfu/g), increased aerobic stability by 75% (77.3h vs 44 h), and prevented production of aflatoxin (5.2 vs. 0 mg/kg). The concentration of aflatoxin in uninoculated, HR silages exceeded action levels stipulated by the US Food and Drug Administration. In conclusion, rust infestation reduced the nutritive value and fermentation of corn silage. Inoculation reduced adverse effects of rust infestation on the fermentation, increased NDFD of NR and MR silages, and decreased mold growth, aerobic spoilage, and aflatoxin production in HR silages.

Key Words: *Puccinia polysora*, inoculant, corn silage

664 Amaferm level and form on digestibility of forage differing in quality. J. Nocek*[1] and H. Jensen[2], [1]*Spruce Haven Research Center, Auburn, NY*, [2]*Biozyme Inc, St Joseph, MO*.

The objective was to determine effects of Amaferm level and form on ruminal DM and NDF digestion of hay and corn silage of different quality. Four hay and corn silage samples with low and high NDF, low and high NDF digestibilities (NDFd, invitro analysis) were utilized to represent ranges in forage quality. Three lactating ruminally canulated cows were used to determine rumen digestibilities. The treatments: Control: 0, 5, 15, 30g dry Amaferm/d or 10ml of liquid Amaferm/d were introduced into the rumen of each cow daily. Forage was mashed prior to bag insertion. Duplicate determinations were used per time point (0, 2, 4, 6, 12, 24, and 48 h). Dry matter and NDF determinations were conducted on each residue, each time in order to calculate relative pool fractions and rate of insoluble potentially digestible (A = water soluble, B fraction = 100-(A+C), KdB, C = 48h ruminal extent) DM and NDF. There was no consistant effect of forage quality within hay or corn silage on DM or NDFd. For hay DM, B fraction was highest (P<.05) for 10ml compared to the Control or 5g with the 15 and 30 being intermediate. The extent of digestion was greatest (P<.05) for 10ml and 15g compared to other treatments. The KdB was also highest (P<.01) for the 15g treatment compared to other treatments. Extent of hay NDFd was highest (P<.05) for 10ml compared to other treatments. Doses of 15g and 10ml yielded higher (P<.05) KdB compared to other treatments. Corn silage DM A and B fraction was not influenced by treatment (P>.10). However, C fraction was lowest (P<.01) for cows receiving 10ml compared to 5g with Control,15 and 30g being intermediate. Extent of corn silage NDFd was highest (P<.05) for cows receiving 10ml, intermediate for 15 and 30g and lowest for Control and 5g. Rates were not influenced by dose. Amaferm fed at 15g/cow/d in a dry form, or 10ml/cow/d in a liquid form, increased ruminal DMd of hay by increasing the extent and rate of digestion for both DM and NDF. The extent of corn silage DM and NDFd was increased when the 10ml/h/d Amaferm was included in the rumen.

Key Words: NDF digestibility, forage

665 The ability of enterococci to survive the ensiling process. S. N. Masiello* and C. S. Petersson-Wolfe, *Virginia Polytechnic Institute and State University, Blacksburg*.

The objective of the current study was to determine the ability of enterococci to survive a 3-wk ensiling process. Harvested grass and corn crops were respectively divided into 3 treatment groups consisting of 2 commercially available silage inoculants and 1 negative control group. Within 24 h of harvest, a uniform amount of forage was added to each of 18 vacuum sealable freezer bags. Inoculants 1 and 2 were applied (according to manufacturer directions) to each of 6 bags and the remaining 6 bags were not inoculated and served as negative controls. An industry grade vacuum sealer was used and 90% nitrogen gas was pumped into the bag to create a pillow pack. Dry matter and bacterial enumeration were performed on the forage prior to ensiling as well as after each week of ensiling. Bacterial enumeration was conducted according to standard bedding sampling procedures with the addition of the Kanamycin Esculin Azide Agar for the enumeration of enterococci. At wk 1, 2, and 3 of the ensiling process, a total of 6 bags were opened; 2 from each of the 3 treatment groups. Preliminary data suggest an increased number of enterococci on inoculated grass samples compared with the negative control after the 3-wk ensiling process. Inoculant 2 (7.3±0.1 log cfu/g DM) displayed a greater count than Inoculant 1 (4.2±1.7 log cfu/g DM) after a 3-wk process and both were greater than the negative control (1.2±1.2 log cfu/g DM). Inoculation of corn silage did not appear to change the enterococci count following the 3-wk ensiling. Enterococci counts for Inoculant 1, Inoculant 2, and the negative control group were 4.3±0.1 log cfu/g DM, 4.4±0.1 log cfu/g DM, and 4.0±0.1 log cfu/g DM, respectively. The addition of a silage inoculant led to greater levels of enterococci in grass silage compared with the negative control at the end of a 3-wk ensiling period. Enterococci levels did not show a marked difference in the inoculated corn silage samples. These preliminary data suggest that enterococci are able to survive the harsh conditions of an ensiling period.

Key Words: mastitis, silage inoculant, *Enterococcus*

666 Expression of genes related to cell wall digestibility of tropical forages. S. S. Stabile[1], L. Jank[2], A. P. Bodini[1], N.S . Oliveira[1], L. V. Março[1], and L. F. P. Silva*[1], [1]*Universidade de São Paulo, Pirassununga, SP, Brazil*, [2]*EMBRAPA, Campo Grande, MS, Brazil*.

Cell wall lignification with advanced maturity is the main limiting factor for ruminant production in tropical systems. Our objective was to iden-

tify genes related to rapid decline in cell wall digestibility with advanced maturity, in order to identify targets for future genetic manipulations. Eleven genotypes of *Panicum maximum* were harvested at 30, 60 and 90 days of regrowth. Samples were divided in three fractions: leaf blades, stems and senescent material. After drying and grinding, the fractions were incubated for 30h at 39°C in ruminal fluid and MacDougall solution for determination of in vitro cell-wall digestibility (NDFD). There was no difference among genotypes for NDFD of leaves, but there was a significant genotype and genotype × maturity interaction for NDFD of stems. From the 11 genotypes, we selected 3 with the slowest decline in stem NDFD and 3 with rapid decline of stem NDFD with advanced maturity for gene expression evaluation. Total RNA was isolated, treated with DNaseI and converted to cDNA for PCR quantification. Real-time PCR was used to quantify the expression of genes from the lignin biosynthesis pathway, using oligonucleotide primers specific for *P. maximum* phenylalanine ammonia lyase (PAL), cafeic acid O-methyltransferase (COMT), cinnamate 4-hydroxylase (C4H), cinnamoyl-CoA reductase, cinnamyl alcohol dehydrogenase and 4-coumarate CoA ligase. Expression of glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was used as a control gene. We were interested in existing treatment x maturity interaction, which would indicate that the referred gene was expressed differentially between the rapid and the slow group of genotypes. There was a significant interaction for the genes C4H, COMT and PAL, where there was larger increase in expression from 30 to 60 days in the rapid group and no difference with 90 days of regrowth. These results indicate that the larger increase in expression of these genes from 30 to 60 days of regrowth could explain the faster decline in NDFD.

Key Words: Guineagrass, lignin, COMT

667 Effect of citrate synthase genes transformed into alfalfa on aluminum tolerance of its cells. F. Fan*, J. J. Li, Y. M. Wu, and J. X. Liu, *Zhejiang University, Hangzhou, P. R. China*.

This study was conducted to investigate the effect of bivalence citrate synthase genes transformed into alfalfa (*Medicago sativa* L.) on aluminum tolerance of its cells. Two different kinds of citrate synthase genes (CS) were cloned from *E. coli* (CSI, 1284bp) and *Oryza sativa* L (CSII, 1425bp), respectively. Bivalence expression vector containing CSI, CSII and the phosphomanose isomerase gene isolated from *E. coli* as the selectable marker gene, was constructed and transferred into *Agrobacterium tumefaciens* LBA4404 strain through electrotransformation method. The expression vector containing CSI alone was also constructed with the same method. Leaf disks of *Medicago sativa* L cultivar Youke were inoculated with *Agrobacterium tumefaciens* LBA4404 and selected on the mannose (30g/L). The callus were grown on the solid SH medium for 6 weeks in a chamber at 25°C with 75% relative humidity, and exposed to 14 h of light and 10 h darkness. Integration of the transgene was detected by PCR with genomic DNA of the callus as template. Transcription of the transgene was determined by cDNA dot blotting analysis. The callus tissues of transgene were cultured in the liquid SH medium under the shake at 150 × *g* and 25°C for 2 days. The activity of the cells and their ATPase were detected when stressed under the different concentrations of Al^{3+}. The specific PCR products of expected size (1284bp and 1425bp) were observed in the genomic DNA from all transformed callus, but not occurred in the non-transformed callus, indicating that two CS genes were integrated into the transformed callus. The cDNA dot blotting of the transformed callus revealed that the interested genes were transcripted. The activity of both the cells and their ATPase was significantly (P<0.05) higher in the transformed than that in the non-transformed cells, with significantly (P<0.05) higher activity in both CSI and CSII transformed than in the CSI transformed cell. It is indicated that expression of the CS gene in the transformed cells could improve the aluminum tolerance of alfalfa cells.

Key Words: citrate synthase gene, aluminum tolerance, alfalfa

668 A survey of condensed tannin concentrations in vegetative and mature legume forages in western Canada. N. Berard[1], K. Ominski*[1], K. Wittenberg[1], D. Krause[1], T. McAllister[2], and Y. Wang[2], [1]*University of Manitoba*, [2]*Agriculture and Agri-Food Canada*.

Condensed tannin (CT) concentrations of legume forages and the potential benefits of inclusion in ruminant diets have been well-documented in semi-arid or tropical regions. To date, there has been limited effort to examine the CT concentration of legume forage species grown in temperate climates such as the prairie region of western Canada. As such, CT concentrations were measured using the butanol-HCl technique in *Medicago sativa*, *Trifolium hybridum*, *Trifolium ambiguum*, *Dalea purpurea*, *Trifolium pratense*, *Onobrychis viciifolia*, *Lotus corniculatus*, and *Trifolium repens* varieties grown in research plots across the prairies. Above ground plant biomass was harvested at vegetative and mature stages for two growing seasons. Statistical analyses were performed using SAS. Significant interactions, LS means, SE and SD for stage of maturity and growing season were determined using PROC MIXED. *Dalea purpurea* (purple prairie clover), a native legume, had the highest mean condensed tannin concentration of 68.7 ± 22.6 g/kg DM, with minimum and maximum values ranging from 37.9 to 92.9 g/kg DM. *Onobrychis viciifolia* (sainfoin) had the second highest mean CT concentration of 46.0 ± 19.3 g/kg DM with a range of 16.3 to 94.4 g/kg DM. The third highest mean CT concentration of 15.1 ± 6.3 g/kg DM was found in *Lotus corniculatus* (birdsfoot trefoil) with a range from 0.0 to 25.7 g/kg DM. No condensed tannin was found in *Medicago sativa* (alfalfa) or *Astragalus cicer* (cicer milkvetch). Forage CT concentrations were higher (P<0.05) when in the mature stage compared to vegetative stage for all species except sainfoin. Growing season did not have a significant effect on plant CT concentration. Potential benefit of inclusion in ruminant diets at the identified concentrations requires further exploration.

Key Words: condensed tannin concentration, forage, western Canada

669 Development of prediction equations to estimate hay intake of beef cows under limited access feeding times. T. S. Dennis*[1], T. D. Nennich[1], R. P. Lemenager[1], C. J. Fleenor[1], S. L. Lake[2], and L. J. Unruh-Snyder[1], [1]*Purdue University, West Lafayette, IN*, [2]*University of Wyoming, Laramie*.

Livestock producers are often faced with limited feed supplies due to drought, disaster, or other shortages and are forced to restrict intake of available feeds. The objective of this study was to develop prediction equations to determine the DMI of forages with differing qualities at limited access feeding times. Forty-five mature, mid-gestation Angus crossbred cows (BW = 602.7 kg; BCS = 5.13) were randomly assigned to pens of five cows by BW, BCS, and breed type. Pens of cows were assigned to one of three limited access times (1, 2, or 4 h) with three replications each. Actual pen intake of LOW (10.9% CP, 60.3% NDF, 59% TDN), MID (12.3% CP, 57.5% NDF, 58% TDN), and then HIGH (18.1% CP, 45.9% NDF, 63% TDN) quality hay was determined three times/wk. On non-sampling days, cows were allowed limited access, according to assigned time, to large round bales of hay (12.8% CP,

56.1% NDF, 60% TDN). All cows were supplemented with soybean hulls and a vitamin-mineral mix to meet NRC requirements for maintenance. Data collected from this study were combined with data from Fleenor et al., 2008 (Abstr.) to develop regression equations. Increased daily access feeding times and/or hay quality resulted in greater hay DMI. Regression equations developed to estimate hay DMI for limited access fed cows were Hay DMI (kg/d) = 1.80 × Hours access - 0.12 × Hay NDF% + 8.34 (n = 72, R^2 = 0.82) and Hay DMI (% of BW) = 0.30 × Hours access - 0.02 × Hay NDF% + 1.34 (n = 72, R^2 = 0.82). These regression equations should provide livestock producers with a valuable tool for formulating diets with differing forage qualities and limited daily access feeding times. Further research is necessary to validate these equations.

Key Words: cows, hay intake, limited access time

670 Whole plant barley NDF digestibility and its relationship with chemical constituents and dry matter yield. M. L. Swift*[1], M. Oba[2], P. E. Juskiw[1], and J. H. Helm[1], [1]*Alberta Agriculture and Rural Development, Lacombe, AB, Canada*, [2]*University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to determine the relationships of 30-h in vitro NDF digestibility (IVFD) of whole plant barley with yield, chemical constituents, and growing environment. Concentrations of ADF, NDF and lignin, and IVFD were determined for 173 samples of whole plant barley harvested in 2005 (n=56), 2006 (n=58) and 2007 (n=59). Correlation coefficients (r) were computed using Proc Corr (SAS) to evaluate the relationships of IVFD with lignin (%DM or %NDF), ADF, NDF, dry matter yield (DMY), growing degree days (GDD) and precipitation during the growing period. To evaluate the effect of hull type (hulled versus hull-less) and row type (2 versus 6) the data were analyzed using Proc Mixed (SAS) with year as a random variable. The IVFD was best related to lignin (%NDF), regardless of hull or row type as shown by r values of -0.80 (hulled 2-row), -0.85 (hulled 6-row), -0.82 (hull-less 2-row) and -0.91 (hull-less 6-row). The r values of IVFD with NDF content were 0.11 and 0.46 for hulled and hull-less barleys, respectively regardless of row. Similarly, there was not a strong relationship between IVFD and DMY (-0.28, 0.22, -0.35, -0.22), GDD (-0.30, -0.13, 0.25, -0.04) or precipitation (-0.39, -0.47, -0.16, -0.30) for hulled 2-row, hulled 6-row, hull-less 2-row and hull-less 6-row, respectively, during the growing period. The hull type (P=0.883) or row type (P=0.545) of barley had no effect on IVFD. The IVFD values ranged from 43.5 to 57.4% for hulled 2-row, 37.9 to 59.5% for hulled 6-row, 39.1 to 55.0 for hull-less 2-row, and 34.9 to 61.5 for hull-less 6-row whole plant barley. The large variation in IVFD within hull and row type of barley indicates that there is scope for genetic selection of cultivars with enhanced fiber digestibility.

Key Words: barley, NDF, digestibility

671 Forage quality of biomass vs. conventional alfalfa cut at early bud or late flower maturity. H. G. Jung*[1,2], K. P. Rock[2], and J. F. S. Lamb[1,2], [1]*USDA-ARS, St. Paul, MN*, [2]*University of Minnesota, St. Paul*.

Cellulosic bioenergy systems will result in large areas planted to biomass crops. An important question is whether biomass crops can also be used for livestock feed. This study compared forage quality of an experimental alfalfa germplasm developed for a biomass production system with a conventional variety when harvested at early bud (four times annually) and late flower (three times annually) maturity stages. Replicated field trials were established at two locations and harvested in 2007 and 2008. Leaf percentage and stem NDF, ADL, and 16- and 96-h in vitro rumen NDF digestibility (IVNDFD) were determined. As expected, delaying harvest to late flower reduced leaf percentage (56.5 vs. 46.7%), and increased stem NDF (58.7 vs. 65.9% DM) and ADL (16.0 vs. 16.7% NDF) concentrations and reduced stem 16-h (22.0 vs. 20.0%) and 96-h (55.5 vs. 50.8%) IVNDFD. When harvested at early bud, biomass alfalfa had less leaf material (55.6 vs. 57.4%) and a lower stem ADL concentration (15.9 vs. 16.0% NDF), was lower in stem fiber digestibility (21.8 vs. 22.1% and 55.4 vs. 55.7% for 16- and 96-h IVNDFD, respectively), and had a higher stem NDF concentration in the first (58.3 vs. 55.7%) and last (61.3 vs. 59.4%) harvests, but not the two mid summer harvests. Harvesting at late flower, biomass alfalfa again had a lower leaf percentage (44.3 vs. 49.2%) and stem ADL concentration (16.6 vs. 16.8% NDF). Stem NDF concentration of the biomass alfalfa was higher (67.0 vs. 64.7% DM) for all three late flower harvests. Stem fiber digestibility was lower for biomass alfalfa at two of three harvests, the first (19.9 vs. 20.7% and 49.6 vs. 51.1% for 16- and 96-h IVNDFD, respectively) and last (19.1 vs. 19.6% and 49.2 vs. 50.3% for 16- and 96-h IVNDFD, respectively). When harvested at late flower for biomass, both alfalfa types were of low quality. While quality of the biomass alfalfa was lower than the conventional variety, the reductions were minor if harvested at early bud. Producers will have some flexibility in how they manage and utilize biomass alfalfa varieties.

Key Words: alfalfa, forage quality, biomass

672 Nutritional evaluation of shrubs as fodder source for ruminants. J. Sultan*, I.-U. Rahim, M. Yaqoob, and H. Nawaz, *University of Agriculture, Faisalabad, Pakistan*.

The intent of the study was the nutritional evaluation of shrubs as fodder source for ruminants. Eight shrub species (Debregeasia salicifolia, Indigoferra gerardiana, Anisomoles indica, Marisine affricana, Desmodiem spp., Impashion bicolor, Dodonia viscosa, Adhatoda vesica) were selected and analyzed for dry matter (DM), organic matter (OM), ash, crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), hemi-cellulose, and lignin contents. The mean percentage values for DM, OM, ash, CP, NDF, ADF, hemi-cellulose and lignin were 31.4±2.16, 27.8±1.83, 11.3±0.67, 17.6±1.06, 59.1±2.05, 30.4±2.04, 28.8±2.33 and 5.7±0.46, respectively. The mean percentage values for Ca, P, K and Mg at were 1.22±0.223, 0.044±0.006, 0.77±0.095 and 0.019±0.004, respectively and mean values for Cu, Zn, Mn and Co were 18.42±1.556, 19.64±5.894, 11.01±1.103 and 0.042±0.007, respectively. In shrub species, the highest ($p<0.05$) potential intake rate (PIR) was observed for Debregeasia salicifolia (67.50±11.00 g/4 minute) and lowest for Adhatoda vesica (8.80±1.54 g/4 minute). However, the highest ($p<0.05$) relative preference (RP) was noted for Debregeasia salicifolia (83.20±1.22%) and lowest for Adhatoda vesica (3.63±0.88%). The mean in vitro dry matter digestibility (IVDMD) and metabolizable energy (ME) of fodder shrubs species were 56.9±2.76% and 7.74±0.31 MJ/kg DM, respectively. The IVDMD, RP and PIR values indicate that fodder shrubs be fed to livestock with some supplementation for different levels of production and types of livestock.

Key Words: shrubs, chemical composition, metabilizeable energy

673 Effects of supplementation of yeast culture to sow diets on reproductive performance and physiological changes in sows and nursing piglets. S. W. Kim*[1], C. Vasquez[2], A. Saraiva[1], and I. Yoon[3], [1]*North Carolina State University, Raleigh*, [2]*Texas Tech University, Lubbock*, [3]*Diamond V Mills, Cedar Rapids, IA*.

Forty-two sows were used to determine the effects of supplementation of yeast culture (XPC™ Yeast Culture, Diamond V Mills, Cedar Rapids, IA) to gestation and lactation diets on reproductive performance and physiological changes in sows and nursing piglets. Sows were allotted to 2 treatments: CON (no yeast culture, n=20) or YC (12 and 15 g XPC/d during gestation and lactation, respectively, n=22). Sows were fed 2 kg/d during gestation and ad libitum during lactation (21 d). On d 5 prior to breeding, d 30 and 110 of gestation, and d 0 (immediately after farrowing) and 21 of lactation, BW, backfat thickness, and blood samples were obtained from sows. Colostrum (d 1) and milk (d 17) samples were collected. On d 18 of lactation, milk yield was measured by weigh-suckle-weigh method. After weaning, conception rate was recorded. Litter BW was measured on d 0 and 21 of lactation. Changes in BW and backfat thickness of sows did not differ between treatments. Yeast culture did not affect litter size at birth or at weaning. Litter birth weight was similar between treatments. However, litter weight at weaning (kg) tended to be greater (P=0.068) for YC (61.1) compared to CON (55.1). Feed intake of sows during lactation did not differ between treatments. Post-weaning conception rate of YC (80.1%) was greater (P<0.05) than CON (68.4%). On d 110 of gestation, plasma urea nitrogen (mg/dL) of YC (1.28) tended (P=0.069) to be smaller than CON (1.46). Milk yield and composition were similar between treatments. Number of neutrophils (10^3 cells/μL) of CON (6.49 and 6.18) was greater (P<0.05) than YC (4.58 and 4.92) on d 110 of gestation and d 21 of lactation, respectively. Collectively, supplementation of yeast culture can improve post-weaning conception rate of sows and increase the litter weight potentially by improving protein utilization without affecting nutrient intake of sows and mobilization of sow body reserves.

Key Words: litter weight, sow, yeast culture

674 Effects of supplementation of yeast culture to diets of sows and offspring on growth and meat quality of offspring. A. C. Chaytor*[1], C. Vasquez[2], V. Fellner[1], I. Yoon[3], and S. W. Kim[1], [1]*North Carolina State University, Raleigh*, [2]*Texas Tech University, Lubbock*, [3]*Diamond V Mills, Cedar Rapids, IA*.

Pigs (n=256) weaned at 21 d of age were used to determine the effects of supplementation of yeast culture (YC; XPC™ Yeast Culture, Diamond V Mills) to diets of sows and pigs on growth, gut environment, and carcass characteristics of pigs. Equal numbers of pigs (n=128) from two sow groups fed diets with or without supplemental YC (12 and 15 g YC/d during gestation and lactation, respectively) were used. Pigs were fed 6 phase diets and the length of each phase was 7, 14, 21, 56, 42, and 27 d, respectively. Pigs from each sow group were allotted to one of two dietary treatments: with or without supplemental YC (0.2% YC for phase 1 to 3 and 0.1% YC for phase 4 to 6). Feed intake and BW were measured during each phase. On d 5, one pig representing the average BW of each pen was euthanized to obtain samples of the jejunum to measure villus height and digesta from the cecum and colon to measure volatile fatty acid (VFA) concentrations. At 115 kg BW, all pigs were slaughtered at a local abattoir to measure carcass characteristics. During the study, growth performance of pigs did not differ between treatments. On d 5, jejunal villus height did not differ between treatments. However, pigs fed YC tended to have greater acetate content (61.2 vs. 57.7%, P=0.084) and reduced propionate content (24.8 vs. 27.4%, P=0.054) in the colon than control-fed pigs. Pigs from sows fed YC tended (8.5 vs. 10.4%, P=0.098) to have greater butyrate content in the cecum than pigs from control-fed sows. When pigs were harvested, loin color, pH, and firmness did not differ between treatments. However, pigs fed YC had greater (P<0.05) loin marbling score (2.4 vs. 1.9) than control-fed pigs. Collectively, dietary supplementation of yeast culture can be beneficial by improving loin marbling score and production of VFA in the hind gut potentially favorable for intramuscular lipogenesis.

Key Words: marbling, pig, yeast culture

675 Use of a phytogenic feed additive in sows during the lactation. Y. Acosta Aragón[1], D. Uribe López[2], A. Pedroche Quevedo[3], and T. Steiner*[1], [1]*Biomin Holding GmbH, Herzogenburg, Lower Austria, Austria*, [2]*Agropecuaria ALFA S.A., Cundinamarca, Colombia*, [3]*NUTRECO S.A., Bogotá, Colombia*.

The aim of this study was to quantify the effects of using a phytogenic feed additive based on a blend of essential oils and prebiotics, hereafter named as PEP, in diets for lactating sows. The experiment was conducted in 2008 in a commercial pig farm in Colombia. The sows (commercial breed) were allocated separately in two treatments. Control sows (n=20) were fed a commercial lactation diet, whereas PEP sows (n=44) were fed the same diet supplemented with a phytogenics feed additive based on essential oils and prebiotics (Biomin® P.E.P. 1000, 2 kg/t). Lactation feed and drinking water were offered ad libitum. Piglets were weaned from 21 to 28 days of age. Measurements included piglets born live and dead, litter weights, feed intake of the sows before and after farrowing, live weights of the sows at farrowing and at weaning, number of weaned piglets as well as their weaning weights and number of dead piglets during lactation. Mortality of piglets at birth and after the lactation, 21-day lactation feed intake and whole lactation feed intake, weight losses of the sows, and the average weaning weights and weight gains of the piglets were calculated. Control and PEP sows were relocated to the farrowing pens 5.7 and 2.75 days before farrowing, respectively. In week 1, feed intake in the control treatment was higher as compared to the PEP treatment. Nevertheless, feed intake in the second and third week was higher in the PEP treatment (up to 21 days, 101.67 vs. 111.64 kg). The increase in feed intake in the second and third week for the treatment with PEP caused a higher feed intake in the first 21 lactation days (+ 10 kg) and also in the whole period (+ 18.27 kg). Although the piglets in the treatment with PEP were 80 g lighter at birth (1.47±0.38 vs. 1.55±0.30 kg), they were heavier than pigs in the control treatment at the end of lactation (7.52±1.20 vs. 6.28±1.38 kg, P<0.05). Average weight gain from birth to weaning was 6.05±2.29 vs. 4.73±1.31 kg in the PEP and control treatment, respectively. In conclusion, lactation feed intake and piglet growth performance was positively affected by supplementation of the lactation diet with the phytogenic feed additive under test.

Key Words: phytogenic, sow, lactation

676 Selection of probiotic strains for combined competitive exclusion treatment in piglets. V. Klose*[1], K. Bayer[1], R Bruckbeck[1], V. A. Sattler[1], A. P. Loibner[1], C. Mair[2], and G. Schatzmayr[3], [1]*BOKU-University, Vienna, Department IFA-Tulln, A-3430 Tulln, Austria*, [2]*BOKU-Uni-*

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In order to develop a feed additive for piglets, various aerobic, facultative and strict anaerobic bacteria were isolated from porcine gastrointestinal tract (GIT) by using semi-selective media and specific conditions, all at 37 °C. Out of 80, 9 aerobes were classified as endospore-forming strains of *Bacillus* or related genera, 66 facultative anaerobes as members of *Lactobacillus* and *Enterococcus*, and five strict anaerobes as members of *Bifidobacterium*. Using an agar spot test, one strain of *E. faecium*, one *L. salivarius*, and one *L. reuteri* with antagonistic effect against a broad panel of pathogens (various *S. enteritidis* serovars and entero-hemorrhagic and –toxigenic *E. coli* serotypes, *C. perfringens*) were selected and combined with one *B. thermophilum* strain, because of its′ capability to suppress *Brachyspira hyodysenteriae*, the main causing agent of Swine dysentery. By determining the minimal inhibitory concentration of ten antibiotics according to the European Guideline (EFSA, 2008), the strains turned out to be susceptible to all antibiotics of human and veterinary importance. In one feeding trial, the effects of their combined use as feed additive on the gut microbiota of weaning piglets (n = 48) was examined by comparing denaturing gradient gel electrophoresis (DGGE) bacterial community fingerprints of different GIT parts in response to the 4-strain probiotic, inulin as non-digestible feed ingredient (prebiotic) and a combination of both (synbiotic). Significant differences ($P < 0.05$) of the pro- and prebiotic fed groups to the control group could be shown, indicating a pro- and/or prebiotic effect of the feed additive. Future work will first involve field trials at various farms, with later work focussing on the in vivo survival and efficiency of bacterial strains when administered to weaning piglets.

Key Words: multi-strain probiotic, porcine pathogens, antagonistic activity

677 Effects of NCG and arginine on organ weight and HSP70 expression in weaned piglets. X. Wu, Y. L. Gao, X. H. Zhou, R. L. Huang, and Y. L. Yin*, *The Chinese Academy of Sciences, Changsha, China.*

To evaluate the effects of N-carbamylglutamate and L-Arginine on organ weight and heat shock protein 70 (HSP70) expressions, eighty-nine Landrace×Yorkshire piglets from 12 pens (average pen weight 5.56±0.51 kg; weaned at 21 d) were grouped into 3 treatments, and fed one of the following diets for 7 d: a standard diet (SD), SD+NCG (0.08%), or SD+Arg (0.6%). Six piglets from each treatment were selected randomly and slaughtered for tissue samples. Compared to the control group, both Arg and NCG increased heart ($P<0.01$), and kidney weight ($P>0.05$). Liver weight was heavier in the NCG group ($P<0.01$), and ratio of pancreas weight/BW was higher in the Arg group ($P<0.05$) (Table 1). HSP70 expression was analyzed by real-time PCR and western blotting. The results showed that HSP70 mRNA was expressed in the liver to a greater extent in the Arg group ($P<0.01$), when compared to the control group. Arg and NCG increased HSP70 mRNA in the kidney by 33.03 and 14.22%, respectively ($P=0.12$). Western blotting results also confirmed that there was a higher level of HSP70 expression in the liver ($P<0.01$) and kidney ($P=0.027$) in the Arg group. These findings indicated that Arg and NCG could prevent tissue dysfunction of weaned piglets and alleviate the weaning stress effectively by inducing HSP70 expression in weaned piglets.

Table 1. Effect of NCG and Arg on organ weight and organ:body weight ratio of piglets (means±SD, n=6)

Items	Control	NCG	Arg
Organ weight (g)			
Heart	25.17±4.22[a]	33.00±3.51[b]	31.75±5.91[b]
Liver	140.92±12.16[a]	161.25±19.31[b]	143.92±12.76[a]
Pancreas	10.42±2.29	9.92±0.74	13.33±3.34
Kidney	15.08±1.83	16.92±2.18	17.83±3.33
Organ:BW (g/kg)			
Heart/BW	0.41±0.064	0.47±0.04	0.48±0.09
Liver/BW	2.27±0.16	2.31±0.28	2.19±0.21
Pancreas/BW	0.17±0.042[a]	0.14±0.010[a]	0.20±0.046[b]
Kidney/BW	0.25±0.025	0.24±0.021	0.27±0.047

a, b means differ ($P<0.05$).

Key Words: N-carbamylglutamate, L-arginine, weaned piglets

678 Digestible energy in resistant starch and dietary fiber sources fed to pigs. S. K. Cervantes-Pahm*, B. G. Kim, and H. H. Stein, *University of Illinois, Urbana.*

An experiment was conducted to measure the concentration of apparent total tract digestible energy (ATT DE) in maltodextrin (MD), 2 sources of resistant starch (PROMITOR™ RS-60 and RS-75), PROMITOR™ soluble corn fiber (SCF), and biogum (BG). All fiber sources were provided by Tate and Lyle, Decatur, IL. A total of 72 castrated male pigs (initial BW: 22.3 ± 1.48 kg) were housed in metabolism crates equipped with a feeder and a nipple drinker and assigned to 6 treatments with 12 replicate pigs per treatment. A basal diet based on corn, soybean meal, and casein was formulated. Five additional diets were prepared by mixing 90% of the basal diet with 10% MD, RS-60, RS-75, SCF, or BG. The daily feed allowance was calculated as 2.5 times the estimated energy requirement for maintenance and pigs were fed 2 equal meals every day. Following a 7-d adaptation period, feces from all pigs were collected quantitatively during a 5-d period using the marker to marker procedure. The ATT DE for each ingredient was calculated using the difference procedure. The ATT DE in RS-60, RS-75, and SCF were less ($P < 0.05$) than in MD and BG, and BG contained less ($P < 0.05$) ATT DE than MD. However, there was no difference in the ATT DE values for RS-60, RS-75, and SCF. The present results indicate that resistant starch and soluble corn fiber can be used as low energy ingredients.

Table 1. Concentration of ATT DE in maltodextrin (MD), 60% resistant starch (RS-60), 75% resistant starch (RS-75), soluble corn fiber (SCF), and biogum (BG) fed to pigs

Item	MD	RS-60	RS-75	SCF	BG	SEM
Gross Energy, kcal/kg	3,914	3,738	3,835	3,760	3,850	-
ATT DE, kcal/kg	3,466[a]	1,776[c]	1,782[c]	1,936[c]	2,795[b]	189
ATT DE, kcal, kg DM	3,559[a]	1,973[c]	1,916[c]	2,062[c]	2,949[b]	200

[a-c]: Means within a row lacking a common superscript letter are different ($P < 0.05$)

Key Words: digestible energy, fiber, pigs

679 Feed additives for the amelioration of aflatoxicosis in growing pigs. A. F. Harper*[1], M. J. Estienne[1], J. B. Meldrum[2], R. J. Harrell[3], and D. E. Diaz[3], [1]*Virginia Polytechnic Institute & State University*, *Blacksburg,*, [2]*VA-MD Regional College of Veterinary Medicine*, *Blacksburg, VA*, [3]*Novus International, Inc.*, *St. Charles, MO*.

A study was conducted to assess a hydrated sodium calcium aluminosilicate and a blend of synthetic antioxidants (AOX) (SOLIS® and AGRADO® Plus Novus International, Inc., St. Charles, MO) for amelioration of toxic effects of aflatoxin in pig feed. Ninety crossbred pigs (31 ± 2 d of age) were allotted to five treatments: 1) positive control with no aflatoxin, 2) negative control contaminated with 500 ppb aflatoxin B1, 3) aflatoxin contaminated diet with 0.5% SOLIS®, 4) aflatoxin contaminated diet with AOX (a blend of ethoxyquin and tertiary butylhydroquinone), and 5) aflatoxin contaminated diet with SOLIS® and AOX. There were six pens with three pigs each per treatment. Feed and water were available ad libitum. The growth assay lasted 21 d after which blood samples were collected for serum indicators of aflatoxicosis. Pigs fed the contaminated negative control diet consumed 29% less feed and grew 27% slower (P < 0.05) than pigs fed the positive control diet. Pigs fed the aflatoxin diets with 0.5% SOLIS® had feed consumption and growth rate greater than pigs fed the negative control diet (P < 0.05) and similar to pigs fed the uncontaminated feed. Pigs fed the aflatoxin diet with AOX alone had feed consumption 22% and growth rate 24% below the positive controls (P < 0.05). Serum protein, albumin, globulins, gamma glutamyltransferase (GGT), and vitamins A and E were altered by feeding the aflatoxin contaminated diet (P < 0.05). Supplementing the diet with SOLIS® returned serum protein, albumin, globulins, and GGT to concentrations similar to the positive control and vitamin A and E to levels intermediate between the positive and negative controls. Serum constituents were less responsive to the AOX supplement. Combining the SOLIS® and AOX restored serum vitamin A and E to concentrations similar to the positive control (7.93 vs. 8.44 ± 0.73 g/dL and 83.88 vs. 75.01 ± 5.87 g/dL, respectively). SOLIS® was highly effective in amelioration of aflatoxicosis. Responses to AOX were limited, but the broadest correction of serum constituents occurred when the supplements were fed in combination.

Key Words: pigs, aflatoxin, antioxidant

680 Xylanase supplementation improves nutrient and energy digestibility in pigs fed corn-soybean meal diets containing 20% corn dried distiller's grains. J. A. Jendza*[1], A. Owusu-Asiedu[2], P. H. Simmins[2], and O. Adeola[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*Danisco Animal Nutrition*, *Marlborough, UK*.

The apparent ileal (AID) and total tract (ATTD) digestibility of nutrients and energy response of pigs to dietary xylanase (Xyl; Porzyme® 9300, endo 1,4 – beta-xylanase) supplementation of a corn-soybean meal diet containing 20% corn dried distiller's grains (cDDG) was investigated in cannulated pigs. Eight 25-kg barrows fitted with T-cannula at the distal ileum were used in a replicated 4 × 4 Latin square, with 4 treatments in 4 periods. A control diet (C) containing 20% cDDG was formulated to contain 3.33 Mcal ME/kg and 0.13% available P. Treatments consisted of the C plus 0, 1,000, 2,000, and 4,000 U Xyl/kg feed. Periods consisted of a 5-d adjustment period, 2 fecal grab samples on d 5, and two 12-h ileal collections on d 6 and 7. The AID and ATTD were calculated via the index method using Ti. Increasing levels of Xyl linearly improved (P < 0.05) AID of energy, Ile, Leu, Phe, Thr, Trp, Glu, Pro, and total amino acids. The respective AID of energy, Thr, and Trp increased (P < 0.05) from 61.5 to 64.7%, 75.2 to 77.9%, and 74.9 to 78.0% for 0 to 4,000 U Xyl/kg feed. Increasing levels of Xyl supplementation from 0 to 4,000 U Xyl/kg feed linearly improved (P < 0.05) ATTD of DM from 80.4 to 81.6% and ATTD of energy from 79.9 to 81.4%. Digestibility of P (P < 0.05) increased 34 to 37% with Xyl supplementation compared to the C diet. In summary, Porzyme® xylanase supplementation improved the apparent ileal digestibility of energy and at least some amino acids, as well as the apparent total tract digestibility of dry matter, energy, and P in pigs fed corn-soybean meal diets containing 20% corn dried distiller's grains.

Key Words: energy, pigs, xylanase

681 Effect of processing method and enzyme supplementation on the apparent metabolizable energy (AME_n) of different oilseed meals. B. Jayaraman* and D. M. Anderson, *Nova Scotia Agricultural College*, *Truro, Nova Scotia, Canada*.

A study was conducted to determine the apparent metabolizable energy (AME_n) of different oil seed meals by broilers. Three hundred and eighty four male broiler chicks were randomly distributed to battery cages (6 birds per cage). A common starter diet was fed from 1-13 days of age. From days 14-21, the birds were fed one of the thirteen treatments (trts), a basal grower diet (4 reps) or the basal grower diet supplemented with 30% of the test ingredients (12 trts, 5 reps/trt). Celite (0.8%) was used as an inert marker in the grower diet. The test ingredients were pre-press solvent extracted meals from full fat seeds of yellow and black canolas and juncea processed by regular (95°C±5 during the desolventization process) and gentle (57°C±5 during the desolventization process) methods with and without a multi-carbohydrase enzyme mixture. A 3 × 2 × 2 factorial design (seed source x processing method × enzyme supplementation) was used. At 21 days of age, excreta were collected from individual cages, freeze-dried and used for subsequent analysis. Method of processing did not affect (P>0.05) AME_n of the oil seed meals. There was an increase (P≤0.05) in AME_n by addition of multi-carbohydrase enzymes to the canola meals only. The mean AME_n (kcal/kg) of regular processed yellow and black canola meals and juncea meals with and without enzymes, respectively, were 1629±124 and 1538±78; 1686±99 and 1450±120; 1629±107 and 1742±160. The mean AME (kcal/kg) of gentle processed yellow and black canola meals and juncea meals with and without enzymes, respectively, were 1791±112 and 1782±51; 1519±191 and 1282±82; 1280±59 and 1413±54. Addition of the carbohydrase enzymes to the canola meals resulted in higher AME_n.

Key Words: apparent metabolizable energy, oil seed meals, enzyme supplementation

682 Effects of dietary aflatoxin on performance of growing barrows. S. M. Rustemeyer*[1], W. R. Lamberson[2], D. R. Ledoux[2], R. R. Cockrum[1], K. L. Kessler[1], K. J. Austin[1], and K. M. Cammack[1], [1]*University of Wyoming*, *Laramie*, [2]*University of Missouri*, *Columbia*.

Dried distillers grains (DDGS) can have high aflatoxin content due to its concentration during ethanol production. Increased use of DDGS in swine diets could potentially lead to aflatoxicosis which causes decreased feed intake, reduced BW gain, and impaired liver function, resulting in substantial losses to the pork industry. The objective of this study was to determine the effects of aflatoxin exposure on performance and blood parameters of growing barrows. Duroc x Yorkshire crossbred barrows (n = 90; age = 35 ± 5 d; initial BW = 14.2 ± 3.031 kg) were randomly assigned in a 3 × 3 factorial design to receive 0, 250 or 500 ppb aflatoxin B1 for 7, 28 or 70 d. Pen feed intake was measured daily,

and pigs were weighed and bled weekly. Serum was analyzed for blood urea nitrogen (BUN), total bilirubin, alanine aminotransferase (ALT), and aspartate aminotransferase (AST). Pen feed intake was lower ($P < 0.01$) in aflatoxin treated barrows (high and low) than control barrows from d 29 onward, and was lower ($P < 0.05$) in high aflatoxin treated barrows than low aflatoxin treated barrows from day 42 onward. Average daily gain was lower ($P < 0.01$) in high aflatoxin treated barrows than control barrows from d 49 onward, and was similar between control and low aflatoxin treated barrows except on d 69, when ADG was lower ($P = 0.0449$) in aflatoxin treated barrows. High aflatoxin treated barrows had lower bilirubin than low aflatoxin treated barrows on d 27 ($P = 0.0372$) and 62 ($P = 0.0030$). Additionally, bilirubin was higher in high aflatoxin treated barrows than control barrows on d 55 ($P = 0.0480$), 62 ($P = 0.0052$) and 69 ($P = 0.0304$). High and low aflatoxin treated barrows had lower BUN ($P < 0.01$) than control barrows on d 6 and low aflatoxin treated barrows additionally had lower ($P = 0.0018$) BUN than control barrows on d 20. These results demonstrate that performance and blood parameters in young growing barrows are affected by consumption of an aflatoxin-contaminated diet, especially when the concentration of aflatoxin is high (≥ 500 ppb) and the diet is fed over an extended period of time (≥ 1month).

Key Words: aflatoxin, swine, production

683 Effects of adding a pelleted protein supplement to processed corn in diets for nursery pigs. S. M. Williams*, E. F. Mader, S. M. Rogers, S. Issa, A. C. Fahrenholz, L. J. McKinney, J. D. Hancock, and K. C. Behnke, *Kansas State University, Manhattan*.

A total of 180 pigs (90 barrows and 90 gilts) were used in a 28-d experiment to determine the effects of adding a pelleted protein supplement to processed corn in diets for nursery pigs. The pigs (average initial BW of 7.5 kg) were weaned and allotted by sex, weight, and ancestry to 30 pens with 6 pigs/pen and 5 pens/treatment. All pigs were fed a common diet for 7 d post weaning and the experimental treatments for the next 28 d. Treatments were a corn-soybean meal-based control in mash form and the corn-soybean meal-based diet as pellets. For the remaining treatments, all ingredients were pelleted together except the corn which was finely ground, cracked, and steam-flaked before mixing with the protein supplement pellets. Pellet durability index for d 0 to 14 of the growth assay was 97 and 98% and for d 14 to 28 was 89 and 94% for the complete feed and protein supplement, respectively. For d 0 to 14, ADG was greater for pigs fed the mash control compared to all thermally processed treatments ($P < 0.06$) and there was a trend ($P < 0.10$) for pigs fed complete pellets to have greater G:F compared to pigs fed the supplement pellets/processed corn treatments. For d 14 to 28 and overall (d 0 to 28), pigs fed the mash control had greater ADG and G:F compared to those given the thermally processed feeds and pigs fed complete pellets had improved ADG and G:F compared to those given the supplement pellets/processed corn treatments ($P < 0.02$). Finally, among pigs fed the processed corn treatments, G:F was greater with steam-flaked corn vs ground corn for d 14 to 28 and overall ($P < 0.007$). For pigs fed the mash, pellets, and protein supplement pellets with ground, cracked, and steam-flaked corn, overall ADG was 496, 472, 444, 421, and 451 g, overall ADFI was 661, 626, 651, 648, and 652 g, and overall G:F was 750, 754, 682, 650, and 692 g/kg. Our results indicated that steam-flaked corn was of benefit compared to ground corn, but compared to a mash diet or complete pellets, the separately processed corn treatments reduced growth performance in nursery pigs.

Key Words: nursery pigs, particle size, steam-flaking

684 Effect of a dry organic acid blend on pig performance during the Paylean® phase of growth. R. J. Harrell*[1], F. Navarro[1], J. Zhao[1], M. Vazquez-Anon[1], B. R. Hinson[2], G. L. Allee[2], and C. D. Knight[1], [1]*Novus International, Inc., St. Charles, MO*, [2]*University of Missouri, Columbia*.

Organic acids have been broadly utilized in young nursery pigs as a growth promotant, presumably by providing antimicrobial activity. Less information is available on the performance benefits of organic acids in grow-finish pigs. The objective of the present study was to determine the effects of a dry organic acid blend (DOAB, ACTIVATE®Starter DA, Novus International, Inc.) on pig performance during the Paylean® (ractopamine hydrochloride) phase of growth, a period of limited antibiotic utilization. Data were generated from two separate trials conducted in the same facility with similar management at two different times. Pigs were fed a nutrient adequate corn-soybean meal based diets with TID lysine levels of 0.95% and 7.5 ppm Paylean for a period of 21 days. In each experiment pigs were fed either 0 or 0.1% of a DOAB throughout the grower and finisher phases. In experiment 1, there were 10 pens of 20-25 pigs/pen and experiment 2 there were 8 pens of 20-25 pigs/pen for control and 0.1% inclusion rate of a DOAB, respectively. No differences in performance were detected by the addition of DOAB from 0 to 63 or 0 to 74 days of study, respectively, for experiments 1 and 2. Initial body weights were not significantly different between trials at the start of the Paylean phase, but ADG, ADFI, and GF were affected by trial ($P < 0.01$). The DOAB did not significantly affect final body weights or GF ($P > 0.20$). The DOAB significantly increased ADG (1006 vs 955±12 g/d) by 5.3% ($P < 0.01$) and tended ($P = 0.12$) to increase ADFI (2651 vs 2563±12 g/d). There were no trial by treatment responses for any parameter tested ($P > 0.25$). In summary, the DOAB increased pig growth rate during the Paylean phase of growth.

Key Words: organic acids, Paylean®, pigs

Physiology and Endocrinology: Livestock Physiology

685 Evaluation of sperm fertilizing capability in stored semen collected from boars fed a diet supplemented with organic selenium. S. Speight*[1], M. Estienne[1], B. Whitaker[2], A. Harper[1], R. Crawford[1], and J. Knight[1], [1]*Virginia Polytechnic Institute and State University, Blacksburg*, [2]*Ferrum College, Ferrum, VA*.

This study compared sperm fertilizing capability in stored semen collected from boars fed diets supplemented with organic or inorganic sources of selenium. At weaning, crossbred boars were assigned to one of three dietary treatments: I. basal diets with no supplemental selenium (controls), II. basal diets supplemented with 0.3 ppm organic selenium (Sel-Plex, Alltech, Inc., Nicholasville, KY) and, III. basal diets supplemented with 0.3 ppm sodium selenite (n = 6 boars/treatment). At sexual maturity, semen was collected, processed and stored in Androhep-Lite (Minitube of America, Inc., Verona, WI; 3 x 10^9 sperm/85 mL semen and extender) at 18° C and was evaluated at d 1 and 8 post-collection (day of semen collection = d 0) using commercially obtained porcine oocytes (Bomed, Madison, WI; 100 oocytes/boar) and in vitro fertilization procedures. Data were analyzed using ANOVA and boar was

the experimental unit. On d 1, fertilization rate was greater (P < 0.01) for the Sel-Plex-fed boars (77.8%) compared with the sodium selenite (67.4%) or control boars (68.5%). Polyspermy rate (16.5%) and male pronucleus (MPN) formation (94.1%) did not differ (P > 0.37) among groups. On d 8, fertilization rates tended to be greater (P = 0.08) for boars fed the diet supplemented with Sel-Plex (63.5%) compared with control (53.3%) or sodium selenite-fed (49.5%) boars. Polyspermy rate (10.7%) and MPN formation (91.2%) did not differ (P = 0.37) among groups. Supplementation of boar diets with Sel-Plex selenium resulted in enhanced sperm fertilizing capability compared with boars fed an equal dietary concentration of selenium from sodium selenite or boars receiving no selenium supplementation. Moreover, enhanced fertility characteristics appeared to be maintained during long-term liquid storage at 18° C.

Key Words: boar, selenium, fertility

686 Use of infrared thermal imaging of the muzzle as a measure of body temperature in sheep and cattle. R. W. Godfrey*[1], R. C. Ketring[1], S. S. Robinson[1], and S. T. Willard[2], [1]*University of the Virgin Islands, Agricultural Experiment Station, St Croix, VI*, [2]*Mississippi State University, Department of Animal and Dairy Sciences and Department of Biochemistry and Molecular Biology, Mississippi State*.

Previous work in our lab has shown a high correlation among rectal, vaginal and eye temperature (RT, VT and ET, respectively) using digital infrared thermal imaging (DITI) in hair sheep ewes. The objective of this study was to evaluate the relationship among VT, RT and ET and muzzle temperature (MT) in hair sheep and cattle. Sheep were evaluated in a state of normothermia (n = 35 rams and 24 ewes) and after the administration of lipopolysaccharide (LPS; 0.2 ug/kg BW i.v) to induce a febrile state (n = 7 treated and 7 control). Cattle (n = 43) were evaluated in a normothermic state. In normothermic sheep and cattle ET and MT were measured using DITI, and RT and VT were measured using a digital veterinary thermometer. In LPS and control ewes VT was measured using data loggers, RT was measured using a digital veterinary thermometer, and ET and MT were measured using DITI. Correlation analysis was conducted to determine the relationship among RT, VT, ET and MT within species. In normothermic sheep, RT was moderately correlated with ET (r = 0.55, P < 0.0001) and MT (r = 0.35, P < 0.006) and MT was correlated with ET (r = 0.64, P < 0.0001). In rams RT and MT were not correlated (r = 0.22, P > 0.10) but they were in ewes (r = 0.55, P < 0.005). In normothermic cattle, RT was correlated with ET (r = 0.58, P < 0.0001) and VT (r = 0.78, P < 0.0001) but not MT (r = 0.22, P > 0.10). MT was only correlated with ET (r = 0.48, P < 0.001). In ewes treated with LPS, RT was correlated with VT, ET and MT (r = 0.97, r = 0.87 and r = 0.79, P < 0.0001). In these ewes MT was correlated with VT and ET (r = 0.79 and r = 0.88, P < 0.0001). These results indicate that DITI can be used to measure ET and MT in sheep as an indicator of body temperature, as measured by RT or VT, in both the normothermic and febrile state. In cattle the relationship between MT and RT was not apparent in the normothermic state, but ET was correlated to RT. This study shows that DITI can be used as a non-invasive method of measuring body temperature in livestock.

Key Words: sheep, cattle, body temperature

687 Relationship of rumen temperature with estrus in beef cows. C. L. Bailey*, M. J. Prado-Cooper, E. C. Wright, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater*.

Angus x Herford cows, 4 to 8 yr of age, were used to evaluate changes in rumen temperature (RT) associated with estrus. Temperature boluses (SmartStock, LLC) were placed in the rumen with a bolus gun during gestation. Boluses were programmed to transmit RT hourly. Estrus of cows (BW = 539 ± 44 kg, BCS = 4.5 ± 0.4) was synchronized with $PGF_{2\alpha}$ at 79 ± 14 d post partum in May (n = 25) or December (Dec, n = 30). The HeatWatch® Estrus Detection System (CowChips, LLC) was used to monitor onset of estrus. Consumption of water decreases RT (unpublished data), therefore, RT < 37.72°C were excluded from analyses. Mean RT for all cows was 38.2 ± 0.1°C and did not differ between seasons. Rumen Temperatures 96 h before to 96 h after estrus in May and 72 h before to 72 h after estrus in Dec were analyzed using the MIXED procedure (SAS). Mean RT the first 8 h after onset of estrus in May cows (39.1 ± 0.1°C, n = 17) was greater (P < 0.001) compared with RT during 16 to 32 h before estrus (38.1 ± 0.1°C, n = 15) or 16 to 32 h after estrus (38.0 ± 0.1°C, n = 19). Similarly, mean RT the first 8 h after onset of estrus in Dec cows (38.9 ± 0.1°C, n = 18) was greater (P < 0.001) compared with RT 16 to 32 h before estrus (38.4 ± 0.1°C, n = 21) or 16 to 32 h after estrus (38.4 ± 0.1°C, n = 19). Increases in RT for any 8 h period ≥0.7°C or ≥0.3°C greater than the mean for that cow during 13 to 84 h proceeding the 8 h period were used as criteria to predict estrus. In Dec, an increase in RT ≥0.3°C predicted 95% of estrous cows while an increase in RT ≥0.7°C predicted 42% of estrous cows; 100% of May estrous cows were predicted using either method. An increase in RT ≥0.3°C falsely identified 36% of May cows and 40% of Dec cows as estrus. An increase in RT ≥0.7°C did not falsely identify any cows as estrus in May or Dec. Mean ambient temperatures (Oklahoma Mesonet) were 20.3°C in May and 2.4°C in Dec, and ranged from 5°C to 33°C in May and -9°C to 19°C in Dec. Ambient temperature may be important to consider when developing a model to predict onset of estrus with RT. The use of RT has potential application for estrous detection in beef cows.

Key Words: rumen temperature, estrus, beef cows

688 Influence of blood sulfate concentrations on uterine pH. G. A. Perry*, B. L. Perry, S. D. Fields, J. A. Walker, and C. L. Wright, *Dept. Anim. and Range Sci., South Dakota State University, Brookings*.

Uterine pH has been reported to influence pregnancy success and early embryonic development. A recent report also indicated a significant correlation between blood sulfate concentrations and sulfate concentrations in oviductal and uterine fluids. Therefore, the objective of the current study was to evaluate the relationship between uterine pH and blood sulfate concentrations. Immediately following detection in estrus, heifers were divided into 3 groups (n = 6 per group). The groups were fed a low (LOW; 6.4 kg hay and 0.01 kg urea/hd), medium (MED; 8.0 kg hay and 0.8 kg DDGS/hd) or high (HIGH; 6.2 kg hay, 2.9 kg DDGS and 0.03 kg urea/hd) sulfur diet (9.6, 18.08, and 31.34 g/d sulfur, respectively). Uterine pH and blood samples were collected on d 7 and 11 after estrus. Uterine pH decreased ($P < 0.01$) from d 7 to d 11. Uterine pH tended to decrease among LOW heifers ($P = 0.06$; 6.9 ± 0.08 and 6.7 ± 0.07 for d 7 and 11), and decreased from d 7 to 11 in MED ($P = 0.01$; 6.9 ± 0.06 and 6.7 ± 0.06) and HIGH ($P < 0.01$; 6.9 ± 0.08 and 6.5 ± 0.07). In addition, there was an effect of time ($P < 0.01$) on blood sulfate concentrations. Sulfate concentrations increased from d 7 to 11 in LOW ($P < 0.01$; 86.7 ± 9.57 and 125.6 ± 8.61 mg/L), MED ($P < 0.01$; 88.9 ± 7.86 and 146.17 ± 7.86 mg/L), and HIGH ($P = 0.01$;

110.82 ± 9.58 and 145.4 ± 8.61 mg/L) heifers. There was a significant positive correlation between time and sulfate concentrations ($P < 0.01$; R^2 0.56) and a significant negative correlation between sulfate concentrations and uterine pH ($P < 0.01$; R^2 0.32). As time on these diets increased blood sulfate concentrations increased and as blood sulfate concentrations increased uterine pH decreased. In summary, on these diets concentrations of blood sulfate increased and uterine pH decreased with time following estrus.

Key Words: blood sulfate, uterine pH, estrus

689 Impact of long-term genetic selection for age at puberty on postpartum reproductive physiology in cows. G. A. Bridges*[1], N. C. Amyes[2], M. C. Berg[2], M. J. D'Occhio[3], and M. L. Day[4], [1]*Purdue University*, *West Lafayette, IN*, [2]*AgResearch, Ruakura Research Centre*, *Hamilton, New Zealand*, [3]*The University of Queensland*, *Brisbane, Australia*, [4]*The Ohio State University*, *Columbus*.

The aim of the present experiment was to determine the impact of > 20 yr of genetic selection for age at puberty on postpartum reproductive function in beef cows. Objective 1 was to compare the duration of postpartum anestrous in mature (≥ 3 yr of age) and 2-yr old (2y) beef cows that had been genetically selected to have either an early age (age-: mature; n = 32 and 2y; n = 17) or late age (age+: mature; n = 27 and 2y; n = 14) of puberty. Blood samples were collected weekly beginning when cows entered their 5th wk postpartum until the 6th wk of the breeding season. Blood was analyzed for progesterone concentrations and the duration of postpartum anestrus was calculated as 7 d before progesterone concentrations in weekly samples were indicative of normal luteal function. Statistical analyses were performed separately for mature and 2y cows. Length of postpartum anestrus was shorter ($P < 0.05$) in age- (least squared mean [LSM]; 81.0 ± 2.0) than age+ (LSM; 88.1 ± 2.2) mature cows, whereas, no difference was detected in 2y cows (92.6 ± 3.5). Objective 2 was to compare follicular wave dynamics during the postpartum anestrus between a subset of age- (mature; n = 11, 2y; n = 4) and age+ (mature; n = 11, 2y; n = 4) cows used for objective 1. Beginning approximately 30 d postpartum, ovarian ultrasonography was conducted daily until a complete follicular wave from each animal was recorded. More ($P < 0.05$) follicles emerged at initiation of this wave in the age+ (15.9 ± 1.4) than the age- (12.3 ± 1.2) cows. However, number of d from emergence to maximum diameter of the dominant follicle (5.8 ± 0.2), maximum diameter of the dominant follicle (14.6 ± 0.4 mm), and length of the follicular wave (7.9 ± 0.2 d) did not differ between genetic lines. In conclusion, long-term, divergent selection for age at puberty resulted in variation in duration of postpartum anestrus between the genetic lines.

Key Words: puberty, beef cattle, genetic selection

690 Liver transcript profiles due to prepartum dietary energy level and bacterial lipopolysacharide challenge in dairy cows early postpartum. D. E. Graugnard*, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, J. K. Drackley, and J. J. Loor, *University of Illinois*, *Urbana*.

Immunosuppression renders cows highly susceptible to mastitis pathogens as well as metabolic diseases after parturition. We hypothesized that plane of dietary energy pre–partum can affect tissue response to inflammatory challenges through changes in gene expression. Twenty–eight Holstein cows with average composite SCC of ~128,000 in the previous lactation were assigned (n = 14/diet) to a control (high–straw; NE_L = 1.52 Mcal/kg) or moderate–energy (ME; NE_L = 1.64 Mcal/kg) diet during the entire dry period. All cows were fed a common lactation diet (NE_L = 1.69 Mcal/kg) postpartum. At 7 DIM, cows (n = 7/prepartum diet) were assigned to receive an intramammary bacterial lipopolysacharide (LPS) challenge (200 µg) in one rear mammary quarter or served as controls. Cows used were bacteriologically–negative in all mammary quarters. A percutaneous liver biopsy was collected at 2 h post–LPS challenge for transcript profiling using a 13,257 annotated bovine oligonucleotide microarray. LPS challenge of cows fed ME prepartum resulted in >140 differentially expressed genes (DEG; $P < 0.01$). The most–enriched biological functions among DEG were regulation of biological process (n = 34) and programmed cell death (n = 18). Genes identified are associated with inflammatory response (e.g. *S100A12*), chemotaxis (e.g. *CXCL2*), and phagocytosis (e.g. *RBED1*) as well as neutrophil apoptosis (e.g. *IFNG*). In the comparison of ME vs. control–fed cows receiving LPS postpartum there were >30 DEG due to prepartum diet. Among the most enriched biological functions were regulation of biological process (n = 10 genes), response to toxin (n = 9 genes), and immune response regulation (e.g. *IL10, ARNT2, IL1R2*). Results showed that a mammary inflammatory challenge early postpartum caused rapid alterations in liver gene expression profiles. However, the hepatic transcriptomic response to inflammation was not greatly affected by prepartum dietary energy level.

Key Words: transcriptomics, inflammation, mastitis

691 Heat stress abatement for dry cows: Does cooling improve immunity status? B. C. do Amaral, S. Tao*, J. Bubolz, J. Hayen, and G. E. Dahl, *University of Florida*, *Gainesville*.

Heat stress during lactation and the dry period reduces milk production of dairy cows. Emerging evidence suggests that heat stress may influence immune status as well. The objective of the study was to evaluate the effect of heat stress prepartum on cellular immune function of periparturient Holstein cows (n=21). Cows were dried off 46 d before expected calving date and assigned to treatment by mature equivalent milk production. The treatments were: 1) Heat stress (HT) and 2) Cooling (CL). Both treatments had a photoperiod of (14L:10D). Rectal temperature was measured 2X daily whereas respiration rate was measured 3X weekly at 1500h during the dry period. After calving, cows were housed in freestalls with cooling, and milk yield was recorded daily up to 140 DIM. Neutrophil function and lymphocyte proliferation were measured in blood collected at dry off, -20, +2, and +20 d relative to calving and production of cytokines (IFN-γ, IL-4, IL-6, and TNF-α) on postpartum samples for cows on HT (n=12) and CL (n=9). HT cows produced less 3.5% FCM (30.8 vs. 35.7 kg/d: $P = 0.07$) and had greater afternoon rectal temperatures (39.4 vs. 39.0°C; $P < 0.01$) and respiration rates (78 vs. 56 respirations/min; $P < 0.01$) during the prepartum period compared with CL cows. Relative to HT cows, lymphocytes had less proliferation (45 vs. 169% of baseline; $P < 0.05$) in CL cows. Lymphocyte production of IFN-γ (69 vs. 52 ng/mL), IL-4 (406 vs. 265 pg/mL), and IL-6 (5 vs. 5 ng/mL) did not differ ($P > 0.05$) among treatments. However, TNF-α production was lower (27 vs. 70 pg/mL; $P < 0.05$) for lymphocytes from HT cows compared to CL cows. Neutrophil phagocytosis (61 vs. 42% and 62 vs. 49% for 2 and 20 DIM, respectively) and oxidative burst (47 vs. 33% and 52 vs. 36% for 2 and 20 DIM, respectively) were greater for CL cows at 2 and 20 DIM compared to HT cows (treatment by DIM interaction; $P < 0.05$). These results supports the concept that heat stress abatement in the dry period increases milk production and improves immune status in the subsequent lactation.

Key Words: heat stress, dairy, immune status

692 Association between seasonality, cleavage timing and gene expression in bovine oocytes. Z. Roth* and M. Gendelman, *Faculty of Agriculture, The Hebrew University of Jerusalem, Israel*.

Developmental competence of bovine oocytes is known to decrease during the hot season. It includes reduced ability to undergo maturation and fertilization, to cleave and to develop to a healthy embryo. The aim of the study was to examine whether seasonal induced alteration is associated with variations in oocyte genes expression. Bovine oocytes were aspirated from ovaries collected from a local slaughterhouse during the hot (Jun-Sep) and cool (Dec-May) seasons. Oocytes were in-vitro matured, fertilized, and cultured (KSOM) for 8 days. The proportion of oocytes cleaved into 2- and 4-cell stages and developed to blastocysts was assessed at 27h, 42-44h and 8 days post-fertilization (PF), respectively. Data was analyzed by one way ANOVA (JMP-6; SAS) followed by student t-test. In each season (4 replicates) and for each developmental stage, samples of 2-, 4-cell stage embryos and blastocyst (n=10, 5, and 3, respectively) were collected. Total RNA was isolated using 500 µl Trizol reagent, cDNA was generated using M-MLV reverse transcriptase (1 h; 42°C) and qPCR was carried out with primers for GDF9, POU5F1, C-MOS and GAPDH using 18S as reference genes and analyzed (MxPRO QPCR). The percentage of embryos developed to the blastocyst stage was higher in the winter than in the summer (23 ± 2.3 vs. 9 ± 3.5%, respectively; P<0.05). The average cleavage rate to the 2- to 4-cell stage (44h PF) did not differ between seasons. However, the proportion of 2-cell stage in the summer was two fold higher than that of 4-cell, suggesting a delayed cleavage. Examination of gene expression in both early (27h PF) and late (42h PF) first-cleaved embryos revealed that the expression of GDF9 and POU5F1 was lower in late- than in early-cleaved embryos in both seasons. At the 4-cell stage embryos (48h PF), opposite patterns were noted between seasons, with decreased expression of GDF9 in the winter and of POU5F1 in the summer. Findings suggest that seasonality has a deleterious effect on the ovarian pool of oocyte as reflected by delayed cleavage and reduced blastocyst formation in association with variation in gene expression.

Key Words: seasonality, oocyte competence, cleavage timing

693 Cytochrome P450 activity, liver blood flow and progesterone clearance in dairy cows fed a high starch versus a high fiber diet. C. O. Lemley*[1], K. A. Vonnahme[2], K. M. Krause[1], and M. E. Wilson[1], [1]*West Virginia University, Morgantown*, [2]*North Dakota State University, Fargo*.

Elevated rates of steroid clearance may lead to lower reproductive success in dairy cows. We have recently demonstrated an insulin induced decrease in the activities of the progesterone catabolic enzymes, cytochrome P450 2C and 3A. The current objectives were to determine liver blood flow, cytochrome P450 activity and metabolic clearance rate of progesterone in dairy cows consuming isoenergetic diets formulated to cause divergent insulin secretion. Holstein dairy cows (n = 11) were randomly assigned to a high starch or high fiber diet in a cross-over experimental design consisting of two 14 d periods. Dry matter intake (25.7 ± 0.7 kg/d), milk yield (38.4 ± 1.4 kg/d) and milk lactose yield were not different between the two diets (P > 0.51). Milk protein yield tended (P = 0.06) to be elevated in cows fed the high starch diet, while milk fat yield was elevated (P < 0.01) in cows fed the high fiber diet. Energy balance was improved (P = 0.03) in cows fed the high starch diet. Insulin concentrations over the 10 h sampling period were increased (P = 0.01) by 22% in cows fed the high starch diet, and both cytochrome P450 2C (P = 0.01) and cytochrome P450 3A (P = 0.03) activities were decreased by 50%. Liver blood flow was not different (P = 0.47) between the two diets (1891 ± 91 l/h). Metabolic clearance rate of progesterone tended (P = 0.06) to be lower in cows fed the high starch diet (25 ± 5 l/h*$BW^{0.75}$) versus the high fiber diet (40 ± 6 l/h*$BW^{0.75}$). The half-life of progesterone was increased (P = 0.01) in cows fed the high starch diet (73 ± 10 min) versus the high fiber diet (24 ± 10 min). In summary, cows with elevated insulin concentrations and lower enzyme activity showed a decrease in progesterone clearance without any changes in liver blood flow, dry matter intake or milk yield. This relationship between insulin and enzyme activity may be a useful approach to decrease high rates of progesterone clearance during pregnancy.

Key Words: insulin, cytochrome P450, progesterone clearance

694 The effect of high and low dos doses of naloxone on the ovulation rate of Suffolk ewes during the breeding season. V. O. Fuentes*, A. Bernal-Canseco, and P. I. Fuentes-Castro, *Centro Universitario de los Altos Universidad de Guadalajara, Tepatitlan, Jalisco, Mexico*.

In previous work it was observed that the administration of low doses of naloxone in the ewe facilitated the expression and duration of estrus. It was considered of interest to study the effect of naloxone in high and low doses on the ovulation rate of Suffolk ewes during the breeding season. During the breeding season of November 2007, 60 ewes were selected from an intensive ovine herd, and allocated at random in to three groups. Group A (n = 20) received an intravaginal sponge with 40 mg of medroxiprogesterona acetate (MAP) for 14 days and since one day before and two days after the sponges were withdrawn, all ewes of this group received an im injection of 2 ml of saline solution at 12 hrs intervals. Group B (n = 20) was treated as ewes of group A but one day before and two days after sponge withdrawal a naloxone iv infusion of 1 mg/kg in saline solution was administered at 12 hrs intervals. Group C (n = 20) was treated as group A, and since one day before and three days after sponge withdrawal they were injected im at 12 hrs interval with 0.5 mg naloxone in saline solution. Between 6 and 10 days after estrus was displayed laparoscopy was carried out under ketalar/xilazine anesthesia and ovulation rate was noted. Ovulation rate in ewes of Group A was 1.8 ± .3, and in ewes of group B ovulation rate was 1.9 ± .5. In ewes of group C ovulation rate was 2.9 ± .6. The statistical analysis showed a high degree of significance when comparing groups C with groups A and B (p< 0.01). Naloxone administered in low doses was more effective to induce an increase in ovulation rate. It was concluded that endogenous opioids are important modulators of reproductive behavior and ovulation in Suffolk ewes.

Key Words: naloxone, ewe, ovulation

695 Tumor necrosis factor alpha increases triglyceride content and alters transcript abundance of metabolic genes in the liver of lactating dairy cattle. B. J. Bradford*, L. K. Mamedova, J. E. Minton, J. S. Drouillard, and B. J. Johnson, *Kansas State University*, *Manhattan*.

Recent data have shown that bovine fatty liver is associated with inflammation, but a causative role of inflammatory mediators has not been demonstrated. To determine whether inflammation can induce fatty liver, recombinant bovine tumor necrosis factor alpha (TNF) was administered to late-lactation Holstein cows in a randomized complete block design. Cows (n = 5 per treatment) were blocked by feed intake and milk production and randomly assigned within block to control (saline), TNF at 2 μg/kg per d, or pair-fed control (saline, intake matched) treatments. Treatments were delivered once daily by subcutaneous injection for 7 d. Plasma samples were collected daily for analysis of glucose and non-esterified fatty acids (NEFA) and a liver biopsy was collected on d 7 for triglyceride (TG) and quantitative real-time PCR analyses. Data were analyzed with mixed models using treatment contrasts to assess effects of TNF administration and decreased feed intake. By d 7, feed intake and milk production decreased by 15% and 12%, respectively, for both TNF and pair-fed cows compared to controls. TNF administration significantly increased hepatic TNF mRNA and protein abundance and increased liver TG content by 103% ($P < 0.05$) without affecting plasma NEFA concentration. TNF tended to decrease hepatic carnitine palmitoyltransferase 1 and increase fatty acid translocase (CD36) and 1-acyl-glycerol-3-phosphate acyltransferase transcript abundance (all $P < 0.10$), effects which are consistent with increased NEFA uptake and storage as TG. TNF also decreased transcript abundance for glucose-6-phosphatase ($P = 0.02$) and phosphoenolpyruvate carboxykinase 1 ($P = 0.09$), genes important for gluconeogenesis. Plasma glucose concentration was not affected by treatment. These findings indicate that TNF promotes liver TG accumulation and suggest that inflammatory pathways may also be responsible for decreased glucose production in cows with fatty liver.

Key Words: fatty liver, tumor necrosis factor, inflammation

696 Effects of feeding colostrum on somatotoropic axis, metabolic traits and vital signs of Holstein bull calves. D. Qadimi, A. Zare Shahne, A. Nikkhah, M. Moradi, and R. Masoumi*, *University of Tehran*, *Iran*.

Bovine colostrum contains various essential nutrients, antibodies, hormones, growth factors and antimicrobial peptides (e.g. Lactoferrin, and Lactoperoxidase) that are important for nutrient supply, host defense, growth and for general neonatal adaptation. In this study, effects of colostrum fed for different durations on somatotropic axis, selected metabolic traits, plasma levels of growth hormone and vital sings in the first week of life in calves were examined. Holstein bull calves (n = 18) with mean body weight of 44.6 kg were randomly assigned into three treatment groups and fed colostrum twice daily for 3d (group GrC6) or colostrum only as their first meal (group GrC1) followed by milk replacer up to day 7, or they received only milk replacer but no colostrum (group GrM). Blood samples were taken on days 1,2 and 7 of experiment five minutes before and 0.5, 2, 4 and 7 h after feeding colostrum. Plasma glucose, urea, creatinine and GH were measured. Data were analyzed by Proc GLM of SAS. Postprandial plasma glucose concentration on day 2 increased significantly ($p<0.05$) in groups GrC6 and GrC1 in compare with group GrM and remained elevated up to day 7. Plasma urea concentration on day 1 decreased significantly ($p<0.01$) in groups GrC6 and GrC1 than in group GrM and remained lowered up to day 7. There was not any significant difference in plasma creatinine ($p<0.05$) concentration between treatment groups. Plasma GH concentration was not changed by feeding different levels of colostrum ($p<0.05$) but there was a increasing trend in plasma GH in GrC6. Calves fed colostrums had significantly higher($p<0.01$) rectal temperatures, heart rates and respiratory frequencies than calves provided by milk replacer. The somatotrophic axis is basically functioning in neonatal calves and may be influenced by nutrition. Furthermore, significantly higher circulating glucose and lower Urea levels in calves fed colostum compared with those fed milk replacer, stimulated anabolic processes.

Key Words: colostrum, metabolism, calves

697 Continuously infused obestatin increased pancreatic β-cell function in response to an intravenous glucose tolerance test. J. R. Roche*[1], A. J. Sheahan[1], L. M. Chagas[1], J. K. Kay[1], and R. C. Boston[2], [1]*DairyNZ*, *Hamilton, NZ*, [2]*University of Pennsylvania*, *Kennett Square*.

At 20 DIM, 51 cows were randomly allocated to one of three treatment groups; a control (CONT) or a group continuously infused with either 0.74 μmol/d of ghrelin (GHRE) or obestatin (OBE) subcutaneously for 8 wk. During wk 5, cows were subjected to an intravenous glucose challenge (300 mg D-glucose/kg BW). Plasma glucose, insulin, NEFA, growth hormone (GH), and ghrelin concentrations were measured prior to glucose infusion and at regular intervals following infusion. Bergman's Minimal Model (MINMOD) and Boston's NEFA model were fitted to each subject's glucose challenge response, and model outputs, area under the curve, peak or nadir concentration, and profile slopes from each hormone/metabolite compared statistically. All treatments exhibited the previously published characteristic post-infusion profiles in plasma glucose, insulin, ghrelin, NEFA, and GH. However, OBE cows produced 50% more ($P< 0.01$) insulin in response to the glucose infusion than either the CONT or GHRE cows (peak insulin at 10 min post-infusion was 22 ± 3.0, 20 ± 1.8, and 35 ± 3.4 μU/mL in CONT, GHRE, and OBE cows, respectively; mean ± SEM). They also had a correspondingly lower nadir plasma NEFA (0.51 ± 0.059, 0.60 ± 0.032, and 0.35 ± 0.033 mmol/L in CONT, GHRE, and OBE cows, respectively), and produced more GH than either GHRE or CONT cows in response to the insulin-mediated decline in blood glucose and NEFA (peak GH 40 to 50 min post-infusion was 7.3 ± 1.10, 10.0 ± 1.53, and 13.2 ± 2.22 ng/mL in CONT, GHRE, and OBE cows, respectively). Model outputs confirm an obestatin effect on insulin and NEFA. The volume of insulin available for glucose disposal (AIRg: a proxy for pancreatic β-cell function) in MINMOD was 45 and 89% greater in OBE cows compared with CONT and GHRE cows, respectively ($P< 0.01$). Boston′s NEFA model highlighted that OBE cows had lower baseline NEFA, and this resulted in a lower nadir NEFA; data imply an effect of obestatin on pancreatic β-cell function, and a corresponding effect on lipid metabolism.

Key Words: glucose tolerance test, ghrelin, obestatin

698 Residual feed intake and heat production of Holstein cows throughout lactation. A. Brosh*[1], A. Asher[1], J. Miron[2], A. Shabtay[1], G. Adin[3], U. Moalem[2], Y. Aharoni[1], and A. Arieli[4], [1]*Agricultural Research Organization*, *Ramat Yishay, Israel*, [2]*Agricultural Research Organiza-*

tion, *Bet-Dagan, Israel*, [3]*Extension Service, Ministry of Agriculture, Bet-Dagan, Israel*, [4]*Hebrew University of Jerusalem, Faculty of Agricultural*, *Rehovot, Israel*.

Serial measurements of cows' individual intake, milk energy, and heat production (HP) using the heart rate Oxygen Pulse method, were obtained from weeks 1 to 11 of lactation (WEL) for 63 Holstein cows, and continue up to WEL 35 for 53 cows. Cows' residual ME feed intake (RFIme, the actual ME intake (MEI) minus the expected MEI, MEIex) were calculated. Similarly cows' residual HP (RHP, the measured HP minus the expected HP, HPex) was calculated. All energy transformation calculations were based on NRC (2001) equations. Dietary NEl concentrations, based on tabular values and not adjusted for level of intake, were 26% higher than the actual dietary NEl based on in vivo measurements of digestibility. Adjusting the tabular dietary NEl concentration for level of intake reduced the magnitude of this overestimation (above the in vivo concentration) by 14.6%, but after this adjustment the calculated dietary NEl concentration was still 8% higher than the NEl concentration based on in vivo digestibility. Milk production in week 1 was 26.8±1 (SE) L/d, 25±0.6 Mcal/d, reached a peak of 55.1±0.9 (L/d), 35.60.5 Mcal/d in WEL 6 and decreased to 36.4±0.8 (L/d), 26.7±0.5 Mcal/d in WEL 35. Cows` BW (kg) and BCS (scale of 1-5) in the first WEL were respectively 658 and 2.98, decreased to the lowest values of 612 and 2.64 in WEL 6 and increased up to 625 and 2.71 in WEL 35. The average MEI (Mcal/d; based on in vivo digestibility) were 41±1 in WEL 1, reached a peak of 64±1 in WEL 11, and decreased to 56±6 in WEL 35. The in vivo values of NEl and ME were used to calculate RFIme and RHP (Mcal/day) for all individual cows. Unexpectedly, a trend of changes was calculated in the RFIme and in the RHP of the weeks' average (N=35), a quadratic regression of RFIme = -0.0061WEL^2^ +0.3272 WEL-1.5155, R^2^= 0.312, (P<0.001) and of RHP = -0.0109WEL^2^+0.3849WEL-5.3623, R^2^=0.285, P<0.001. RHP was positively correlated to the cows` HP (R^2^=0.67, P<0.001). It can be concluded that the tested cows were less efficient than expected according to NRC (2001), and that coefficients of transforming MEI to energy in milk may not be constant during lactation.

Key Words: cow, lactation, efficiency

699 IGF-1 concentrations following sustained release growth hormone treatment in ewes. T. A. Wilmoth*, J. M. Koch, C. O. Lemley, and M. E. Wilson, *West Virginia University*, *Morgantown*.

Low birth weight lambs have higher mortality rates in the first few days following birth than normal birth weight lambs. Treatment of ewes with growth hormone (GH) around the time of conception increases birth weight of lambs, therefore increasing their chance of survival. Treatment of ewes with GH at the time of conception does not cause a difference in the number of cells in the trophectoderm or inner cell mass of the embryo compared to embryos from control ewes. However, treatment of ewes with GH caused an increase in placental efficiency compared to control ewes, which may indicate prolonged alterations in uterine environment. Growth hormone causes an increase in insulin like growth factor-1 (IGF-1), which increases cell growth and somatostatin production, but causes a decrease in growth hormone releasing hormone and GH. Concentrations of IGF-1 in the serum are correlated to the concentration of GH at peak amplitude. The objective of this experiment was to determine the effective duration of sustained release GH using IGF-1 as a proxy for GH. Ewes were synchronized with 2 prostaglandin injections 8 days apart and penned with a fertile ram. At the time of the second injection, rbST (Posilac) was administered and a blood sample collected (week 0). Jugular blood samples were collected weekly and plasma was used for determining IGF-1. For weeks 1, 2, 3 and 4, treated ewes had an increased IGF-1 concentration compared to control ewes (3, 5, 4 and 2.5-fold, respectively). By week 8, control and treated ewes had similar concentrations of IGF-1. Periconceptional treatment with sustained release GH causes IGF-1 to remain elevated for the first half of gestation, potentially altering the uterine environment during a crucial developmental period. The timing of the elevation in IGF-1 following periconceptional GH treatment leads us to suggest that its effect on birth weight is mediated by a change in placental function as IGF-1 concentrations are similar in control and treated ewes during the second half of gestation in which the fetus will undergo the most growth.

Key Words: growth hormone, IGF-1, fetal programming

700 Transcriptional adaptations in mesenteric and subcutaneous adipose tissue from non-lactating cows in response to plane of dietary energy. M. Mukesh, J. K. Drackley, P. Ji*, M. Bionaz, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, and J. J. Loor, *University of Illinois*, *Urbana*.

The transcriptional machinery of cow adipose tissue depots and the role of dietary energy on gene networks remain poorly characterized. Effects of moderate excess (M) or low dietary energy (L) on mesenteric (MES) and subcutaneous (SubQ) adipose tissue transcript profiles were assessed in 10 non-pregnant dry cows. Cows were assigned to either an M (NE_L = 1.61 Mcal/kg) or L (NE_L = 1.37 Mcal/kg) diet for 8 wk. The M diet contained 74.5% (DM basis) forage without straw, while the L diet contained 84.6% forage including 41.9% wheat straw and met cow NE_L requirements at ad libitum DMI. At slaughter, SubQ and MES were sampled and used for microarray analysis using a 13,000 annotated bovine oligonucleotide microarray. Cows fed M had greater MES weight. Statistical analysis (FDR $\leq$ 0.2; unadjusted $P < 0.007$) revealed 427 and 312 differentially expressed genes (DEG) due to tissue site and diet. Pathway analysis showed that the most-enriched functions among DEG between tissues were cellular growth (greater in MES), synthesis and accumulation of lipid (greater in MES), and transcription regulation (e.g. NFκB binding site activation, greater in MES). Network analysis among DEG higher in MES suggested a central role of CCAAT/enhancer binding protein beta (CEBPB). Among DEG due to energy intake were several involved in cell viability (greater in L), development of leukocytes (greater in M), cytostasis of connective tissue (greater in M), and activation and binding of cells (both immune and non-immune; greater in M). Pathways of synthesis and sensitivity to growth factors (FGF, HGF) as well as sphingolipid synthesis had more DEG with M than L. Most DEG due to energy intake level were involved in response to stimulus (e.g., immune response; greater in M) and components of protein complex (e.g., translation; greater in L). Glucocorticoid receptor (GRLF1) and E2F transcription factor 7 (E2F7) were the transcription factors most affected by dietary energy. Results provide evidence of adipose site-specific and energy-responsive transcriptomic signatures.

Key Words: genomics, overnutrition, lipogenesis

701 Effect of plane of nutrition and feed deprivation on insulin responses in dairy cattle during late gestation. K. M. Schoenberg*, R. M. Ehrhardt, and T. R. Overton, *Cornell University*, *Ithaca, NY*.

Nonlactating Holstein cows (n=12) in late pregnancy were used to determine effects of plane of nutrition followed by feed deprivation on

responses to insulin. Beginning 48±4.5 d prior to calving, cows were fed either a high (H) or low (L) diet to meet 139 and 84% of calculated energy requirements, respectively. Cows were subjected to an intravenous glucose tolerance test (GTTa; 0.25 g dextrose/kg BW) on d 14 of treatment and a hyperinsulinemic-euglycemic clamp (HECa; 1μg/kg of BW/h) on d 15. Following a 24 h fast, cows were subjected to GTTb on d 17 and HECb on d 18. During the feeding period, NEFA were higher for cows fed L vs. H (73.1, 163.6 μEq/L; P<0.001). For all cows, glucose was lower after 48 vs. 24 h of fasting (54.6, 67.6 mg/dL; P<0.001) but NEFA were higher (792.6, 219.3 μEq/L; P<0.02). Glucose area under the curve (AUC) across both GTT were higher for cows fed L than cows fed H (5437, 4532 mg/dL x 180 min; P <0.04) and was higher during GTTb (6778, 3192; P<0.001) than GTTa, suggesting slower clearance of glucose during negative energy balance either pre- or post-fast. This corresponded with a higher dextrose infusion rate during HECa than HECb (203.3, 90.1 ml/hr; P = 0.001). Plasma NEFA decreased at a faster rate during GTTb than GTTa (-22.5, -4.8 μEq/L*min; P<0.001). NEFA suppression was highest for cows on the L diet during GTTb, and lowest for cows fed H during GTTa (68.6, 50.3 μEq/L; P = 0.07). Cows fed L had greater NEFA AUC than those fed H (-48726, -26068 μEq/L x 180 min; P< 0.02), as did cows during GTTb vs. GTTa (-64016, 10778 μEq/L x 180 min; P<0.001). During HECa, NEFA were 21% below basal for cows fed the H diet, 69% below basal for cows fed the L diet and NEFA were 88 and 66% below basal respectively during HECb (treatment x HEC; P<0.001). These results suggest that cows fed below energy requirements or feed-deprived have slower clearance of glucose and larger NEFA responses to glucose challenge; overall, effects of feed deprivation were larger than plane of nutrition.

Key Words: insulin clamp, glucose tolerance test

702 The acute phase response: Differentiating corticotrophin-releasing hormone (CRH)- versus lipopolysaccharide (LPS)-induced proinflammatory cytokine and acute phase protein profiles in beef calves. J. A. Carroll*[1], L. E. Hulbert[1], N. C. Burdick[1,2], L. C. Caldwell[2,3], M. A. Ballou[4], J. D. Arthington[5], R. C. Vann[6], A. N. Loyd[2,3], T. H. Welsh, Jr.[2], and R. D. Randel[3], [1]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX*, [2]*Texas AgriLife Research, Texas A&M System, College Station*, [3]*Texas AgriLife Research Center, Texas A&M System, Overton*, [4]*Department of Animal and Food Sciences, Texas Tech University, Lubbock*, [5]*University of Florida - IFAS, Range Cattle Research and Education Center, Ona*, [6]*MAFES, Mississippi State University, Raymond*.

Development of methods to effectively attenuate potentially detrimental effects of various stressors encountered by livestock depends on understanding unique stressor-specific responses. The objective of this study was to profile indicators of the acute phase immune response to compare and contrast potential differences between CRH- and LPS-induced stress responses. Purebred Brahman bull calves (n = 11; 226.9±12.6 kg) were transported 770 km from Overton, TX to Lubbock, TX and fitted with indwelling jugular catheters after 24 h of rest. Twenty-four h afterwards, blood samples were collected at 30-min intervals from -2 to 8 h, and again at 12 and 24 h, relative to an i.v. infusion of either LPS (0.25 μg/kg BW) or CRH (0.5 μg/kg BW) at 0 h. Serum was stored at -80°C until analyzed for tumor necrosis factor-alpha (TNF-α), interleukin 6 (IL-6), interferon gamma (IFN-γ) and haptogolobin (Hp). Compared to pre-challenge concentrations, CRH induced a single peak in serum TNF-α starting at 2.5 h (P≤0.01) and lasting until 4 h (P≤0.07) whereas LPS induced a biphasic response beginning at .5 h (P≤0.04) with peaks at 1.5 and 3.5 h, and lasting until 7.5 h (P≤0.01). For IL-6, CRH induced a single peak beginning at 3 h (P≤0.01) and only lasting for .5 h. In contrast, LPS induced a biphasic IL-6 response beginning at 1.5 h (P≤0.01), peaking at 2.5 h and 6 h, and lasting until 12 h (P≤0.03). For IFN-γ, CRH induced a single peak at 3 h (P≤0.01), beginning at 2.5 h (P≤0.07) and lasting until 3.5 h (P≤0.01). LPS induced a multiphasic IFN-γ response beginning at .5 h (P≤0.01) and lasting until 24 h (P≤0.01) with peaks at 2.5, 3.5 and 6 h. For Hp, CRH-induced a single spike at 4 h (P≤0.02) that had ended by 6 h (P≥0.14) whereas LPS induced Hp concentrations continued to escalate even at the 24 h time period (P≤0.01). These data demonstrate that the stress response in beef calves either simulated by CRH or induced by endotoxin is comprised of specific immunological profiles that may be as unique as the stressor itself.

Key Words: cattle, immunity, stress

703 Fibroblast growth factor 21 (FGF21) expression is increased in hepatic tissue of feed-restricted cows and during the transition from pregnancy to lactation. K. J. Harvatine*[1] and Y. R. Boisclair[2], [1]*Penn State University, University Park*, [2]*Cornell University, Ithaca, NY*.

Fibroblast growth factor 21 (FGF21) is a recently discovered hormone that is induced in liver during fasting. FGF21 promotes adaptations to the fasted state, including coordination of hepatic oxidation of free fatty acids with their mobilization from adipose tissue. Interestingly, exogenous administration of FGF21 reduced hepatic triglyceride concentration and improved insulin sensitivity in obese mice. Our objective was to determine if FGF21 is regulated similarly in the cow. To investigate the role of FGF21 in regulation of energy homeostatis in the dairy cow we measured hepatic FGF21 expression in liver during positive and negative energy balance. First, liver biopsies were collected from five non-pregnant late-lactation cows when fed 120% of energy requirement or restricted to 30% of maintenance requirement. Statistical analysis included the random effect of cow and the fixed effect of treatment. Feed restriction resulted in a 37 fold increase in hepatic FGF21 expression compared to control (P<0.001). Secondly, liver biopsies were collected from ten cows during the transition from pregnancy to lactation. Statistical analysis included the random effect of cow and the fixed effect of stage of lactation. Hepatic FGF21 expression was increased over 10 fold 8 d after parturition compare to 28 d prior to calving (P = 0.001). Feed restriction and the transition to lactation resulted in a large negative energy balance, increased adipose tissue mobilization, and increased plasma NEFA concentration. Hepatic FGF21 synthesis may play a determinant role in regulating the rate of utilization of lipid reserves in energy-deficient dairy cows.

Key Words: FGF21, transition cow

704 Expression of thyroid hormone responsive spot 14 and a homologous protein (MIG12) are dynamically regulated in adipose tissue of dairy cows during modification of energy balance. K. J. Harvatine*[1], Y. R. Boisclair[2], and D. E. Bauman[2], [1]*Penn State University, University Park*, [2]*Cornell University, Ithaca, NY*.

Thyroid hormone responsive spot 14 (S14) and MID1 interacting protein 1 (MIG12) share sequence homology and may encode proteins with redundant function, although a specific biochemical function of their gene products is not clear. Regulation of S14 is well described in other species where it is predominantly expressed in lipogenic tissue and dynamically altered by transcriptional regulation under dietary conditions affecting energy balance. Expression and regulation of MIG12 has not been well described. Our objective was to characterize

the metabolic responsiveness of S14 and MIG12 in the bovine using real-time RT-PCR. Our initial study compared the expression of S14 and MIG12 in a panel of 9 tissues collected from lactating dairy cows. S14 was predominantly expressed in adipose tissue and moderately expressed in liver, mammary tissue, and skeletal muscle. MIG12 was predominantly expressed in skeletal muscle and moderately expressed in adipose tissue and liver. Next, we investigated the regulation of S14 and MIG12 in the adipose tissue of dairy cows experiencing periods of positive and negative energy balance. Firstly, adipose tissue biopsies were collected from five non-pregnant late-lactation cows when fed 120% of energy requirement or restricted to 30% of maintenance requirement. Feed restriction resulted in over a 90% and 78% decrease in the expression of S14 and MIG12, respectively ($P = 0.02$ and $P < 0.01$). Secondly, adipose tissue biopsies were collected from ten cows during the transition from pregnancy to lactation. Expression of both S14 and MIG12 was decreased over 95% by 8 d postpartum as compared to 28 d prepartum (both $P < 0.001$). Overall, results indicate both S14 and MIG12 are responsive to energy status and that the induction of a negative energy balance, whether by feed restriction or the transition from pregnancy to lactation, results in a down regulation in the expression of S14 and MIG12 in adipose tissue.

Key Words: S14, MIG12, ;ipogenesis

705 TNFα and factors related to insulin signaling in adipose tissue of dry- and early lactating dairy cows. H. Sadri[1,2], A. van Dorland[1], G. R. Ghorbani[2], H. R. Rahmani[2], and R. M. Bruckmaier*[1], [1]*University of Bern, Vetsuisse Faculty, Veterinary Physiology*, *Bern, Switzerland*, [2]*Isfahan University of Technology, Department of Animal Science*, *Isfahan, Iran*.

This study was conducted to clarify the mechanisms of insulin resistance in adipose tissue during late gestation and early lactation in dairy cows. The mRNA expression of TNFα, insulin receptor (INSR), insulin receptor substrates (IRS1 and IRS2), regulatory (p85) and catalytic subunit of PI-3 kinase (p110), insulin independent (GLUT1) and responsive (GLUT4) glucose transporters in adipose tissue was measured by real-time RT-PCR, and their relationship with plasma NEFA concentrations was evaluated. Biopsies from subcutaneous fat were taken at the tail head from 30 dairy cows in wk 8 antepartum (a.p.), on d 1 postpartum (p.p) and in wk 5 p.p.. Blood samples were collected every two weeks. The mRNA abundance of TNFα was higher ($P < 0.05$) during p.p. compared to that in a.p. The mRNA encoding for GLUT1 and GLUT4 on d 1 p.p. was lower ($P < 0.05$) compared to the other time-points. There was a trend ($P = 0.09$) for increased mRNA abundance of INSR in p.p. relative to a.p., and decreased mRNA abundance of IRS1 on d 1 compared to wk 5 p.p. The mRNA encoding for IRS2, p85 did not change over time. A tendency ($P<0.15$) was observed for a negative correlation between plasma NEFA concentration and GLUT4 mRNA abundance in wk 8 a.p., and on d 1 p.p. There was a trend ($r = 0.30$, $P = 0.11$) for a positive correlation between TNFα mRNA abundance and plasma NEFA concentration in wk 5 p.p.. Results show a local role for adipocyte-derived TNFα, and suggest its contribution in adaptation of adipose tissue towards catabolism. Down regulation of GLUT4 expression may be involved in insulin resistance shortly after calving, and may be mediated in part by TNFα and elevated NEFA concentration. The slight decrease in mRNA abundance of IRS1 on d 1 compared to wk 5 p.p. may show an involvement of IRS1 in insulin resistance at the onset of lactation. Changes in gene expression of INSR, IRS2 and p85 show no involvement in promoting insulin resistance in adipose tissue of dairy cows.

Key Words: TNF, adipose tissue, cow

706 Differential effects of propionate on mRNA abundance of adiponectin receptors and G protein-coupled receptor GPR41 in bovine subcutaneous and perirenal adipose tissue explants *in vitro*. A. Hosseini*, H. Sauerwein, and M. Mielenz, *University of Bonn*, *Bonn, Germany*.

Ruminants entirely depend on the ruminal production of short-chain fatty acids (SCFA) as the main energy source. The SCFA propionate (C3) is an important stimulus to insulin secretion in ruminants. Insulin (100 nM) increases leptin mRNA in bovine adipose tissue (AT) explants (1). C3 activates members of the family of fatty acid binding receptors, e.g. GPR41, which in turn stimulates leptin mRNA in mice (2). In goats, we have previously demonstrated that C3 differentially increases the mRNA abundance of putative GPR41 in subcutaneous (SC) and perirenal (PR) AT *in vivo*. The adiponectin system improves insulin sensitivity in monogastrics but less is known about the situation in ruminants. Therefore, we established an AT explant model for both SC and PR for characterizing the response of the adiponectin receptors (AdipoR1 and AdipoR2) mRNA to C3 *in vitro*. SC and PR AT were obtained from 7 slaughtered Holstein Friesian cows. The tissue was incubated 4 h in basal medium (DMEM/Ham's F-12 with L-Glutamine) or in medium supplemented with either 100 nM insulin or with 0.5, 1, 2, or 3 mM C3. The mRNA of AdipoR1, AdipoR2 and GPR41 was quantified by real-time-PCR. The data were analyzed using the Paired-samples t-test ($P\leq0.05$; trend: $P\leq0.11$). C3 significantly, or as a trend, increased the mRNA expression of AdipoR1 and AdipoR2 dose dependent only in SC AT explants. No influence of C3 on the mRNA of GPR41 was observed. Insulin did not influence the mRNA expression of AdipoR1 and AdipoR2, but a trend was observed for GPR41 in SC AT. Our results indicate that short-term C3 treatment *in vitro* affects AdipoR1 and AdipoR2 mRNA only in SC AT which might increase glucose uptake and lipid metabolism or accumulation under increased energy load. Likewise *in vivo* studies, an influence of C3 treatment on GPR41 mRNA in SC AT might not be ruled out. (1) Houseknecht et al. 2000. J Endocrinol 164. 51 (2) Xiong et al. 2004. Proc Natl Acad Sci U S A. 101. 1045

Key Words: adipose tissue explants, adiponectin receptors, GPR41

Ruminant Nutrition: Dairy 2

707 Effect of grain type and processing method on rumen fermentation and milk rumenic acid production. R. Mohammed*[1], J. J. Kennelly[1], J. K. G. Kramer[2], K. A. Beauchemin[3], C. S. Stanton[4], and J. J. Murphy[4], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Guelph, ON, Canada*, [3]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [4]*Teagasc*, *Moorepark, Co. Cork, Ireland*.

Eight Holstein cows in mid-lactation were assigned to 4 diets - rolled barley, ground barley, rolled corn and ground corn containing similar starch contents in two 4 × 4 Latin squares with 21-day periods to investigate the effect of grain type and processing method on milk rumenic acid (RA) production. Diets were supplemented with sunflower seed and had forage:concentrate ratios of 42:58. Rumen and milk samples were collected in the third week of each period. Data were analysed by the

MIXED procedure of SAS. Dry matter intakes were greater (P =0.01) for corn-based diets (CBD) than for barley-based diets (BBD). Milk yield was not influenced by grain type or processing method. Milk fat content (P < 0.01) and yield (P = 0.03)were less for BBD than for CBD with greater values observed for rolling compared to grinding. Mean rumen pH was not different; however, daily minimum pH was less (P = 0.01; 5.2 ± 0.1 vs 5.5 ± 0.1) and pH duration < 5.8 (h/d) greater (P 0.03; 7.4 ± 2.1 vs 4.3 ± 2.1) for BBD than for CBD. Rumen acetate concentrations (mmol/100mol) were greater (P < 0.01; 48.4 ± 0.9 vs 45.5 ± 0.9) and propionate concentrations lesser (P < 0.01; 22.7 ± 1.2 vs 28.3 ± 1.2) for CBD than for BBD. Rumen ammonia concentration was greater (P < 0.01) for CBD than for BBD with greater (P = 0.04) values observed for rolling compared to grinding. The concentrations of t10-18:1 and t11-18:1 (% total FAME) were greater for BBD than for CBD in rumen (t10-18:1 - 3.5 ± 0.8 vs 1.3 ± 0.8, P < 0.01; t11-18:1- 3.2 ± 0.5 vs 1.9 ± 0.5, P = 0.01) and milk (t10-18:1- 3.8 ± 1.3 vs 1.0 ± 1.3, P = 0.03; t11-18:1- 2.6 ± 0.3 vs 1.7 ± 0.3, P < 0.01). Milk RA concentrations were greater (P < 0.01) for BBD than for CBD (1.46 ± 0.2 vs 0.89 ± 0.2). This study demonstrates the significance of the effect of grain type and processing method on rumen fermentation, PUFA biohydrogenation and milk RA concentration.

Key Words: grain processing, milk rumenic acid, cow

708 Feeding dairy cows barley grain treated with lactic acid and heat increased milk fat content and prevented the decline of rumen pH to sub-clinical ruminal acidosis (SARA) values. Q. Zebeli*, S. M. Dunn, and B. N. Ametaj, *University of Alberta*, *Edmonton, AB, Canada*.

Rapid degradation of barley grain in the rumen is often related to SARA and low milk fat. The objective of this study was to evaluate effects of feeding barley grain treated with lactic acid (LA) and heat on rumen pH and milk composition in dairy cows. Eight rumen-fistulated Holstein cows (170 DIM) were fed once daily a TMR containing rolled barley grain (32.8%, DM basis) steeped for 48h in equal quantity of water (CTR-diet) or with 1% LA (v/v) and oven-heated at 55°C (TRT-diet) in a crossover design with two 21-d periods. After 11-d of adaptation period, samples of rumen fluid (at 0730) and milk (at 0500 and 1500) were collected on d 1, 3, 5, 7, and 10 of measurements period. Diurnal rumen pH was measured in rumen fluid collected every 2h up to 12h post-feeding on d 10. Data were analyzed statistically by SAS accounting for effects of period, cow, sampling time, treatment, and carryover influences as well as by considering measurements at different sampling days as repeated measures with an autoregressive covariance structure. Results showed higher preprandial (P<0.02) and diurnal (P=0.01) rumen pH for cows fed the TRT diet. Also, cows fed the TRT diet maintained higher rumen pH (5.92 vs. 5.67) at the nadir (8h post-feeding) up to 12h post-feeding (6.10 vs. 5.78) lowering the risk of SARA. Interestingly, across 10-d measurements the treatment increased milk fat content (3.58 vs. 3.12%; P<0.01), fat yield (0.97 vs. 0.83 kg/d; P=0.02), fat-to-protein ratio (1.12 vs. 1.00; P=0.02), and tended to increase fat-corrected (27.4 vs. 25.0 kg/d; P=0.06) as well as the energy-corrected milk (P=0.07) resulting in greater milk energy efficiency (P=0.01). Additionally, cows fed the TRT diet had lower MUN (14.4 vs. 16.8 mg/dL; P<0.01) indicating a better N utilization of the TRT diet. The DMI, milk yield, and other milk variables measured were not affected by diet (P>0.10). In summary, feeding dairy cows 32.8% rolled barley grain treated with 1% LA and heat increased milk fat content and energy efficiency as well as prevented rumen pH from falling at SARA levels.

Key Words: dairy cow, milk composition, lactic acid

709 Overfeeding energy prepartum dramatically affects peripartal expression of mRNA transcripts in subcutaneous adipose tissue compared with controlling energy intake prepartum. N. A. Janovick*[1], J. J. Loor[1], P. Ji[1], R. E. Everts[1], H. A. Lewin[1,2], S. L. Rodriguez-Zas[1], and J. K. Drackley[1], [1]*University of Illinois*, *Urbana*, [2]*Institute for Genomic Biology*, *Urbana, IL*.

A bovine oligonucleotide microarray was used to determine the effects of prepartum plane of energy intake on patterns of mRNA expression in subcutaneous adipose. Fourteen Holstein cows were fed either a moderate-energy diet for ad libitum intake (OVER) to provide at least 150% of NRC (2001) energy requirement for dry cows in late gestation or a diet including chopped wheat straw to limit intake to 100% of energy requirements at ad libitum intake (CON). After parturition, all cows were fed the same lactation diet. Subcutaneous adipose tissue was biopsied before cows were assigned to prepartum diets and on d -14, 1, and 14 relative to parturition. Statistical analysis revealed 3,423 differentially expressed mRNA transcripts as a result diet and day interactions at a FDR-adjusted *P*-value ≤ 0.05. K-means clustering revealed 13 unique clusters with functional categories including insulin signaling, lipid metabolism, immune system or inflammatory processes, glucocorticoid signaling, cell death, and free radical scavenging. The largest number of differences between dietary groups occurred on d -14 relative to parturition, where 27 transcripts were downregulated at least 2.5-fold or greater and 55 were upregulated at least 3.0-fold or greater in OVER compared to CON cows. The most notable changes in transcripts of genes related to lipid synthesis were *SCD*, *DGAT2*, *LPL*, *FASN*, *ADIPOQ*, and *LEP*, which were upregulated, and *ADRB3*, which was downregulated in OVER compared with CON cows. Transcript expression patterns on d -14 relative to d 1 revealed very different effects of prepartum diet; cows in the CON group had a much smaller magnitude of fold changes and markedly fewer affected transcripts during this period compared with OVER cows. Most notable was the 5- to nearly 50-fold decreases in expression for 25 lipid synthesis and storage genes in OVER cows on d 1 relative to d -14. Large changes such as these may be detrimental to metabolic adaptation during the periparturient period.

Key Words: prepartum energy intake, mRNA transcript profiling, subcutaneous adipose tissue

710 Effect of antioxidant and energy density on antioxidant status and postpartum performance in transition cows. Y. M. Wang*, C. Wang, J. H. Wang, and J. X. Liu, *Institute of Dairy Science, Zhejiang University*, *Hangzhou, P. R. China*.

This study was conducted to investigate the effect of antioxidant and energy density on oxidative status and postpartum performance in transition cows. Forty Chinese Holstein dairy cows 3 weeks prepartum were allocated to 4 blocks of 10 cows based on parity, expected calving date, body condition score and previous milk yield, with a 2 × 2 factorial design. Treatments were antioxidant (AOX, 0 or 5 g/day) and prepartum energy density (1.42 or 1.3 Mcal/ kg DM). After calving, all cows were fed the similar lactating diets, except for AOX addition until 3 week postpartum. Feeding high energy prepartum diets decreased the DMI prepartum and 1 week postpartum (*P*<0.05). Energy balance of dairy cows and birth weight of their calves were unaffected by energy density and AOX. Compared with low energy diet, high energy diet prepartum reduced the milk yield of the first 3 weeks postpartum (*P*=0.03), and AOX tended to increase the milk yield (*P*=0.06). There was an interaction of energy density and AOX on milk protein (*P*<0.01) and total solids contents (*P*=0.02). Addition of AOX reduced the β-hydroxybutyrate level during 2 and 3 week postpartum (*P*<0.05). Diet with high energy

increased glutathione peroxidase activity 1 week prepartum ($P<0.05$), while AOX decreased this enzyme activity during 1 and 2 week before calving, and malondialdehyde contents around calving. Both energy density and AOX affected fatty acids composition of erythrocyte membrane 1 week postpartum. The improvement in fluidity of erythrocyte membrane was observed in high energy treatment. It is suggested that feeding high energy prepartum diets may negatively affect the antioxidant status, DMI and subsequent performance, while addition of AOX may partially alleviate the negative effects by improving the antioxidant status and metabolism.

Key Words: antioxidant, energy density, transition cows

711 Effects of replacing corn grain with molasses on ruminal fermentation and milk component production in dairy cows. C. A. Martel*, E. C. Titgemeyer, and B. J. Bradford, *Kansas State University*, *Manhattan*.

Previous research demonstrated that replacing corn with 5% molasses partially alleviated milk fat depression (MFD), but also decreased milk protein yield. Six cannulated, multiparous, late-lactation Holstein cows (220 ± 18 DIM) were used to evaluate effects of adding molasses to a high-concentrate diet containing 20% distiller's grains, with or without supplemental amino acids (AA), on ruminal parameters and milk composition. Cows were randomly assigned to dietary treatment sequence in a crossover split plot design with 0% and 5% molasses diets. Dietary treatments were fed for 28 d, with 16 d for diet adaptation, and the final 12 d for 2 abomasal infusion periods in a crossover arrangement. Abomasal infusions of water or AA (5 g/d L-Met + 15 g/d L-Lys-HCl + 5 g/d L-His-HCl-H2O) were administered 3 times daily for 5 d, with 2 d between infusion periods. Milk production data and samples were collected during d 18-21 and 25-28 for analysis of milk components and fatty acid (FA) profiles. Ruminal fluid was collected on d 26-28. Milk fat percent increased with addition of molasses (P=0.01; 2.71% vs. 2.94%), but molasses had no effect on yield of milk fat (P=0.25; 0.80 vs. 0.84 kg/d) or protein. Administration of AA had no effect on concentration or yield of any milk components. Dietary molasses decreased total VFA concentration (P<0.01; 141 vs. 133 mM), decreased molar proportion of propionate, and increased molar proportion of butyrate in ruminal fluid. Molasses also increased ruminal pH (P=0.01; 5.73 vs. 5.87). Analysis of milk FA profile demonstrated a tendency for an increased proportion of de novo synthesized FA (P=0.06), but yield of de novo FA was not altered. Molasses decreased yield of trans-10 C18:1 and increased yield of trans-11 C18:1, consistent with previous findings. Molasses also decreased delta-9 desaturase index (C14:1/C14). Data provide evidence that molasses may promote mammary de novo FA synthesis in high-energy rations by moderating ruminal pH and promoting normal biohydrogenation of dietary FA.

Key Words: milk fat depression, molasses, biohydrogenation

712 Effects of feeding increasing levels of wet corn gluten feed on digestibility, rumen pH, and VFA concentrations of lactating Holstein cows. C. R. Mullins*[1], L. K. Mamedova[1], K. N. Grigsby[2], and B. J. Bradford[1], [1]*Kansas State University*, *Manhattan*, [2]*Cargill Inc.*, *Blair, NE*.

Numerous studies have reported production responses to dietary inclusion of wet corn gluten feed (WCGF), but few have reported ruminal effects. Measures of ruminal fermentation and total-tract digestion were evaluated in four primiparous and four multiparous Holstein cows (90 ± 13 DIM; mean ± SD) fed differing levels of WCGF. Cows were randomly assigned to square and sequence within square in a replicated 4 × 4 Latin square design balanced for carry over effects. Treatment periods were 28 d, with the final 8 d used for in situ work, data collection, and sample collection. Treatments were diets containing 0, 12, 24, or 36% WCGF on a DM basis, with alfalfa hay, corn silage, corn grain, soybean meal, expeller soybean meal, and mineral supplements varying across diets to maintain uniform CP, RUP, NDF, and mineral concentrations. Linear and quadratic treatment effects were evaluated using mixed models. Increasing the amount of WCGF in the diet tended to linearly decrease rumen pH (P = 0.07; 6.18, 6.12, 6.14, and 5.91). Ruminal acetate concentration decreased linearly and propionate increased linearly (P < 0.001) as WCGF inclusion rate increased. Treatment also had a quadratic effect on ammonia concentration (P < 0.01), with greater concentrations in the 0% and 36% WCGF diets. In situ digestibility of soybean hulls showed a significant diet by time interaction (P < 0.001), and increasing WCGF linearly decreased in situ NDF disappearance at 24 hrs (P < 0.01). No differences were observed in total-tract digestibility of DM, organic matter, NDF, ADF, CP, or ether extract. Replacement of both starch and forage fiber with non-forage fiber apparently resulted in increased ruminal fermentation and accumulation of volatile fatty acids, decreasing ruminal pH; however, relatively low mean particle size of experimental diets may have contributed to these effects.

Key Words: corn gluten feed, dairy cows, rumen

713 Effects of wet corn gluten feed inclusion rates on productivity of lactating Holstein cows. C. R. Mullins*[1], K. N. Grigsby[2], and B. J. Bradford[1], [1]*Kansas State University*, *Manhattan*, [2]*Cargill Inc.*, *Blair, NE*.

Four primiparous and four multiparous ruminally cannulated Holstein cows (90 ± 13 DIM; mean ± SD) were monitored to evaluate the effects of differing dietary inclusion rates of wet corn gluten feed (WCGF). Cows were randomly assigned to square and sequence within square in a replicated 4 × 4 Latin square design balanced for carryover effects. Treatment periods were 28 d, with the final 8 d used for data collection and sample collection. Treatments were diets containing 0, 12, 24, or 36% WCGF on a DM basis, with alfalfa hay, corn silage, corn grain, soybean meal, expeller soybean meal, and mineral supplements varying across diets to maintain similar CP, RUP, NDF, and mineral concentrations. Feed intake, milk production, body weight, and body condition score were monitored, and linear and quadratic effects of increasing WCGF inclusion rate were assessed using mixed models. Increasing dietary WCGF increased dry matter intake (P = 0.03; 26.7, 25.9, 29.3, and 29.7 kg/d for 0, 12, 24, and 36% WCGF, respectively) and milk production (P < 0.01; 36.8, 37.0, 40.1, and 38.9 kg/d). Concentrations of milk components did not differ among treatments (P > 0.10); however, protein and lactose yields linearly increased, and fat yield tended to increase linearly when more WCGF was fed. Production of energy corrected milk (P = 0.01; 38.2, 38.8, 41.7, and 40.4 kg/d) and solids corrected milk (P = 0.01; 35.2, 35.7, 38.5, and 37.2 kg/d) also increased linearly. Efficiency of milk production measured as ECM/DMI linearly decreased as cows consumed greater proportions of WCGF, and change in body condition score increased linearly. As expected, increasing the inclusion rate of WCGF decreased the proportion of particles > 19 mm in the TMR, but all TMR had small proportions of particles > 19 mm (mean 3%). This did not adversely affect milk fat concentrations (mean 3.7%). Results indicate that adding WCGF to dairy rations can increase

ECM yield, and this increase in production is likely driven at least in part by an increase in DMI.

Key Words: dairy nutrition, co-products, gluten

714 Response of lactating dairy cows to high protein distillers grains or three other protein supplements. K. A. Christen*[1], D. J. Schingoethe[1], K. F. Kalscheur[1], A. R. Hippen[1], K. Karges[2], and M. L. Gibson[2], [1]*South Dakota State University*, *Brookings*, [2]*Dakota Gold Research Association*, *Sioux Falls, SD*.

High protein dried distillers grains (HPDG) was compared against soybean meal (SBM), canola meal (CM), and dried distillers grains with solubles (DGS) as protein supplements in diets for lactating dairy cows. A trial comparing these protein sources utilized 12 multiparous Holstein cows, averaging 78 d in milk at the start of the experiment, in a 4 × 4 Latin square design with 28-d periods. Weeks 1 and 2 of each period were for adjustment and wk 3 and 4 for data collection. Each treatment diet consisted of 55% forage and one of the four protein supplements provided in a concentrate mix. Diets contained 15.3% CP with 38% of the CP supplied by a respective protein supplement. Dry matter intake (24.4 kg/d) was similar for all four treatments (P > 0.05). Milk production (31.8 kg/d), protein yield (1.05 kg/d), and fat yield (1.29 kg/d) were similar for all four treatment diets (P > 0.05). Milk protein percent was lower (P < 0.05) when fed DGS (3.23) than when fed the other three diets (3.34). Total milk nitrogen and true milk protein were higher (P < 0.05) when fed the HPDG diet than when fed the other diets. Milk fat percentage was lower (P = 0.02) when fed DGS (3.78) than when fed SBM or HPDG (4.21), but similar with CM (4.07). Feed efficiency and nitrogen efficiency were similar for all diets (P > 0.05). Molar proportions of acetate, propionate, and the acetate to propionate ratio in ruminal contents were similar for all diets (P > 0.05). Total essential AA concentrations in arterial plasma were similar with all diets while concentrations in venous plasma were lower (P < 0.05) when fed CM. Extraction efficiency indicated that Met was the first limiting AA by the mammary gland when fed the SBM diet, whereas Lys was first limiting for the other diets. For the milk components measured, HPDG was equal to or better than SBM, CM, and DGS as a protein supplement.

Key Words: high protein distillers grains, canola meal, lactating cows

715 Lactation performance and amino acid utilization of early lactating cows fed regular or de-oiled dried distillers grains with solubles. K. Mjoun*, K. F. Kalscheur, A. R. Hippen, and D. J. Schingoethe, *South Dakota State University*, *Brookings*.

The objective of this study was to evaluate lactation response and AA utilization in early lactating cows fed either regular or de-oiled distillers grains with solubles (rDGS and dDGS, respectively). Thirty-six Holstein cows 19.7 ± 2.6 DIM at the start of the experiment were used in a randomized complete block design for 14-wk including a 2-wk covariate period. Diets consisted of 1) Control based on soybean products; 2) 22% inclusion of rDGS; and 3) 20% inclusion of dDGS. Distillers grains replaced soybean meal, expeller soybean meal and soyhulls from the control diet. Diets were formulated to contain similar concentrations of CP, RUP, EE, NDF and NEL. Dry matter intake (24.2 kg/d) and milk yield (39.2 kg/d) were similar for all diets. Milk fat, protein, and lactose percentages were unaffected by diets; however, protein yield was greater ($P < 0.001$) for diets containing either DGS diets compared with control diet (1.14 *vs.* 1.04 kg/d). Milk urea nitrogen decreased ($P < 0.001$) for cows fed DGS diets and averaged 11.8, 10.8 and 10.1 mg/dl, respectively, for control, rDGS, and dDGS. The efficiency of milk production (1.46, 1.54, and 1.61 ECM/DMI) was different ($P < 0.01$) across diets. Efficiency of N utilization for milk protein was decreased ($P = 0.01$) for cows fed control compared with DGS diets (24.3 *vs.* 26.8%). Body weight (711 kg) and body condition score (3.38) were similar for all diets. Arterial Lys concentration was lower ($P < 0.001$) with DGS diets (80.0, 58.7 and 55.6 μM/L). Cows fed DGS had higher ($P < 0.001$) arterial Met concentration (21.7 μM) compared with (15.2) for control. Arteriovenous difference of Lys was similar across diets, whereas that of Met was greater for the DGS diets compared with control diet 13.3 *vs.* 10.7 μM/L. Extraction efficiency of Lys by the mammary gland was greater for DGS compared with control (76.1 *vs.*65.4%). Mammary uptakes of Lys (2.73) and Met (0.80) were similar for all diets. Despite the apparent deficiency of Lys in DGS diets, milk production and milk components were similar to a soybean-based diet.

Key Words: amino acids, distillers grains with solubles, early lactation

716 Effects of forage type on nitrogen utilization in dairy cows consuming diets high in wet distillers grains with solubles. A. M. Gehman* and P. J. Kononoff, *University of Nebraska*, *Lincoln*.

The objectives of this experiment were to determine the effects of forage type when feeding high levels of wet distillers grains with solubles (WDGS). Primiparous (n = 8) and multiparous (n = 20) Holstein cows averaging (mean &plumn; SD) 598 ± 64 kg BW and 99 ± 28 DIM were used in a replicated 4 × 4 Latin square. Treatments were arranged in a 2 × 2 factorial with factors WDGS (0 or 25% DM) and forage type [high corn silage (CS) or high alfalfa haylage (AH)]. Animals were fed one of 4 treatments during each 21-d period: 1) CONT-CS, 0% DM WDGS and high CS; 2) CONT-AH, 0% DM WDGS and high AH; 3) WDGS-CS, 25% DM WDGS and high CS; and 4) WDGS-AH, 25% DM WDGS and high AH. Intake and milk data was collected daily and averaged for d 15 – 21 of each period. There was an interaction ($P < 0.01$) between forage type and WDGS for DMI with AH stimulating DMI for rations without WDGS, while no effects were observed for rations with WDGS (22.5, 24.6, 24.6, and 24.8 ± 0.4 kg/d for CONT-CS, CONT-AH, WDGS-CS, and WDGS-AH). Digestibility of DM, OM, NDF, and N were not affected by treatment, averaging 59.6 ± 0.45, 62.3 ± 0.27, 40.1 ± 0.60, and 58.6 ± 0.15% across treatments. Excretion of urinary purine derivatives were ($P < 0.01$) elevated for treatments with WDGS compared to control (487.1 vs. 390.5 ± 20.6 mmol/d) but were not affected by forage type. Mass of fecal N was not different among treatments (averaging 287.1 ± 14.8 g/d), but urinary and manure N was ($P < 0.01$) reduced with WDGS compared to control (252.0 and 538.7 vs. 318.4 ± 14.8 and 603.5 ± 21.3 g/d). There were no effects of forage type on N utilization. There was an effect of WDGS ($P < 0.01$) and forage type ($P = 0.01$) on 4% fat-corrected milk with rations containing WDGS or AH having higher milk than control or CS (27.2, 28.3, 29.7, and 30.7 ± 1.0 kg/d for CONT–CS, CONT-AH, WDGS-CS, and WDGS-AH). This research demonstrated rations can be formulated to contain 25% WDGS and result in reduced N excretion regardless of forage type. These rations may also result in improved DMI and milk production.

Key Words: distillers grains, forage, N utilization

717 Effect of management and milk yield on the incidence of lameness in dairy cattle. C. Lira Diaz and J. K. Margerison*, *Massey University*, *Palmerston North, New Zealand.*

Data was collected from 14 commercial farms, comprising a total of 6412 cows (mean 458 cows per farm). Farms were nominated by a nutrition consultant in 4 districts of the North Island, New Zealand. Data was collected weekly over the period of 1st July 2007 until 31st July 2008 by the same observer during farm visits to monitor overall productivity, nutrition and health. Cows were classified into either Holstein Friesian (HF), Jersey (J) or Jersey cross Friesian (X). Lameness cause, type of lesion, locomotion scoring and location of any lesions were recorded using a 5 point scale and lame cows were inspected to determine the type of lesion and classified into five groups: (1) White line; (2) Sole damage; (3) Foot rot; (4) Laminitis; (5) Tender feet (LS 2-3). Data each cow on the farm was available throughout the lactation and dry cow period, or until any animal was no longer in the herd. Holstein Frisian cows were 7.9 (95% CI=4.18-12.02) times more likely to become lame compared to Jersey cows. Likewise, Crossbred cows were 4.64 (95% CI=2.82-7.63) times more likely to be lame than Jersey cows. Of the cows were lame 0.74 were hind feet compared to 0.14 for fore feet. A higher percentage of cows lame was during winter and spring time, whereas summer time had significantly lower mean percentages than the other seasons. In winter cows were 2.78 (95% CI= 2.58-2.99) more likely to be lame than cows in summer. There was no significant effect of walking distance on frequency of lameness (P=0.5726). Cows in early lactation had the highest mean percentages of lameness and were 1.68 (95% CI=1.66-1.70) times more likely to be lame than cows in middle stage of lactation. Higher yielders were 1.95 (95% CI= 1.80-2.11) times more likely to be lame than low yielders and moderate producers were 1.35 (95% CI= 1.35-1.61).

Key Words: lameness, breed, management

718 Competition at the feed bunk affects DMI and feeding behavior of metritic dairy cows. K. L. Proudfoot*, D. M. Weary, and M. A. G. von Keyserlingk, *University of British Columbia*, *Vancouver, BC, Canada*.

Cows at-risk for metritis after calving decrease dry matter intake (DMI) in the weeks before and after calving. It remains unclear how competition at the feed bunk may impact the DMI and feeding behavior of cows at-risk for metritis. Our aim was to test the effect of a competitive feeding environment on the feeding behavior of cows that become sick after calving versus those that remain healthy. Using an electronic feeding system we monitored DMI and feeding behavior of 76 Holstein cows from 1 wk before to 2 wk after calving. Cows were assigned to a competitive (2:1 cows:bin) or non-competitive (1:1 cow:bin) treatment and were examined for clinical metritis every 3 d after calving. Multiparous cows on the competitive (n=8) and non-competitive treatments (n=8) diagnosed with clinical metritis after calving were matched with healthy cows on each treatment (n=8/treatment). Using PROC MIXED we tested fixed effects of treatment and health, and a treatment*health interaction for DMI, feeding time and rate of intake for the following 3 periods: wk-1 (d-8 to d-1 pre-calving), wk+1 (d1 to d8 post-calving) and wk+2 (d9 to d16 post-calving). We detected an effect of health on DMI and feeding time where sick cows, regardless of treatment, ate less and spent less time feeding than cows that remained healthy. During wk-1, competitively fed cows tended to eat less than non-competitively fed cows (13.4±0.8 kg/d vs 14.8±0.8 kg/d, P=0.07). We found no effect of health on feeding rate, but there was a trend for a health*treatment interaction for feeding rate during the wk+1 (P=0.10). When tested separately, competitively fed metritic cows ate faster than healthy cows (139±7 g/min vs 116±8 g/min, P=0.04). There were no differences in feeding rate between non-competitive health groups (P=0.77). We provide the first evidence that competition at the feeder can alter the DMI and feeding behavior of cows at-risk for metritis after calving. Future work should examine the effect of competition on social behavior before calving, and the links between social status and disease.

Key Words: transition, competition, DMI

Ruminant Nutrition: Minerals

719 Thirty-eight years of vitamin D and calcium research: From dairy cows to humans. R. L. Horst*, *Heartland Assays, Inc.*, *Ames, IA*.

There is a long-standing and continuing interest in the relationship between vitamin D status and calcium nutrition. In that regard, several facts have been well established: 1.) Vitamin D must be converted in the liver to form 25-hydroxyvitamin D, which is consider the most clinically useful metabolite in evaluating vitamin D status and 2.) 25-hydroxyvitamin D must be converted to its active metabolite, 1,25-dihydroxyvitamin D. In mammals and birds, the 1,25-dihydroxyvitamin D acts to maintain calcium homeostasis by stimulating intestinal calcium transport and bone calcium mobilization. All of the compounds in the vitamin D activation cascade (including vitamin D itself) have been used in some form in attempts to prevent periparturient hypocalcemia (milk fever) in dairy cows. These attempts were met with varying degrees of success, which has lead to more interest in controlling milk fever by dietary measures. Although vitamin D in mainly associated with calcium metabolism and bone health, it has recently received at lot of attention regarding its relationship with heart health, cancer and infectious diseases. Several epidemiologic studies in humans have suggest that vitamin D may account for several thousand premature deaths due to colon, breast, ovarian, prostate cancer. The active form of vitamin D, 1,25-dihydroxyvitamin D, has also been shown to up-regulate the innate immune response triggering direct antimicrobial activity against intracellular bacteria such as Mycobacterium tuberculosis. So, what was once thought to be a simple vitamin affecting only bone and calcium metabolism is now seen as a complex pre-hormone that is involved not only in calcium homeostasis but also in maintaining, down to the cellular level, the integrity various organ systems throughout the body.

Key Words: vitamin D, calcium, functions

720 The optimum dietary Ca concentration to minimize the risk of hypocalcaemia in dairy cows is affected by dietary cation-anion difference. M. Oba*[1], A. Oakley[1], and G. Tremblay[2], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Quebec, QC, Canada*.

The objective of this study was to determine whether dietary Ca concentration affects the ability to maintain Ca homeostasis in dairy cows fed diets differing in dietary cation-anion difference (DCAD). Eight non-lactating and non-pregnant multiparous Holstein cows (594 ± 80.3 kg

BW; 34.5 ± 11.4 month old) were fed diets low or high in DCAD (-5.4 vs. 9.7 mEq/100g DM, respectively) in combinations with low or high dietary Ca concentration (0.30 vs. 0.90% of dietary DM) in a duplicated 4×4 Latin square design with 14-d periods. Diets consisted of low or high DCAD timothy hay (70% of dietary DM) supplemented with low or high Ca concentrate mix (30% of dietary DM). Following 13-d diet adaptations, cows were subjected to an EDTA challenge; intra-jugular infusion of EDTA solution to decrease blood Ca concentration. In this protocol, the time required to reduce blood Ca concentration to 60% of the pre-challenge values and the time required to recover to 90% of the pre-challenge values after EDTA infusion is stopped were determined as resistance and recovery time, respectively. Blood pH (7.41 vs. 7.44; $P < 0.01$) and urine pH (5.67 vs. 6.86; $P < 0.01$) were lower for cows fed low DCAD diets compared to those fed high DCAD diets, but plasma parathyroid hormone concentration was not affected by treatment, averaged at 22.1 p*M*. Although dietary treatments did not affect the resistance time, feeding high Ca diet shortened the recovery time (106 vs. 134 min; $P < 0.05$) when DCAD is low, while low Ca diet shortened the recovery time (125 vs. 159 min; $P < 0.05$) when DCAD is high. Cows fed low DCAD diets mitigated metabolic alkalosis, but the ability to maintain Ca homeostasis was improved only for cows fed the high Ca diet. These results suggest that the optimum dietary Ca concentration to minimize the risk of hypocalcaemia in dairy cows is likely different depending on the DCAD value.

Key Words: DCAD, dietary Ca, EDTA challenge

721 Effects of copper deficiency on gene expression profiles of copper transporters and chaperones in steers. R. S. Fry*[1], M. S. Ashwell[1], S. L. Hansen[1], T. E. Engle[2], H. Han[2], and J. W. Spears[1], [1]*North Carolina State University*, *Raleigh*, [2]*Colorado State University*, *Fort Collins*.

An experiment was conducted to evaluate the gene expression profiles of Cu transporters and chaperones in the intestine and liver of steers in response to long-term Cu deficiency. Angus calves (n = 14) were born to cows fed one of the following dietary treatments for 410 d prior to calving: 1) Cu-adequate (+Cu; 10 mg supplemental Cu/kg DM) or 2) Cu-deficient (-Cu). Copper deficiency was produced by providing no supplemental Cu and supplementing the Cu antagonist Mo at 2 mg/kg DM. Calves remained on the same dietary treatments as their dams after weaning, and were individually fed treatment diets for an additional 310 d. Calves were harvested on d 493, and duodenal scrapings and liver samples were collected from steers and flash frozen for Cu content and analysis of several genes encoding proteins necessary for Cu metabolism. These Cu transporters and chaperones have been shown in rodents to regulate Cu entry into the cell (CTR1), deliver Cu to cytochrome c oxidase (COX17), to the trans-golgi network (ATOX1), and for Cu export into cuproenzymes (ATP7A and ATP7B). Plasma Cu (0.2 vs. 1.3 mg/L) and liver Cu (6.3 vs. 217.6 mg Cu/kg DM) on d 490 was lower ($P < 0.001$) in -Cu steers compared to +Cu steers. Duodenal expression of *Ctr1*, *Atox1*, *Cox17*, and *Atp7b* was not different due to Cu deficiency. There was a trend ($P = 0.12$) for duodenal *Atp7a* to be up-regulated in -Cu steers. Liver expression of *Ctr1* and *Atox1* was not different; however, *Cox17*, *Atp7a*, and *Atp7b* were differentially expressed. Copper deficiency markedly ($P < 0.01$) reduced the relative expression of *Cox17* and tended ($P \leq 0.10$) to reduce relative expression of *Atp7a* and *Atp7b*. Results from this study indicate that Cu deficiency decreases expression of certain Cu transporters and chaperones in cattle. Furthermore, it appears that Cu transporters in the liver are affected to a greater extent than duodenal Cu transporters.

Key Words: cattle, copper, transporters

722 Strategic use of naturally selenium-rich milling coproducts to manage selenium deficiency. J. B. Taylor*, *USDA, Agricultural Research Service*, *Dubois, ID*.

The objective was to use Se-rich milling coproducts to enhance the long-term Se status of ewes and their lambs. A complete randomized design experiment was used to test the null hypothesis that diets formulated with Se-rich wheat middlings will not alter the Se status of lactating ewes and their lambs. Mature Columbia x Polypay ewes (n = 28; BW = 76.9±1.9 kg) with twin lambs were placed in individual pens 6 h after parturition. Selenium treatments were assigned randomly to each ewe. Treatments were adequate or elevated dietary Se. The adequate-Se treatment was fortified with Na_2SeO_3 and the elevated-Se treatment was formulated with Se-rich wheat middlings to provide (DM basis) 0.02 and 0.11 mg of Se per kg of BW per day, respectively. Treatments commenced when ewes were placed in pens and continued for 19 d. Ewe feeding and watering receptacles were placed out of reach of the lambs; thus, the lambs' nutrition was restricted to their dam's milk. Milk samples were collected at 18 d of treatment. Skeletal muscle samples were collected from anesthetized ewes and lambs at the end of the 19-d treatment period, and 108 d later. The following data are least squares means with SEM in parentheses. Muscle Se was greater ($P<0.04$) in elevated-Se than in adequate-Se ewes; muscle Se (DM basis) was 0.88 and 0.46 (0.04) mg/kg at the end of the treatment period and 0.49 and 0.38 (0.04) mg/kg 108 d later, respectively. Milk Se was greater ($P<0.01$) in elevated-Se than in adequate-Se ewes; milk Se was 0.53 and 0.06 (0.03) mg/L at the end of the treatment period, respectively. Muscle Se was greater ($P<0.01$) in lambs nursing elevated-Se ewes than in lambs nursing adequate-Se ewes; muscle Se was 2.96 and 0.43 (0.07) mg/kg at the end of the treatment period and 0.74 and 0.25 (0.02) mg/kg 108 d later, respectively. Through strategic use of Se-rich milling coproducts, skeletal muscle in ewes and their lambs were simultaneously enriched with Se within a 19-d period. Selenium enrichment remained significant for 108 d. This information will enable livestock producers to utilize Se-deficient rangelands for extended periods of time without having to provide supplemental Se.

Key Words: deficiency, lactation, selenium

723 Effects of nutritional plane and selenium supply on intestinal mass, cellularity, and proliferation in the ewe. A. M. Meyer*[1], J. J. Reed[1], T. L. Neville[1], L. R. Coupe[1], J. B. Taylor[2], L. P. Reynolds[1], D. A. Redmer[1], K. A. Vonnahme[1], and J. S. Caton[1], [1]*North Dakota State University*, *Fargo*, [2]*USDA-ARS, U.S. Sheep Experiment Station*, *Dubois, ID*.

Objectives were to investigate the effects of maternal nutrition and Se supply during gestation on intestinal mass and growth in ewes at parturition and during early lactation. Rambouillet ewe lambs (n = 84) were allocated to treatments arranged as a 2 x 3 x 2 factorial. Factors were dietary Se (adequate Se [ASe, 8.5 µg/kg BW] or high Se [HSe, 80 µg/kg BW]), nutritional plane (60% [RES], 100% [CON], or 140% [HIGH]), and necropsy period (parturition or d 20 of lactation). At parturition, lambs were removed, and 42 ewes (7/treatment) were necropsied. Remaining ewes were transitioned to a common diet that met requirements of lactation and mechanically milked until necropsy on d 20. The small intestine was dissected and tissues were harvested at both necropsy periods. Where interactions were present ($P \leq 0.10$), least square means from the highest order interaction are presented. At parturition, small intestinal mass was greater ($P < 0.002$) for HIGH fed ewes than RES and CON (629 vs. 447 and 492 ± 32 g) and was greater ($P < 0.01$) for ASe than HSe (572 vs. 473 ± 25 g). Small intestinal mass increased (*P*

< 0.02) from parturition to lactation (523 vs. 732 ± 18 g). Ewes fed the HIGH diet had greater ($P \leq 0.02$) jejunal mass than RES and CON. At parturition, jejunal mass was greater ($P = 0.04$) for ASe than HSe fed ewes and jejunal mucosal density was less ($P \leq 0.01$) for RES fed ewes than CON and HIGH. Jejunal mucosal DNA concentration in ewes fed HSe was greater ($P < 0.001$) at parturition than lactation. Ewes fed the CON diet had greater ($P < 0.003$) jejunal mucosal RNA:DNA than RES and HIGH at parturition. Mucosal protein:DNA decreased ($P = 0.03$) from parturition to lactation. Jejunal cell proliferation was greatest ($P < 0.09$) in RES, intermediate in CON, and least in HIGH fed ewes during lactation. Total number of proliferating jejunal cells was greater ($P \leq 0.04$) in HIGH fed ewes than RES and CON at parturition, and was greater ($P < 0.05$) in RES fed ewes than CON and HIGH on d 20 of lactation. Results indicate that maternal intestinal growth is responsive to nutritional plane, dietary Se, and periparturient period.

Key Words: gestational nutrition, intestine, selenium

724 Mineral balances in California dairy farms. A. R. Castillo*[1], N. St-Pierre[2], and N. Silva del Rio[1], [1]*University of California, Cooperative Extension, Merced*, [2]*The Ohio State University*, *Columbus*.

Forty commercial dairy farms in Merced County (CA) were selected to study mineral balance in lactating animals (mean 787±592 lactating cows/farm). Dairies were selected based on total salt (TS) drinking water content (mean 560±343.3 TS mg/L, from 100 to 1680 mg/L) and on daily milk average yield per cow (mean 31.5±5.31 kg milk/cow per day, ranging from 20.6 to 43.5 kg milk/cow per day). Pearson correlation analysis was used to study the mineral balance and the milk utilization efficiency for each mineral. Duplicated samples of total mixed rations (TMR), water and milk were collected in each farm on two non-consecutive days, and analyzed for Ca, P, Mg, Cl, K, Na, S, Cu, Fe, Mn, Se, and Zn. Dry matter intake was calculated for each lactating group or farm based on the total daily amount of TMR supplied, divided by the number of cows in each feeding group, and corrected by estimated refusal. Milk yield per cow was obtained from Dairy Herd Improvement (DHI) records and when not available, from the total daily milk produced/number of milking cows. Dietary mineral content per farm was calculated according to TMR mineral content weighted by the proportion of animals in each production group. The daily mineral balance and gross utilization efficiency (%GUE) were calculated for each mineral as follow: balance = total mineral daily intake – total mineral milk output, and %GUE = mineral milk output/total mineral intake x 100. The dietary mineral contents were positively correlated to mineral balance (no less than r=0.90) and negatively correlated to %GUE (no less than r=-0.55), all the correlations were P<0.001. These results indicate that mineral contents in the diet might be used to estimate its correspondent mineral balance, the mineral milk utilization efficiency, and its possible excretion.

Key Words: mineral balance, dairy cows, mineral utilization efficiency

725 Effects of trace mineral amount and source on aspects of oxidative status and immune function in dairy cows. T. Yasui*[1], R. M. Ehrhardt[1], G. R. Bowman[2], M. Vázquez-Añon[2], J. D. Richards[2], C. A. Atwell[2], T. D. Wineman[2], and T. R. Overton[1], [1]*Cornell University*, *Ithaca, NY*, [2]*Novus International*, *St. Charles, MO*.

Multiparous Holstein cows (n=48) were used to determine effects of trace mineral amount and source on aspects of oxidative status and immune function. Cows were fed a basal diet meeting NRC (2001) requirements except for no added Zn, Cu, or Mn. After a 4-wk preliminary period, cows were assigned to one of four topdress treatments in a randomized complete block design: 1) NRC 2001 levels of Zn, Cu, and Mn using sulfates only; 2) NRC 2001 levels of Zn, Cu, and Mn using MINTREX® organic trace minerals (Novus International, Inc.); 3) Commercial inorganic (approximately 2X NRC) using sulfates only; and 4) Commercial organic using MINTREX®. Final concentrations of Zn, Cu, and Mn were similar between the inorganic and MINTREX® treatments and averaged 55, 8.3, and 21 ppm, respectively, for the NRC level and 75, 16, and 35 ppm for the commercial level. Cows were fed the respective mineral treatments for 6 wk. During wk 1 of treatment, cows fed Zn, Cu, and Mn at commercial levels tended (P<0.15) to have decreased activity of glutathione peroxidase in erythrocyte lysate (27,698 vs. 28,932 nmol/min*ml of packed cell volume), cows fed inorganic sources at NRC levels tended to have lower plasma total antioxidant capacity (1.25, 1.59, 1.58, and 1.55 mM; level x source, P<0.15), and cows fed MINTREX® tended to have decreased concentrations of plasma thiobarbituric acid reactive substances (TBARS; 5.26 vs. 4.39 μM; P<0.13). Cows fed MINTREX® had higher plasma IgG across the experimental period (2.35 vs. 2.68 g/dl; P < 0.01). All cows were administered an intramammary lipopolysaccharide challenge during wk 5; during wk 6 cows fed commercial levels of Zn, Cu, and Mn had higher plasma total antioxidant capacity (1.34 vs. 1.48 mM; P < 0.09) and cows fed MINTREX® had decreased plasma TBARS (4.16 vs. 3.60 μM; P<0.05). Overall, results suggest that varying level and source of dietary trace minerals can affect parameters related to oxidative status.

Key Words: trace minerals, oxidative status

726 Impact of phosphorus form on utilization in lactating dairy cows. K. J. Lager*, M. J. Brouk, B. J. Bradford, and J. P. Harner, *Kansas State University*, *Manhattan*.

Supplementation of phosphorus (P) in varying forms was compared to test the effects on intake and utilization. Twelve multiparous Holstein cows producing approximately 43 kg of milk (115 ± 55 DIM) were utilized in a 4x4 Latin square design with 21d periods. Four total mixed rations (TMR) were formulated for similar P concentrations. The forms of supplemental P chosen were a pellet, meal and liquid. Wheat middlings were used as a carrier for dicalcium phosphate in the pellet and meal forms while a cane molasses based liquid was the delivery form in the third diet. Corn dried distiller′s grains with solubles (DDGS) were used in the fourth diet for comparison between organic and inorganic P mineral sources. Cows were randomly assigned to treatments and blocked by parity, lactation number, and milk production. Data were analyzed using the Mixed model of SAS. Dry matter intake (DMI) was not affected by diet and intake of P was similar for the pellet, meal, liquid and DDGS diets (116, 116, 119 and 118 g/d, respectively). Cows consuming the liquid supplementation diet showed increased sugar intakes (P<0.001) and also the lowest daily milk production. Daily fat intake was significantly greater (P<0.001) for the DDGS than the pellet, meal, and liquid supplemented diets (1.15, 1.15, 1.12 and 1.36 kg, respectively). The distiller's grains replaced a portion of the corn grain in the DDGS diet which decreased (P<0.03) starch intakes of cows consuming that diet, but intake of NE_L was similar (P=0.55) for all diets. Differences (P=0.05) in milk production were noticed with the DDGS supplemented diet resulting in the greatest milk production (34.6, 35.5, 34.1 and 36.5 kg/cow). Percentage of butterfat in milk was greatest for the meal diet but no difference was observed between diets for milk protein percentage (P=0.32) or lactose production (P=0.22).

These data show that supplemental P form does not affect DMI or P intake and that an organic source of P in DDGS shows similar response as inorganic P mineral supplements.

Key Words: liquid feed, mineral supplementation, distiller's grains

727 Effect of 4-Plex® on milk production, reproduction and claw integrity of dairy cows. J. M. DeFrain*[1], M. T. Socha[1], D. J. Tomlinson[1], and D. Kluth[2], [1]*Zinpro Corporation*, *Eden Prairie, MN*, [2]*Standard Dairy Consultants*, *Omaha, NE*.

On a commercial dairy, 366 Holstein cows were blocked by parity and expected calving date and assigned to an experiment with a randomized complete block design to determine the effect of treatment on lactation, reproduction and claw integrity. Treatments were 1) all supplemental Zn, Mn, Cu and Co supplied by sulfates and 2) 360 mg Zn, 200 mg Mn, 125 mg Cu and 25 mg Co from sulfates replaced by similar amounts of trace minerals supplied by 4-Plex (Zinpro Corporation, Eden Prairie, MN). All cows were fed inorganic trace minerals for 4 months prior to initiation of treatments. Cows received treatments from 3 wk prepartum through 250 d postpartum. Treatments were mixed into a supplement then blended into a TMR. The TMR was delivered to 4 pens prepartum (2 pens/trt) and 4 pens postpartum (2 pens/trt). Cows were milked three times per day and milk yield recorded at each milking. Milk was sampled twice monthly and composition determined. All claws of cows were examined prior to initiation of treatments and at 17 and 36 wk postpartum by personnel trained in identifying claw lesions. Individuals involved with daily animal care and/or data recording were blinded to treatment assignments. The MIXED procedure of SAS® was used to analyze the data. There was no effect of treatment (P>0.10) on yields of milk, 3.5% fat-corrected milk or energy corrected milk. Cows fed sulfates tended (P<0.10) to produce more milk fat and milk with a greater fat content (P<0.05). Feeding cows 4-Plex tended (P<0.10) to reduce SCC content of milk and linear SCC scores. Survival curve analysis indicated that more cows fed 4-Plex became pregnant and these cows became pregnant at a faster rate (P<0.10) than cows fed only sulfate trace minerals. Feeding sulfates decreased (P<0.05) severity of sole hemorrhages, while feeding 4-Plex decreased (P<0.05) incidence of heel erosion. There was no other effect (P>0.10) of treatment on claw lesions. In conclusion, replacing a portion of the inorganic sulfate sources of Zn, Cu, Mn and Co with those trace minerals supplied by 4-Plex improved milk quality and reproductive performance.

Key Words: trace minerals, dairy cattle, reproduction

728 Metabolic and productive responses to supplemental chromium in early-lactation heat-stressed cows. M. Mirzaei[1], G. R. Ghorbani[1], M. Khorvash[1], H. R. Rahmani[1], and A. Nikkhah*[2,1], [1]*Isfahan University of Technology*, *Isfahan, Iran*, [2]*Zanjan University*, *Zanjan, Iran*.

An enormous challenge to the dairy industry is the coincidence of metabolic pressures of early lactation with heat stress. The effects of a chromium (Cr) supplement on feed intake, blood metabolites and hormones, and productivity of early lactation heat-stressed cows were determined. Fifteen Holstein cows at 38 ± 6 d in milk were grouped based on parity and randomly assigned to 3 levels of 0, 0.05 and 0.10 mg of Cr per kg of $BW^{0.75}$. Cows received a basal total mixed ration with a forage to concentrate ratio of 57.7:42.3, twice daily at 0900 and 1600 h. The Cr supplement was mixed with 100 g ground corn and top dressed with the morning feed. Blood was collected weekly at 1130 h via coccygeal vein for 7 wk. Milk was sampled weekly for 3 consecutive milkings. Data were analyzed as a mixed model with the best fit covariance structure for repeated measurements i.e., AR(1) for IGF-1, NEFA and cortisol, and ARH(1) for other measurements. Dry matter intake increased (24.2 vs. 21.8 kg/d ± 0.5, P<0.01) when 0.05 mg Cr per $BW^{0.75}$ was provided. As a result, milk fat (1.46 vs. 1.32 kg/d ± 0.05), protein (1.13 vs. 1.04 kg/d ± 0.03) and total solids (4.96 vs. 4.59 kg/d ± 0.12) yields increased (P<0.05) by providing supplemental Cr at 0.05 mg per $BW^{0.75}$. Respective milk yield was 38, 39.6 and 37.8 kg/d for the 3 groups. Both doses of Cr increased (P>0.05) milk protein (2.85% and 2.82% vs. 2.73% ± 0.02), but the higher Cr dose reduced (P<0.05) feed efficiency compared to when no supplemental Cr was provided (1.45 vs. 1.62 ± 0.05). Cows receiving 0.05 Cr per $BW^{0.75}$ lost body weight (-142 vs. 317 g/d, P=0.05) and tended (P<0.10) to have greater respiration rate than control cows (58.6 vs. 56.4 ± 1.2 per min). Blood insulin (8.2 vs. 8.9 ± 0.3 μIU/ml) and NEFA (145 vs. 159 ± 4.7 μEq/l) concentrations and the insulin to glucagon ratio (0.108 vs. 0.123 ± 0.005) decreased but serum albumin increased (3.91 vs. 3.77 ± 0.05 mg/dl, P<0.05) when cows received 0.05 mg of supplemental Cr per $BW^{0.75}$. Findings suggest that providing supplemental Cr to early lactation cows under heat stress improves feed intake and milk secretion

Key Words: chromium, early lactation, heat stress

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SYMPOSIA AND ORAL SESSIONS

Animal Behavior and Well-Being: Animal Behavior and Well-Being 2

729 Behavior-nutrition interaction in swine. J. N. Marchant-Forde*, *USDA-ARS, West Lafayette, IN*.

Swine nutrition management aims to maximize output for minimal input. With the breeding sow, the aim is to maximize reproductive output, with easy farrowing, large and heavy litters, good lactation, and quick recovery and re-breeding. For the wean-to-finish pig, the aim is to maximize growth efficiency, with pigs growing as fast as potential allows on as little food as possible. Under commercial conditions, the pig can meet its daily energetic requirements quickly with a highly nutritious, uniform food source, which may or may not be accessible ad libitum and which may or may not be accessible by all animals at the same time. Under natural conditions, the pig is a foraging omnivore, spending a large proportion of the day rooting and searching for a varied, relatively low energy food source, usually eating in groups. Thus, some aspects of nutrition management in commercial production depart from the nutritional strategy of the wild pig, negatively affecting well-being. For example, with sows, there may be issues of chronic hunger, as the sow is fed her daily ration in a single meal. Also, feeding system design may influence aggressive behavior in group housing, as food becomes a limited resource and subject to competition. At weaning, piglets are weaned abruptly and undergo a sudden change from milk-only diet to solid food, impacting gut morphology and also behavior, as the pigs adapt to the change. Their ability to cope with weaning can be influenced by the pre-weaning management and weaning age. With growing and finishing pigs, there may be issues with feed availability as it pertains to the number of pigs per feeding space, placement of feeders within the pen and group size. The physical properties of the feed (ingredients, particle size, pelleting versus meal versus mash) may impact the behavior, health and well-being of the pigs. The diet may contain feed additives, such as repartitioning agents and growth promoters, some of which may affect the pigs′ physiology and behavior, again leading to potential well-being concerns. Overall, a clearer understanding of how behavior interacts with nutrition can enable husbandry to be adjusted to better safeguard and improve swine welfare and production.

Key Words: swine, behavior, nutrition

730 Effect of distance moved during loading, lairage time, and distance moved to stun on blood lactate concentration of pigs in a commercial slaughter plant. L. N. Edwards*[1], T. Grandin[1], T. E. Engle[1], M. J. Ritter[2], A. Sosnicki[3], B. A. Carlson[1], and D. B. Anderson[1], [1]*Colorado State University, Fort Collins*, [2]*Elanco Animal Health, Greenfield, IN*, [3]*PIC, Hendersonville, TN*.

Two studies were conducted to assess the relationship between management and blood lactate concentration (LAC) of pigs. A 2 × 2 × 2 repeated measures factorial design was used (Exp. 1, n = 64; Exp. 2, n = 144; pig = experimental unit) exploring distance moved at the farm (T1), lairage time (T2) and distance moved to stun (T3) on LAC of pigs in a commercial slaughter plant. Pigs were moved a short (15 m) or a long (46 m) distance (T1) during loading at the farm. Pigs were transported for approximately 2.5 h to the packing facility where they were rested for a short (30 min) or long (4.5 h) period (T2). After lairage, the pigs were moved a short (20 m) or long (300 m) distance to stun (T3). Pigs from each treatment subclass were equally distributed on each truckload. Pigs were electrically stunned and exsanguinated. A lactate analyzer was used to measure LAC at seven time points during the marketing process: baseline, post-load, pre-unload, post-unload, post-lairage, post-movement to the stunner and at exsanguination. In Exp. 1 and 2 LAC changed ($P < 0.0001$) during the marketing process; the highest LAC was observed at loading and exsanguination. Long distance moved during loading resulted in higher (8.3 & 6.0 mM; $P = 0.0001$) LAC during loading (Exp. 2). Unexpectedly, in Exp. 2, pigs rested for a longer period had higher LAC post-lairage (3.6 & 3.0 mM; $P = 0.02$), post-movement to stun (4.7 & 3.8 mM; $P = 0.01$) and at exsanguination (8.1 & 5.5 mM; $P = 0.0001$). In Exp. 1, pigs rested for a long period had greater increases (change between time points) in LAC during the immediate pre-stun handling (+5.6 & +3.6 mM; $P = 0.003$). Differences between experiments could be explained by difference in season, facility design and specifics of experimental protocols. Blood lactate was greater in pigs moving a short distance to stun (7.6 & 5.8 mM, Exp. 1; 7.2 & 6.0 mM, Exp. 2; $P < 0.04$) than those moving the long distance. This study emphasized the impact that pre-slaughter management has on LAC of pigs from farm to stun and demonstrates that the greatest handling stress is at loading and exsanguination.

Key Words: lactate, lairage, pre-stun

731 Validation of saliva sampling techniques in swine in order to assess stress responses. S. M. Hayne*[1], N. J. Cook[2], and H. W. Gonyou[1,3], [1]*Prairie Swine Centre, Saskatoon, SK, Canada*, [2]*Alberta Agriculture and Rural Development, Edmonton, AB, Canada*, [3]*University of Saskatchewan, Saskatoon, SK, Canada*.

Salivary cortisol is an outcome measure that can be used as an indication of what pigs are experiencing when exposed to various production methods. Saliva sampling has the potential to be a relatively non-invasive method of determining cortisol concentration. However, techniques have not yet been validated or standardized for use in grower-finisher pigs. The purpose of this study was to determine the effect that different sampling regimes have on salivary cortisol concentration. The first regime involved sampling individually housed pigs as many times as possible over 30 min. The second regime involved sampling individually housed pigs every 30 min for three hours. The third regime involved sampling pigs housed in groups of five. During group sampling, only one focal pig was sampled every 30 min for three hours. The other pigs were all sampled at the beginning and either at 30, 60, 120, 150 or 180 min (interval-sampled). Sampling difficulty was also recorded. For the pigs that were sampled intensively for 30 min, sampling difficulty did not have an effect on cortisol concentration ($P>0.05$). However, cortisol concentration increased over time ($P<0.05$). This could indicate that this sampling method is stressful for pigs. For individually housed pigs that were sampled every 30 min, cortisol concentration increased when sampling was difficult ($P<0.05$). However, over time, cortisol concentration decreased ($P<0.05$). This could indicate that the sampling method was

not stressful for the pigs. For group-housed pigs, cortisol concentration also increased when sampling was difficult (P<0.05), but did not change over time. The cortisol concentration did not differ between the focal and interval-sampled pigs in the group setting. Group/interval sampling appears to be the least stressful regime for collecting saliva samples. These results increase confidence that salivary cortisol concentration indicates a stress response to the situation being tested (for example, the effect of crowding) and not a response to the sampling procedure.

Key Words: cortisol, stress, pigs

732 Influence of season on the behaviour of market weight pigs transported 2 hours to slaughter. S. Torrey*[1], S. Hayne[2], R. Bergeron[3], L. Faucitano[1], T. Widowski[3], N. Lewis[4], T. Crowe[5], C. Dewey[3], and H. Gonyou[2,5], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*, [2]*Prairie Swine Centre*, *Saskatoon, SK, Canada*, [3]*University of Guelph*, *Guelph, ON, Canada*, [4]*University of Manitoba*, *Winnipeg, MB, Canada*, [5]*University of Saskatchewan*, *Saskatoon, SK, Canada*.

There is evidence that season plays an important role in pig death losses during transportation, although little is known about the seasonal effects on pig behaviour after transportation, and whether there is an interaction between trailer design and season. This experiment was designed to examine the influence of season on unloading and lairage behaviour of market weight pigs transported on two different trucks. Over the course of 12 weeks during winter and summer, 3,192 pigs were transported for 2 h on either a three-deck pot-belly truck with internal ramps to upper and lower levels (PB; n=181 pigs per week in 8 experimental compartments; 0.40 m2/pig) or a double-decker hydraulic truck without internal ramps (DD; n=85 pigs per week in 4 compartments; 0.40 m2/pig) to a commercial abattoir. Pigs were unloaded by compartment at the abattoir and driven into lairage pens segregated by truck compartment. Behaviour during unloading (slips and falls), time to unload each compartment, and latency to rest (75% of pen lying) during the first hour of lairage were observed. Behaviour data were analyzed using the mixed model procedure in SAS, with season and truck as fixed effects and week within season as random effect. Data were weighted for the number of pigs in each compartment. Pigs took longer to unload in winter (P=0.04; summer: 59 ± 3s; winter: 68 ± 3s) and from the PB truck (P<0.001; PB: 74 ± 2s; DD: 53 ± 4s), although the seasonal effect tended to be more pronounced for pigs unloading from the DD (Season × Truck, P=0.08). During unloading, there were more slips and falls during winter (P<0.0001; summer 1.1 ± 1.6 slips/falls; winter: 8.0 ± 1.6 slips/falls) regardless of truck (P=0.66). Latency to rest in lairage was shorter (P=0.006) in winter (31 ± 2 min) than summer (40 ± 2 min) but there was no effect of truck (P=0.40) or truck by season (P=0.19). In summary, season influences unloading and lairage behaviour of market-weight pigs, making unloading more difficult in winter. These results may help interpret the variation in animal welfare and meat quality.

Key Words: pig, transportation, season

733 Effects of linoleic and α-linolenic acid intake on pig behaviour, and its relationship with brain DHA. J. E. Bolhuis, I. van Kerkhof, and W. J. J. Gerrits*, *Wageningen University*, *Wageningen, the Netherlands*.

Effects of linoleic acid (LA) and α-linolenic acid (ALA) on behaviour of individually housed pigs (15-30 kg BW) were studied. In a 2×2 factorial arrangement, 32 gilts from 4 litters were assigned to one of four dietary treatments, varying in LA and ALA intake. Differences between low and high intake levels were designed to be identical for LA and ALA: Low ALA and LA intakes were 0.15 and 1.30, and high ALA and LA intakes were 1.45 and 2.60 g/(kg $BW^{0.75}$.d), respectively. Intakes of saturated and mono-unsaturated fatty acids (FA), and other nutrients were kept constant. Pigs were subjected to an open field test (d 15) and a novel object test (d 16). In addition, behaviour in the home pen was observed using 2-min instantaneous scan sampling for 5 h per day (d 12 and d 18). After 28 d on the dietary treatments, pigs were sacrificed and brain tissues were sampled and analyzed for FA composition. The latencies to approach and touch the novel object were reduced by ALA intake, but at the low LA intake only (LA*ALA, P<0.05). The low LA-high ALA combination also tended to reduce standing alert in the open field (P=0.08). The percentage of time spent nosing in the open field, and exploratory behaviours in the home pen were reduced by LA intake (P<0.05). Although dietary treatments did not greatly influence DHA concentrations in the hippocampus and frontal cortex (P>0.05), DHA concentrations in the frontal cortex were positively correlated with explorative behaviour (r = 0.56, P<0.001). In conclusion, an increase in ALA intake, specifically at low LA intake levels, causes consistent changes in behavioural patterns, indicating reduced fear and increased exploration. It is unclear to what extent DHA concentrations in the brain are important for mediating these effects.

Key Words: DHA, pig, behaviour

734 The motivation of gestating sows for environmental enrichment in a stall. M. R. Elmore*[1], J. P. Garner[1], A. K. Johnson[2], R. D. Kirkden[1], E. G. Patterson-Kane[1], B. T. Richert[1], and E. A. Pajor[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*Iowa State University*, *Ames*.

Sows are often housed in barren stalls during breeding and gestation. Providing environmental enrichments for which sows are highly motivated should improve welfare. The aim of this study was to compare the motivation of Yorkshire x Landrace gestating sows (32, n=8/reward) housed in standard gestation stalls for access to 1 of 4 rewards. Environmental enrichments: spent mushroom compost (C, 2.27 kg) or straw (S, 0.45 kg) were tested. Additionally, food (F, 0.91 kg) and an empty trough (T) were included as positive and negative controls, respectively. We predicted that enrichments for which sows were highly motivated would be similar to F and/or significantly different from T, while low motivation enrichments would resemble T. While in visual and olfactory contact with rewards, sows were trained to press an operant panel on an increasing schedule. The highest schedule pressed indicated motivational strength. Sows were given 1 hr to press the panel and 23 hr to interact with the reward. Data were analyzed using GLM and post-hoc Tukey tests. The C sows showed higher motivation (# of presses) for the reward (196.88 ± 46.38, LS means ± S.E.) than T (55.85 ± 46.75; P=0.017), S and T did not differ (P>0.05). The F sows pressed more than all other treatments (462.87 ± 46.38; all P<0.01). The C sows started pressing the panel more quickly (sec; 5.00 ± 156.40) than S (332.88 ± 156.40) and T (271.43 ± 157.70; P=0.069 and P=0.011, respectively), while F pressed more quickly (11.25 ± 156.40) than T (P=0.046); all other latency comparisons did not differ (P>0.05). The F sows used a higher proportion of the reward (1.00 ± 0.08) compared to C (0.80 ± 0.08) and S (0.70 ± 0.08; P=0.042 and P=0.007, respectively), C and S did not differ (P=0.682). Gestating sows housed in stalls were highly motivated for C and F, but showed low motivation for S and T. The C and F sows pressed the panel sooner, while F sows used a higher proportion of the reward, which may indicate increased motivation. The provision of

compost is of value to sows housed in barren stalls and may improve their welfare in production settings.

Key Words: enriched housing, gestating sows, motivation

735 Effect of premolar eruption on growth and behaviour of weaned piglets. A. L. Tucker* and T. M. Widowski, *University of Guelph, Guelph, ON, Canada*.

Standard profiles for the deciduous dental eruption of our `modern' commercial pigs have recently been shown to have later eruption as compared to reports from the 1970's. Additionally, premolar eruption was found to influence the amount of time young piglets spent at the creep feeder during the pre-weaning period, making dental eruption of interest to the commercial sector. The objectives of this study were to determine whether premolar eruption or occlusion at time of weaning at 28 days of age influenced piglets' growth or behaviour over the following 2 weeks. A total of 112 Yorkshire piglets (16 litters of 7 piglets) had their dentition examined the day prior to weaning (age 27 days) with eruption and contact between opposing premolars being scored as occurring or not. Weight was recorded at birth, weaning, and on days 3 and 7 after weaning. Behaviour data was collected from video recordings on days 2, 4, 6, 8, 10 and 12 after weaning using scan sampling every 5 min during three 2-hr time periods (0600:0800, 1100:1300, 1600:1800). Mixed model ANOVAs (SAS) were employed to test how premolar eruption and occlusion influenced piglet growth 3 and 7 days after weaning, while repeated measures ANOVAs were employed to examine associations between dentition and ingestive behaviours (time spent at the feeder and time spent at the drinker) and oral-nasal behaviours (rooting of the pen, rooting of pen-mates, belly nosing) over the following 2 weeks. By 27 days, all piglets had their maxillary p^3 and mandibular p_4 erupted. Occlusion between 3 opposing premolars was achieved by 48.2% of the population, and eruption of the mandibular p_3 and maxillary p^4 had occurred in 96.4% and 81.2% of the population, respectively. None of the dental measures influenced post-weaning growth rates ($P > 0.10$) or the performance of any behaviour ($P > 0.10$). This study demonstrates that variability in premolar eruption by 27 days of age is low and does not influence either the time spent in any behaviour over the following 2 weeks or growth in the first 3 and 7 days of weaning.

Key Words: teeth, feeding, weaning

736 Pen and stall-housed gestating sows prefer unlocked to locked free-access stalls. L. M. W. Jones*[1], J. P. Garner[1], J. N. Marchant-Forde[2,1], and E. A. Pajor[1], [1]*Purdue University, West Lafayette, IN*, [2]*USDA Livestock Behavior Research Unit, West Lafayette, IN*.

Animal controlled stalls, such as free-access stalls, provide sows with individual protection but also provide access to a common group area. Preference testing determines the extent to which sows prefer or are averse to different housing methods. The objective of our study was to determine if sows showed a preference for locked or unlocked free access stalls and if that was influenced by their housing background. Two experiments gave 32 sows from 2 different housing backgrounds a choice between locked and unlocked free access stalls. In the unlocked stall, sows could stay in the stall or use a 3.6 m^2 area outside the stall. The 1st experiment used 16 pen-housed sows while the 2nd experiment used 16 sows from standard gestation stalls. Sows were 2nd or 3rd parity and within the 1st mo of gestation. Pen location was balanced in both experiments. Other than housing background, the methodology for each experiment was the same. On d1, each sow was given 3 h to habituate to both sides of a T-maze. On d2, the sow was trained to each side of the maze twice, for 30 min. On d3, the 1st day of testing, sows experienced each side once before being tested with 8 free choices. During free choices, the time sows were kept in the chosen stall was reduced to 15 min. On d4, sows rested. On d5, the last 8 free choices were conducted. This resulted in a total of 16 free choices for each sow to demonstrate a preference. Data were analyzed, after angular transformation, using the mixed model procedure in SAS. In experiment 1, sows housed in pens showed a preference for the unlocked free access stall (10.000 ± 0.713, $P=0.0193$). In experiment 2, sows housed in standard gestation stalls also showed a preference for unlocked free access stalls (10.875 ± 0.464, $P=0.0002$). The results of both experiments demonstrated that regardless of housing background, sows had a strong preference for some characteristic of the unlocked free access stall, which might include access to space, and the freedom of choice and movement. These characteristics should be considered when designing sow housing systems.

Key Words: preference testing, sow housing, welfare

737 Making sense of fear testing– Validating common behavioral tests used in swine. D. C. Lay Jr.*[1] and J. P. Garner[2], [1]*Agricultural Research Service - USDA, West Lafayette, IN*, [2]*Purdue University, West Lafayette, IN*.

In lab animals, fear tests assay the influence of drugs, genes, and environments on an animal's fearfulness. Livestock welfare researchers have adopted many of these tests to measure the fearfulness of animals. Tests used to assess fear in swine include the Approach/Avoidance Test, Novel Object test, and the Startle test. These tests place animals in conflict situations where less fearful individuals should express fewer behaviors believed to be indicative of fear. For these data to be meaningful, the tests should be both reliable and valid. However, they have not been validated in swine. Although behaviors in these tests might resemble a fearful human in a similar situation, we do not know whether the behaviors measured are actually indicative of fear. In addition, welfare certification programs often include fear assessment in their auditing, although the methods may not be reliable or valid. This causes confusion for producers, who need accurate, conclusive information. Some members of the NC-1029-Applied Animal Behavior and Welfare committee designed research to address this problem. Three tests were chosen for validation: 1) Approach/Avoidance Test, 2) Novel Object Test, and 3) the Startle Test. Care was taken to replicate the tests as precisely as possible, controlling for: the size of the pigs, the gender, the size of the test pen, the color of clothes the researchers wore, time of testing, etc. Factor analysis (with varimax rotation) identified 7 factors with eigen scores greater than 1, accounting for 72% of the variation in behavior. Behaviors with loadings >0.4 were considered to be influenced by a factor. Factors labeled "elimination", "searching for contact", and "vocalization", loaded urination, defecation, vocalizations and number of squares crossed consistently across tests. In contrast, other purported measures of fear, such as distance and latency to approach a person or object, loaded consistently within tests, but onto separate factors between tests ("Object freezing", "object investigation", "human freezing", "human exploration"), indicating that these measures are specific to the test rather than generalizable indicators of fear.

Key Words: fear, swine, tests

738 Jersey × Holstein crossbred cows compared to pure Holstein cows for fertility and survival during the first three lactations. B. J. Heins*, L. B. Hansen, A. R. Hazel, A. J. Seykora, D. G. Johnson, and J. G. Linn, *University of Minnesota, Saint Paul*.

Jersey × Holstein crossbred (**J×H**, n = 80) cows were compared to pure Holstein (n = 77) cows for days to first breeding, number of inseminations, days open, pregnancy rate, survival to second lactation, and survival to third lactation during the first three lactations. Cows were in two research herds of the University of Minnesota and calved from September 2003 to June 2008. The J×H cows were mated to Montbeliarde sires, and Holstein cows were mated to Holstein sires. For days open, cows were required to be at least 250 d in milk and those with greater than 250 d for days open were truncated to 250 d. Independent variables for statistical analysis of days to first breeding, number of inseminations, and days open were the fixed effects of herd, season (fall or spring) nested within herd, breed group, lactation number nested within breed group, and cow within breed group was a random effect. For pregnancy rate, survival analysis was used to assess breed differences. For survival, a Chi-square test was used to evaluate breed differences. The JxH cows had significantly ($P < 0.05$) fewer days to first breeding in first (79 d vs. 90 d), second (78 d vs. 86 d), and third (64 d vs. 77 d) lactation. Additionally, JxH cows were not significantly different from pure Holstein cows for number of inseminations in first and third lactations. However, in second lactation, J×H cows had significantly ($P < 0.05$) fewer number of inseminations (2.21 vs. 2.73) than pure Holstein cows. For days open, J×H cows had significantly ($P < 0.05$) fewer days open than pure Holstein cows in first lactation (124 d vs. 148 d), second lactation (121 d vs. 163 d), and third lactation (158 d vs. 200 d). Furthermore, J×H cows had significantly ($P < 0.05$) higher pregnancy rates in first (20% vs. 12%) and second (25% vs. 13%) lactations. For survival to second calving, J×H cows (80%) were not significantly different from pure Holstein cows (71%). However, more JxH cows (64%) tended ($P < 0.10$) to calve a third time than pure Holstein cows.

Key Words: crossbreeding, heterosis, Jersey

739 Jersey × Holstein crossbred cows compared to pure Holstein cows for production, SCS, and udder measurements during the first three lactations. B. J. Heins*, L. B. Hansen, A. R. Hazel, A. J. Seykora, D. G. Johnson, and J. G. Linn, *University of Minnesota, Saint Paul*.

Jersey × Holstein crossbred (J×H, n = 76) cows were compared to pure Holstein (n = 73) cows for 305-d milk, fat, and protein production, lifetime production, SCS, and udder measurements during the first three lactations. Cows were in two research herds of the University of Minnesota and calved from September 2003 to June 2008. The J×H were mated to Montbeliarde sires, and Holstein cows were mated to Holstein sires. Best Prediction was used to determine lifetime production (to 1220 d after first calving) and actual production for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Independent variables for statistical analysis were the fixed effects of herd, season (fall or spring) nested within herd, breed group, lactation number nested within breed group, and cow within breed group, which was a random effect. During first lactation, JxH (518 kg) and pure Holstein (526 kg) cows were not significantly different for fat plus protein production. However, during second (605 kg vs. 630 kg) and third (609 kg vs. 660 kg) lactations, JxH cows were significantly ($P < 0.05$) lower for fat plus protein production than pure Holstein cows. The JxH cows were not significantly different from pure Holstein cows for SCS during first and second lactations; however, JxH cows (3.80) tended ($P < 0.10$) to have higher SCS than pure Holstein cows (3.40) during third lactation. The J×H cows were not significantly different from pure Holsteins for lifetime milk (19,194 kg vs. 21,448 kg) and lifetime fat plus protein (1,361 kg vs. 1,455 kg) production. For udder measurements, JxH cows had significantly ($P < 0.01$) less udder clearance from the ground than pure Holstein cows in first (47.8 cm vs. 54.8 cm), second (42.4 cm vs. 51.4 cm), and third (40.4 cm vs. 48.9 cm) lactations. Furthermore, JxH cows had significantly ($P < 0.01$) greater distance between front teats in first (15.7 cm vs. 14.0 cm), second (17.0 cm vs. 14.7 cm), and third (17.7 cm vs. 15.6 cm) lactation than pure Holstein cows.

Key Words: crossbreeding, heterosis, Jersey

740 Positive percent heterosis for fat-corrected milk per day of life from Holstein-Jersey diallel. R. D. Shanks*[1], B. G. Cassell[2], K. M. Olson[2], A. J. McAllister[3], and S. P. Washburn[4], [1]*University of Illinois, Urbana*, [2]*Virginia Polytechnic Institute and State University, Blacksburg*, [3]*University of Kentucky, Lexington*, [4]*North Carolina State University, Raleigh*.

Objective was to estimate heterosis for performance of a population of dairy cows from a diallel crossbreeding experiment [S-1040 regional research project]. Fat-corrected milk was proposed almost a century ago to evaluate breeds on an energy basis. Milk per day of life can evaluate efficiency by combining the effects of lifetime milk production and length of life. Integrating the two concepts identified fat-corrected milk per day of life (FCMPD) as the variable of choice for the estimation of heterosis. Residuals for FCMPD were more normally distributed than were residuals for lifetime milk production or length of life. The 230 cows for this analysis were born between June 2003 and September 2006, housed in North Carolina (NC)(34), Kentucky (KY)(49) and Virginia (VA)(147), and were required to have initiated at least one lactation. Most cows were alive in January 2009, NC (31), KY (45) and VA (98). Holsteins (H) and Jerseys (J) defined the four breed groups, with sire breed first, of 66 HH, 55 HJ, 65 JH, and 44 JJ cows. The general linear model for analysis included effects of herd (KY, NC, or VA), alive status (alive or dead), birth year (2003, 2004, 2005, or 2006) and breed group (HH, HJ, JH, or JJ). The model accounted for 71% of the variation in FCMPD and all factors were significant. The KY herd had the greatest FCMPD and the NC herd had the smallest FCMPD. Older cows had longer opportunities for performance and had higher FCMPD. Least squares means (standard errors) for FCMPD ranged from 14.0 kg (.6) for cows born in 2003 to 3.2 kg (.5) for cows born in 2006. Cows still alive had higher FCMPD than dead cows. Percent heterosis for FCMPD was estimated as 16.8%. Least squares means (standard errors) for FCMPD for the breed groups were 10.18 kg (.41) for HJ, 10.34 kg (.42) for JH, 9.84 kg (.39) for HH, and 7.72 kg (.43) for JJ indicating overdominance of the crossbreds. Actual FCMPD is expected to rise as more cows complete their lifetimes and the percent of active cows is reduced.

Key Words: fat-corrected milk per day of life, heterosis, crossbreeding

741 Energy balance in first lactation Holsteins, Jerseys, and reciprocal crosses estimated using random regression. K. M. Olson*, B. G. Cassell, and M. D. Hanigan, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

The Virginia Tech crossbreeding project mated Holstein and Jersey females to four Holstein and four Jersey bulls to create HH, HJ, JH, and JJ breed groups (sire breed listed first). Intakes were measured from September 2005 to March 2008 for two weeks out of every six week period on cows in first lactation and less than 306 days in milk. Cows with intake observations numbered 44, 32, 29, and 13 for HH, HJ, JH, and JJ, respectively. NEL (Mcal) was calculated from ration analyses. Body and milk weights were collected daily with milk components measured monthly. NEL requirements for maintenance, growth, production, and pregnancy were calculated using NRC (2001) equations. Random regression models were used to estimate NEL of consumption and NEL required for production, maintenance, and body weight at every week in lactation (WOL). Energy required for growth was calculated for each cow at each stage of lactation (five two month stages). Energy balance was estimated at every WOL by subtracting energy required for production, maintenance, growth, and pregnancy from NEL consumed. A linear model with fixed effects of breed group, year-season of freshening group, and a linear and quadratic effect of age at calving was used to analyze energy terms. HJ and JH were not different in any analyses for energy terms. The HH cows consumed more energy than HJ and JJ. There were no breed group differences for total energy required for pregnancy. The HH, HJ, and JH were not different for energy required for production but were different from JJ. No differences were found for percent energy used for pregnancy and growth. The JH allocated less energy to maintenance than the HH (25.8% versus 27.6%). There were no breed group differences for week of return to positive energy balance or positive cumulative energy balance. Breed group explained significant variation for cumulative energy balance at the end of lactation ($P < 0.10$), but no pair of breed groups differed significantly.

Key Words: crossbreeding, dairy cows, energy balance

742 Calving traits, gestation length, and birth weight of Montbeliarde sires mated to Holstein or Jersey × Holstein crossbreds. B. J. Heins, L. B. Hansen*, A. R. Hazel, A. J. Seykora, D. G. Johnson, and J. G. Linn, *University of Minnesota*, *Saint Paul*.

Pure Holstein cows (HOL) and Jersey × Holstein crossbred cows (J×H) were compared for calving difficulty (CD), stillbirths (SB), gestation length (GL), calf birth weight (BW), and twinning rate (TR). Cows were in two research herds of the University of Minnesota and calved from August 2003 to December 2008. HOL (n=415) bred to either Holstein or Montbeliarde AI bulls during second and later lactation were compared to determine the effect of breed of sire. Statistical models for analysis of CD, SB, GL, and BW included the fixed effects of herd, sex of calf, breed group, and cow, which was a random effect. For CD and SB, respectively, calves (n=138) sired by Montbeliarde bulls (9.3%, 4.3%) were not significantly different from calves (n=277) sired by Holstein bulls (5.9%, 4.1%). The Montbeliarde-sired calves (283.2 d) also had significantly ($P < 0.01$) longer GL than Holstein-sired calves (278.4 d). Montbeliarde-sired calves (n=134) had significantly ($P < 0.01$) higher BW (48.3 kg vs. 43.3 kg) compared to Holstein-sired calves (n=266). Additionally, HOL mated to Holstein sires and J×H mated to Montbeliarde sires were compared during their first three lactations. Statistical models for analysis of CD, SB, GL, and BW included fixed effects of herd, season (fall or spring) nested within herd, sex of calf, breed group, lactation number nested within breed group, and cow within breed group, which was a random effect. However, a Chi-square test was needed to evaluate breed differences for TR. For CD and SB, JxH (n=177) were not significantly different from HOL (n=160) during the first three lactations. GL was significantly ($P < 0.05$) longer for J×H than HOL in first (280.3 d vs. 277.7 d), second (280.7 d vs. 278.4 d), and third (283.8 d vs. 278.8 d) lactation. Across lactations, JxH had a significantly higher ($P < 0.05$) TR than HOL (7.7% vs. 3.0%). J×H tended ($P < 0.10$) to have Montbeliarde-sired calves (n=71) with less BW (37.6 kg vs. 38.9 kg) than pure Holstein calves (n=74) during first lactation.

Key Words: calving difficulty, crossbreeding, stillbirths

743 Montbeliarde-sired crossbred cows compared to pure Holstein cows for body weight, body condition score, hip height, dry matter intake, and production during the first 150 days of first lactation. A. R. Hazel*, B. J. Heins, L. B. Hansen, A. J. Seykora, D. G. Johnson, and J. G. Linn, *University of Minnesota*, *Saint Paul*.

Differences in body weight (BW), body condition score (BCS), hip height (HH), dry matter intake (DMI), and milk, fat, and protein production were compared for Montbeliarde-sired crossbred cows (MX, n = 57) and pure Holstein cows (HOL, n = 40). MX consisted of 33 F_1 crossbreds of Montbeliarde x Holstein (MH) and 24 3-breed crossbreds of Montbeliarde x Jersey/Holstein (MJH). Data was collected during the 147-d interval from 4 d to 150 d postpartum of first lactation. Cows were housed at the University of Minnesota research facility, St. Paul, and calved during fall seasons between October 2005 to December 2007. BW and BCS were recorded bi-weekly, and HH was measured once between 20 and 172 DIM. Cows were individually fed a TMR twice daily, and feed weighbacks were collected once daily during a 147-d interval from 4 d to 150 d postpartum. Independent variables for the statistical analysis of BW, BCS, HH, DMI, and production were age at calving (mo, linear), year of fall calving, breed of sire (Holstein vs. Montbeliarde), and MH vs. MJH nested within breed group for all dependent variables. Furthermore, period postpartum (14-d for BW and BCS and 7-d for DMI) within breed of sire (Holstein vs. Montbeliarde), and random effect of cow nested within breed of sire and MH vs. MJH were added to the model for BW, BCS, and DMI. MX had significantly ($P < 0.01$) more BW than HOL (537 kg vs. 514 kg, respectively), and MH (550 kg) had more BW ($P < 0.01$) compared to MJH (524 kg). For BCS, MX had more BCS ($P < 0.01$) than HOL (3.28 vs. 2.72). However, MX (139 cm) had significantly ($P < 0.01$) shorter HH than HOL (141 cm). DMI did not differ for MX and HOL (19.3 kg vs. 20.0 kg, respectively). Fat plus protein production during the interval from 4 d to 150 d postpartum did not differ for MX and HOL (305 kg vs. 308 kg), nor did MH (303 kg) differ from MJH (308 kg). In summary, DMI and production did not differ between MX and HOL, but MX maintained more BCS and BW in early lactation than HOL.

Key Words: crossbreeding, Montbeliarde, dry matter intake

744 A comparative study of Holstein and Jersey crossbred cows in 14 Australian dairy herds. M. F. Pyman*, G. A. Anderson, and K. L. Macmillan, *University of Melbourne*, *Werribee, Victoria, Australia*.

Production, reproduction and somatic cell count (SCC) data were analysed in a study of Australian seasonally calving, pasture-based dairy herds with at least 15% crossbred cows of first cross Jersey × Holstein (JJFF) and backcross Holstein x Jersey Holstein (FFJF) breed type. Proc GLIMMIX of SAS was used for analysis. Production and

reproduction data from 669 JJFF and 305 FFJF cows in 14 herds were analysed to produce least squares means adjusted for herd, age group and calving to the start of mating. Over 305 days the backcross FFJF cows produced a similar amount of fat (4.9 ± 3.8 kg difference, p=0.20) but significantly more litres (515 ± 100L difference, p<0.0001), protein (10.5 ± 3.3 kg, p=0.0014) and fat plus protein (15.4± 6.9 kg, p=0.026) than the JJFF cows. The JJFF first cross cows had superior reproductive performance compared to the FFJF backcross cows for conception rate to first service (n=615, 57.6% versus 48.2%, n=279, p=0.012) and pregnancy rate after 42 days of breeding (67.6% versus 60.5%, p=0.039) but similar performance in pregnancy rate after 14 weeks of breeding (84.3% versus 82.6%, p=0.48) and not pregnant at the end of breeding (13.7% versus 13.9%, p=0.93). Ln(lactation mean SCC) from 13 herds was analysed in a linear model to produce geometric means of SCC after adjusting for herd and age group. The 199 FFJF backcross cows had a geometric mean significantly lower than the 501 first cross JJFF cows (50.8′000 cells/ml versus 60.1′000 cells/ml, p=0.035). Results indicate that expression of hybrid vigour was variable in the FFJF backcross as it achieved a similar reproductive performance to the first cross JJFF after 14 weeks of breeding and at the end of the breeding period while attaining superior production and a lower geometric mean SCC for the lactation. The backcross FFJF cow would appear to be a viable breed type for pasture-based, seasonally calving dairy herds.

Key Words: seasonal calving, first cross, backcross

745 Preliminary analysis of NRF-Holstein crossbred cattle in Israel. E. Ezra[1], Y. Zeron[2], and J. I. Weller*[3], [1]*Israel Cattle Breeders Association*, *Caesaria, Israel*, [2]*Sion*, *Shikmim, Israel*, [3]*ARO, The Volcani Center*, *Bet Dagan, Israel*.

Approximately 99% of all dairy cows in Israel are Holsteins. Over the last decade samples of Holstein cows have been inseminated with imported semen from several different breeds, including Montbeliard and Jersey. Importation of Norwegian Red (NRF) semen began in 2005. This is the first report on the performance of F1 NRF-Holstein crosses in Israel. The analysis was based on 27 herds with at least 4 crossbred cows with at least 75 DIM per herd-year-season. Cows were included only if their sires had reliability > 0.75 for production traits. Two seasons were defined within each herd-year beginning in April and October. The analysis was based on 1425 purebred and 168 crossbred first parity cows, daughters of 108 Holstein and 3 NRF sires. Mean DIM were 231 and 246, respectively. There were two bases for comparison: the mean phenotypic values of first parity purebred and crossbreed cattle in these herds, and the mean breeding values of the sires of these cows, weighted by the number of daughters per bull. Breeding values for milk, fat and protein production were computed by the multitrait animal model, with parities 1 through 5 as correlated traits. Only purebred Holsteins had records for later parities. Results of the two comparisons are presented in Table 1. Differences were very similar for both criteria for all five traits, even though the purebred breeding values were based on multiple parities. Direct effects of sire breed on dystocia and calf mortality were compared based on 6009 purebred and 2112 crossbred calvings in these herds. Purebred Holsteins were 0.45% lower for mean dystocia, and 0.08% higher for calf mortality. Differences in the mean weighted breeding values were the same for dystocia. Mean breeding values for calf mortality were 0.25% higher for purebreds.

Table 1. Comparison of the purebred and crossbred cows for milk production traits

Comparison	Cow type	Milk (kgs)	Fat (kgs)	Protein (kgs)	Fat %	Protein %
Phenotypic	purebred	12,122	428.5	384.5	3.55	3.18
	crossbred	11,500	406.9	373.9	3.55	3.26
	difference	622	21.6	10.6	0.00	-0.08
Breeding values	purebred	97	9.7	8.1	0.06	0.05
	crossbred	-555	-14.3	-5.2	0.05	0.12
	difference	653	23.9	13.3	0.01	-0.07

Key Words: crossbreeding, Israeli Holsteins, NRF

746 Brown Swiss × Holstein crossbreds compared to pure Holsteins for production, SCS, milking speed, days to first breeding and days open. S. Bloettner*[1], M. Wensch-Dorendorf[1], H. H. Swalve[1], B. J. Heins[2], and L. B. Hansen[2], [1]*Group Animal Breeding, Halle (Saale), Saxony-Anhalt, Germany*, [2]*Department of Animal Breeding, University of Minnesota, Saint Paul*.

The objective of the study was to assess the competitiveness of Brown Swiss x Holstein crossbreds (BSH) with respect to dairy production traits. BSH (n = 55) were compared to pure Holsteins (HOL, n = 50) during the first three lactations for 305-d milk, fat and protein production, SCS, days to first breeding and days open at the experimental station in Iden, Germany. First calvings started in September 2005. All animals originated from a designed experiment. Best Prediction was used to determine actual production for milk, fat, protein and SCS. Data was pre-adjusted for age at calving and records less than 305 d were extended to 305 d. Variables in the model for statistical analysis of production and fertility were the fixed effects of breed group, lactation number, lactation number nested within breed group, season of calving (fall or spring) nested within lactation number, and cow within breed group was a random effect in the model. For 305-d milk production, BSH and HOL were not significantly different in first (8,689 kg. vs. 8,889 kg.) or second (10,251 kg. vs. 10,446 kg.) lactation. During third lactation, BSH (10,450 kg) were significantly ($P < 0.05$) lower than pure HOL (11,096 kg) for milk volume. BSH and HOL were not significantly different for fat plus protein production in first (668 kg vs. 674 kg), second (786 kg vs. 801 kg) and third lactation (812 kg vs. 794kg). Across lactations, BSH and HOL were not significantly different for SCS (2.72 vs. 2.68). BSH had significantly ($P < 0.01$) lower average milk flow (kg/min) than HOL (1.91 vs. 2.19, respectively) across the three lactations. Average milking time was significantly ($P < 0.01$) greater for BSH (5.68 min) than for HOL (5.05 min). Over all lactations, BSH had significantly ($P < 0.01$) fewer days to first breeding than HOL (78 d vs. 84 d, respectively). For days open, BSH and HOL did not differ significantly during first (94 d vs. 107 d), second (102 d vs. 116 d) and third (119 d vs. 121 d) lactation. Summarizing, BSH were equal in production and had lower cell counts in first lactation than HOL.

Key Words: crossbreeding, Brown Swiss, production

747 Brown Swiss × Holstein crossbreds compared to pure Holsteins for body weight, back fat thickness and udder measurements during the first two lactations. S. Bloettner*[1], M. Wensch-Dorendorf[1], H. H. Swalve[1], J. Guehne[2], B. J. Heins[3], and L. B. Hansen[3], [1]*Group Animal*

Breeding, Halle (Saale), Saxony-Anhalt, Germany, [2]Technical College for Agriculture, Haldensleben, Saxony-Anhalt, Germany, [3]Department of Animal Science, University of Minnesota, Saint Paul.

The objective of the study was to assess the competitiveness of Brown Swiss x Holstein crossbreds (BSH) with respect to body weight and body measurements. BSH (n = 55) were compared to pure Holsteins (HOL, n = 50) for body weight (BW), backfat thickness (BF), udder clearance, teat length, and teat placement during first and second lactation. BF was measured with ultrasonography between the hooks and the thurl. Udder clearance was measured from the floor to the bottom of the udder. All animals originated from a designed experiment. Variables in the model for statistical analysis were the fixed effects of breed group, lactation number, lactation number nested within breed group, season (fall and spring) nested within lactation number, and days in milk nested within lactation number. Cow within breed group was a random effect in the model. Across lactations, BSH had significantly ($P < 0.05$) more BW than HOL (669 kg vs. 648 kg). During first (620 kg vs. 594 kg) and second (678 kg vs. 656 kg) lactations, BSH had significantly ($P < 0.05$) more BW than HOL. For BF, BSH (17.7 mm) tended ($P < 0.10$) to have more BF than HOL (16.3 mm) across the two lactations. However, BSH had significantly ($P < 0.01$) more BF (18.2 mm vs. 15.8 mm) than HOL in first lactation. HOL had significantly more udder clearance ($P > 0.01$) than BSH in first (60.0 cm vs.62.4 cm) and second lactation (52.3 cm vs. 56.9 cm). Rear udder clearance was significantly less ($P > 0.01$) for BSH than HOL in first (59.9 cm vs. 62.7 cm) and second lactations (52.0 cm vs. 57.1 cm), respectively. Teat length was significantly ($P < 0.05$) longer for BSH in first lactation (5.10 cm, front; 4.29 cm, rear) than for pure HOL (4.81 cm, front; 3.96 cm, rear). During second lactation, BSH had significantly ($P < 0.05$) longer front teats (5.0cm vs. 4.6 cm) and rear teats (4.0 cm vs. 3.6 cm) than HOL. Across first and second lactation, BSH (2.21 cm) had ($P < 0.05$) wider rear teats than HOL (2.11 cm). Summarizing, BSH had more body weight across lactation and differed in various body measurements from HOL.

Key Words: crossbreeding, Brown Swiss, heterosis

Dairy Foods: Dairy Foods Processing/Enzymes

748 Whey—From gutter to gold. P. J. Jelen*, *University of Alberta, Edmonton, AB, Canada*.

Whey.. oh whey! Where are the days when whey was a bothersome liquid resulting from the manufacture of cheese or casein and when pigs loved it! Careers were built on research projects aimed at utilization of this golden-green fluid, and descriptions of its magic properties were recorded in the literature since the days of Hippocrates. When nutrition became king, products based on whey started appearing on the market with increased frequency. Use of whey by modern dairy and food industries has developed along four main avenues: 1-products based on whole whey (principally whey cheeses and drinks); 2-products based on whey protein; 3-traditional and novel uses of lactose; and 4- everything else the whey research community came up with. Historically, the first attempts to utilize whey were aimed at "cutting the losses" of the cheesemakers by finding the least expensive disposal route, including uses as spraying onto pastures, transforming whey into animal feed, or simply discharging it into nearby streams. Crystallizing lactose from whey added some value, but brought the problem of what to do with the lactose. Nowadays, lactose is being crystallized mainly from the ultrafiltration permeates which replaced whey as the bad boy of the dairy industry, while whey itself is becoming the main product of interest in cheesemaking. Development of the various whey protein-based products advanced along two parallel and sometimes intertwined lines, technological and/or physiological functionality, and brought about the needed valorization aspect of whey usage for the mainstream processors. Whey drinks and whey cheeses, the traditional routes for turning whey into profitable products, are still important mainly in local markets as shown by the continued success of the Swiss whey drink, Rivella, or the popularity of the various whey cheeses in many countries. Some of the more unusual avenues for whey valorization, some of which are still in the "pipedream stage" include direct or indirect conversion into methane, economical production of unique high value lactose-based ingredients (e.g. "humanized oligosaccharides") or profitable utilization of the main whey ingredient, the cow-water.

Key Words: whey, history, products

749 Protein-interactions in heat-treated milk and effect on rennet coagulation. P. Kethireddipalli*, D. G. Dalgleish, and A. R. Hill, *University of Guelph, Guelph, ON, Canada*.

The underlying molecular processes that cause impaired rennet clotting of heat-treated bovine milk were investigated. Firstly, the effect of whey protein(WP)/κ-casein complexes bound to the casein micelle on the elastic modulus (G′) and gelation times (T) of renneted heat-treated milk was examined. Milks with different levels of micelle-bound WP (<5% to ~80%) were produced by heating skim milk at 90°C for 10 min at pH values ranging from 6.3 to 7.1. WP was quantified using SDS-PAGE. Lower pH produced higher micellar WP association and vice versa. Using oscillatory rheometry, we found that compared to unheated milk (G′, 83.5 Pa; T, 10 min) all heat-treated milks, after renneting, showed a remarkable reduction in G′ (0.1 to 2.1 Pa) and a large increase in T (55 to 130 min). It did not seem to matter if the WP/κ-casein complexes were predominantly bound to the casein micelle (pH 6.3) or were largely present as soluble protein complexes in the lactoserum (pH 7.1). In the second part, the individual effects of casein micelles and lactoserum on the rennet gelation properties of heated milk were investigated. Two different milk systems were examined; one was prepared by re-suspending casein micelles from milk heated at pH values 6.3, 6.7, or 7.1 in native serum from unheated milk, and the other contained native micelles from unheated milk in the serum from the various pH- and heat-treated milks. Heat- and pH-modified casein micelles suspended in native serum significantly lowered the G′values of the resulting rennet gels. With the exception of pH 6.3, the heated lactoserum also interfered with gelation of heat-treated milks. In the final part of our study, the serum from heat-treated milks was further examined after its ultrafiltration (removes WP/κ-casein complexes) or its dialysis against unheated milk (restores ionic composition). Both these processes significantly improved serum performance. This clearly demonstrated that not only serum ionic factors, but also serum WP/κ-casein complexes, and heat-modified casein micelles (with or without associated WP) significantly interfere with the rennet gelation of heat-treated milks.

Key Words: heat-treated milk, rennet, WP/κ complexes

750 Effect of processing aids on mineral balance and fouling during ultrafitlration of cheese whey. C. Marella*, L. E. Metzger, and K. Muthukumarappan, *South Dakota State University*, *Brookings*.

The conventional membrane based manufacturing process for whey protein concentrate (WPC) and whey protein isolate (WPI) utilizes a three stage process that includes ultrafitlration, microfiltration and ultrafitlration. Although most manufacturers use a similar process, conventional WPC and WPI vary widely in their composition and salt content. These variations lead to variability in functionality that limits the use of WPC and WPI in some applications. The objective of the present study was to determine if mineral chelating processing aids have an impact on the removal of divalent ions and membrane fouling during the first ultrafitlration step of whey processing. Ultrafiltration experiments were conducted in triplicate using disodium phosphate, citric acid and ethylenediamine tetra acetic acid at three levels each. The level of each processing aid was based on its ability to chelate 2.5 mM (L1), 5 mM (L2) and 10 mM of calcium (L3) present in the whey. All the experiments were conducted in a lab scale plate and frame separation unit using a 10 kDa Polyether sulfone membrane, 172.4 kPa transmembrane pressure, 6.2 pH and 25° temperature. The effect of mineral chelating processing aids on membrane fouling was expressed in terms of overall and irreversible fouling resistances while the effect of these processing aids on divalent ions was expressed in terms of rejection coefficients at the end of ultrafitlration and after diafiltration. Statistical analysis of the fouling resistances showed no significant effect ($P>0.05$) of addition of processing aids on fouling of ultrafitlration membranes. Addition of citric acid at L2 resulted into the lowest rejection of calcium at the end of ultrafitlration (0.25) and after diafiltration (0.265). Addition of disodium phosphate at L3 resulted into the lowest rejection of magnesium at the end of ultrafitlration (0.175) and after diafiltration (0.24). The results demonstrate that mineral balance during the first ultrafitlration step can be modified with the addition of mineral chelating processing aids.

Key Words: ultrafiltration, mineral balance, processing aids

751 Impact of bleaching on the flavor of whey protein concentrate. A. E. Croissant*[1], J. Kang[1], R. E. Campbell[1], E. Bastian[2], and M. A. Drake[1], [1]*North Carolina State University*, *Raleigh*, [2]*Glanbia Nutritionals*, *Twin Falls, ID*.

The increasing use and demand for whey protein as an ingredient requires a bland-tasting, neutral-colored final product. The bleaching of colored Cheddar whey is necessary to achieve this goal. Currently, hydrogen peroxide (HP) and benzoyl peroxide (BPO) are approved for bleaching liquid whey prior to spray drying. There is no current information on the impact of this process on flavor of spray dried whey protein concentrate (WPC). The objective of this study was to characterize the impact of bleaching on flavor of liquid and spray dried Cheddar whey. Cheddar cheeses colored with annatto were manufactured in triplicate. Four bleaching treatments (HP: 250 and 500 ppm and BPO: 10 and 20 ppm) were applied to liquid whey for 2 h at 60 C followed by cooling to 5C. A control whey with no bleach was also evaluated. Flavor of liquid wheys were evaluated by sensory and instrumental volatile analysis. One HP and one BPO treatment were subsequently incorporated into liquid whey and processed into spray dried WPC along with an unbleached control. WPC were evaluated by sensory and instrumental analyses as well as color and proximate analyses. Liquid whey and WPC that were bleached had higher concentrations of lipid oxidation products including heptanal, hexanal, octanal, and nonanal compared to unbleached liquid whey or WPC ($p<0.05$). HP products were higher in oxidation products compared to BPO products. HP liquid whey and WPC were also higher in fatty and cardboard flavors compared to the controls or BPO samples. Color values (L, a, b) of WPC powders were distinct ($p<0.05$) on all three color scale parameters with HP WPC having the highest L values. These results indicate that bleaching of liquid whey does affect the flavor of WPC and that type of bleaching agent may also impact flavor and color of WPC.

Key Words: whey protein, bleaching, flavor

752 An on-line light backscatter sensor at 980 nm for monitoring curd moisture and whey solids contents with a cooking step during syneresis in a cheese vat. M. J. Mateo*[1], C. D. Everard[1], C. P. O'Donnell[2], M. Castillo[3], F. A. Payne[3], and D. J. O'Callaghan[1], [1]*Teagasc*, *Cork, Ireland*, [2]*University College Dublin*, *Dublin, Ireland*, [3]*University of Kentucky*, *Lexington*.

The aim of this study was to use on-line light backscatter at 980 nm to monitor curd moisture and whey solids contents with a cooking step as an experimental treatment during syneresis. Milk was renneted at 32°C and, following gel cutting, the temperature was raised by 1 degree every 5 min until the temperature reached 38°C (the cooking step) or held at 32°C in the case of the control. A full factorial experimental design having two final temperatures (32 or 38°C), with three replicates ($n = 6$) was performed. The trials were carried out using recombined whole milk in an 11 L cheese vat, in which a light backscatter on-line sensor was installed. Samples of curd / whey mixture were taken from the vat during syneresis using an on-line sampler at 10 min intervals and curd was separated from whey using a stainless steel 75-micron sieve. The effect of added shrinkage due to cooking of the curd is shown by its negative effect on curd moisture content. A model was developed which explained 86% of the variation in curd moisture content, involving three significant factors, namely time after gel cutting, the sensor response and final temperature, in order of standardised coefficient. By comparison, the sensor response alone predicted curd moisture content with $R^2 = 0.74$. The sensor response predicted whey solids content with $R^2 = 0.81$, without relying on any other factors. Theses results contribute to understanding the effect of cooking on the monitoring of curd moisture and whey solids contents when using an online light backscatter sensor.

Key Words: curd moisture, whey solids, light backscatter

753 Development of rapid method for measurement of lactose in model solutions using a hand-held blood glucose biosensor. J. Amamcharla*, K. Shah, and L. Metzger, *South Dakota State University*, *Brookings*.

Current methods for lactose measurement in dairy products are time consuming, tedious and may require expensive equipment and skilled technicians. The aim of this research was to develop a novel, rapid method for measurement of lactose in model solutions. The method is based on rapid hydrolysis of lactose using β-galactosidase and subsequently measuring the glucose using a blood glucose meter. Blood glucose meters were developed after decades of research. Initially, lactase concentration, temperature and time required for near complete hydrolysis were determined. We found that the hydrolysis of lactose was complete in 10 minutes at 40°C using 2% enzyme. A randomized factorial experimental design with two factors, i.e. glucose meters (meter 1 & 2), test strips (lot 1 & 2), and three replications was performed. Each measurement was performed with three test strips from the same

lot using the same meter under different concentrations of lactose (50 – 400 mg/dL) in model solution. After incubation with lactase, the sample was applied onto the test strip and the glucose concentration was determined. We found that meters and replications were not significantly different ($P<0.05$). However, the test strip lots were significantly different from each other. A standard curve using all the data was linear and had a slope of 0.855 and intercept of -18.77 (R^2=0.99). In order to verify the predictive ability of the method, different concentrations of lactose (1.9 –6.5%) were prepared independently and analyzed using the proposed method as well as by HPLC. Since, the glucose meter reading was significantly influenced by test strip lot, six different lots were utilized in this experiment. Simultaneously, standard curves were also developed for each of the six test strip lots. Lactose concentration was then calculated from the combined and individual standard curves. The average absolute bias, calculated for 25 samples, was found to be between 0.08–0.17 for individual standard curve and 0.1 –0.36 for the combined standard curve. The proposed method shows potential in rapid measurement of lactose in dairy products.

Key Words: lactose, glucose meter, rapid measurement

754 Persistency of conjugated linoleic acid and vaccenic acid on Sardo cow cheese. G. A. Gagliostro*[1], M. Martínez[2], V. I. Cejas[3], M. A. Rodríguez[3], and M. Balán[4], [1]*Instituto Nacional de Tecnologíia Agropecuaria, Balcarce, Buenos Aires, Argentina*, [2]*Instituto Nacional de Tecnología Agropecuaria, Salta, Argentina*, [3]*Instituto Nacional de Tecnología Industrial, PTM MIguelete, Buenos Aires, Argentina*, [4]*PRODEO S.R.L., Chivilcoy, Buenos Aires, Argentina*.

Persistency of 9-cis 11-trans C18:2 (CLA), trans-11 C18:1 (VA) and other fatty acids (FA) was tested on Sardo cheese elaborated from milk with high CLA and VA contents. The same feeding trial and cows were also used when transfer of FA to Tybo cheese was tested. Milk was obtained from eight Holstein cows (570 kg, 109 days in milk) producing 24.8 kg milk/d and consuming (DM basis) 7.3 kg/cow of concentrate, 1.94 kg/cow/d of a TMR (corn silage, 70%, soybean oil, 22%, fish oil 5.4% and urea, 2.6%) and 8 kg of pasture. After 25 days of adaptation, milk was collected and transformed into Sardo cheese reproducing industrial conditions. Milk and chesse FA composition was analyzed by GLC and differences in FA content between milk and cheese were stated using the T-test for paired observations. Milk fat, protein and lactose contents were 23, 35.1 and 47.1 g/kg respectively, with a fat/protein ratio of 0.65. Intake of 427 g/d of soybean oil (229 g of C18:2) and 105 g of fish oil contained in the TMR reduced the atherogenicity index (AI = [(C12 + 4C14 + C16)/total unsaturated)] of milk from a pre supplementation basal value of 2.06 to 1.16. Basal concentration (g/100g) of the atherogenic FA C12:0 (4.04) C14:0 (12.52) and C16:0 (29,16) were decreased by intake of oils (C12:0 = -1,66, 41%, C14:0 = -3,48, 28% and C16:0 = -4.89, 11%). After oil supplementation milk CLA content increased from a basal value of 1.42 to 3.58 g/100g and VA from 2.56 to 3.58 g/100g FA. Elaborated Sardo cheese contained 26.73% fat and 31.23% protein (w/w) with an atherogenicity index of 1.22. Significant differences between milk FA and cheese FA content were not detected. Transfer of 9-cis 11-trans CLA to Tybo cheese averaged 98%. Assuming that the cheese fat contain 95% FA, intake of 90 g/d of Sardo cheese rich in CLA may allow to obtain the suggested anticancer dose (800 mg) of CLA. These results were obtained using a feeding strategy that may be easy carried out by the farmer and the grazed forage represented about 46.4% of total dry matter intake.

Key Words: Sardo cheese, conjugated linoleic acid, vaccenic acid

755 Dairy food intake among historically African American college campus students. A. M. Patterson* and S. A. Ibrahim, *North Carolina A & T State University, Greensboro*.

Dairy foods, such as milk, cheese, and yogurt are one of the greatest sources of essential nutrients such as potassium and calcium. Dairy foods are also mostly known for their importance in bone health and overall diet health. Previous studies have shown a low consumption of dairy foods among African American, but no recent studies have been conducted with African American college campus students. The purpose of this study was to survey a sample of students about the consumption of dairy foods from a historically African American college campus. Fifty four male and female students provided information on their intake of dairy products by completing the Food Frequency Questionnaire (FFQ). The section of the FFQ of interest to this study related to what type of dairy products (cheese, yogurt, ice cream, liquid milk) and other food items that include dairy products (pizza, hamburgers, etc.) are eaten and how often consumed. The survey also inquired about their intake amounts, and their feelings and attitudes about those foods that are consumed and the ones that are not consumed. Our results indicated that there was a low dairy products intake among the students that participated. Ninety percent of the respondents reported consuming less than the recommended daily amount; males tended to consume more than females. Both males and females received most of their dairy from cheeses that were included on foods such as pasta, pizza, cheeseburgers, but the most popular dairy product that was consumed was ice cream. The results suggest that African American college campus students need to increase their dairy food consumption, but do so by choosing healthy dairy foods such as yogurt, low-fat cheeses and milk.

Key Words: historically African American, dairy products

Forages and Pastures: Grazing and Pasture Utilization

756 Effect of fall grazing system on annual ryegrass quality and beef cattle performance. J. M. Kelzer*[1], S. Bird[2], R. D. Mathison[2], P. R. Peterson[1], and R. S. Walker[3], [1]*University of Minnesota, St. Paul*, [2]*University of Minnesota, Grand Rapids*, [3]*University of Minnesota, Andover*.

Windrowed and stockpiled annual ryegrass as fall grazing systems were evaluated for forage quality and beef cow performance over two separate years. In 2007 and 2008, two 6-acre paddocks were seeded in early spring with annual ryegrass, rotationally grazed during summer, fertilized, and stockpiled in August. In mid-October, forage from one-half of each replicated 6-acre paddock was cut while the other half was left standing. Two windrows in each cut section were raked together 1 d following swathing to represent the windrow treatment. Dry, pregnant Angus beef cows (n = 32 each year) averaging 651 ± 75 kg BW, 5 ± 2 yr of age, 125 ± 22 d pregnant, and BCS of 5.5 ± 0.5 for 2007 and 582 ± 80 kg BW, 4 ± 3 yr of age, 131 d pregnant, and BCS of 5 ± 0.4 were assigned randomly to one of four 3-acre paddocks representing one of two grazing treatments: 1) windrowed annual ryegrass (WIN), and 2) stockpiled annual ryegrass (STO). Data for forage quality and animal performance were collected and analyzed by year. Forage CP, ADF,

and NDF were greater ($P < 0.05$) over time, whereas percent TDN and relative feed value were lower ($P < 0.05$) over time for WIN vs. STO paddocks for both years. Compared to WIN, cattle on STO paddocks grazed 8 and 10 d longer ($P < 0.05$) in 2007 and 2008. Animal BW gain and ADG were similar for cows grazing STO and WIN paddocks in 2007 and averaged -1.4 ± 26.4 kg BW and 0.02 ± 0.8 kg/d; however, animal BW gain (39.9 vs. 20.0 ± 11.9 kg BW) and ADG (1.0 vs. 0.7 ± 0.4 kg/d) were greater ($P < 0.05$) for STO than WIN in 2008. Results of this study indicate forage CP, TDN, ADF, NDF, and relative feed value are affected by fall grazing system over time. Thus, stockpiling forage may be a viable system to retain forage quality and maintain beef cow performance later in the grazing season.

Key Words: annual ryegrass, grazing system, beef cattle

757 Economic potential of stocker cattle grazing legume-interseeded bermudagrass. J. Guretzky*, R. Reuter, J. Biermacher, J. Springer, T. Butler, H. Aljoe, J. Rogers, and B. Cook, *The Noble Foundation, Ardmore, OK*.

Planting legumes is a forage management strategy that may offset N fertilization costs and improve stocker cattle gains on pasture. Our objectives were to document herbage availability, average daily gain, and net returns to land, labor, and management from stocker cattle grazing N-fertilized and legume-interseeded bermudagrass pastures. Research was conducted in nine, 1.4-ha paddocks, continuously stocked with 204-kg steers at 2.8 steers/ha, near Ardmore, OK, in 2008. Treatments arranged in a completely randomized design included: bermudagrass fertilized with urea at 112 kg N/ha; bermudagrass interseeded with a grazing-type alfalfa at 6.9 kg PLS/ha; and bermudagrass interseeded with a mixture of winter annual legumes (hairy vetch, crimson clover, and arrowleaf clover at 12.3, 9.4, and 5.8 kg PLS/ha, respectively). Legumes were no-till drilled into dormant bermudagrass on 11 Oct. 2007. The N-fertilized system supported 84 grazing days (23 May to 15 August) and gains of 1.12 ± 0.22 kg/d. The alfalfa system supported 56 grazing days (23 May to 18 July) and gains of 1.21 ± 0.23 kg/d. The annual legume system allowed 66 grazing days (24 April to 28 June) and gains of 1.43 ± 0.33 kg/d. Average daily gain and gain/ha were similar among systems (P = 0.65 and 0.13, respectively). Planting annual legumes improved average herbage availability in April and May (2709 ± 223 kg/ha) compared to N-fertilized (1638 ± 134 kg/ha) and alfalfa (1378 ± 184 kg/ha) systems. Average herbage availability in June and July, however, peaked within the N-fertilized system (3683 ± 344 kg/ha) compared to the alfalfa (1339 ± 204 kg/ha) and annual legume systems (1276 ± 180 kg/ha). Net returns were $292, $109, and $227/ha for N-fertilized, alfalfa, and annual legume systems, respectively. Net returns between the N-fertilized and the annual legume system were sensitive to price of N, gain/ha, value of gain, and grazing days. Poor establishment limited herbage availability, grazing days, and net returns within the alfalfa system. The annual legume system has economic potential based on the first year data.

Key Words: forage systems, forage ecology, grazing systems

758 Economic feasibility of stocker cattle grazing tall fescue infected with a novel endophyte in the Southern Great Plains of the USA. J. T. Biermacher*[1], R. Reuter[1], B. J. Cook[1], M. A. Islam[2], A. Hopkins[1], J. H. Bouton[1], and T. J. Butler[1], [1]*Samuel Roberts Noble Foundation, Ardmore, OK*, [2]*University of Wyoming, Laramie*.

The objective of this study was to compare the net return of stocker cattle grazing either novel endophyte-infected tall fescue or annual rye/ryegrass pastures. In a randomized complete block design, four paddocks of cereal rye and ryegrass were planted in early September 2005, 2006 and 2007. Additionally, four paddocks of an experimental tall fescue were planted in late September 2005. Each fall, beef steers (245 kg BW) were randomly assigned to paddocks. Animals were weighed every 28 days of each grazing season, and forage availability and nutritive value samples were collected. Stocking rates were adjusted periodically throughout the grazing season to attempt to maintain equal forage availability among paddocks. Total costs for the perennial system includes the 5-yr amortized cost of establishing the tall fescue and the annual expenses for fertilizer and weed control. Average daily gain between treatments was similar (1.1 kg/d, Table 1.); however the annual system produced 43% more grazing days. Average total cost of the perennial system was 101 USD / ha less than the rye/ryegrass system. The annual system realized a total economic advantage of 92 USD / ha over the perennial system. Although the perennial tall fescue system cost less, the additional grazing days available in the annual system compensated for this relative cost advantage. The economic results are sensitive to the number of grazing days, stand life expectancy and prices of rye and ryegrass seed.

Table 1. Average daily gain, grazing days, total gain, total cost and net return to land, labor and management for annual and perennial forage systems for stocker cattle

	Rye/ryegrass		Tall Fescue	
Performance measure	Avg.	St. Dev.	Avg.	St. Dev.
Average daily gain (kg / ha)	1.1[a]	0.1	1.1[a]	0.1
Grazing days	225[a]	73	157[b]	64
Total gain (kg / ha)	520[a]	258	362[b]	116
Total cost (USD / ha)	367[a]	99	266[b]	96
Net return (USD / ha)	264[a]	410	172[b]	55

Letters that differ were statistically different at the 95% level of confidence.

Key Words: economics, stocker grazing systems, novel endophyte-infected tall fescue

759 Utilization of switchgrass in a dual purpose stocker cattle and bioenergy system. J. A. Guretzky, J. T. Biermacher, R. R. Reuter, J. R. Blanton Jr.*, J. Mosali, M. Kering, and B. J. Cook, *The Samuel Roberts Noble Foundation, Ardmore, OK*.

The objective of this study was to determine if switchgrass (*Panicum virgatum*) produced for bioenergy production could serve as a dual crop for stocker cattle management programs. Switchgrass is a native grass that produces sufficient biomass on marginal lands to serve as a bio-refinery feedstock. Stocker cattle production generally involves lightweight calves developed on forage-based diets for feedlot production or cow replacements. In May 2007, 9.7 ha of Alamo switchgrass was established in southern Oklahoma on sandy soil and divided into twelve, 0.8 ha paddocks to evaluate stocker cattle performance and switchgrass utilization at 4 stocking densities. In April 2008, steers (n = 36) weighing 348 kg, were randomly assigned to control (0 steers/ha), low (2.5 steers/ha), medium, (5 steers/ha) and high (7.5 steers/ha) stocking density paddocks. Herbage mass and nutrient composition was measures bi-weekly during the grazing period and at completion of switchgrass growing season (September). Animal weights were collected

on d 0 and at completion of grazing. Grazing was terminated when forage height was less than 10 cm. Overall, ADG and total gain per ha was not significantly affected (P = .34) by treatment but a numerical trend was observed with the higher stocking density (1.5 kg/d) outperforming both the low (0.8 kg/d) and medium (1.2 kg/d) stocking densities. Stocking density significantly affected (P<.001) total grazing days with the high density (21d) resulting in fewer days than either low (98d) or medium (30d) stocking densities. Stocking density did not affect (P>.05) biomass availability at conclusion of growing season, however grazing significantly (P<.01) reduced overall biomass. Control paddocks contained 14,100 kg/ha at conclusion of growing season, whereas grazed paddocks averaged 7,615 kg/ha. Nutrient composition was not significantly affected by grazing (P<.05). While grazing reduced biomass availability of switchgrass, the significant animal performance gained could impact producer profitability.

Key Words: switchgrass, stocker cattle, grazing

760 Effects of supplemental cottonseed meal versus part-time annual ryegrass grazing on performance of beef heifers grazing stockpiled limpograss pastures. J. M. B. Vendramini* and J. D. Arthington, *University of Florida*, *Ona*.

Limpograss [(*Hermathria altissima* (Poir.) Stapf & C.E. Hubb.] is an important perennial forage in Florida because of its adaptation to poorly drained soils and better cool-season growth than other available warm-season grass varieties. The objective of this study was to evaluate the performance of heifers grazing stockpiled limpograss pastures supplemented with cottonseed meal or grazing part-time annual ryegrass (*Lolium multiflorum* Lam.). The experiment was conducted over 2 consecutive years from Feb. to April. Twelve 0.5 ha limpograss pastures were staged at a 10 cm stubble height and fertilized with 60 kg N / ha in Oct., and stockpiled from Oct. to Feb. of the subsequent year. Three Angus crossbred yearling heifers (338 ± 30 kg LW) were assigned to each pasture. Treatments consisted of 3 supplementation rates, 0 (control), 1.1, and 2.2 kg/heifer daily of cottonseed meal, or part-time grazing ryegrass on a completely randomized design with three replicates. Ryegrass pastures were planted in Nov. and fertilized with 30 kg N/ha. Heifers were allowed to graze ryegrass three 24-h periods each week (Mon, Wed, and Fri.). Ryegrass pastures were 0.4 ha. Limpograss herbage mass was greater in pastures where the heifers part-time grazed ryegrass than in other treatments (2100 vs.1800 ± 50 kg/ha). Herbage mass accumulation (24 ± 3 kg/heifer daily), CP (12 ± 1%), and IVDOM (50 ± 1%) were similar among treatments. There was a linear increase in ADG of heifers receiving crescent levels of cottonseed meal from 0.14 and 0.67 kg/d, but there was no difference in ADG of heifers grazing part-time ryegrass and supplemented with 2.2 kg CSM/d (0.64 kg/d). There was no difference in BUN concentrations between heifers receiving the control treatment (19 ± 1 mg/dL) and part-time grazing ryegrass (21 ± 1 mg/dL); however, heifers receiving 1.1 and 2.2 kg of cottonseed meal/d had greater BUN concentration compared with control (23 and 27 ± 1 mg/dL, respectively). Part-time grazing ryegrass may be an economically viable option for the supplementation of beef cattle in the southeast US.

Key Words: limpograss, annual ryegrass, supplementation

761 Prediction of rumen function measures from plant constituents in lactating cows fed pasture-based diets. R. E. Vibart*, B. A. Barrett, and D. Pacheco, *AgResearch Limited*, *Palmerston North, New Zealand*.

A greater concentration of water-soluble carbohydrates (WSC) in grasses has shown promise in improving the asynchronous supply of nitrogen (N) and carbohydrates for microbial protein synthesis in the rumen, enhancing N capture in the grazing ruminant. Data from experiments with lactating cows (17 publications, 42 treatment means) where freshly-cut or grazed pasture comprised more than 70% of the total dry matter consumed, were used to evaluate the effects of plant constituent concentrations and nutrient ratios [organic matter (OM), WSC, crude protein (CP), neutral detergent fiber (NDF), non-fibre carbohydrate (NFC), WSC/CP, NFC/CP] on rumen function indicators. Regression was performed using the stepwise selection method restricted to $P = 0.05$ for variables to enter and remain in the model. Response equations were also examined by combining results from all studies using meta-analysis methods. Response variables included ruminal pH (mean 6.2 ± SD 0.24), total volatile fatty acids concentration (tVFA; 121.6 ± 17.0 mmol/L), ammonia N concentration (11.8 ± 6.1 mmol/L), microbial N flow (236.1 ± 57.6 g/d), and efficiency of microbial protein synthesis (EMPS; 24.0 ± 5.1 g microbial N/kg OM apparently digested in the rumen). No plant constituent variable met the significance level of entry for ruminal pH, whereas OM (microbial N flow: adj. $R^2 = 0.21$; RMSE = 51.2; $P = 0.004$), OM and CP (EMPS: adj. $R^2 = 0.23$; RMSE = 4.5; $P = 0.007$), and OM, CP, WSC, and NDF (tVFA: adj. $R^2 = 0.61$; RMSE = 10.6; $P < 0.001$; ammonia N: adj. $R^2 = 0.84$; RMSE = 2.4; $P < 0.001$) were selected predictors. No additional variation was explained by nonlinear analysis. Out of the variables studied, forage components were better at explaining the variability of tVFA and ammonia N concentration (adj. R^2 values > 0.6) compared with microbial N flow and the EMPS (adj. R^2 values < 0.3). These last results highlight the challenge of enhancing N capture in pasture-based systems through breeding programmes aimed at modifying the chemical composition of temperate forages.

Key Words: rumen function, ryegrass, nitrogen capture

762 Prediction of nitrogen utilization efficiency from plant constituents in lactating cows fed pasture-based diets. R. E. Vibart*, B. A. Barrett, and D. Pacheco, *AgResearch Limited*, *Palmerston North, New Zealand*.

Identifying suitable dietary predictors of the efficiency of nitrogen (N) utilization (ENU, g N per kg of N intake) is critical to develop management strategies to optimize N capture in grazing ruminants. Data from experiments with lactating cows consuming ryegrass-based diets were used to evaluate the effects of plant constituent concentrations and nutrient ratios on the ENU in milk (ENU_m) and manure (ENU_{ma}). The data set used (36 publications, 153 treatment means) was derived from studies where freshly-cut or grazed pasture comprised more than 70% of the total dry matter consumed. Regression and mixed models were performed using the stepwise selection method constrained to $P = 0.05$ for variables to enter and remain in the model, and meta-analysis methods, respectively. Total N intake (mean 516 ± SD 105 g/d) was partitioned into milk N (115 ± 22 g/d) and manure N (398 ± 103 g/d). Crude protein (CP) concentration was the best single predictor of both ENU_m and ENU_{ma}($P < 0.001$; adjusted $R^2 = 0.59$ and 0.39; RMSE = 31.6 and 49.0 g N/kg N intake, respectively). Stronger relationships (increased adj. R^2 and reduced RMSE values) were obtained by adding water soluble carbohydrates (WSC) alone (ENU_m; adj. $R^2 = 0.64$; RMSE = 29.6 g milk N/kg N intake) or with neutral detergent fiber (NDF) to the models (ENU_{ma}; adj. $R^2 = 0.51$; RMSE = 43.9 g milk N/kg N intake). Within studies, the ratio of WSC to CP and the concentrations of CP,

WSC, and NDF, as well as N intake, were suitable predictors of both ENU_m and ENU_{ma}($P < 0.05$; adj. R^2 ranged from 0.64 to 0.93), indicating the consistency of these relationships within numerous studies. Results herein suggest that the partitioning of carbon between soluble and structural carbohydrates within the plant affects N utilization in grazing ruminants. Although WSC provide the most readily available source of energy for grazing ruminants, the highly-digestible nature of NDF from these diets provide for additional energy in the rumen that also contributes in reducing N in manure.

Key Words: efficiency of nitrogen utilization, ryegrass, dairy

763 Effects of stocking rate and supplementation on lactation and reproduction in pasture-based dairy systems in Eastern North Carolina. R. E. Vibart*[1], S. P. Washburn[2], G. A. Benson[2], and J. T. Green[2], [1]*AgResearch Limited, Palmerston North, New Zealand*, [2]*North Carolina State University, Raleigh*.

A balance between stocking rate and per cow performance is required to optimize grazing strategies and profitability in pastoral dairying. Beginning September 2003, a seasonal, fall-calving, pasture-based system was established on a research station dairy herd to address the effects of stocking rate (supplementation rate adjusted accordingly) on lactation and reproduction performance for three years. Eighty lactating cows including Holstein (H); Jersey (J); and crosses of H and J were assigned to one of two stocking rate (SR) groups and balanced for breed group. Cows were assigned to either a low stocking, low supplementation group (LSR; 2.2 cows per ha) or a high stocking, high supplementation group (HSR; 3.3 cows per ha). Proportional amounts (1.0x and 1.5x; mean 4.6 and 7.6 kg DM/cow for LSR and HSR, respectively) of a corn-based concentrate mix were offered daily in amounts that varied according to pasture quality and availability. Estimates of grazed herbage DM intake, obtained from weighed pasture removal within a 24-h period and grazing area allocated per cow, were 35% greater for cows on LSR (14.3 vs. 10.6 kg DM/d). Lactation performance, however, was greater ($P < 0.05$) for cows on HSR: mature-equivalent milk yield (6,010 vs. 6,733 kg); milk fat yield (205.8 vs. 229.3 kg); protein yields (179.5 vs. 208.7 kg) for cows on LSR vs. HSR, respectively. Reproduction efficiency (conception rate at first and all services, pregnancy rate) was not affected by stocking rate. Although concentrate prices also affect farm profitability, with similar reproduction efficiency, a greater per cow milk yield along with increased productivity per unit of land favored the greater stocking rate.

Key Words: stocking rate, lactation, reproduction

764 Sequence grazing of perennial and annual cool-season grasses to extend the grazing season for stocker calves. B. K. Northup[1], W. A. Phillips*[1], and A. A. Hopkins[2], [1]*USDA-ARS Grazinglands Research Laboratory, El Reno, OK*, [2]*Noble Foundation Inc., Ardmore, OK*.

Grazing of cool-season grasses by beef calves before entry into the feedlot for finishing is an important component of the US beef production system. The length of time in the feedlot and the quantity of feed grain required to reach market BW would be reduced if more BW was gained during the grazing season. The objective of these experiments were to evaluate the feasibility of using perennial cool-season grass in early fall and late spring to extend the winter wheat stocker calf grazing season. In Experiment 1, six 1.8-ha pastures of non-toxic endophyte infected fescue (*Festuca arundinacea Schreb.*) were established at the Grazinglands Research Laboratory and allowed one year of deferment for establishment. A different set of calves were used each fall (BW = 250± 44 kg) and spring (BW = 326± 34 kg). Calves were randomly assigned to pastures and stocking rate was based on the amount of forage available for grazing. Pasture was the experimental unit and data were analyzed using PROC MIXED procedures with year (n=3)being random. Pastures were grazed for 38 ± 7.4 d in the fall (mean start date = Oct. 22) and for 33 ± 6.2 d in the spring (mean start date = Apr. 23). Average daily gain (0.56 vs. 0.99 kg) and stocking rate (1460 vs. 2200 kg BW/ha) was lower (P = 0.03) in the fall than in the spring. In Experiment 2, 144 Angus steers were divided into 6 groups, and grazed on 2.1-ha fescue pastures (n=6) for 29 d in the fall, a common wheat pasture for 134 d in the winter and spring and returned to fescue pastures for 29 d in late spring. Initial BW (Nov. 14) in the fall was 248 kg. Steers gained 19.7 ± 1.5 kg in the fall on fescue, 118.0 ± 2.6 kg in the winter and spring on wheat pasture and 32.1 ± 1.7 kg in the late spring on fescue. We conclude that fescue pasture can be used in a sequence grazing system under short intensively grazing management during the fall and spring to extend the winter wheat grazing season by approximately 60 d and can add as much as 52 kg of BW.

Key Words: wheat pasture, fescue, stockers

765 Comparison of fescues versus orchardgrass—Forage characteristics and stocker performance. M. H. Ramos*[1], J. W. Lehmkuhler[2], and K. A. Albrecht[3], [1]*University of Missouri, Columbia*, [2]*University of Kentucky, Lexington*, [3]*University of Wisconsin, Madison*.

Since both tall fescue and orchardgrass are well accepted by beef producers, and comparison of reported grazing results being inconsistent, a grazing study was designed to compare non-entophyte infected tall fescue, a novel soft-leaf tall fescue variety (soft leaf) and orchardgrass in a rotational grazing system using stocker cattle. Crossbred beef steers, crossbred beef heifers and Holsteins steers were allowed to graze during 2005, 2006 and 2007. Dry matter availability was not different between treatments at any of the three years (P > 0.05). During the year of 2006 only the dry matter production of fescue grasses were higher (P < 0.05) than the orchardgrass grass. No significant differences (P > 0.1) could be observed between treatments for NDF. During the three years no differences (P > 0.10) could be seen between treatments for IVDMD. Orchardgrass pastures had lower (P < 0.05) ADG than SL (soft leaf) pastures during the 2005 grazing season. While in 2006 gains for cattle grazing orchardgrass and tall fescue were not different (P > 0.05). Tall fescue pastures supported daily gains less than orchardgrass (P <0.05) only in 2007 with 2005 and 2006 showing no differences in ADG between orchardgrass and tall fescue. Soft-leaf tall fescue pastures supported ADG greater than both tall fescue and orchardgrass (P < 0.05) in 2005 and gains for cattle consuming soft-leaf tall fescue were also higher in 2007 (P < 0.05) compared to tall fescue. Orchardgrass pastures supported fewer animals (lower Stocking density, SD) for most of the grazing season all three years. It can be concluded that DM production for fescues were higher than orchardgrass pastures and that forage quality did not differ due to forage. Quality indicators for forage showed the expected pattern of higher quality during the spring and fall and lower quality during the summer months. Fescues and orchardgrass pastures allow for similar ADG when using stocker animals. Fescue pastures support higher carrying capacity than the orchardgrass which will translate into more animal output per ha.

Key Words: fescue, pasture, nitrogen

766 Use of N fertilization versus interseeded legume—Forage characteristics and stockers performance. M. H. Ramos*[1], J. W. Lehmkuhler[2], and K. A. Albrecht[3], [1]*University of Missouri, Columbia*, [2]*University of Kentucky, Lexington*, [3]*University of Wisconsin, Madison*.

Due to increasing prices of N an experiment was conducted to compare the response of stocker beef animals grazed on an interseeded legume to a pasture with N application. The legumes interseeded were Kura Clover with Soft Leaf Fescue, White Clover with Soft leaf fescue and Soft leaf tall fescue only. During all three years of the experiment no differences in dry matter availability ($P > 0.05$) were observed between treatments, with DM production of legumes being lower ($P < 0.05$) than grass during 2006 but not ($P > 0.05$) during 2007. Both NDF and ADF of grass was higher ($P < 0.05$) than legumes during 2006 but no differences were measured the other two years. The IVDMD was higher ($P < 0.05$) for legumes than grass during 2006 with a tendency to follow the same pattern in 2005 but not ($P > 0.05$) during 2007. Lignin, CP, and ASH were not different ($P > 0.05$) among treatments. No significant differences ($P > 0.05$) were observed between treatments for ADG and gain/ha during the 2005 grazing season. End weights and ADG were higher ($P < 0.05$) for the legume treatments than the fescue treatment during 2006 although no significant difference ($P > 0.05$) was measured between treatments for gain/ha in 2006. End weights were not significantly ($P < 0.05$) different between treatments for the 2007 grazing season. It can be concluded that pastures containing a mixture of grass and legume, with the legume representing at least 40% of the mixture, will have better forage quality (lower NDF and higher IVDMD) while still providing the same amount of dry matter compared with pastures that contain only grass and nitrogen fertilizer. Pastures that contain a mixture of legume will allow for higher ADG when compared with pastures that contain grasses only and that can or cannot be translate in higher gains/ha.

Key Words: grass, legume, nitrogen

767 Performance of Holstein steers, beef steers and beef heifers under rotational grazing. M. H. Ramos*[1], J. W. Lehmkuhler[2], and K. A. Albrecht[3], [1]*University of Missouri, Columbia*, [2]*University of Kentucky, Lexington*, [3]*University of Wisconsin, Madison*.

A grazing experiment was conducted where Holstein steers, beef steers and beef heifers (both Angus crossed) were intensively grazed during the grazing season of 2005, 2006 and 2007. Animals had access to pasture of tall fescue, soft leaf tall fescue, orchardgrass (all received nitrogen) and soft leaf tall fescue with Kura clover and white clover. All three types of animals were implanted with growth promoting implants during the first two years but not 2007. The initial weight of animals were not different ($P > 0.05$) for 2006, for 2005 heifers started heavier than steers which were heavier than Holsteins, and for 2007 Holstein started the experiment heavier than heifers which were heavier than steers. Since beginning weight was different it was used as covariate in the Statistical model. For two out of three years Holstein steers gained as well ($P < 0.05$) as beef steers and heifers, which were similar. In one year beef steers had higher ADG than Holsteins and heifers. End weight was not different ($P > 0.05$) during 2005, Holstein steers finished as heavy ($P > 0.05$) as beef steers and both were heavier than heifers in 2006. In 2007 Holstein steers finished as heavy as beef heifers but lighter than beef steers. It can be concluded that Holsteins steers have the potential to perform as well as beef steers under managed intensive grazing.

Key Words: grazing, Holstein, beef

Horse Species

768 The welfare of horses during transport. J. Woods*, *J. Woods Livestock Services*.

In the past three years, we have seen an increasing focus on the welfare of horses during transport. This trend is due to a combination of several factors. First, the closing of the three remaining horse slaughter plants in the United States has forced horses to be transported further distances to Canada and Mexico. Second, these closures and current economic restraints have increased the number of unwanted and abandoned horses throughout North America. And finally, several animal rights groups have launched campaigns focusing on the transport of all livestock. With the increase of horses being transported north, Canada has come under even more of a microscope regarding the welfare of the horses not only within our borders, but also those crossing into our country. This increasing scrutiny has brought the horse industry together and to the table to work with enforcement agencies, animal welfare groups, processors and transporters to help ensure our horses are being transported humanely and safely, no matter their destination. Out of this collaboration has also come a campaign to take responsibility for the welfare of horses during transport clear back to the farm through education and awareness to stop the transportation of unfit animals.

Key Words: transportation, horse, welfare

769 Expression of intestinal monosaccharide transporters and the sweet taste receptor in equine small intestine. D. Arora*, M. Al-Rammahi, K. Salmon, C. Proudman, and S. Shirazi-Beechey, *University of Liverpool, Liverpool, UK*.

Glucose and sodium are co-transported by the Na^+-glucose cotransporter, SGLT1, across the luminal membrane of intestinal absorptive cells (enterocytes). Na^+ and glucose exit the cell across the basolateral membrane of enterocytes by Na^+/K^+-ATPase and the monosaccharide transporter, GLUT2, respectively. Co-transport of water along with Na^+ and glucose accounts for 50% of the total water absorption across the intestinal luminal membrane. It has been shown that expression of SGLT1 is upregulated in response to increased lumenal monosaccharide concentration. This upregulation is achieved through a signalling pathway initiated by the gut sweet taste receptor. Aim: To determine if the gut sweet taste receptor and the signalling elements involved in SGLT1 upregulation are expressed in equine intestine. Intestinal tissue samples from 8 horses, maintained on either a forage pasture or grain based diet, and euthanased for conditions other than intestinal disease were used. Histological examination confirmed the integrity of the tissue. Using immunohistochemistry with antibodies to equine SGLT1 and GLUT2, it was shown that, in all dietary conditions, SGLT1 is expressed on the brush border and GLUT2 on the basolateral membranes of entire villus enterocytes indicating that the transcellular route for absorption of glucose in equine intestine is accomplished by luminally located SGLT1 and basally residing GLUT2. Furthermore, utilising

antibodies to equine T1R2 + T1R3 (the sweet taste receptor subunits) and their partner G-protein, gustducin, it was demonstrated that the sweet taste receptor is located in the enteroendocrine cells of equine small intestine. The presence of the sweet taste receptor in the equine gut provides a potential route for manipulating the capacity of the gut to absorb glucose and water, with attendant promise to enhance energy and hydration for racing horses.

Key Words: intestine, glucose transporters, sweet taste receptor

770 Fatty acid synthesis in equine adipose and liver tissue explants. J. K. Suagee*[1], B. A. Corl[1], M. V. Crisman[2], J. G. Wearn[2], L. J. McCutcheon[3], and R. J. Geor[3], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Virginia-Maryland Regional College of Veterinary Medicine*, *Blacksburg*, [3]*Michigan State University*, *East Lansing*.

Glucose and acetate can both be used to synthesize fatty acids with difference in preference noted between species. Ruminants preferentially use acetate, while humans and pigs preferentially use glucose- a difference that may be due to variations in gastrointestinal physiology. Equids possess the ability to absorb both dietary glucose from the small intestine and acetate from the hindgut, thus both substrates should be available for lipogenesis. Additionally, fatty acid synthesis can occur in either adipose or liver tissue. The objective of this study was to determine tissue depot and substrate preference for fatty acid synthesis in horses. Adipose (subcutaneous and mesenteric) and liver tissue was collected immediately post-euthanasia from six horses (3 BCS=7-8; 3 BCS=3) in order to determine substrate preference and tissue lipogenic activity. Tissue slices (100-150 mg) were incubated for two hours in buffer containing 1 μCi of either [U-^{14} C] D-glucose or sodium [1-^{14} C] acetate. Incubations were carried out at 37°C in a shaking water bath. Following incubations, total lipids were extracted and incorporation of radiolabel into fatty acids was measured. Data were analyzed using mixed models ANOVA. Lipogenesis was greater in the adipose depots than liver ($P = 0.002$). Within depot, glucose and acetate were used equally by both mesenteric and subcutaneous adipose tissue. Adiposity did not affect lipogenesis in mesenteric adipose; however, lipogenesis was reduced in the subcutaneous adipose of BCS 3 animals ($P < 0.001$). Lipogenesis in the liver was not affected by adiposity, but there were substrate differences, with acetate used to a greater extent than glucose ($P = 0.021$). In conclusion, horses primarily synthesize free fatty acids in adipose tissue and are capable of using both glucose and acetate as substrates. The low capacity of the liver to synthesize free fatty acids may suggest that this organ functions primarily in gluconeogenesis.

Key Words: horse, lipid

771 Effects of the insulin sensitizing drug, pioglitazone, on genes regulating glucose and fat metabolism in horses. J. K. Suagee*[1], R. J. Geor[3], L. J. McCutcheon[3], J. G. Wearn[2], M. V. Crisman[2], B. A. Corl[2], and M. W. Hulver[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksbug*, [2]*Virginia-Maryland Regional College of Veterinary Medicine*, *Blacksburg*, [3]*Michigan State University*, *East Lansing*.

Pioglitazone hydrochloride (PG), a thiazolidinedione antidiabetic agent, improves insulin sensitivity in humans by enhancing glucose and free fatty acid uptake from plasma and reducing pro-inflammatory cytokine expression. As a synthetic ligand for the peroxisome proliferator-activated receptor-γ (PPARg), PG alters the expression of genes involved in glucose and lipid metabolism and inflammation in skeletal muscle and adipose tissues. Our objective was to determine the influence of 10 d of PG treatment on 1) the expression of genes regulating glucose and lipid metabolism in equine adipose and skeletal muscle tissue and 2) lipopolysaccharide (LPS) induced insulin resistance. Sixteen mature (8 – 21 yr), non-pregnant mares with an average (± SEM) BCS of 5.9 ± 0.8 were used for this study. Treatment (n=8) horses received a 1 mg/kg dose of PG at 0700 hr, p.o. for 14 d. Muscle (mid gluteal) and adipose (nuchal crest) tissues were collected on d 0, 11, and 13. On d 12, all horses received an infusion of LPS (35 ng/kg, i.v., over 30 min). Following RNA isolation, 30 ng of total RNA was used in a one step PCR reaction to determine gene expression changes of glucose and lipid metabolism genes (GLUT4, GLUT1, insulin receptor [INSR], FATP, CD36, and PPARg). Fold changes were calculated as $2^{-\Delta\Delta Ct}$ and all data were analyzed using the mixed models procedure of SAS. Treatment with PG increased expression of muscle INSR ($P = 0.023$) and GLUT1 ($P = 0.053$), and adipose tissue FATP ($P = 0.034$). Infusion of LPS decreased expression levels of GLUT4 in muscle ($P = 0.054$) in both groups and in adipose of control animals ($P = 0.026$). Pioglitazone potentially increases mechanisms of insulin and non-insulin mediated glucose disposal in muscle, and free fatty acid uptake in adipose tissue, in addition to protecting against LPS induced reductions in insulin mediated glucose uptake into adipose tissue.

Key Words: horse, glucose, lipid

772 The use of a handheld glucometer for measuring glucose concentrations from whole blood collected from the horse. C. D. Gunkel*, J. S. Drouillard, and T. L. Slough, *Kansas State University*, *Manhattan*.

The objective of this experiment was to determine if a handheld glucometer could be used to accurately measure blood glucose concentrations in horses. Six four-year-old Quarter horse geldings (488 ± 20 kg BW) were used in the study. Horses were fed a diet consisting of ad libitum native prairie hay and 2.25 kg/d of concentrate. Half of the concentrate was fed in the morning, and the remainder was fed in the afternoon. Whole blood was collected in vacuum tubes via jugular catheter on two consecutive days at 30-min intervals for 4 h, beginning 1 h before introduction of concentrate feeding, thus resulting in a total of 120 individual samples. Approximately 10 μL of whole blood was utilized to obtain glucose readings using a One Touch Ultra handheld glucose monitor. The remaining blood was centrifuged at 876 × g for 10 min. Serum then was separated and frozen at -21° C. Serum was later thawed and subjected to a glucose assay performed with an Auto Analyzer 3 digital colorimeter. The glucose measurements obtained with the One Touch Ultra and the Auto Analyzer 3 were compared by repeated measures using a mixed model analysis of covariance, with glucose measurements obtained from the Auto Analyzer 3 as the response, measurements obtained with the One Touch Ultra as the covariate, horse as a random effect, and sampling day as a fixed effect. Initially, first order autoregressive covariance structure was utilized, but serial correlation between times was not significant. Residuals were found to normal. Whole blood glucose measurements determined on the One Touch Ultra system and serum glucose measured with the Auto Analyzer 3 were correlated ($R^2 = 0.48$; $P<0.0001$). Serum glucose concentration from the Auto Analyzer 3 can be estimated as: 3.61 + 0.3814 × whole blood glucose concentration from the One Touch Ultra. While the exact concentrations obtained by the standard colorimetric assay and the One Touch Ultra were not identical, both methods detected similar trends. Thus, the One Touch Ultra is a convenient method of monitoring blood glucose in the field.

Key Words: horse, glucose, glucometer

773 The effect of consuming endophyte-infected tall fescue on lameness in the horse. K. C. Gradert*[1], J. M. Bormann[1], S. F. DeWitt[2], L. W. Lomas[3], J. M. Kouba[1], and T. L. Slough[1], [1]*Kansas State University, Manhattan*, [2]*Woodside Equine Clinic, Ashland, VA*, [3]*Southeast Agricultural Research Center, Parsons, KS*.

The objective of this study was to assess the effect of endophyte-infected tall fescue consumption on equine soundness. Researchers have shown a vasoconstrictive effect of ergovaline on equine tissue *in vitro*. If circulation to the hoof is reduced *in vivo* then soundness may be compromised. Animals consisted of 12 clinically sound, three-year-old American Quarter horses with a mean BW of 459 ± 31 kg. They were blocked by weight, sex, and HYPP status and divided into two cohorts: control horses (n = 6) received an endophyte-free diet (E-) and treatment horses (n = 6) received an endophyte-infected (E+) diet. Fescue seed was integrated into the concentrate at a rate sufficient to bring daily ergovaline consumption in the E+ diet to a minimum of 0.20 ppm. The E- concentrate contained an equal amount of endophyte-free fescue seed. Horses had *ad libitum* access to native prairie hay. From d 30 to d 60 the native hay was replaced by a low- (E-) or high-endophyte (E+) variety of fescue hay. Based on assumed daily DM consumption of 2% BW, inclusion of fescue hay brought total dietary ergovaline consumption to 0.19 ppm (E-) and 1.04 ppm (E+). Lameness exams were conducted by a DVM blinded to treatment and occurred on d 0, d 30, d 60 and d 90. Animals were trotted in a straight path, tested for hoof sole and frog sensitivity, and longed in both directions on a concrete surface. Horses on the E+ diet tended (P = 0.06) to have increased hoof sensitivity to hoof testers on d 60 compared to E- horses. While numerically there appeared to be a treatment effect, limited numbers of observations resulted in no significant difference between groups. Further research with increased numbers of horses or increased treatment duration may better elucidate whether the consumption of endophyte-infected fescue has a negative impact on equine soundness.

Key Words: lameness, fescue, horse

774 The use of thermal imaging to monitor temperature in the hoof of horses consuming endophyte-infected tall fescue. K. C. Gradert*[1], J. M. Bormann[1], S. F. DeWitt[2], L. W. Lomas[3], J. M. Kouba[1], and T. L. Slough[1], [1]*Kansas State University, Manhattan*, [2]*Woodside Equine Clinic, Ashland, VA*, [3]*Southeast Agricultural Research Center, Parsons, KS*.

The objective was to evaluate blood flow in the hoof of horses consuming endophyte-infected tall fescue. A digital thermography camera was used to measure temperature in the hoof as an indicator of blood perfusion. Twelve clinically sound three-year-old Quarter horses with a mean BW of 459 ± 31 kg were blocked by weight, sex, and HYPP status and divided into two groups: those receiving an endophyte-free diet (E-; n = 6) and those receiving an endophyte-infected diet (E+; n = 6). Fescue seed was fed twice daily to bring daily ergovaline consumption in the E+ diet to a minimum of 0.20 ppm. The E- diet contained an equal amount of endophyte-free fescue seed. Horses had *ad libitum* access to native prairie hay, which was replaced with a high-endophyte (E+) or low-endophyte (E-) fescue hay from d 30 to d 60. Based on assumed daily DM consumption of 2.0% BW, total daily ergovaline consumption was calculated to be 0.19 ppm (E-) and 1.04 ppm (E+). Temperature was recorded at the center of both front hooves just below the coronary band on d 0, d 30, d 60 and d 90. Following the morning meal, ten serial temperature readings were taken on each hoof. On d 60, lower temperatures were noted in horses consuming the E+ diet compared to E- horses (P = 0.04). On d 90, E+ horses had higher hoof temperatures than E- horses (P = 0.03), and the regression coefficient for weight was positive (P = 0.05) indicating heavier horses exhibited higher temperatures compared to lighter horses. Regardless of diet, horses with HYPP status of NH had higher temperature readings on d 60 and d 90 than NN horses (P < 0.04). Adding the fescue hay to the diet prior to the d 60 measurements, and thus increasing total ergovaline content, appeared to alter the hoof temperature response in E+ horses. Consequently, if there is a vasoactive effect of ergovaline, it may be a dose dependent response.

Key Words: thermography, fescue, hoof

Nonruminant Nutrition: Fats and Oils

775 Effect of rice oil supplementation in diets for weanling pigs. G. J. M. M. Lima*[1], L. Wortmann[2], and A. Mior[2], [1]*Embrapa, Concordia, SC, Brazil*, [2]*Helmut Tessmann Vegetable Oils, Camaquã, RS, Brazil*.

Natural vitamin E (E) has been shown to be a superior source for young pigs to synthetic forms. This study was conducted to determine the effects of feeding high nutrient rice oil (RO) for weaned pigs. RO was extracted from bran to preserve E (166.79 mg total E/100 g and 37.47 mg α-tocopherol/100 g). Other natural constituents such as γ-oryzanol (1.1%) and n-3 fatty acids (16.3%) were present, too. Four hundred and thirty two weaned pigs, 21 days old and 6.49 ± 0.30 kg average weight (wt), were allotted to 2 treatments according to a randomized complete block design with 7 blocks, defined by wt and sex. Treatments were: T1- control diet, based on ensiled corn grain, soybean meal, porcine plasma, lactose sources, soybean oil, supplemented with minerals, vitamins and growth promoters, formulated to meet or exceed 1998 NRC levels; T2- same diets of T1, except for the inclusion of 2% RO in partial replacement of soybean oil. Pigs were raised on a three phase feeding program with free access to feed and water until the end of trial (42 days). Diarrhea frequencies were not different between treatments (X2 test, P>0.05). Pigs fed T2 diets showed heavier final wt (P=0.02) compared to T1, even when data were adjusted to initial weight (P=0.05) by analysis of covariance. RO dietary supplementation improved (P=0.02) average daily gain (ADG) and feed consumption (ADFC), but had no significant effect on feed:gain ratio (FCR, P=0.29). It is difficult to delineate the importance of each RO component (E, n-3 fatty acids, γ-oryzanol) for the obtained performance improvement, but these results confirm previous positive effects of supplementing natural E and n-3 fatty acids for young pigs.

Table 1. Effects of partial replacement of soybean oil by rice oil in diets for weaning pigs.

Variable	T1 - 2% SBO	T2 - 2% RO	SEM	CV%	P
Initial wt, kg	6.376	6.601	0.143	5.86	0.31
Final wt, kg	28.610	31.078	0.556	4.93	0.02
Adj. final wt, kg[1]	28.821	30.866	0.559	4.72	0.05
ADG, kg/d	0.442	0.487	0.010	5.60	0.02
ADFC, kg/d	0.893	0.956	0.015	4.19	0.02
Adj. ADFC, kg/d[1]	0.896	0.952	0.016	4.42	0.07
FCR	2.029	1.972	0.035	4.60	0.29

[1] Data adjusted to initial body wt. SEM=Standard error of the mean. CV=Coefficient of variation.

Key Words: swine, γ-oryzanol, n-3 fatty acids

776 Apparent and true ileal digestibility of acid hydrolyzed ether extract in various feed ingredients fed to growing pigs. B. G. Kim*, D. Y. Kil, and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was conducted to measure the apparent (AID) and true ileal digestibility (TID) of acid hydrolyzed-ether extract (AEE) in extracted corn oil (CO), high-oil corn (HOC, 7.1% AEE), full-fat soybeans (FFSB, 21.4% AEE), distillers dried grains with solubles (DDGS, 11.8% AEE), corn germ (CG, 18.1% AEE), and high protein-distillers dried grains (HP-DDG, 6.8% AEE). The ileal digestibility of AEE in these ingredients was determined using 19 barrows (initial BW: 52.2 ± 3.81 kg) that were fitted with a T-cannula in the distal ileum. Pigs were allotted to a 19 × 12 incomplete Latin square design with 19 diets and 12 periods. A basal diet (0.67% AEE) based on cornstarch, casein, sucrose, and corn bran was formulated. Fifteen additional diets were formulated by adding 2.0, 4.0, or 6.0% AEE from CO (2 to 6%), HOC (24 to 72%), FFSB (9 to 28%), DDGS (17 to 51%), and CG (11 to 33%) to the basal diet at the expense of corn starch, casein, and corn bran. In the remaining 3 diets, 1.1, 2.2, and 3.2% of AEE was added to the basal diet by including 16, 32, and 48% HP-DDG, respectively. The AID of AEE increased with increased concentrations of AEE from CO and FFSB ($P < 0.05$; linear and quadratic), and from DDGS and HP-DDG ($P < 0.05$; linear). However, the inclusion level of AEE from HOC and CG did not affect the AID of AEE. The average AID of AEE was 85.8, 48.1, 76.6, 59.8, 49.4, and 66.5% (SEM = 1.68) in CO, HOC, FFSB, DDGS, CG, and HP-DDG, respectively. The ileal endogenous excretion of AEE was 0.695, 0.112, 0.525, 0.137, -0.021, and 0.427 g/100 g DMI, and the TID of AEE was 96.8, 50.8, 86.1, 62.6, 48.9, and 76.3% (SEM = 1.63) for CO, HOC, FFSB, DDGS, CG, and HP-DDG, respectively. In conclusion, the digestibility of AEE in DDGS and HP-DDG is greater than in HOC or CG, implying the distillation process may improve the digestibility of AEE in corn. However, all the sources of intact corn oil that were used in this experiment had lower AID and TID values for AEE than extracted corn oil.

Key Words: acid hydrolyzed ether extract, ileal digestibility, pigs

777 The impact of dried distillers grains with solubles withdrawal programs on swine carcass fatty acid profiles and bacon quality. J. Stevens, A. Schinckel, B. Richert, and M. Latour*, *Purdue University*, *West Lafayette, IN*.

Crossbred pigs (N=112; initial BW = 29.0 kg) were blocked by initial BW and sex and assigned to 1 of 7 dietary treatments to assess the impact of removing dried distillers grains w/ solubles (DDGS) the last 26 d and adding fat to the late finishing diet on carcass fatty acid (FA) profiles, belly processing, and bacon cooking traits. Dietary treatments were: 1) Corn-soybean meal (CS) control d 0-103; 2) 20% DDGS d 0-103; 3, 4, and 5) 20% DDGS d 0-77 and CS, CS+5% beef tallow (BT), or CS+5% choice white grease (CWG) from d 77-103, respectively; 6 and 7) 20% DDGS+5% CWG d 0-77 and CS+5% BT or CS+5% CWG d 77-103, respectively. All diets were formulated on an equal dig. Lys to calorie ratio and were phase fed (2 grower and 2 finisher diets). Belly firmness was tested by placing bellies over a 7.6 cm pipe. Bellies were pumped, smoked and the center slices were baked at 204°C for 12 min to evaluate cooking properties of the bacon. The FA profiles of the belly, loin, outer backfat, and inner 2 layers of backfat were determined. Pigs fed treatment 1 had firmer bellies than pigs fed treatment 2 (Avg. 8.4 vs 5.8 cm vertical flex scores; P = 0.001). Feeding treatment 4 during the 26 d withdrawal tended to improve belly firmness over all other withdrawal programs (P<0.10). The high levels of linoleic acid in the DDGS resulted in the greatest difference between treatments 1 and 2 in linoleic acid (Belly; 9.3 vs 16.2%) in all adipose tissues measured (P = 0.001), resulting in a higher carcass calculated iodine value (belly; 57.1 vs 66.4), increased omega 6 to omega 3 ratios, and decreasing (P= 0.037) saturated to unsaturated ratios (belly; 0.70 vs 0.59) in all adipose tissues. Dietary treatments had minimal effects on belly yields or bacon cook scores. Feeding a CS or CS + 5% fat diet during a 26 d DDGS withdrawal program partially recovered some of the adverse fat quality effects caused by the increase in linoleic acid in the diet from the DDGS, however longer withdrawals are required for complete recovery of pork fat quality.

Key Words: swine, distillers dried grains, fatty acid profile

778 Analysis of iodine value in pork fat by Fourier transform near infrared spectroscopy for pork fat quality assessment. R. A. Cocciardi*[1], J. M. Benz[2], H. Li[1], S. S. Dritz[2], J. M. DeRouchey[2], M. D. Tokach[2], J. L. Nelssen[2], R. D. Goodband[2], and A. W. Duttlinger[2], [1]*Bruker Optics Inc.*, *Billerica, MA*, [2]*Kansas State University*, *Manhattan*.

The inclusion of dried distillers' grains with solubles (DDGS) in swine diets has rapidly increased in recent years because of increased availability. Because DDGS is high in linoleic acid, dietary intake by pigs has resulted in pork fat with higher levels of unsaturated fatty acids, adversely affecting pork fat firmness and quality. In this study, Fourier transform near infrared (FT-NIR) spectroscopy was used to measure iodine value (IV), a measure of the degree of unsaturation of fat. A total of 168 pork belly and jowl fat samples from pigs fed DDGS or ractopamine HCl were cut into pieces, placed on a glass petri dish and analyzed by FT-NIR spectroscopy in diffuse reflectance. Partial-least-squares (PLS) calibration models were developed for measuring IV in fat derived from pigs fed DDGS and ractopamine HCl by correlating their FT-NIR spectra to their respective gas chromatography-mass spectrometry reference values. Leave-one-out cross validation of the PLS models yielded R2 values of 89.0 and 90.6 and a root mean square error of cross validation of 1.04 IV and 1.26 IV for pork fat samples from pigs fed ractopamine HCl and DDGS, respectively. When the ractopamine HCl pork fat model was used to predict the DDGS pork fat model, a bias of 1.41 IV was obtained due to the compositional differences between the two types of samples. To obtain a more robust PLS calibration model, both data sets were merged and a test set validation of this model using half the samples as a validation set yielded an R2 value of 90.9, a root mean square error of prediction of 1.10 IV and a bias of 0.02 IV. This study demonstrates that FT-NIR spectroscopy combined with a robust PLS calibration model can measure IV in pork fat samples directly with an accuracy of approximately 1.1 IV. Conventional methods for measuring IV in pork fat are time consuming and costly, while this method allows processors to obtain IV results for quality assessment of pork fat on-site in under a minute.

Key Words: near infrared spectroscopy, iodine value, pork fat

779 The role of linoleic and α-linolenic acid for synthesis of long chain polyunsaturated fatty acids in liver and brain: A model study with growing pigs. W. Smink, J. Van Baal, R. Hovenier, and W. J. J. Gerrits*, *Wageningen University*, *Wageningen, the Netherlands*.

The effects of linoleic acid (LA) and α-linolenic acid (ALA) as precursor and inhibitor in the chain of n-3 and n-6 polyunsaturated fatty acids (LC PUFA) were studied in liver and brain of growing pigs (15-30 kg BW). In a 2x2 factorial arrangement, 32 gilts from 4 litters were

assigned to one of four dietary treatments, varying in LA and ALA intake. Differences between low and high intake were designed to be identical for LA and ALA: Low ALA and LA intakes were 0.15 and 1.30, and high ALA and LA intakes were 1.45 and 2.60 g/(kg $BW^{0.75}$/d), respectively. Intakes of saturated and monounsaturated FA, and other nutrients were kept constant. Consequently, energy intake increased with LA and ALA additions. After 28d on the dietary treatments, pigs were sacrificed. Liver and brain tissues were sampled and analyzed for FA composition and mRNA levels of Δ5 and Δ6 desaturase and elongase 2 and 5. In the liver, LA intake substantially increased C20:4n-6 (ARA) and ALA intake increased C20:5n-3 (EPA) concentrations, but decreased C22:6n-3 (DHA) (all P<0.01). Competition between n-3 and n-6 pathways was evidenced by substantial reductions of ARA at high ALA intakes (>40%) and EPA (>35%) and DHA (>20%) by increased LA intake (all P<0.001). Liver mRNA levels of Δ5 and Δ6 desaturase were increased by LA intake, and elongase 2 by both ALA and LA (P<0.01). Brain DHA was virtually unaffected by the dietary treatments, but C22:5n-3 was increased by ALA and decreased by LA (all P<0.001). mRNA levels of Elongase 2 were increased by ALA intake. In conclusion, ALA is a strong regulator in both the n-3 and n-6 LC PUFA chains. In addition to desaturation (Δ6), elongation from EPA and ARA may be rate limiting in brain and liver. Finally, brain DHA is virtually unaffected by ALA and LA.

Key Words: fatty acids, pig, brain

780 Comparing oxidation of fatty acids in pigs fed starch, animal fat or soy oil using ^{13}C labeled fatty acids. J. J. G. C. van den Borne[1], E. M. A. M. Bruininx[1], E. van Heugten[2], J. van Milgen[3], and W. J. J. Gerrits*[1], [1]*Wageningen University, Wageningen, the Netherlands*, [2]*North Carolina State University, Raleigh*, [3]*INRA, UMR1079, Systèmes d'Elevage, Nutrition Animale et Humaine, St Gilles, France*.

A study was conducted to compare oxidative loss of dietary starch, unsaturated and saturated fats in growing pigs. Eighteen barrows (28 kg BW) were assigned to one of 3 dietary treatments, in which starch (20%), animal fat (9.7%) or soy oil (9.1%) were exchanged isocalorically. Diets were fed twice daily at a rate of 1200 kJ DE/(kg $BW^{0.75}$.d) for an adaptation and experimental period of 7d each. A bolus dose of [U-^{13}C] labeled glucose was administered 1 h after feeding on d 1, and [U-^{13}C] bolus doses of linoleic (C18:2), stearic (C18:0) and oleic acid (C18:1) with the feed on d 2, 4 and 6, respectively. Pigs were housed individually in climate-respiration chambers. Based on $^{13}CO_2$ measurements by non-dispersive infrared absorption, ^{13}C recoveries of tracers were calculated (Table 1). Complete energy balances were measured using indirect calorimetry. Exchanging starch for fat, regardless of its source, reduced heat production by 4%. Cumulative recovery of ^{13}C from labeled glucose was unaffected. Replacing starch by fat increased the ^{13}C recovery of all fatty acid tracers used (P<0.01). Exchanging animal fat for soy oil did not affect the recovery of any of the tracers used. Recovery of ^{13}C from C18:0 was markedly lower compared with that of C18:1 and C18:2, which may result from a reduced tracer digestibility, but more likely reflects a reduced β oxidation of C18:0. In addition, these results indicate that exchanging starch for fat, regardless its source, increases fatty acid oxidation but reduces heat production.

Table 1. Treatment effects on heat production (HP, kJ/(kg $BW^{0.75}$.d)) and on recovery[1] of an oral bolus of ^{13}C tracers as $^{13}CO_2$ in pigs (% of dose)

	Diet			P-value
Item	starch	animal fat	soy oil	diet
C18:0	3.6[a]	9.5[b]	6.6[ab]	<0.01
C18:1	7.6[a]	14.4[b]	20.4[b]	<0.01
C18:2	8.5[a]	15.0[b]	15.7[b]	<0.01
glucose	49.1	48.4	46.9	0.69
HP	692[a]	664[b]	665[b]	<0.05

[a,b] means within a row without common superscript differ (P<0.05); [1] 24h (glucose) or 48h (fatty acids)

Key Words: pig, fatty acid, stable isotopes

781 Essential oil micro encapsulation increases stability during pelleting and premix and feed storage. D. Bravo, C. Ionescu*, A. Vienne, and S. Oguey, *Pancosma, Geneva, Switzerland*.

This experiment evaluated the influence of micro encapsulation technologies and encapsulate formulation on recovery of essential oils during the feed production process. Encapsulate formulations incorporated carvacrol (CA) into silica (SI), fat with a large particle size (HYB), modified starch (MS), maltodextrin (MA), arabic gum combined with maltodextrin (MAG) or as maltrodextrin coated with either salts (MAS) or with fat (MAF). Encapsulates were produced using adsorption (SI), spray granulation (MA, MS, MAG), spray cooling (HYB), or their combination (MAS, MAF). Encapsulates were then blended into mineral premixes and meal feeds. Unblended encapsulates were stored at room temperature for 20 wks, premixes were stored at 20C or 40C for 3 and 5 wks. Meals were expanded at 120C and then pelleted (75C). Pelleting stability was checked and samples of meals and pellets stored at 25C or 40C for 3, 6 and 20 wks. CA level was measured in feed samples. Under the most stringent condition for mineral premixes (40C for 5 wks), CA recovery was greater ($P < 0.01$) for MAG, MAS and MA (100, 97 and 97%, respectively) than for MAF (91%), with lower recovery from HYB, SI and MS ($P < 0.01$, 74, 72 and 70%, respectively). Pelleting stability was higher ($P < 0.001$) for MS, MAG and HYB (97, 96 and 96%, respectively) than for MA, MAF, MAS and SI (89, 87, 86 and 81%, respectively). After 6 weeks at 25C, CA recoveries in meal feed were higher ($P < 0.001$) for MA, MAG, MAS, MS and MAF (100, 100, 100, 97, 97%, respectively) than for HYB and SI (91 and 84%, respectively). Under the same conditions, recoveries in pellets were higher ($P < 0.001$) for MA and MAG (100 and 98%, respectively) compared with MAF, MAS, MS, HYB and SI (94, 93, 92, 92 and 90%, respectively). These results show that micro encapsulation method and formulations of the encapsulated additive itself are important determinants of essential oil recovery during feed production.

Key Words: Carvacrol, microencapsulation, stability

782 An evaluation of residual feed intake estimates obtained with computer models versus empirical regression. C. B. Williams*, C. L. Ferrell, and T. G. Jenkins, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

Data on individual daily feed intake, bi-weekly BW, and carcass composition were obtained on 1,212 crossbred steers, in Cycle VII of the Germplasm Evaluation Project at the U.S. Meat Animal Research Center. Within animal regressions of cumulative feed intake and BW on linear and quadratic days on feed were used to quantify average daily feed intake (ADFI) and ADG over a 120-d period. Residual feed intake (RFI) was estimated from predicted values of expected feed intake obtained by, a) empirical regression of ADFI on ADG and average $BW^{0.75}$ (RFI_{REG}), b) Cornell Value Discovery System (RFI_{CVDS}), c) National Research Council 2000 beef model (RFI_{NRC}), and d) Decision Evaluator for the Cattle Industry (DECI, RFI_{DECI}). Observed data on growth and carcass composition were used as input to the 3 computer models. Phenotypic correlations (r = 0.95, 0.87, 0.78) for RFI_{REG} with RFI_{CVDS}, RFI_{NRC}, RFI_{DECI}, respectively, suggest that RFI_{DECI} may be a different trait from RFI_{REG}. Additionally, RFI_{REG}, RFI_{CVDS}, RFI_{NRC}, and RFI_{DECI}, respectively, were correlated with ADG (r = 0.00, -0.20, -0.41, -0.48), and ADFI (r = 0.58, 0.50, 0.27, 0.09). These results show further differences between RFI_{DECI} and RFI_{REG}, and similarity between RFI_{CVDS} and RFI_{REG}, with RFI_{NRC} in between. Some animals that eat very little and grow slowly were identified as efficient based on their RFI_{REG} values, but ranged from less efficient to inefficient based on their RFI_{CVDS}, RFI_{NRC}, and RFI_{DECI} values, respectively. These results may be due to the fact that computer models predict performance on an individual animal basis in contrast to empirical regression. Also, the formulation of maintenance in DECI results in increasing maintenance requirements with increasing BW and ADFI. Animals with very low ADFI have lower maintenance requirements with DECI and in some cases, this results in expected feed intake being lower than ADFI. Finally, the results suggest that selection for RFI_{DECI} would tend to increase ADG with no change in ADFI.

Key Words: computer models, feed efficiency, beef cattle

783 Influence of feed management on random herd curves from random regression test-day model. M. Caccamo*[1], R. F. Veerkamp[2], J. D. Ferguson[3], R. Petriglieri[1], F. La Terra[1], and G. Licitra[1,4], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*Animal Breeding and Genomics Centre, ASG, WageningenUR, Lelystad, The Netherlands*, [3]*University of Pennsylvania, Kennett Square*, [4]*D.A.C.P.A. University of Catania, Italy*.

Earlier studies indentified large between-herd variation in lactation curve parameters in Ragusa province. The objective of this study was to identify sources of variation that explain these differences between herds in milk production curves, by estimating effect of animal breed (Holstein Friesian vs Brown Swiss), feeding system (separate feeding vs TMR), and TMR chemical composition on milk and milk components yield herd curves. Data for test day (TD) milk (Kg), fat (g), and protein (g) production from 1,287,019 TD records of 148,951 lactations of 51,489 cows in 450 herds, recorded from 1992 through 2007 were processed using a random regression TD model. Random herd curves (HCUR) for milk, fat, and protein yield were estimated for each herd per year from the model using 4-order Legendre polynomials. Information on herd management practices was monthly collected from 37 farms in Ragusa province from March 2006 through December 2007. TMR samples were collected every 3 months and analyzed for dry matter (DM), ash, crude protein (CP), soluble nitrogen (SN), acid detergent lignin (ADL), sequential NDF (NFDS), sequential acid detergent fiber (ADFS), and starch. The traits used to describe the curves were: peak, DIM at peak, persistency, and mean. Influence of feeding system and animal breed on herd curve traits was investigated using the GLM procedure of SAS. Influence of TMR chemical composition on HCUR traits was investigated using multivariate analysis with SAS REG and stepwise option. Feeding system had the largest influence ($P<0.05$) on HCUR peak and mean for all traits and parities, with higher values for TMR. Animal breed had the largest influence ($P<0.05$) on HCUR persistency, with higher values for Brown Swiss herds. Results from multivariate analysis showed that CP had the largest impact on HCUR peak and mean for all traits and for all parities, whereas the interaction between CP and DM had the largest impact on persistency for all traits and for all parities.

Key Words: herd curve, feeding management, test day model

784 Effects of programmed growth on yearling Brangus and Angus heifers. I. Performance and body composition. B. R. Austin, M. J. Hersom*, and J. V. Yelich, *University of Florida, Gainesville*.

The objective of this study was to examine the effects of programmed growth with deferred supplementation on BW gain and body composition of yearling Brangus and Angus heifers consuming Tifton 85 bermudagrass round bale silage (RBS; CP=7.9%, IVDMD=45.5%). Sixty heifers (n=30, Angus; n=30, Brangus) were stratified by initial BW, breed, and age and randomly allocated to 12 pens. Pens were randomly assigned to one of two treatments: 1) RBS and dried distillers grains (DDG) supplemented 3 d/wk for duration of experiment (174 d, CON) or, 2) RBS ad libitum for the first 88 d and RBS and DDG supplemented 3 d/wk from d 89–174 (L–H). CON heifers were provided supplement to gain 0.75 kg/d. When supplemented, L–H heifers were supplemented to gain 1.5 kg/d. Full BW and hip heights (HH) were obtained on d 0, 89, and 174. Ultrasound measurements of ribeye area (REA) and rump fat were obtained on d 16, 89, and 174. Data were analyzed using the MIXED procedure of SAS. Total DDG intake was greater ($P<0.05$) for L–H (1,662 kg) compared to CON (1,442 kg). Total RBS offered was greater ($P<0.05$) for CON (7,966 kg) compared to L–H (6,606 kg). ADG for the first 89 d of the trial was greater ($P<0.05$) for CON (0.57 kg/d) compared to L–H (0.003 kg/d). The ADG for the last 85 d of the trial tended ($P=0.07$) to be greater for the L–H (0.74 kg/d) compared to CON (0.61 kg/d). HH on d 174 was greater ($P<0.05$) for CON (122.8 cm) compared to L–H (119.6 cm). The CON had greater ($P<0.05$) REA compared to L–H on d 89 (18.4 vs 13.8 cm^2) and on d 134 (20.6 vs. 17.8 cm^2), respectively. Rump fat was greater ($P < 0.05$) for CON (0.42 cm) compared to L–H (0.31 cm) on d 89 but were similar ($P > 0.10$) for CON (0.43 cm) compared to L–H (0.38 cm) on d 174. Programmed growth with deferred supplementation of yearling heifers fed low–quality forage and supplemented with DDG had negative effects on growth patterns and body composition.

Key Words: beef heifers, supplementation, growth

785 Effects of programmed growth on yearling Brangus and Angus heifers. II. Puberty and reproductive performance. B. R. Austin, M. J. Hersom*, and J. V. Yelich, *University of Florida*, *Gainesville*.

The objective of this study was to examine the effects of programmed growth with deferred supplementation on the onset of puberty, estrous synchronization response, and pregnancy rates of yearling Brangus and Angus heifers consuming bermudagrass round bale silage (RBS, CP=7.9%, IVDMD=45.5%). Sixty heifers (n=30, Angus; n=30, Brangus) were stratified by initial BW, breed, and age and randomly allocated to 12 pens. Pens were randomly assigned to one of two treatments: 1) RBS and dried distillers grains (DDG) supplemented 3 d/wk for duration of experiment (174 d, CON) or 2) RBS ad libitum for the first 88 d and RBS and DDG supplemented 3 d/wk from d 89–174 (L–H). Blood samples were collected on d –2, 8, 79, and 89 to determine plasma progesterone concentrations and onset of puberty. Weekly blood samples were collected from d 89–174 to determine plasma progesterone concentrations to determine onset of puberty. Heifers were synchronized for AI on d 174 with a CIDR concomitant with GnRH (100 ug; i.m.) with CIDR removal and PG (25 mg; i.m.) 7 d later. Estrus was detected using HeatWatch for 72 h after PG, and heifers were AI 8–12 h after the onset of estrus. Heifers not exhibiting estrus by 72 h were timed–AI + GnRH. Estrous detection and AI continued for 30 d after synchronization. Heifers were divided by breed and exposed to clean–up bulls for 30 d. Pregnancy was diagnosed by ultrasonography 31, 62, and 95 d after PG. Percentage of heifers that attained puberty on d 89 (13 vs 3%) and at initiation of breeding (33 vs 7%) was greater (P<0.01) for CON compared to L–H, respectively. Estrous response (73 vs 40%), 30–d AI pregnancy rates (83 vs 56%), and overall pregnancy rates (93 vs 66%) were greater (P <0.05) for CON compared to L–H, respectively. Synchronized pregnancy rates (46 vs 33%) and conception rates (50 vs 53%) were similar (P>0.05) between CON and L–H, respectively. Programmed growth with deferred supplementation of yearling heifers fed low-quality forage and supplemented with DDG had negative effects on reproductive performance.

Key Words: beef heifer, supplementation, reproduction

786 Predicting the success of fixed-time AI from passive monitoring of body temperature in beef heifers. J. A. Small*[1,4], A. D. Kennedy[2], L. M. Pfeifer[3], and J. Singh[3], [1]*Agriculture and Agri-Food Canada*, *Brandon, MB, Canada*, [2]*University of Manitoba*, *Winnipeg, MB, Canada*, [3]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [4]*Nova Scotia Agricultural College*, *Truro, NS, Canada*.

The objective was to determine if the body temperature (Trr) and number of monitoring events (ME) from passive acquisition of data logged by transponder boluses differed between heifers that were, retrospectively, pregnant (PR, N=30) or not-pregnant (NP, N=33) to fixed-time artificial insemination (TAI). Yearling heifers (12.5 ± 0.5 mo., 421 ± 32 kg body weight, 5.4 ± 1.2 mm backfat thickness) with magnetic, inductively coupled full duplex RFID transponder boluses containing thermistors (Phase IV Engineering Inc., Boulder, CO) were housed in one pen with two panel readers in an outdoor shed-lot facility and provided a mixed ration (59% dry matter) at 1500h daily. Fencing was arranged for water motivated acquisitions by one panel reader, and activity motivated acquisitions by the other (Small et al. Can. J. Anim. Sci. 88:225-235, 2008). All heifers were administered estradiol benzoate (1 mg im) on the 8th d after the second of two doses of PGF (500 ug im) given 11 d apart, two groups were given progestin inserts (1/2 Cue-mate) removed concurrent with PGF (25 mg im; 1100h, Day 0), and a third group was given a temperature recording device (HOBO ProV2) anchored in the vagina and programmed to record temperature (Tv) every 15 min from Day -7 to Day 7; all received pLH (12.5 mg im) concurrent with TAI 54h after PGF (Day 0). Current Trr and Tv were compared to the previous 3-d baselines for each window of time. For PR, Tv decreased to nadir within 24h of PGF and peaked above baseline at 58h (Day 2) returning to baseline at 78h (Day 3); for NP peaks occurred 78 to 90h returning to baseline at 96h (Day 4). Mean Trr was 0.3°C higher (P<0.05) for pregnant than non-pregnant heifers at 60h (Day 2) and vice-versa at 114h (Day 4). The number of Trr ME was greater (P<0.05) for PR than NP at 30, 36 and 60h windows after PGF (7.9 vs 12.8 ± 0.8 ME/6h at 60h). Passive monitoring of Trr could improve the efficacy of TAI in heifers by facilitating a management decision to re-inseminate or observe for return to estrus.

Key Words: body temperature, beef heifers, fixed-time artificial insemination

787 Does fertility-associated antigen on sperm collected from Nellore *(Bos indicus)* bulls affect fertility at first-service timed AI? J. C. Dalton*[1], L. Deragon[2], J. L. M. Vasconcelos[3], and A. Ahmadzadeh[4], [1]*University of Idaho*, *Caldwell*, [2]*Alta Genetics Brazil*, *Uberaba, MG, Brazil*, [3]*FMVZ-UNESP*, *Botucatu, SP, Brazil*, [4]*University of Idaho*, *Moscow*.

The objective was to determine whether the presence of fertility-associated antigen (FAA; a 31 kDA heparin binding protein) on sperm collected from Nellore bulls can be used to assess potential fertility of sperm for use at first-service timed AI (TAI). Following determination of FAA status by use of a lateral flow cassette, 6 Nellore bulls (4 to 7 yr old) were selected based on FAA status (FAA-negative: n = 3; FAA-positive: n = 3) and their ability to produce neat semen with characteristics equal to or greater than 70% morphologically normal sperm and 60% estimated progressive motility before cryopreservation. Ejaculates were collected by artificial vagina and were extended to 120×10^6 sperm/mL. The extended semen was packaged and cryopreserved in 0.25-mL straws (30×10^6 sperm). Multiparous lactating Nellore cows (n = 835) at a commercial beef farm in Mato Grosso do Sul, Brazil, were evaluated for body condition score (BCS;1-5 scale) and enrolled in a first-service TAI program. On d 0 cows began the synchronization protocol with an intravaginal progesterone device (CIDR) + an injection of 2.0 mg of estradiol benzoate. On d 9, the CIDR was removed, 12.5 mg of $PGF_{2\propto}$ + 0.5 mg of estradiol cypionate were administered, and calves were removed for 48 h until TAI. Two technicians performed TAI, with each technician using semen from each bull. Fertility, as measured by pregnancy/TAI (P/TAI), was not different between FAA-positive and FAA-negative bulls (41.5% vs. 39.3%, respectively). There was an effect of AI technician on P/TAI (36.0% vs. 43.9%; n = 375 and n= 460, respectively; P<0.05); however, there was no AI technician by FAA status (treatment) interaction. BCS affected P/TAI (P<0.05). Cows with BCS < 2.5 were three times less likely to become pregnant to first TAI compared with cows with BCS ≥ 2.5. In this study using a limited number of bulls, there was no effect of FAA status on fertility at first-service TAI.

Key Words: sperm, timed AI, fertility

788 Mastitis in beef bulls caused by *Arcanobacterium pyogenes*. S. C. Nickerson*[1], E. Rollin[2], D. T. Ensley[2], and R. D. Berghaus[2], [1]*University of Georgia, College of Agricultural and Environmental Sciences, Department of Animal and Dairy Science*, *Athens*, [2]*University*

of Georgia, College of Veterinary Medicine, Department of Population Health, Athens.

As part of a trial at a university bull test station, data were collected from 101 animals 7 to 10 mo of age including daily weight gain, scrotal circumference, and body frame score. In the process of measuring scrotal circumference, technicians observed that teats of 2 bulls were swollen and leaking a thick pus-like fluid. Upon subsequent culture by university personnel 2 mo later, 14 of 58 bulls sampled (24.1%) were observed to have abnormal, swollen teats, and an examination of teat skin surfaces revealed the presence of scabs and abrasions typical of those caused by horn flies. The culture of teat skin scabs revealed numerous coagulase-negative staphylococcal (CNS) species. No systemic clinical signs were observed, but affected bulls exhibited expressible mammary secretions ranging from a clear, serum-like fluid to a viscous, pus-like secretion. A total of 19 mammary secretion samples were collected for culture, plated on blood agar, and identified following procedures recommended for the diagnosis of mastitis in dairy cows. Results demonstrated the following distribution: Uninfected- 26.3%, *Arcanobacterium pyogenes*- 52.6%, gram-negative rods- 10.5%, CNS- 5.3%, and dual infections with CNS/environmental streptococci- 5.3%. Approximately 1 mo later, 21 of 97 bulls (21.6%) were found to have mastitis, and 26 mammary secretion samples were collected with the following distribution: Uninfected- 11.2%, *A. pyogenes*- 57.7%, gram-negative rods- 7.7%, CNS- 7.7%, *Staphylococcus aureus*- 7.7%, and environmental streptococci- 8%. Although a limited number of *A. pyogenes* infections was treated, teat infusions with a cephalosporin-based nonlactating cow product was ineffective, but infusion of 2% chlorhexidine digluconate resulted in a cure in one bull. Because *A. pyogenes* mastitis is known to be initiated by horn flies in dairy cows and heifers, greater control of these insect vectors may be necessary to manage this form of mastitis in beef bulls.

Key Words: *Arcanobacterium pyogenes*, beef bulls, mastitis

Ruminant Nutrition: Dairy 3

789 Short-term changes in forage dry matter affect milk production responses in dairy cows. D. R. Mertens*[1] and P. Berzaghi[2], [1]*US Dairy Forage Research Center, Madison, WI*, [2]*University of Padua, Italy*.

Our goal was to quantify the effect of one-day changes in forage DM on ration imprecision and milk responses. Forty eight cows (days of lactation = 121 ±52d; BW = 591 ±63 kg) were blocked in 12 groups for parity and milk production and two were assigned to a control (CON) or treatment (TRT) group. The TRT consisted of changing forage DM to simulate a rain event on a bunker silo and feeding an imprecise ration based on as-fed ratios of ingredients for one day of each week. The CON ration was adjusted to maintain DM ratios of ingredients on that day. Each period consisted of three days for baseline, one day (d4) with ration differences, and three days of recovery. The ration changes were repeated 5 times by changing DM of corn silage or alfalfa silage or both by 8%-units. Production was recorded and samples were taken at each milking (2 ×/d) between days 2 and 6 of each period. Milk production and composition during days 4 to 6 were expressed as difference from those of the baseline period. Forages, TMR and refusals were sampled daily and concentrates were samples weekly. Chemical composition (DM, CP, NDF) of samples were determined by NIR after updating in-house calibrations with 58 samples from the experiment. Data were analyzed using Proc Mix of SAS with cow-within-block and TRT group as random variables. The DMI of TRT was reduced ($P<0.01$) on d4 (-2.2 kg) compared to the baseline, but cows returned to baseline level during recovery. Overall DMI was similar between CON and TRT (25 kg/d). Compared to baseline, milk production, but not composition, of TRT was affected ($P<0.001$) in the two days following d4 (-0.86 kg/d) compared to an increase ($P<0.05$) of 0.43 kg/d in the CON group. On d5, TRT milk depression averaged 1 kg and remained depressed (-0.7 kg) on d6. Using DMI change as a covariate ($P<0.001$), the loss of one kg of DMI on d4 resulted in 0.57kg/d less milk in each of the following two days. We concluded that improving ration precision by adjusting rations for forage DM changes enhances DMI and milk production.

Key Words: dry matter, intake, precision feeding

790 Meta-analysis of influence of dietary NDF on energy partitioning in dairy cows. D. Sauvant*[1], O. Martin[1], and D. Mertens[2], [1]*Agroparistech-INRA, Paris, France*, [2]*US Dairy Forage Center, Madison, WI*.

The objective of this study was to evaluate the influence of dietary NDF on dairy cow energy intake and partitioning. A database of 88 published experiments (nexp) with 219 treatments (n) where dietary NDF was the factor (34.9 ±8.6, min = 28.8, max = 40.0%DM) was compiled. Experiments were selected that measured diet organic matter digestibility (OMD = 70.7 ±5.9, min = 54.6, Max = 83.6%) to predict as accurately as possible dietary metabolizable energy intake (MEI). Milk yield ranged from 9.2 to 45.2 kg/d (27.6 ±7.8). Milk fat content ranged from 2.1 to 5.1% (3.7 ±0.6). Energy secreted in milk (Emilk) and in milk lactose (Elact), protein (Eprot) and fat (Efat) was calculated using 4.0, 5.6 and 9.3 Mcal/kg, respectively. Data were analyzed using GLM to separate inter- and intra-experiment variances. Daily MEI (48.7 ±9.9 Mcal/d) was negatively linked to the dietary NDF (MEI = 72.3 – 0.693 NDF, n = 219, nexp = 88, R2 = 0.90, RMSE = 15.3). Energy secreted as lactose was linearly linked to MEI (Elact = 2.40 + 0.0665 MEI, n = 80, nexp = 34, R2 = 0.98, RMSE = 0.22), and the regression was similar for Eprot (Eprot = 1.18 + 0.074 MEI, n = 197, nexp = 78, R2 = 0.98, RMSE = 0.23). The global and inter-experiment regressions were not statistically different, thus, the marginal efficiency of MEI transformation to Elact and Eprot is of 6.7 and 7.4% respectively. For energy secreted as fat, the relationship was curvilinear (Efat = – 3.20 + 0.45 MEI – 0.0038 MEI2, n = 219, nexp = 88, R2 = 0.95, RMSE = 0.59). Marginal efficiency of MEI to Efat decreased from 26% (MEI = 25) to – 8% (MEI = 70). Therefore the milk energy response was curvilinear (Emilk = 2.49 + 0.48 MEI – 0.0027 MEI2, n = 219, nexp = 88, R2 = 0.98, RMSE = 0.78). Energy balance (EB) was also curvilinearly related to MEI (EB = –3.3 – 0.23 MEI + 0.0062 MEI2, n = 219, nexp = 88, R2 = 0.94, RMSE = 1.09), and EB of zero was achieved for MEI = 50 Mcal/j. In conclusion, dietary NDF strongly influences energy partitioning in dairy cows through its impact on MEI.

Key Words: NDF, milk energy, energy partitioning

791 Effect of feeding low-starch, low-forage diets to mid-lactation dairy cows on lactational performance and ruminal characteristics. E. R. Myers*[1], H. M. Dann[2], K. W. Cotanch[2], C. S. Mooney[2], R. J. Grant[2], A. L. Lock[1], and K. Yagi[3], [1]*University of Vermont, Burlington*, [2]*William H. Miner Agricultural Research Institute, Chazy, NY*, [3]*ZEN-NOH National Federation of Agriculture Co-Operative Associations, Tokyo, Japan*.

We have shown that corn grain can be replaced with byproduct feeds in lactating cow diets resulting in a low-starch [18% of dry matter (DM)] diet without adverse effects on ruminal fermentation and lactational performance. Previous research has not addressed how little forage can be fed with a low-starch diet. Sixteen lactating Holstein cows (116 ± 5 days in milk; 8 ruminally fistulated) were used in a replicated 4×4 Latin square design study with 21-d periods (9-d collection) to determine the effect of feeding diets containing low-starch (19% of DM) and different amounts of forage (52, 47, 43, and 39% of DM) on lactational performance and ruminal characteristics. The primary ingredients (DM basis) in the 52 to 39% forage diets were corn silage (37 to 28%), alfalfa-grass silage (14 to 1%), wheat straw (0 to 10%), beet pulp (6.2%), distillers dried grains with solubles (11 to 9%), soybean meal (11 to 12%), wheat middlings (7 to 19%), and corn meal (5 to 6%). Data were analyzed as a replicated Latin square design using the MIXED procedure of SAS. Diet affected ($P \leq 0.05$) dry matter intake [DMI, % of body weight (BW)], feed efficiency, total tract digestibility (TTD) of organic matter (OM) and neutral detergent fiber (NDF), and ruminal turnover rate (RTR) of OM and NDF. Diet did not affect ($P > 0.10$) milk yield, milk composition (fat = 3.60 ± 0.09%; protein = 3.02 ± 0.04%), mean ruminal pH (6.07 ± 0.07), microbial N yield (450 ± 17 g/d), ruminal digesta mass (95.1 ± 8.3 kg), or ruminal pool size (OM = 12.2 ± 1.1 kg; NDF = 8.4 ± 0.7 kg). For high producing cows the limit to decreasing forage in low-starch diets appears to be between 39 and 43% forage.

Table 1.

Item	52% forage	47% forage	43% forage	39% forage	SEM	P
DMI, kg/d	22.8	23.4	23.4	24.1	0.5	0.07
DMI, % BW/d	3.47^{b}	3.55^{ab}	3.54^{ab}	3.67^{a}	0.1	0.03
Milk, kg/d	42.5	42.6	42.8	42.6	1.3	0.99
Milk/DMI, kg/kg	1.87^{a}	1.82^{ab}	1.84^{ab}	1.77^{b}	0.04	0.02
TTD of OM, %	64.5^{a}	63.3^{ab}	62.0^{bc}	61.0^{c}	0.7	<0.01
TTD of NDF, %	39.4^{a}	35.9^{ab}	34.0^{b}	29.1^{c}	1.3	<0.01
RTR of OM, %/h	7.0^{b}	7.5^{bc}	8.1^{a}	8.0^{a}	0.5	0.01
RTR of NDF, %/h	4.0^{b}	4.4^{ab}	4.6^{a}	4.5^{ab}	0.3	0.03

^{abc} $P \leq 0.05$

Key Words: starch, forage, dairy cow

792 Assessment of dietary ratios of red clover and corn silages on milk production and milk quality in dairy cows. J. M. Moorby*, N. M. Ellis, D. W. R. Davies, and D. R. Davies, *Institute of Biological, Environmental and Rural Sciences, Aberystwyth, UK*.

Twenty-four multiparous Holstein-Friesian dairy cows at 106 (± 16.1) DIM were used in a replicated 3×3 Latin square changeover design experiment to test the effects of changing from corn silage to red clover silage in graded proportions on feed intake, milk production and milk quality, and whole-body partitioning of N and P. The 3 dietary treatments comprised ad libitum access to 1 of 3 forage mixtures plus 4 kg dairy concentrates/d. The 3 forage mixtures (on a DM basis) were: 1) 90% corn silage:10% red clover silage, 2) 50% corn silage:50% red clover silage, and 3) 10% corn silage:90% red clover silage. In each of 3 experimental periods there were 21 d for adaptation to diets and 7 d for measurements. Results were analyzed by ANOVA with polynomial contrasts and are given in order of diets 1, 2 and 3. Diet CP intakes increased, and starch intakes decreased, as the silage mixture changed from 90% corn to 90% red clover. Highest total DM intakes (19.6, 20.5, and 19.5 kg/d; SED = 0.32; $P_{quad} < 0.001$) and milk yields (26.1, 27.3, and 25.7 kg/d; SED = 0.54; $P_{quad} < 0.01$) were achieved on the 1:1 silage mix. Although milk fat concentrations were unaffected by diet, milk protein concentrations decreased as the proportion of red clover silage in the diet increased (3.09, 3.06, and 2.99%; SED = 0.024; $P_{lin} < 0.001$). Apparent secretion of dietary N into milk (33, 28, and 25%; SED = 1.1; $P_{lin} < 0.001$) decreased, while apparent urinary excretion of dietary N (19, 23, and 31%; SED = 1.3; $P_{lin} < 0.001$) and urinary allantoin excretion (408, 440, and 481 mmol/d; SED = 28.5; $P_{lin} = 0.04$) increased, with more red clover in the diet. There was no treatment effect on whole body N balance, although P balance was greatest on the 1:1 forage mix (10, 17, and 12 g P/d; SED = 1.6; $P_{quad} = 0.03$). In conclusion, optimum feed intakes and milk yields were achieved on a diet that contained a 1:1 DM mixture of corn and red clover silages.

Key Words: red clover silage, corn silage, N use efficiency

793 Determining fiber requirements in dairy cows by modeling digestive responses to dietary physically effective NDF. Q. Zebeli*[1,2], D. Mansmann[1,2], H. Steingass[2], W. Drochner[2], and B. N. Ametaj[1], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*University of Hohenheim, Stuttgart, Germany*.

Predicting requirements for dietary fiber is crucial in optimizing digestion and preventing occurrence of sub-acute ruminal acidosis (SARA). The aim of the study was to determine requirements of physically effective fiber in dairy cows by modeling its effects on digestive responses using a meta-analytical approach. A database was compiled from 65 recently published studies (n=242 dietary treatments) with lactating Holstein cows (112 DIM, 33.7 kg milk/d) fed TMR (35.1% NDF and 25.0% starch in DM). The content of $peNDF_{>8}$ was calculated by amount of DM retained on 2 sieves (19 and 8mm) of PSPS multiplied by dietary NDF. Average amounts of dietary particles retained on screens 19 and 8 mm were 12.8 and 37.1%, respectively, while average content of $peNDF_{>8}$ was 16.9±5.5%. Digestive response variables modeled included rumen pH, chewing activities, passage rate, and fiber digestibility. Results showed that total chewing time increased linearly with increasing dietary $peNDF_{>8}$ (R^2=0.40). The analysis revealed a curvilinear response of rumination time (RT) to dietary $peNDF_{>8}$ [RT (min/d)=512-243$e^{-0.077*peNDF_{>8}}$; R^2=0.42]. Increasing the content of dietary $peNDF_{>8}$ quadratically decreased chewing time per unit of $peNDF_{>8}$ ingested with the latter reaching a plateau at 160 min/kg $peNDF_{>8}$. Interestingly, results showed a linear response of rumen pH to diet $peNDF_{>8}$ (pH=5.57+0.034*$peNDF_{>8}$; RSME=0.12; R^2=0.62) up to a content of 18.5% (95% CI: 16.4 to 20.6% $peNDF_{>8}$). The latter threshold of $peNDF_{>8}$ corresponded to plateau values of 6.22 for daily mean rumen pH and <1 h/d for duration in which rumen pH was <5.8. Both pH-variables and passage rate out of reticulorumen were accurate predictors of NDF and ADF digestibility (R^2=0.47 to 0.62). In summary, results suggested that a minimum of 16.4% $peNDF_{>8}$ in diet DM is required to maintain chewing activities, prevent SARA, and optimize fiber digestion in dairy cows.

Key Words: dairy cow, physically effective fiber, meta analysis

794 Nutritional value of bahiagrass, bahiagrass-alfalfa, or brown mid rib sorghum baleage for lactating Holstein cows. M. E. McCormick*[1], V. R. Moreira[1], D. C. Blouin[2], and K. J. Han[1], [1]*Louisiana State University Agricultural Center, Southeast Research Station, Franklinton*, [2]*Louisiana State University Department of Experimental Statistics, Baton Rouge*.

Forty eight Holstein cows were stratified according to lactation number, days in milk (115 ± 17), and daily milk yield (34.3 ± 7.2 kg) and randomly assigned to the following forage treatments:1) bahiagrass baleage, 2) bahiagrass-alfalfa (78%:22%) baleage, 3) brown mid rib (BMR) sorghum baleage, or 4) corn silage. The first objective of the 56-day feeding study was to assess the feeding value of a bahiagrass-alfalfa baleage derived by interseeding 'Amerigraze 702' alfalfa in 30 cm rows into an existing stand of 'Argentine' bahiagrass relative to the feeding value of baleage from a pure stand of similar bahiagrass. A second objective was to evaluate the nutritional value of 'BMR 106' forage sorghum (vegetative, 1.4m ht) stored as baleage compared to corn silage. Baleage crops were ground with a flail-type hay processor. All forages were incorporated into total mixed rations (TMR) and individually fed once daily. Lactation performance data were statistically analyzed using Proc Mixed of SAS with data from a 7-day standard feeding period used as covariables. Forage dry matter, pH, CP, ADF, NDF, water soluble carbohydrate, and IVTD means were 57.2%, 5.69, 10.1%, 38.4%, 69.5%, 2.2% and 67.8%; 52.6%, 5.42, 11.4%, 37.6%, 64.8%, 3.7% and 71.0%; 35.2%, 4.54, 12.9%, 38.8%, 61.7%, 8.0% and 79.8%; 29.2%, 3.8, 8.6%, 24.0%, 41.4%, 10.3%, and 80.6% for treatment 1-4, respectively. The TMR dry matter intake (DMI) was similar between diets 1 and 2 (20.3 vs 22.1 kg/d), but milk yield (26.1 vs 28.5 kg/d) tended ($P < 0.10$) to favor the bahiagrass-alfalfa mixture, presumably due to improved forage nutritive value. The TMR DMI and daily milk yield were lower ($P < .05$) for diet 3 than 4 (21.3 and 30.6 kg/d vs 25.7 and 33.1 kg/d, respectively). Milk composition, rumen pH, body weights, and body condition scores were not affected by diet. The data indicate that modest concentrations of alfalfa in bahiagrass baleage may improve lactation performance of Holstein cows. The BMR sorghum baleage failed to generate as much milk as corn silage due to lower TMR DMI.

Key Words: baleage, nutrition, Holstein

795 Diurnal patterns of rumen pH and function in dairy cows on high quality temperate pastures of the South Island of New Zealand. J. Gibbs* and J. Laporte, *Lincoln University, Canterbury, New Zealand*.

This experiment was undertaken to describe the diurnal patterns of rumen, urinary and faecal pH, SCFA and ammonia in dairy cows under a specific grazing management typical of the new, large herd systems of the South Island of NZ, and to compare these to accepted patterns of rumen function in traditional, lower intensity grass based dairy systems. For a 48h period in mid-spring, six high production (425 kg MS/ yr), ruminally fistulated, lactating Holstein Friesian cows free-grazing very high quality ryegrass pasture in a typical NZ large herd scenario had indwelling rumen pH and temperature probes recording to a datalogger every 15s and were also manually sampled for rumen fluid, faeces and urine every 2h. Samples obtained were analysed for: rumen - SCFA and ammonia; faeces - pH, SCFA and ammonia; urine - pH and ammonia. Cow grazing behaviour was recorded every 15min over the 48h. Results showed a consistent, marked diurnal wax and wane pattern of rumen, faecal and urinary pH, SCFA and ammonia associated with grazing behaviour. Rumen pH varied from 5.1-7.0, faecal pH from 6.2-7.1, and urinary pH from 7.0-8.5. Total rumen SCFA concentrations varied from 84-223mmol/L, lactic acid was absent or below 10mmol/L, and ammonia varied from 35-528mg/L. Faecal total SCFA concentrations varied from 15-50mmol/L, and ammonia from 47-325mg/L, and urinary ammonia from 5-102mg/L. The results suggest grazing behaviour under intensive pasture management conditions typical of the South island in NZ produces an atypical rumen function of extreme diurnal variation in metabolic activity. However, this previously undescribed pattern in rumen, faecal and urinary pH and metabolites does not appear inimical to either rumen function or milk production, suggesting physiological adaptation.

Key Words: rumen pH, pasture grazing, grazing management

796 Effect of pre-grazing herbage mass and daily herbage allowance on rumen, plasma and milk fatty acids. R. A. Palladino[1], M. O'Donovan[2], J. J. Murphy[2], M. McEvoy[1,2], and D. A. Kenny*[1], [1]*University College Dublin, Belfield, Dublin, Ireland*, [2]*Teagasc, Fermoy, Co. Cork, Ireland*.

Conjugated linoleic acid (CLA) in milk is dictated by intake of dietary precursors and the extent of ruminal biohydrogenation. Grazing management may change both precursor intake and biohydrogenation through its influence on pasture composition. This study evaluated the effect of two levels of pre-grazing herbage mass (HM; 1700 and 2500 kg/ha) and two levels of daily herbage allowance (DHA; 16 and 20 kg/cow/d) on the fatty acid (FA) composition of rumen fluid, plasma and milk in grazing dairy cows. Four rumen fistulated Holstein dairy cows were randomly allocated to four treatments (high HM, high DHA; high HM, low DHA; low HM, high DHA; low HM, low DHA). Rumen (0700, 1100, 1500 and 2000 h), plasma (0700 and 1500 h) and milk (pm milking) samples were collected during each of four periods from June to August in a Latin square design. Samples were analyzed for FA by gas chromatography. Data were analyzed by mixed model ANOVA with cow as a random effect. The model included terms for HM, DHA, period and the interaction HM x DHA. For rumen and plasma samples, time of sampling was included as well as the interaction of HM x time, DHA x time and HM x DHA x time. No CLA was detected in either rumen or plasma samples. The milk CLA concentration was in agreement with previous reports under grazing conditions (12.8 × 2.20 g/kg of total FA) but was not affected by treatment ($P>0.05$). Rumen concentration of vaccenic acid (VA) was highest in cows grazing the low HM, high DHA pasture (17.0 g/kg of total FA; $P<0.05$). Additionally, rumen VA concentration increased from 0700 to 2000 h (from 13.1 to 14.7 g/kg of total FA; $P<0.01$). Concentrations of VA in plasma were not affected by treatment or time of sampling ($P>0.05$). Milk VA was higher in cows grazing low HM ($P<0.01$). Linolenic acid (LNA) in plasma or rumen fluid was not affected by time ($P>0.05$). However, milk LNA was higher for cows grazing low HM (3.6 vs. 5.6 g/kg of total FA for high and low HM respectively). In conclusion, under the conditions of the present study, there was little effect of grazing management on the concentration of health promoting FA in milk.

Key Words: conjugated linoleic acid, herbage mass, daily herbage allowance

797 Comparison of energy expenditure, physical activity and feeding behavior in dairy cows grazing pasture grass or fed the same grass indoors. L. D. Kaufmann[1], A. Münger[1], M. Rérat[1], P. Junghans[2], S. Görs[2], C. C. Metges[2], and F. Dohme*[1], [1]*Agroscope Liebefeld-Posieux,*

Research Station ALP, Posieux, FR, Switzerland, [2]*Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany.*

The objectives of the study were to compare energy expenditure (EE) of dairy cows fed grass either on pasture or in the barn and to evaluate the influence of physical activity on EE. Fourteen dairy cows (BW: 658 ± 64.3 kg; milk yield: 45.5 ± 1.78 kg/d) were randomly assigned to a cross over study, with two 2-wk experimental periods consisting of an adaptation and a data collection period of 1 wk each. Cows either grazed on pasture or had ad libitum access to grass from the same paddock, fed in a free-stall barn. All cows were supplemented with a cereal-based concentrate. Milk yield and milk components were recorded daily. In the collection period EE of each cow was determined on 1 d from 0700 to 1300 h using the ^{13}C bicarbonate dilution technique. After administration of the tracer (0.7 mg $NaH^{13}CO_3$ /kg BW) into the jugular vein, blood was sampled either manually in the barn or with an automatic blood sampling system on pasture. During the same time cow′s physical activity was recorded with a pedometer and feeding behavior was investigated using a behavior recorder. Milk (42.8 kg/d), fat (1.58 kg/d) and protein yield (1.31 kg/d) did not differ ($P > 0.05$) between treatments. Within the 6-h measurement period, cows on pasture produced more ($P < 0.01$) CO_2 and consequently expended more energy ($P < 0.01$) than cows fed grass in the barn (251 vs. 204 kJ/kg $BW^{0.75}$). Number of steps was higher ($P < 0.001$) and the proportion of time spent walking (28 vs. 9%) increased ($P < 0.001$) for cows on pasture compared to those in the barn, which, conversely, spent more ($P < 0.01$) time standing (37 vs. 48%). Feeding behavior of the treatment groups changed in such a manner that the proportion of time spent eating (47 vs. 37%) was higher ($P < 0.001$) and that of time spent ruminating (22 vs. 29%) lower ($P < 0.01$) for grazing cows compared to cows fed grass in the barn. In conclusion, positive correlations ($P < 0.01$) between EE and walking (r = 0.63) and eating time (r = 0.59) suggest that higher physical activity accounts for a considerable part of the higher energy requirements of cows on pasture.

Key Words: dairy cows, energy expenditure, pasture

798 Relationship between milk fat and nutrition in lactating Holstein cows. M. Vazirigohar*, A. Nejati Javaremi, and A. Nikkhah, *University of Tehran, Karaj, Tehran, Iran.*

The objective of this study was to evaluate production and nutritional factors that influence milk fat (MF) and milk fat depression (MFD) in lactating Holstein dairy herds. Production data were obtained from the Iranian Dairy Herd Improvement Center (n=33540), which in 2005 and 2006. Programmed total mixed ration (731 herd-month rations) on milk test day were collected from 3 large dairy herds. Diets were evaluated for nutrient composition using CPM Dairy. Milk fat: protein ratio was divided into four different categories (<0.8, 0.8 to 1, 1 to 1.2 and >1.2), which the ratios less than 1 defined as MFD. Data were analyzed with univariate and multivariate regression models. Significant negative ($p<0.01$; estimate= -0.018) relationship was found between MF concentration and milk yield; MF levels were lower during the summer months and increased as lactation progressed. Milk fat was increased ($p<0.01$) with dietary levels of forage neutral detergent fiber, effective neutral detergent fiber and sugar contents; it was decreased ($p<0.01$) with non forage neutral detergent fiber, rumen undegradable protein, and linoleic acid contents. In the ratios lower than 0.8, least squares means of effective neutral detergent fiber, soluble fiber and forage neutral detergent fiber were in the lowest levels (20.81±0.009, 10.43±0.01 and 17.58±0.04 respect.; as %DM), non fibrous carbohydrate, non forage neutral detergent fiber, crude protein, rumen undegradable protein, linoleic acid and dry matter intake were in the greatest levels (40.58±0.01, 15.35±0.02, 15.69±0.02, 5.99±0.009, 1.62±0.003; as %DM, and 22.41±0.04; as kg of DM). In the ratios of lower than 0.8, least Squares means of milk yield was in the greatest (31.47±0.1 kg) and milk fat percentage was in the lowest (2.15±0.007%) level.This study showed that DMI and linoeleic acid were the main factors that influence milk fat depression.

Key Words: milk fat depression, nutrition, dairy cows

799 Profitability and milk yield response to protein supplementation in mid-lactation dairy cows. A. E. O. Malau-Aduli* and J. C. Beattie, *School of Agricultural Science, University of Tasmania, Hobart, Tasmania, Australia.*

This study utilized 120 Holstein-Friesian dairy cows in mid-lactation in a randomized block experimental design. The aim was to evaluate milk yield and composition responses to protein supplementation and profitability over an eight-week lactation period. The cows were blocked according to milk yield, days in milk and parity before being randomly assigned to three treatment groups: Control, 15% and 30% protein supplementation. Weekly average daily milk yield (WMY), total milk yield (TMY), income from milk sales, profitability, fat and protein percentages were subjected to statistical analyses to test the effects of treatment, block, parity, week and their second order interactions fitting days in milk as a random effect in mixed model procedures. Multiple regressions with quadratic contrasts were fitted to predict income and profitability from total ration fed and days in milk. The 30% protein supplemented cows gave the highest milk responses (WMY, 27.1 ± 0.80; TMY, 1479.9 ± 38.01litres), fat percentage (2.6 ± 0.3%), total income ($597.4 ± 40.23) and profitability ($54.4 ± 5.04 per cow), while the control group gave the least responses and incurred a loss of -$24.30 ± 4.95. Third parity cows also gave the highest milk yield responses (WMY, 28.1 ± 0.51; TMY 1562.1 ± 28.24 litres) and profitability ($65.7 ± 15.37). Residual phenotypic correlations (r) between milk yield, composition and profitability were almost all highly significant (P<001) with the highest positive r=0.96 between WMY and TMY. Total ration and days in milk within treatment group alone were very poor predictors of profitability (r^2=0.02-0.12) compared to within parity groups (r^2=0.14-0.90) for income, WMY and TMY. It was concluded that even though a positive profit margin was evident, long-term feeding of mid-lactation cows with 30% protein supplement is unrealistic because of the prohibitive cost of protein. Furthermore, protein requirements for milk synthesis at this stage of lactation can be adequately met by a 16-17% protein diet since energy would be the most limiting nutrient.

Key Words: protein supplementation, milk yield response, profitability

800 Pigeon peas as a supplement for lactating dairy cows fed corn silage based diets. V. A. Corriher*[1], G. M. Hill[1], J. K. Bernard[1], T. Jenkins[2], and B. G. Mullinix[1], [1]*University of Georgia, Tifton,* [2]*Clemson University, Anderson, SC.*

Holstein rumen canulated cows (n=7; initial BW 640.56 ±71.43 kg) were fed a corn silage basal diet with one of three concentrates (C=control; P10=10% pigeon peas; P20=20% pigeon peas). Cows were randomly assigned to treatments in a replicated 3 × 3 Latin square design and individually fed using Calan®gates. Each experimental period was 21 d with 7 d for adaption and 14 d for sample collection. Ruminal fluid samples were taken the last day of each experimental period and analyzed for

pH, ammonia, long chain fatty acids (LCFA) and VFA. Consecutive a.m. and p.m. milk samples were taken from each cow during last 2 wk of 21-d period and analyzed for fat, protein, LCFA and somatic cell count (SCC). Dietary DMI (kg/d) was lower during second period and higher for the 10% pigeon pea diet ($P < 0.05$). Milk protein was higher for cows fed the 20% pigeon pea diet compared with 10% diet ($P < 0.05$). Milk ECM was higher for cows fed control diet compared with 10% pigeon peas ($P < 0.05$). Treatment had no effect on milk yield ($P > 0.10$). Diets did not affect ruminal fluid pH ($P > 0.10$); however, pH was different for sampling periods ($P < 0.01$). Ruminal ammonia decreased until 8h post-feeding at which time it peaked consistent with changes in ammonia concentrations that usually peak 3-5h post-feeding on diets high in plant proteins. Dietary treatments altered ruminal fluid VFA with lower concentrations of acetate and higher concentrations of propionate for the control diet, resulting in lower acetate: propionate ratio ($P < 0.05$). The P10 diet resulted in higher ruminal isovalerate ($P < 0.05$). Ruminal cis 9, trans 11 and trans 10, cis 12 conjugated linoleic acid (CLA) isomers were not affected by dietary treatments ($P > 0.10$). The P10 diet had highest ruminal synthesis of c9, t11, but control cows had highest ruminal synthesis of t10, c12 ($P > 0.10$). Milk CLA isomers were similar ($P > 0.10$) among treatments. Trends were observed for greater ($P > 0.10$) c9, t11 and t10, c12 for P10 diet. Pigeon peas may be used as a protein supplement in dairy diets without affecting milk production, DMI or ruminal environment when they replace corn and soybean meal.

Key Words: dairy, forage, fatty acids

Ruminant Nutrition: Research Methods

801 Everting the omasum into the reticulum to identify the sensory receptors in the omasum of the sheep. W. L. Grovum*, *Department of Biomedical Sciences, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada*.

The purpose of this work was to expose the inner surface of the omasum to identify its sensory receptors. Such work has been precluded to date because there was no technique for displaying its epithelia while keeping their circulation and vagal innervation intact. The main problem has been the location of the omasum under the liver, caudal to the diaphragm between the cranial sac of the rumen and the ribs on the right. Also, the reticulo-omasal orifice is nearly closed whereas the bean-shaped omasum is approximately 16 cm in diameter. To evert the omasum, sheep were anesthesized with sodium pentobarbital, intubated and placed on a ventilation pump to first remove 7 ribs (6-12) along with associated tissues on the left and thus expose the reticulum. Then, it was incised from its apex upwards on its left and right sides between major blood vessels and opened like a clam-shell, care being taken to prevent contamination of the thoracic and abdominal cavities with digesta. The cut edges of the reticulum and the skin incision were clipped together to close the large opening in the animal. The reticulo-omasal orifice thus exposed was stretched to 4 - 5 cm in diameter to elute the omasal contents between the leaves into the reticulum by pumping warm normal saline through a 2 mm ID copper tube while dislodging the particles with 2 fingers. The much shrunken omasum was then gently pushed from behind and pulled into the reticulum. The omasal leaves now projected outwards from the omasal body and were easily manipulated to identify neuronal receptors sensitive to stretch and tactile stimulation.

Key Words: omasum, sensory function, sheep

802 Standardization of an in vitro method using *Streptomyces griseus* enzyme to predict rumen undegraded protein. I. Schadt*[1], P. J. Van Soest[2], and G. Licitra[1,3], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*Cornell University, Ithaca, NY*, [3]*D.A.C.P.A. University of Catania, Italy*.

In situ rumen protein degradation might change relative to feed intake and production. Incubation times of an in vitro method to achieve equal extents should be adapted, consequently. However, a continuous change of enzyme time is not practical for laboratory use. The purpose of the present study was the development and validation of a calibration curve to predict undegraded protein (UP) at any necessary enzyme time from one measurement at a single incubation time of 18 hours (1T). UP of 32 feeds was determined using *S. griseus* enzyme (40.6 U per gram true protein) at 4, 8, 12, 18, 24, 36 and 48 hours. The feeds were divided into 18 calibration and 14 validation feeds. UP of calibration feeds at incubation times was subtracted from UP at 18 hours and mean deviations at individual times were calculated. Deviations were plotted upon the natural logarithm of respective times to obtain the calibration curve. UP of validation feeds at 4, 8, 12, 24, 36 and 48 hours was predicted from the measured residue at 18 hours. The 1T method was validated against methods using two incubation times of 18 and 36 hours (2T) and all seven incubation times (7T). Individual calibration curves for all 32 feeds were generated by plotting UP either after 18 and 36 hours (2T) or after all seven incubation times (7T) upon the natural logarithms of the respective times. All three methods were examined for predictive capacity by plotting measured values upon predicted values and by calculating proportional deviations (PD) of calculated from measured values. Calculated and measured UP was generally highly correlated with $R^2 = 0.96$ ($n = 98$), $R^2 = 0.96$ ($n = 224$), and $R^2 = 0.99$ ($n = 224$), at 1T, 2T, and 7T, respectively. PD was decreasing ($p < 0.01$) with values of $0.066 > 0.049 > 0.030$ at 1T, 2T, and 7T, respectively. PD was highest at 48 hours using 1T and 7T. Elimination of times longer than 36 hours decreases PD at 1T to 0.054 being not different from PD at 2T.

Key Words: in vitro method, rumen protein degradation

803 Methodology to improve the sensitivity and repeatability of in vitro gas production. D. R. Mertens*, *US Dairy Forage Research Center, Madison, WI.*

The goal of this research was to improve the measurement of in vitro gas production during early fermentation and reduce variability among runs. Eleven forages (immature and mature grasses and legumes) were used in four in vitro runs over a six week period. Ruminal contents were collected from four lactating cows, and inoculum preparation was initiated within 20 min after collection. Ruminal fluid was separated from solids by squeezing through two layers of cheesecloth. Solids weighing one-half of the required ruminal fluid was blended for 60 s with twice their weight of CO_2-purged, reduced and warmed media. Ruminal fluid and blended solids were combined and squeezed through four layers of cheesecloth. Inoculum was kept warm using a jacketed beaker with circulating water at 39°C and purged with CO_2. Bottles (50 ml) containing samples and 6 ml of buffered media were purged with CO_2, reduced and warmed in a waterbath. Each bottle was inoculated with 4 ml of blended inoculum, closed with a septum and crimp

cap, and immediately placed in an incubator and attached to pressure transducer via needle puncture. Inoculum weight was recorded for each bottle. Blended inoculum actively fermented during inoculation and gas pressure increased within .01 hr of inoculation. Pressure was measured every .01 h during inoculation to identify zero times, then every .1 h for 3 to 6 h of fermentation and every .5 h thereafter (44 to 48 h). Blended inoculum generated significant gas in blanks. A flexible sigmoid function was used to fit blank data and calculate a blank-correction for each bottle based on weigh of inoculum. Asymptotic gas production of blanks varied from 2.7 to 3.2 mls per gram of inoculum and was different among runs using PROC GLM (P<.05). Rapid fermentation was indicated by 28% of total gas produced within 3 h of fermentation. Coefficients of variation among-runs were 8.1, 6.5, 6.0, 5.5, and 5.2% at 3, 6, 12, 24 and 36 h, respectively. It was concluded that this method has the sensitivity and repeatability necessary to detect small differences in digestion kinetics.

Key Words: gas production, digestion kinetics, in vitro methods

804 Effect of lignin linkages with other plant cell wall components on in vitro and in vivo NDF digestibility of forages. E. Raffrenato*[1], R. Fievisohn[2], K. W. Cotanch[2], R. J. Grant[2], L. E. Chase[1], and M. E. Van Amburgh[1], [1]*Cornell University, Ithaca, NY*, [2]*W. H. Miner Agricultural Research Institute, Chazy, NY*.

Lignin limits forage digestibility and imparts this effect by decreasing digestible energy and limiting dry matter intake. Measurements of acid detergent lignin (ADL) do not always account for variability in digestibility, especially at fermentation times representing rumen residence times of forages. The chemistry of ADL cross-linkages with cell wall polysaccharides rather than amount of ADL has been suggested as a better predictor of NDF digestibility (NDFD). The objective of our work was to evaluate the effects of ester and ether linked p-coumaric (PCA) and ferulic acid (FA) on in-vitro and in-vivo NDFD. Twenty-four corn silages (CS) were incubated in-vitro for 24hr NDFD. Digested residues were analyzed for NDF, ADF and ADL and ester and ether linked PCA and FA were determined in those fractions. Three of the CS were fed to 6 fistulated cows for 3 wks in three iso-NDF diets. Diet, rumen and feces samples were taken every 3hr for three days, 10d from the start of the study. Intact samples, NDF and ADF residues were analyzed for ester and ether linked PCA and FA. Extraction of phenolic acids was by 2N and 4N NaOH treatment, followed by HPLC equipped with a diode array detector using a reverse-phase column. Ether-linked PCA and FA were calculated as the difference between total and ester-linked phenolic acids. The content of ester and ether linked PCA and FA in both NDF and ADF residues showed negative correlations with 24hr NDFD, -0.16 to -0.87 for NDF and -0.71 to -0.95 for ADF. In particular, the ester linked PCA content of ADF explained 92% of the variation in 24hr NDFD. Correlations decreased for longer fermentation lengths, demonstrating that PCA and FA limit only rate and not extent of in-vitro digestion. The analyses from the in-vivo study confirmed the in-vitro results, demonstrating the highest total tract NDFD (70%) for the CS with the lowest phenolic acid and ester linked PCA content in the ADF fraction.

Key Words: digestibility, lignin, phenolic acids

805 Do the time of access to food, the supplementation with additives and the graze affect ruminal inocula used for *in vitro* gas production trials? A. Pérez-Ruchel[1], A. Britos[1], E. Almanza[1], J. L. Repetto[2], N. Pomiés[1], and C. Cajarville*[1], [1]*Departamento de Nutrición Animal, Facultad de Veterinaria, Montevideo, Uruguay*, [2]*Departamento de Bovinos, Facultad de Veterinaria, Montevideo, Uruguay*.

The objective of this study was to evaluate if the time of access to food (TAF), the supplementation or not with buffer or yeasts, and the graze affect rumen inocula of ruminants consuming pastures. Twenty cannulated wethers consuming forage from a temperate pasture (*Lotus corniculatus*, CP 14%) were allocated into 5 groups: AD had forage available all day; R, RB, RS, RG had forage available 6h/d. AD, R, RB, RS were housed in metabolic cages; RG was grazing. RB ate buffers (2% DMI, 75% NaHCO3-25% MgO); RS yeasts (6.2×10^9 UFC/d of *Saccharomyces cerevisiae*). Rumen inocula was collected at hour 2 after the beginning of the ingestion from each animal and mixed within grups. 0.5 g of 3 substrates (*Avena sativa*, *Lotus corniculatus* and wheat straw) were introduced in flasks by triplicate for each inoculum and incubated at 39.5°C. Gas pressure was measured during 96 h. Cumulative gas production data were fitted to the model: gas= a+b{1-exp[-kd(t-L)]} (a+b (mL): potential gas production; kd (h^{-1}): rate of gas production; L (h): lag time). Parameters were analysed by GLM considering 'substrate', 'inocula' and its interaction. Means for 'inocula' were separated by orthogonal contrasts studying the effect of TAF (AD *vs* R), use of additive (R + RG *vs* RB + RS), additive used (RB *vs* RS), and graze (R *vs* RG). Non interactions 'substrate' × 'inocula' were detected. Animals fed during all day presented higher kd (P=0.046) and lower L (P<0.001), which should indicate a more stable microbial population. Instead offered food and TAF were the same, grazing animals presented lower a+b (P=0.024) but with a higher kd (P=0.002), suggesting different ruminal environments. The use of additives had no effect, instead RS tended to have higher kd and lower L. We concluded that TAF and grazing affected the inocula characteristics. *Acknowledgements: PDT-DICyT (78/12 and S/PSP/02/48), CSIC, and CODENOR S.A.*

Key Words: in vitro fermentation, temperate pastures, additives

806 *In vitro* assessment of effects of microalgae type, protection of microalgae, and dilution rate on dry matter disappearance and methane emission in a rumen simulation system. R. Kinley*[1], K. Glover[1], R. Teather[2], S. Iverson[3], and A. Fredeen[1], [1]*Nova Scotia Agricultural College, Truro, Nova Scotia, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*, [3]*Dalhousie University, Halifax, Nova Scotia, Canada*.

The impact of microalgae type, microalgae protection against microbial degradation, and fluid turnover rate was evaluated *in vitro* using five continuous culture fermentors in a 3 times replicated factorial of control + 3 alga × 3 flow rates × 3 protection levels, completed over 18 periods. Mixed inoculums from 5 lactating cows were maintained at pH 6.8 and 39°C, with rotary mixing (13 rpm), in 1200 mL (working capacity) Versatec fermentors. Thirty grams of a dry 50/50 forage/concentrate mix (2 mm screen) and 1.2 g of microalgae were fed daily in equal 12 h increments. Each period consisted of 12 d of stabilization followed by repeated measurements over the final 4 d. The production of CH_4 was determined by gas chromatography by measuring its concentration in the head space with constant gas flow. A 3–way interaction (alga × flow rate × protection) effect on methane emission was significant (P<0.001). Compared to the control all 3 algae reduced overall DM disappearance (DMD; P<0.001) but not NH_4–N concentration (P=0.285). Production of NH_4–N was significantly reduced by increasing flow rate (P=0.002), while both overall DMD and CH_4 emissions were increased (P<0.001). Algae–1 significantly reduced CH_4 production at lower levels of pro-

tection and flow rate combined ($P<0.001$). The level of protection of algae had no significant effect on DMD, CH_4 or NH_4–N ($P>0.374$), but lower CH_4 emissions were generally observed with increasing protection level. Slower turnover rate and lower protection level may serve to promote toxic effects of the algae on rumen microbes, as indicated by the observed onset of floating digesta mat instability, which may reflect reduced production of fermentation gases (CH_4 and CO_2).

Key Words: methane, microalgae, rumen

807 Comparing real-time PCR to purine analysis in regard to estimation of bacterial crude protein. E. Castillo-Lopez*, J. Miner, and P. Kononoff, *University of Nebraska*, *Lincoln*.

The objectives were to evaluate the estimation of rumen bacterial crude protein (BCP) based on two methods, real-time PCR (RTPCR) and purine analysis, and, secondly, to determine the impact of yeast on estimation of BCP. In the first trial, an *in vitro* fermentation was carried out. Treatments were I) Control: grass hay and corn, II) Added distillers dried grains (DDG) and III) Added DDG with added solubles (DDG+S). After 48 h of fermentation, the amount of BCP was estimated based on purine analysis and RTPCR. The RTPCR probe targeted DNA encoding the bacterial 16S rRNA to establish the ratio of bacterial DNA:BCP. Data were analyzed as a completely randomized design arranged in a 2X3 factorial. Estimates of BCP production were 0.383 and 0.285 ±0.013 g BCP/L of fermentation fluid based on purine analysis and RTPCR, respectively, and were different ($P < 0.01$). There was ($P < 0.01$) an effect of treatment on BCP production estimates, 0.39, 0.35 and 0.26 ±0.016 g BCP/L for the control, DDG, and DDG+S respectively. The method by treatment interaction tended to be different ($P = 0.06$). Specifically, BCP of the control was 0.41 and 0.38 ±0.023 g BCP/L for purine analysis and RTPCR respectively, and were not different ($P = 0.34$). The BCP estimated for DDG were 0.43 and 0.26 ±0.023 g BCP/L for purine analysis and RTPCR respectively, and were different ($P < 0.01$). The BCP estimated for DDG+S were 0.30 and 0.22 ±0.023 g BCP/L for purine analysis and RTPCR and were different ($P = 0.04$). In the second trial, bacteria were isolated from ruminal fluid from one steer and split into six samples. Yeast was added to three samples at one third of total DM, DNA was extracted from all samples, and BCP was estimated using RTPCR. Data were analyzed as a completely randomized design. Estimates for BCP were 0.29 and 0.27 ±0.013 g/L digesta for samples with and without yeast, respectively, and were not different ($P = 0.38$). Results suggest purine analysis may overestimate BCP due to the presence of yeast cells, while RTPCR is unaffected by the presence of yeast. Thus, RTPCR may be a more accurate method to measure BCP.

Key Words: bacterial crude protein, distillers grains, purine analysis

808 Evaluation of supplementation or controlled-release capsule (CRC) to supply *n*-alkane as an intake marker in steers fed switchgrass or alfalfa hay. S. Chavez*, C. Lane, M. Braxton, A. Bruner, E. Leonard, J. Burns, and G. Huntington, *North Carolina State University*, *Raleigh*.

The objective was to evaluate *n*-alkanes as intake markers provided either in supplement or CRC. Seven ruminally fistulated beef steers (BW = 422 ± 36 kg) were fed 1 kg of soyhulls supplement once daily and alfalfa (n =3) or switchgrass (n=4) twice daily (18 g/kg BW). Each steer received dotriacontane (C32) in supplement or intraruminal CRC in a balanced changeover of 16-d periods. Delivery from the CRC was periodically measured with calipers. Fecal grab samples and total feces were collected during the last 5 d of each period. Fecal grab samples were divided into aliquots that were freeze-dried (FD) or oven-dried (OD) to a constant weight at 60°C. Forage and fecal alkanes were saponified, extracted with heptane, and analyzed by gas chromatography. The two forages were used to evaluate different levels of forage hentriacontane (C31) to predict intake. Overall, predicted intake (6.21 ± 1.26 kg DM/d) did not differ ($P = 0.12$) from measured intake (5.88 ± 1.27 kg DM/d). Fecal C31 (1,037 ± 55 mg/kg DM) and C32 (141 ± 13 mg/kg DM) did not differ ($P < 0.26$) between OD and FD in alfalfa. Fecal C31 (124 ± 18 mg/kg DM) and C32 (112 ± 10 mg/kg DM) did not differ ($P < 0.75$) between OD and FD in switchgrass. Intake predicted by fecal grab samples (6.21 ± 0.34 kg DM/d) did not differ ($P < 0.89$) from intake predicted by 5-d total fecal collection (6.28 ± 0.34 kg DM/d). Intake predicted by supplementation (6.29 ± 0.34 kg DM/d) did not differ ($P < 0.82$) from intake predicted by measured release of C32 from the CRC (6.13 ± 0.34 kg DM/d). Measured CRC delivery was appreciably less than manufacturer's specifications. Use of manufacturer's specifications would increase predicted intake from 1.18 to 1.35 times among the steers. In conclusion, alkanes can be used as markers to predict intake by using fecal grab samples rather than collecting total feces. Hay intake can be predicted accurately with once daily alkane supplementation, and samples can be OD or FD with no difference in alkane concentrations.

Key Words: alkanes, intake, steer

Swine Species: Symposium: Environmental Concerns Based on Swine Production

809 Research and extension needs in air and water quality. D. J. Meisinger*, *US Pork Center of Excellence*, *Ames, IA*.

The US Pork Center of Excellence in cooperation with the National Pork Board′s Environmental Committee hosted two invitational workshops to develop research and extension needs, one for air quality and one for water quality. These workshops had perfect attendance of the invitation list with the result being an exhaustive set of research and outreach needs. The air quality group organized themselves into breakout groups by gases, odors, and particulate matter. The water quality group did the same with the topics of nutrients and sediments, pharmaceuticals and hormones, and pathogens. Each breakout group answered the following questions:

- Identify research that is underway or has already been completed.
- Identify what is known and can be developed into extension materials and programs.
- Identify what still needs to be answered by further research efforts.
- Work to form a consensus targeting future research investments and efforts.
- Work to identify opportunities for soliciting research funding from external sources.

The deliverables from these two meetings were as follows:

- Identification of producer materials that should be developed based on available research.
- A recommended priority list for development of producer educational and informational materials based on available research.

- Identification of research efforts needed to fill gaps in information.
- A recommended priority list for identified research needs.

A document comprised of all these results is available as an environmental quality research and extension needs publication. Another module on nutrient management is being developed.

Key Words: air quality, water quality, research & extension needs

810 Occupational and environmental concerns in swine production. K. Donham*, *University of Iowa, Iowa City*.

The term: Confined Animal Feeding Operation (CAFO) is used to describe animal feeding operations (AFOs) over a specified size that are a risk as a point source for water pollution, and therefore require regulation (US Environmental Protection Agency). In regard to water, air, and solid waste pollution, CAFOs have many of the same concerns as described for other agricultural operations. However, there are special concerns in regards to CAFOs because of the sheer size, the concentration of animals, feed, manure (usually handled in liquid form), dead animals, flies, and associated gases, particulates, odors and odorants, and infectious diseases all concentrated on a small land area. There are concerns that the manure cannot be recycled without pollution on such a small area, and that local and regional air and water quality suffers. Public concerns relative to adverse consequences of livestock production have been increasingly voiced since the late 1960s (Thu, 1998). Numerous regional, national and international conferences have been held on the subject since 1994 (Merchant, 2002, 2008; Thu, 1995). An in-depth review of the literature on the subject (Donham, 2000) will be updated. One reason large scale livestock production has raised concern is that it has separated from family farming and has developed like other industries in management, structure, and concentration. The magnitude of the problem cited by environmental groups has often been criticized by lack of science based evidence. Additional to general environmental concerns, occupational health of workers has become more relevant as many operations now are employing more than 10 employees, which brings many operations under the scrutiny of the Occupational Safety and Health Administration. In this presentation the scientific literature is reviewed relative to the science basis of occupational and environmental impacts on community and individual health. Further, recommendations are made to help promote sustainability of our livestock industry within the context of maintaining good stewardship of our environmental and human capital.

Key Words: swine, health, environment

811 The potential ability of swine nutrition to influence environmental factors positively. S. T. Petersen*, *Land O'Lakes Purina Feed LLC, Shoreview, MN*.

Environmental issues are a growing concern. Several of them can be categorized under the following headings; manure storage and handling, air quality, manure nutrient concentration and soil nutrient levels. Recently introduced, EcoCare feed is a dedicated and affordable feed program addressing manure management, ammonia emissions and nutrient excretion, while optimizing pig performance. Components in EcoCare feed reduce manure solids and viscosity resulting in improved physical uniformity of the manure that is easier to agitate and handle through equipment. Internal research trials have indicated a reduction of 14% in solids and 22% in viscosity over a 45 collection day period; these physical changes may have positive implications on manure pit pump-out and facility sanitation. EcoCare feed also has the potential to reduce ammonia emissions. This is achieved primarily by using crystalline amino acid inclusion, specific Bacillus bacteria and saponin-derived compounds. Emissions measured in a manure pit simulation trial, performed at LongView Animal Nutrition Center, demonstrated that pigs consuming EcoCare feed excreted manure with reduced ammonia volatilization by 18% over a 45 day period when compared to the control pigs. Over time, EcoCare feed may result in reduced production of ammonia by up to 40% in commercial situations. Nutrient manipulation of feeds can greatly reduce nutrient waste. For example, reduced nitrogen excretion can be achieved by incorporating crystalline amino acids, using specific feed additives can lower the volatilization of nitrogen-containing ammonia from manure pits and by using phytase, we can reduce inorganic phosphorus in the diet thus improving phosphorus digestibility. These types of formulation can be achieved without limiting swine growth performance. In fact, EcoCare feed has been shown to improve feed conversion rate by up to 4% over other standard feeds in field conditions. EcoCare is a registered trademark of Land O'Lakes Purina Feed LLC.

Key Words: swine, environment, nutrition

812 Potential of anaerobic digestion to address current environmental concerns on swine operations. D. I. Massé*, *Agriculture and Agri-Food Canada, Sherbrooke, Québec, Canada*.

Recently, there have been concerns raised about the potential impact of livestock production on natural resources. According to the FAO report, Livestock's Long Shadow, the rapidly growing and intensifying livestock sector contributes negatively to climate change and air pollution, soil and water degradation, and biodiversity depletion. The FAO report also indicates that the demand for animal food products is expected to double by 2050. This will further increase pressure on natural resources. These concerns are leading to a renewed interest in environmental biotechnologies that can minimize environmental impact and valorize livestock operations' by-products. An anaerobic digestion process called Psychrophilic Anaerobic Digestion (PAD) in Sequencing Batch Reactor (SBR) has been developed at Agriculture Canada. This very stable biotechnology recovers usable energy, stabilizes, deodorizes, and increases the availability of plant nutrients. Experimental results indicated that PAD of swine manure slurry at 15 – 25°C in an intermittently-fed SBR reduced the pollution potential of swine manure slurry by removing 84 to 93% of the soluble chemical oxygen demand (COD). The process performs well under intermittent feeding, once to three times a week, and without external mixing. Therefore, feeding activities could be integrated with the routine operation of manure removal from the barn, thereby minimizing interferences with other farm operations and allowing the use of existing manure handling equipment for feeding the bioreactors. The process stability was not affected by the antibiotics commonly used in livestock production. The anaerobic digestion process was also effective in eliminating populations of zoonotic pathogens and parasites present in raw livestock manure slurries. The biotechnology produces biogas at rates exceeding 0.20 L of CH4 per gram of soluble COD fed and the biogas produced is of high quality with a methane concentration ranging between 70 and 80%. The recovery of green energy and the production of a value added odorless fertilizer will substantially reduce the carbon footprint on products of animal origin.

Key Words: anaerobic digestion, swine manure

813 Fate and transport of zoonotic bacterial, viral, and parasitic pathogens during swine manure treatment, storage, and land application. C. Ziemer*[1], J. Bonner[2], Task Force Members for CAST Special Publication No. 29[2], D. Cole (Cochair)[3], and J. Vinjé (Cochair)[4], [1]*National Soil Tilth Lab ARS-USDA, Ames, IA*, [2]*Council for Agricultural Science and Technology, Ames, IA*, [3]*Georgia Division of Public Health, Atlanta, GA*, [4]*Centers for Disease Control and Prevention, Atlanta, GA*.

The public is always somewhat aware of foodborne and other zoonotic pathogens; however, recent illnesses traced to produce and the emergence of another avian influenza virus have increased the scrutiny on all areas of food production. The Council for Agricultural Science and Technology has recently published a comprehensive review of the fate and transport of zoonogic pathogens that can be associated with swine manure. The majority of microbes in swine manure are not zoonotic but a number of bacterial, viral and parasitic pathogens have been detected. Awareness of the potential zoonotic pathogens in swine manure and how treatment, storage and handling affect their survival and potential to persist in the environment is critical to ensure that producers and consumers are not at risk. This review will cover the primary zoonotic pathogens associated with swine manure; including bacteria, viruses and parasites; as well as their fate and transport. Because the ecology of microbes in swine waste is still poorly described, a number of recommendations for future research are made to better understand and reduce human health risks. These recommendations include examination of environmental and ecological conditions that contribute to off-farm transport and quantitative risk assessments.

Key Words: swine manure, zoonotic pathogens, manure handling

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